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# **Mapping of SUMO sites and analysis of SUMOylation changes induced by external stimuli**

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**Running Title :** SUMO sites mapping by quantitative proteomics

## **Abstract**

**SUMOylation is an essential ubiquitin-like modification of eukaryotic cells involved in important biological processes. Identification of SUMO-conjugated residues in proteins is critical to understand the role of SUMOylation but remains experimentally challenging. Here, we have set up a powerful and high throughput method combining quantitative proteomics and peptide immunocapture to map SUMOylation sites and analyze SUMOylation changes in response to stimuli. With this technique, we identified 295 SUMO1 and 167 SUMO2 sites on endogenous substrates of human cells. We further used this strategy to characterize changes in SUMOylation induced by Listeriolysin O, a bacterial toxin that impairs the host cell SUMOylation machinery, and identified several classes of host proteins specifically deSUMOylated in response to this toxin. Taken together, our approach constitutes an unprecedented tool, broadly applicable to various SUMO-regulated cellular processes in health and disease.**

## **SIGNIFICANCE STATEMENT**

SUMO is a post-translational modification essential for many functions in eukaryotic cells. To better understand the role of this ubiquitin-like modification, identification of proteins modified by SUMO and knowledge of the exact sites of SUMO conjugation is critical, but remains however experimentally challenging. Here, we developed a new proteomic strategy allowing proteome-wide identification of SUMOylation sites and quantification of cell SUMOylation changes in response to diverse stimuli. Identification of yet unknown SUMO targets as well as characterization of SUMOylome alterations in response to environmental stresses, drugs, toxins, or bacterial and viral infections will help deciphering new roles of SUMOylation in cell physiology and diseases.

## INTRODUCTION

Post-translational modifications (PTMs) are key mechanisms used by both prokaryotes and eukaryotes to specifically, locally and temporally regulate protein activity. Ubiquitin and Ubiquitin-like proteins (UBLs) constitute a specific class of small protein modifiers that can be covalently attached to a target protein via the formation of an isopeptide bond in a reversible manner. SUMO, one of these UBLs, is an essential PTM in eukaryotic cells that is involved in various cellular functions including gene expression regulation, DNA repair, intracellular transport and response to viral and bacterial infections (1-5). The human genome encodes 3 different functional SUMO isoforms (SUMO1, SUMO2 and SUMO3), that are conjugated to distinct, but overlapping sets of target proteins (1, 2, 6). Conjugation of SUMO to its targets requires in humans an E1 activating enzyme (the SAE1/SAE2 heterodimer), an E2 conjugating enzyme (Ubc9) and several E3 SUMO enzymes. Once conjugated to its target, SUMO can be deconjugated by several different SUMO isopeptidases that tightly regulate the SUMOylation levels of proteins (7).

Since the discovery of SUMO two decades ago, much effort has been dedicated to the identification of SUMO-conjugated proteins in different organisms including yeast, plants and mammals (8). However, isolation of SUMOylated proteins has proven to be challenging. Indeed, for most SUMO substrates, only a small proportion of the total amount of protein is SUMO-modified. In addition, the high activity of SUMO isopeptidases in cell lysates results in the rapid loss of SUMO-conjugation in the absence of appropriate inhibitors. Thus, the most common approach to isolate SUMOylated proteins is based on expression of His-tagged versions of SUMO allowing for purification of SUMO-conjugated proteins by nickel chromatography under denaturing conditions (8, 9). Denaturing conditions inactivate SUMO isopeptidases and also prevent contamination by proteins interacting non-covalently with

SUMO via specific domains such as SUMO interacting motifs (SIMs) (2). Once isolated, analysis of SUMOylated proteins by mass spectrometry (MS) has been widely used to identify SUMO-modified proteins and, albeit less successfully, SUMO conjugation sites.

Mapping of the exact lysine residue to which SUMO is attached in modified proteins is a critical step to get further insight into the function of SUMOylation. Indeed, identification of SUMO sites allows for the generation of non SUMOylatable mutants and the study of associated phenotypes. Identification of SUMO sites by MS is not straightforward (8). Unlike ubiquitin that leaves a small diglycine signature tag on the modified lysine residue after trypsin digestion, SUMO leaves a larger signature, which severely hampers the identification of modified peptides.

In addition to SUMO site identification *per se*, comparison of the SUMOylation status of sites in different cell growth conditions is also critical to better characterize the biological implications of SUMOylation. For example, analysis of SUMOylation changes induced after heat shock, arsenic treatment, inhibition of the proteasome or during cell cycle has led to numerous insights into the role of SUMOylation in cell physiology ((10-14) and reviewed in ref. 2). Here, we devised a novel approach which combines the use of SUMO variants, peptide immunocapture and quantitative proteomics for high throughput identification of SUMO sites. We then show that our approach is able to characterize global changes in the cell SUMOylome in response to a given stimulus, such as exposure to a bacterial toxin, listeriolysin O (LLO).

## RESULTS

### *A proteomics-based strategy to map SUMO-modified lysines*

In contrast to ubiquitylated proteins, SUMOylated proteins upon trypsin digestion lead to large signature tags of 19 or 32 amino acids for human SUMO1 and SUMO2/3,

respectively, on peptides containing the modified lysine residue. These tags generate complex ion patterns during MS/MS fragmentation of the peptides, thus preventing their straightforward identification by common search algorithms. To circumvent this problem, we generated variants of mature human SUMO1 and SUMO2 with one arginine introduced immediately before the C-terminal diglycine motif, thereby mimicking the sequence of human ubiquitin (SUMO1 T95R, SUMO2 T91R; Fig 1a). Trypsin digestion of proteins modified by these SUMO variants generate SUMO-modified peptides with a simple diglycine tag (GG tag) easily identifiable by classical LC-MS/MS, as previously described for other similar SUMO variants (Fig. 1b) (11, 14-17). We also tagged these SUMO variants with 6xHis stretches thereby allowing affinity purification of SUMOylated proteins from cell lysates under denaturing conditions (9).

To verify that SUMO1 T95R and SUMO2 T91R variants behave similarly to their wild-type counterparts, we transfected HeLa cells with wild-type or variant His<sub>6</sub>-SUMO1 and His<sub>6</sub>-SUMO2 and pulled down SUMOylated proteins from cell lysates using nickel chromatography. Immunoblot analysis of SUMOylation patterns revealed a slight decrease in the global intensity of proteins SUMOylated by SUMO variants compared to wild type, which may indicate that these SUMO variants are less efficiently conjugated by the SUMOylation machinery. Nevertheless, the relative distribution of SUMOylated proteins in these patterns (*i.e.* number and size of observed bands) does not show major difference between wild type and SUMO variants, strongly suggesting that the sets of proteins conjugated by these different SUMO forms are similar. We further verified that the SUMOylation of a known SUMO target, RanGAP1, was similar with wild type or variant SUMOs (Fig. 1d). Strikingly, the isoform preference observed with wild-type SUMO (*i.e.* preferential modification of RanGAP1 by SUMO1 compared to SUMO2) (7) was also observed with SUMO1 T95R and SUMO2 T91R variants (Fig. 1d). We finally tested if SUMO1 T95R and SUMO2 T91R

interacted with SIMs as their wild-type counterparts (2). We used an established assay based on split-luciferase complementation to detect non-covalent interactions between SUMO and SIMs from two different proteins, Daxx and PIAS2 (18). We observed that wild-type and variant SUMO interact similarly with the different SIMs tested in this assay, strongly suggesting that the introduced mutations in SUMO1 and SUMO2 do not alter their ability to be recognized by SIMs (Fig. S1).

Trypsin digestion of proteins after His-purification of SUMOylated proteins generates a mixture of SUMO-modified and non-modified peptides. Under these conditions, identification of SUMO-modified peptides is challenging as they represent a very small fraction of the total amount of peptides. Indeed, after direct MS analysis of His-pulled down samples, we were able to identify only very few GG-modified peptides (<0.1% of total identified peptides). We thus added an additional enrichment step for GG-modified peptides to our protocol by taking advantage of antibodies directed against GG-modified lysines (anti-K- $\epsilon$ -GG antibodies). Although these antibodies were initially used to capture and enrich GG-modified peptides from trypsinized ubiquitylated proteins (19-21), we decided to broaden their application to the study of SUMOylation sites by combining them with the aforementioned SUMO variants.

To rule out that identified GG-modified peptides in our study came from endogenous ubiquitin, NEDD8 or ISG15-modified proteins (as these three modifiers also leave GG-tags on modified proteins), we used SILAC labeling to compare peptides derived from cells expressing wild-type or variant SUMO. SILAC (for Stable Isotope Labeling by Amino acids in Cell culture) (22) allows for differential isotope labeling of proteins during cell culture by metabolic incorporation of essential amino acids (predominantly lysine and arginine) that carry light or heavy isotopes. After mixing light and heavy labeled cell lysates, isolated SUMO-targets are subjected to trypsin digestion and the resulting peptide mixture is analyzed



by tandem mass spectrometry. Proteins are then identified by searching the recorded MS/MS spectra against protein databases, while quantification is obtained by comparing the light and heavy intensity for each peptide. In our experimental set up, all GG-modified peptides identified from cells expressing wild-type SUMO are expected to correspond to non-SUMO sites, as trypsin digestion of SUMOylated proteins in these conditions does not produce GG tags. Only GG-modified lysines identified specifically with SUMO variants were considered as *bona fide* SUMOylation sites (Fig. 2). A third labeling condition can be added to this experiment to study SUMOylome changes in response to external stimuli. As described below, we treated cells expressing SUMO variants with the bacterial toxin listeriolysin O (LLO) (Fig. 2).

#### *Proteome-wide identification of SUMO1 and SUMO2 sites*

HeLa cells cultivated in different SILAC media ( $\sim 2 \times 10^7$  cells/SILAC condition) were transfected with wild-type ('light' labeling) or variant His<sub>6</sub>-SUMO ('medium' and 'heavy' labeling) (Fig. 2a). Two independent experiments were performed to identify SUMO1 and SUMO2 sites, respectively. Two days after transfection, cells were lysed in denaturing buffer, SUMOylated proteins were affinity purified by nickel chromatography and digested by trypsin. GG-modified peptides were then enriched by peptide immunoprecipitation before MS analysis. Inclusion of this last step resulted in an enrichment of GG-modified peptides by more than 300 fold, as previously observed for studies focusing on ubiquitin (21).

SUMO sites were determined by comparing the data obtained from cells transfected with wild-type and variant SUMO. To this end GG-modified peptides were quantified by comparing intensities of the different SILAC labels in the MS spectra. More than 70% of these peptides showed no detectable signal in the light channel and were therefore considered as markers of *bona fide* SUMO sites (Fig. 2). Together, these analyses led to the identification

of 295 SUMO1 sites from 227 endogenous targets and 167 SUMO2 sites from 135 endogenous targets (see Table S1 and S2 for list of identified SUMO sites), and therefore constitute the most comprehensive list of human SUMO sites to date (8) (Table S1). Among the 332 different SUMO sites identified in our screen, 130 sites (39%) were found both with SUMO1 and SUMO2, 165 sites (50%) were found only with SUMO1 and 37 sites (11%) only with SUMO2 (Fig. 2d). These percentages are in agreement with previously observed isoform preferences (6).

86 of our 332 identified sites (26%) were previously reported in proteomic screens for SUMO sites (11, 14, 16, 17, 23, 24) and 82 (25%) are reported in the PhosphoSitePlus database (a resource for human PTM, including SUMOylation) (25), thereby validating our approach (Table S1). Thus, to our knowledge, 227 novel SUMO sites (203 for SUMO1 and 82 for SUMO2) were identified here for the first time (Table S1). To validate the reproducibility of our approach, we repeated our analysis for SUMO1 in a smaller scale experiment ( $\sim 1 \times 10^7$  cells/SILAC condition). We identified 132 SUMO1 sites of which 115 (87%) were in common with the 295 SUMO1 sites found in the first analysis, indicating a high degree of reproducibility (Fig. S2).

To further validate the SUMOylated proteins identified in our screens as well as their associated SUMO sites, we selected several candidates: the transcriptional repressors ZBTB20 (Zinc Finger and BTB domain containing 20), HMBOX1 (Homeobox Containing protein 1), NACC1 (Nucleus accumbens-associated protein 1), the transcription factor TFAP2A (Transcription factor AP-2 alpha), the microtubule-binding protein MAP7/ensconsin and the lamin-B1 (LMNB1) protein. ZBTB20, HMBOX1, NACC1, MAP7 and LMNB1 were previously reported to be SUMOylated but their SUMOylation sites had not been characterized (6, 12, 13, 26). We generated expression vectors for HA-tagged version of each of these six proteins and mutated the SUMO-modified lysines identified in our screens into

arginines to obtain non SUMOylatable mutants. We cotransfected HeLa cells with plasmids encoding the different HA-tagged candidates and the corresponding mutants, and His<sub>6</sub>-tagged SUMO1 or SUMO2. After cell lysis, SUMOylated proteins were nickel purified and the presence of SUMOylated forms of the different candidates was assayed by immunoblotting experiments using anti-HA antibodies. For each tested candidate, slower migrating bands corresponding to SUMO-modified forms of these proteins were detected in the His pulled-down fraction from cells expressing His<sub>6</sub>-SUMO1 or His<sub>6</sub>-SUMO2, thus demonstrating that all these proteins are indeed modified by SUMO (Fig. 3). As already observed for many other SUMO targets (2), the percentage of SUMOylated versus non SUMOylated proteins is rather low (~5% for ZBTB20, ~2% for TFAP2A and below 1% for HMBOX1, NACC1, MAP7 and LMNB1). For ZBTB20, HMBOX1 and TFAP2A, we did not observe SUMO-modified forms in cells expressing the different non SUMOylatable mutants, thus validating that the sites identified in our proteomic screen are *bona fide* SUMO sites (Fig. 3). For NACC1, MAP7 and LMNB1, expression of non SUMOylatable mutants led to a decrease in SUMOylation of these proteins, even though some SUMOylated forms could still be detected (Fig. 3). These data argue that the mutated residues correspond to real SUMO sites but also suggest that either additional SUMO sites are present in these targets or that compensatory events may lead to SUMOylation of different lysines in these mutants. Together, these experiments confirm the previously described SUMO site of TFAP2A (27) and provide the first identification of SUMO sites for ZBTB20, HMBOX1, NACC1, MAP7 and LMNB1.

We then classified the identified SUMOylated proteins from our screens by Gene Ontology (GO) terms analysis. Proteins annotated as ‘nuclear’, ‘nuclear lumen’ or ‘nucleolus’ were significantly enriched in the list of SUMO-identified proteins relative to the whole human proteome (Fig. 4a). This confirmed the well established finding that a high proportion

of SUMOylated proteins are nuclear factors. In particular, we identified several SUMO-conjugated DNA binding proteins and transcription factors, consistent with the essential role of SUMO in the regulation of gene expression (1, 28). Apart from these classes of proteins, we identified a significant enrichment for cytoskeletal proteins in our list of identified SUMOylated proteins (modified fisher exact p-value= $4.1 \times 10^{-4}$  for SUMO1 and  $1.6 \times 10^{-2}$  for SUMO2; Fig. 4a and Table S1). In particular, we identified several SUMO targets implicated in the architecture of the actin cytoskeleton, such as actin itself, anillin, cortactin or RhoGDI. Of note, actin was already reported to be SUMOylated (albeit on different residues) (29), whereas cortactin and anillin were not known as being SUMOylated. We also identified several intermediate filament proteins as SUMO targets, including keratins, lamins, nestin and vimentin, for which we provide data on yet uncharacterized SUMO sites. Finally, besides nuclear and cytoskeletal proteins, we identified examples of other classes of proteins, such as plasma membrane proteins or proteins from intracellular organelles that can also be targeted by SUMOylation (Table S1).

#### *'Consensus' and 'non-consensus' SUMO sites*

Analysis of the aminoacids surrounding SUMOylated lysines showed that 65% of SUMO sites lie in a Kx[DE] environment, and that 48% conformed to the previously established SUMO consensus motif ([FILMV]Kx[DE]) (30, 31) (Fig. 4b). It has been established that residues constituting this SUMO consensus motif directly interact with the E2 SUMO conjugating enzyme (reviewed in ref. 2). For SUMO sites located in such a motif, we observed a marked preference for valine or isoleucine for the hydrophobic residue preceding the modified lysine (Fig. 4c).

In addition to this general SUMO consensus motif, extended motifs have been characterized in several SUMO targets. Among them, PDSM motifs (Phosphorylation-

Dependent SUMO Motifs) are characterized by the presence of a phosphorylated residue downstream of a classical consensus motif, which was shown to increase SUMOylation efficiency by mediating interactions between the target and a basic patch on Ubc9 (32, 33). To further study the link between SUMOylation and phosphorylation, we also analyzed our mass spectrometry data taking into account phosphorylation as a possible peptide modification. We identified thirteen SUMO-conjugated peptides that may be phosphorylated. Interestingly, six other of these peptides were found only in their phosphorylated state, which probably reflects the importance of phosphorylation in the SUMOylation efficiency of the corresponding targets (Table S3). For each of these SUMOylated/phosphorylated peptides, the phosphorylated residue is a serine located downstream of a lysine lying in a SUMO consensus motif. As previously reported for some SUMOylated/phosphorylated targets, the sequence motif surrounding the phosphorylated residue slightly diverges from the initially described PDSM ( $\Psi K x E x x S P$ , where K is the SUMO-conjugated lysine and S the phosphorylated serine) (17, 32, 34). Indeed, we observed that the distance between the phosphorylated and SUMOylated residues can vary between four and fourteen residues, and, even though we noticed a marked preference for proline after the phosphorylated residue, glutamate or aspartate residues were also present (Table S3).

In parallel to PDSM, negatively charged residues can also be found downstream of SUMO-conjugated lysines, which may substitute for the phosphorylated serine side chain of PDSMs and maintain a constitutively active motif for SUMO conjugation. Among our list of identified SUMO sites, we frequently observed aspartate and glutamate residues in position +4 to +8 downstream of the modified lysine and 58 sites (37% of sites in SUMO consensus motif) are accordingly located into NDSM motifs (Negatively charged amino acid-Dependent SUMO Motifs) (35) (Fig. 4c and Table S1).

Finally, 29 of our identified sites (18% of sites in SUMO consensus motif) match the HCSM motif (Hydrophobic Cluster SUMOylation Motif), which is characterized by the presence of at least 3 residues with hydrophobic properties upstream of the modified lysine, instead of the single hydrophobic residue usually present (17) (Table S1).

By analyzing sites which lack a Kx[DE] motif, we confirmed the existence of an ‘inverted SUMOylation consensus motif’ (defined as [DE]xKx[no DE]) (17) for 42 sites (13% of total SUMO sites) (Fig. 4b and c). Interestingly, this ‘inversion’ not only concerns the D/E residue but also the negatively charged residues, which are, in this case, frequently found upstream of the SUMO-conjugated lysine sites (Fig. 4c). A significant number of sites (73 sites; 22%) did not lie either in a Kx[DE] motif or in an ‘inverted SUMOylation consensus motif’. Analysis of these sites did not reveal any marked preference for surrounding amino acids, as it is the case for ubiquitin sites (Fig. 4c). Whether the specificity of the modified lysine is directed by the flanking residues of these ‘non-consensus’ SUMO sites interacting with Ubc9 or by other factors such as SUMO E3 enzymes still requires further investigation. The absence of motif for these ‘non consensus’ sites renders their prediction by bioinformatic analysis almost impossible, thus strengthening the utility of an untargeted approach such as the one described here for their identification.

Finally, we observed no significant differences in the frequencies of the various motifs identified for SUMO1 and SUMO2 sites (Fig. 4b). This indicates that the selection of the SUMO-conjugated lysine is not influenced by the sequence of SUMO isoform itself but is probably imposed by the interactions between the target, the E2 and the E3 SUMO enzymes.

We cross-referenced our data with previously established databases of other PTMs (25). Interestingly, we observed that an important fraction of our identified SUMO sites are also reported to be acetylated (20%) or ubiquitylated (37%) (Table S1). This highlights the

importance of the cross-talks between SUMOylation and other post-translational modifications that can either compete for the same lysine or occur sequentially at a given site.

*Analysis of SUMOylome changes induced by an external stimulus*

One powerful aspect of our strategy is that it enables comparison of the SUMO landscape of two cell populations in different biological conditions. We thus decided to apply our technique to elucidate changes in SUMOylation induced by a bacterial toxin, listeriolysin O (LLO). This toxin is secreted by the Gram-positive bacterial pathogen *Listeria monocytogenes*, the etiological agent of human listeriosis (36), and has a potent signaling activity through pore formation in the host plasma membrane during infection (37). Among the different cellular responses triggered by LLO, we have previously shown that this toxin induces the degradation of Ubc9, the unique E2 enzyme of the host SUMOylation machinery (38). This degradation leads to a blockade in SUMOylation and a global decrease in the level of host SUMOylated proteins, which is beneficial for efficient infection by *Listeria* (38). In order to get further insight into the extent of deSUMOylation events in response to LLO and to identify deSUMOylated proteins, we added in our protocol, as discussed above, a third SILAC condition corresponding to cells transfected with variant His<sub>6</sub>-SUMO, treated with a sublytic concentration of LLO for a short time (*i.e.* 3 nM for 20 min; Fig. 2). Immunoblot analysis using antibodies specific for SUMO1 and SUMO2/3 confirmed that these conditions lead to a global decrease in the level of SUMO1- and SUMO2-conjugated proteins (Fig. 5a). Quantitative analysis of our proteomic data confirmed this global decrease in SUMO-conjugated proteins (Table S4). More specifically, we identified 35 SUMO1 sites and 90 SUMO2 sites with a medium/heavy (M/H) ratio >2, indicative of a decrease in SUMOylation in response to LLO (Table S4). In contrast, very few proteins are associated with M/H

ratios<1, indicating that *de novo* SUMOylation of host proteins in response to LLO is very limited.

Analysis of SUMO motifs frequencies for sites highly deSUMOylated in response to LLO shows an overrepresentation of lysines lying in SUMO consensus motifs, compared to the total list of identified SUMOylated sites (Fig. S3). Functional enrichment analysis of highly deSUMOylated proteins (31 proteins for SUMO1 (M/H ratio>2) and 35 proteins for SUMO2 (M/H ratio>4)) showed that several classes of targets annotated ‘nucleus’, ‘DNA-binding’, ‘zinc-finger’ or ‘transcription regulation’, are significantly over represented in the list of highly deSUMOylated proteins relative to the total list of identified SUMOylated proteins (Fig. 5b). This result suggests that SUMOylated host factors are not similarly sensitive to LLO-induced loss of SUMOylation. In particular, several nuclear factors are strongly deSUMOylated in response to LLO, whereas other classes of proteins, such as cytoskeletal proteins for example, are less affected. SUMOylation of transcription factors is known to either positively or negatively regulate their transcriptional activity (1, 28). LLO-induced modification of the SUMOylation state of these proteins may thus alter the transcriptome of the cell in response to toxin exposure. Alteration of the host transcriptome in response to LLO has already been described (39) but the exact role of deSUMOylation in this response remains to be determined. The identification of proteins deSUMOylated upon LLO treatment thus provides candidate host factors for which SUMO-regulation may play an important role during establishment and persistence of *Listeria* infection.



## DISCUSSION

In the last decade, several strategies have been developed to identify SUMOylation sites. Site-directed mutagenesis of lysine residues in the SUMOylated target constitutes one of the most common strategies to identify SUMO-conjugated lysines. This technique is however time-consuming and often limited to ‘predicted’ SUMO sites, based on SUMO consensus motif analysis. In addition, this technique does not formally differentiate between *bona fide* SUMO sites and residues involved in SUMOylation of distal lysines (*e.g.* residues mediating interactions with the SUMOylation machinery that are not modified themselves). Mass spectrometry constitutes an untargeted and high-throughput approach to identify SUMO sites. Different strategies have been used to circumvent the difficulties of SUMO-conjugated peptide identification due to the complexity of the associated MS/MS spectra. These approaches essentially rely on either elucidation of the complex MS/MS spectra or on use of modified SUMO versions leaving simpler tags on SUMO-modified peptides, more easily identified by classical MS ((11, 14-17, 23, 24) and reviewed in ref. 8). Despite these efforts, only a limited number of SUMO sites have been identified by these different approaches so far.

Here, by combining SILAC-based quantitative proteomics and immunocapture of SUMO-modified peptides, we developed a powerful method for identification of SUMO sites. Using this approach, we identified 295 SUMO1 and 167 SUMO2 sites in human endogenous proteins. Of note, we identified 227 SUMO sites not described before that will provide a useful database for the SUMO community. Furthermore, by taking advantage of quantitative proteomics, our method allows SUMOylome comparison between two different cell populations and thus may open new avenues for studying the role of SUMOylation in

response to variations in environmental conditions, exposure to drugs or toxins, or infection by various pathogens.

During the reviewing process of this manuscript, a similar strategy using cells stably expressing a His<sub>6</sub>-SUMO2 T91K variant and allowing mapping of SUMO2 sites has been published (40). In this study, His<sub>6</sub>-SUMO2 T91K-conjugated proteins were isolated by nickel affinity chromatography and then digested by endoproteinase Lys-C, leaving a specific GG-tag on SUMO2 T91K-modified peptides (while proteins modified by endogenous Ubiquitin, Nedd8 or ISG15 give rise to peptides modified by a larger tag, as endoproteinase Lys-C only cuts after K and not R residues; (40) and Fig. 1a). GG-modified peptides were then enriched using anti-K-ε-GG immunoprecipitation prior to mass spectrometry analysis. This approach was successfully used to identify SUMO2 sites in proteins from HEK293 cells after heat shock, a stress condition known to strongly enhance SUMO2-conjugation (10, 13, 40). The independent success of both our approach and the one from Tammsalu *et al.* (40) demonstrates that the use of SUMO variants in combination with enrichment of resulting SUMO-modified peptides constitute a powerful and broadly applicable strategy to study SUMOylation. The additional use of SILAC-based quantitative proteomics in our approach further allows analysis of SUMOylation changes in response to external stimuli.

Finally, these methods, although developed for the study of SUMO, can be further broadened to investigate conjugation sites of other UBL proteins by using similar combinations of variants leading to the presence or absence of GG-modified peptides after digestion by trypsin or by endoproteinase Lys-C. These approaches constitute therefore a generalizable tool to study Ubiquitin-like modifications and to provide further insight in the role of these PTMs in cell physiology.

## **METHODS**

Description of plasmids, bacterial strains and antibodies, as well as detailed experimental procedures used in this study are provided in SI Material and Methods.

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## FIGURE LEGENDS

### **Figure 1 : Generation of SUMO variants compatible with quantitative diGlycine capture proteomics**

**a**, C-terminal sequence comparison of mature SUMO1, SUMO2, Ubiquitin, Nedd8 and ISG15. C-terminal diglycine motifs are highlighted in purple. Positions of mutations introduced in SUMO1 and SUMO2 are indicated in green. **b**, Schematic representation of the signature tags left after trypsin digestion on peptides modified either by wild-type or T95R SUMO1. **c**, Comparison of SUMO-conjugated protein patterns of cells expressing wild-type or variant SUMOs. SUMOylated proteins from HeLa cells transfected with wild-type or variant His<sub>6</sub>-SUMOs were pull-downed and analyzed by immunoblot using anti-SUMO1 or anti-SUMO2/3 antibodies. **d**, Detection of RanGAP1 SUMO-conjugated forms by immunoblot analysis of HeLa cells expressing wild-type or variant His<sub>6</sub>-SUMOs. Input fractions are shown as control.

### **Figure 2 : Method used for quantitative mapping of SUMO sites**

**a**, Schematic representation of the approach. **b**, Theoretical MS spectra expected for peptides conjugated to SUMO or non-SUMO modifiers and to peptides overSUMOylated or deSUMOylated in condition #2 versus condition #1. (rel. ab., relative abundance) **c**, MS spectra obtained for two different GG-modified peptides. The peptide from Polyubiquitin B is present in its light labeled form and therefore considered as a contaminant, most likely derived from K63-linked polyubiquitin chains. The peptide from General transcription factor II-I (GTF2I) displays a SUMO1 site on K221. The absence of the peptide in its light labeled form excludes GG-modification by a non-SUMO modifier (*i.e.* Ubiquitin, Nedd8 or ISG15). The decrease in intensity of the heavy labeled form of this peptide indicates a decrease in the



SUMOylation level of this site after LLO treatment. **d**, Overlap between SUMO1 and SUMO2 sites identified in this study.

### **Figure 3 : Validation of identified SUMOylated proteins and SUMO sites**

HeLa cells were cotransfected with His<sub>6</sub>-SUMO1 or SUMO2 and HA-tagged wild-type or K to R mutants expression vectors for selected candidates. Cell lysates were subjected to His-pull down (His PD) and the presence of SUMOylated forms of the different candidates was assayed using anti-HA antibodies. Input fractions are shown as control.

### **Figure 4 : Analysis of identified SUMO1 and SUMO2-conjugation sites**

**a**, Gene Ontology (GO) terms enrichment analysis of proteins conjugated to SUMO1 or SUMO2 compared to all human proteins. Bars correspond to the percentage of proteins annotated with each GO term (\*, groups with significant enrichment; modified fisher exact p-value<0.0001). **b**, Distribution of sites over different types of SUMOylation motifs. **c**, IceLogo representations showing the amino acids surrounding SUMO-conjugated lysine residue in different motifs (41). Imposed amino acids for each type of motif are marked by an asterisk (\*). Frequencies of non-imposed amino acids at every subsite are compared with sampled frequencies in the human proteins stored in the Swiss-Prot database (negative control). Only residues that are statistically over-represented (upper part of the iceLogo) or under-represented (lower-part of the iceLogo) at a 95% confidence level are depicted. Residues that were never observed at specific positions are shown in pink.

### **Figure 5 : Analysis of targets deSUMOylated in response to the LLO toxin**

**a**, Immunoblot analysis of SUMO-conjugated patterns from cells transfected with His<sub>6</sub>-SUMOs variants and exposed to LLO. **b**, Functional enrichment analysis of highly

deSUMOylated proteins after LLO treatment compared to all SUMO-conjugated proteins. Bars correspond to the percentage of proteins annotated with each SP-PIR keyword (\*, groups with significant enrichment; modified fisher exact p-value<0.05).

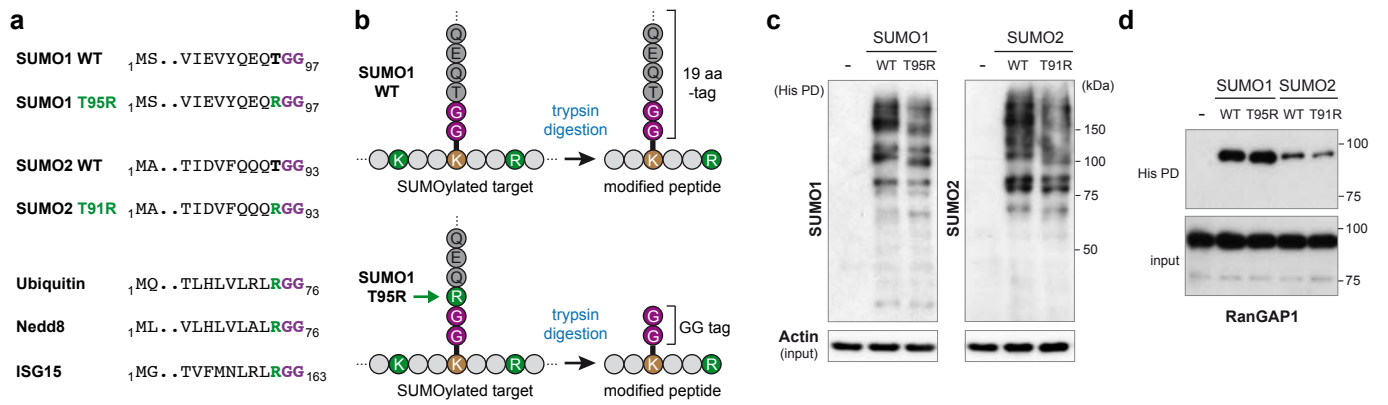


Figure 1

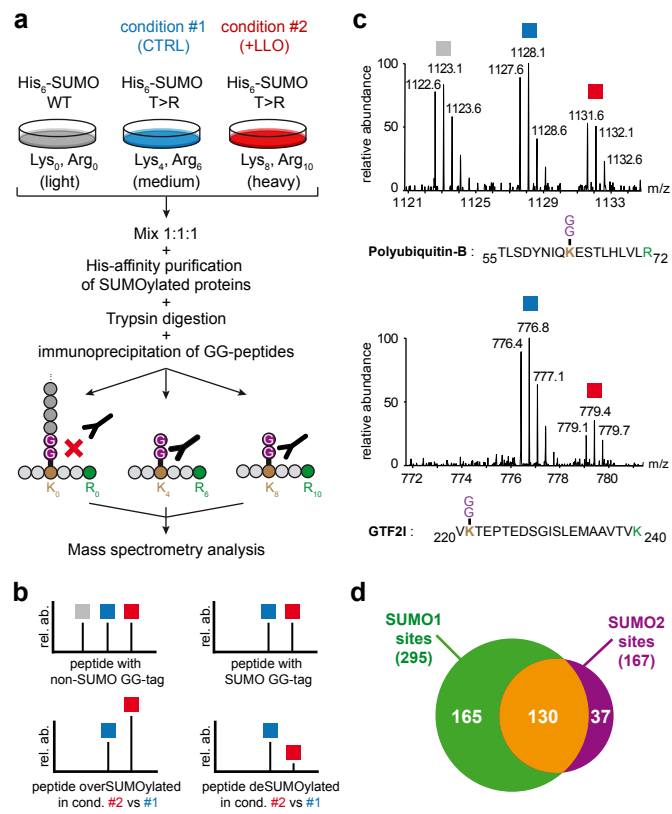
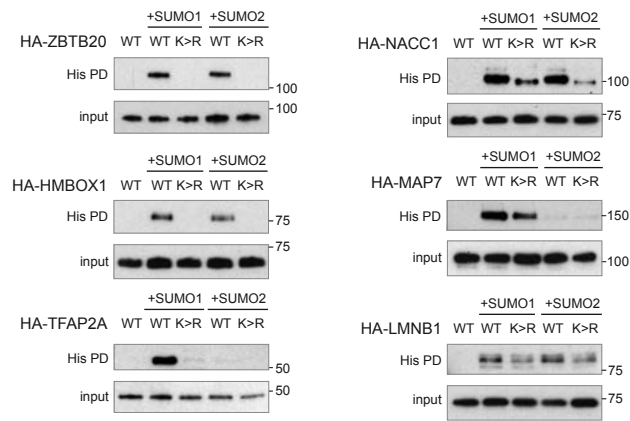


Figure 2



**Figure 3**

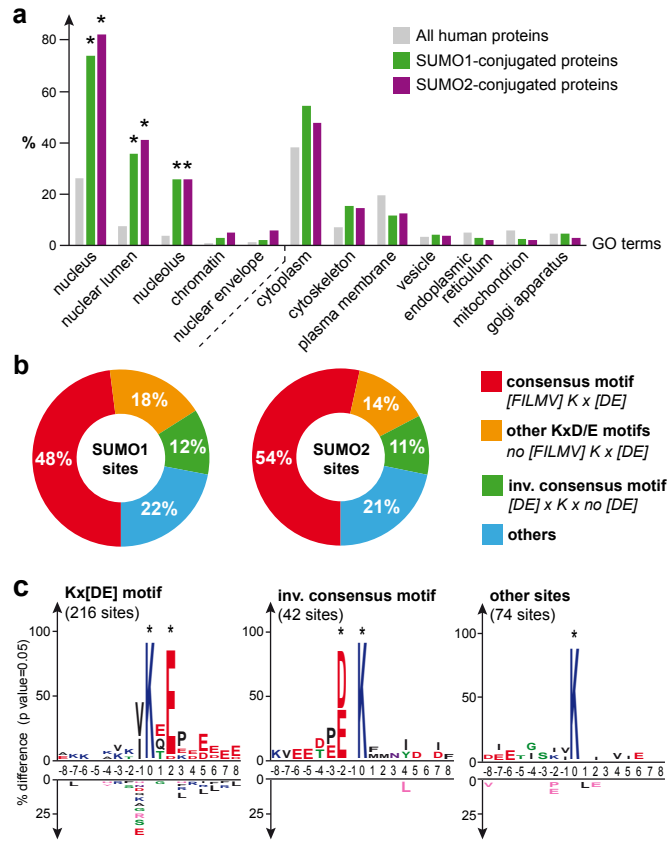
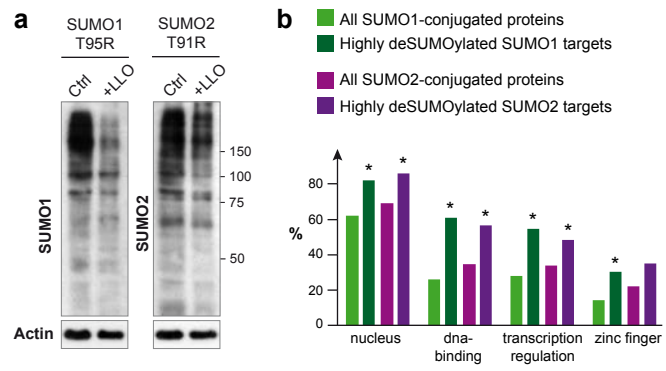


Figure 4



**Figure 5**

## Material and Methods

### Plasmids

pSG5-His<sub>6</sub>-SUMO1 plasmid encodes N-terminal His<sub>6</sub>-tagged mature SUMO1 isoform (kind gift by A. Dejean). From this plasmid was derived, using PCR mutagenesis, pSG5-His<sub>6</sub>-SUMO1 T95R. pSG5-His<sub>6</sub>-SUMO2 was obtained by inserting the cDNA corresponding to human mature SUMO2 isoform with an N-terminal His<sub>6</sub> tag in pSG5 vector (Stratagene). pSG5-His<sub>6</sub>-SUMO2 T91R was derived from this plasmid by PCR mutagenesis. N-terminally HA-tagged human cDNA of ZBTB20 isoform 2 (UniProt identifier Q9HC78-2), HMBOX1 isoform 1 (HMBOX1A, UniProt identifier Q6NT76-1), NACC1 (UniProt identifier Q96RE7), MAP7 isoform 1 (UniProt identifier Q14244-1) or LMNB1 (UniProt identifier P20700) and C-terminally HA-tagged human cDNA of TFAP2A isoform 1 (AP-2A, UniProt identifier P05549-1) were introduced into pCDNA3 vector (Invitrogen). From these plasmids were derived by PCR mutagenesis expression vectors for HA-ZBTB20 K257R, HA-HMBOX1 K413R, HA-NACC1 K167R, HA-MAP7 K406R, HA-LMNB1 K241R and TFAP2A K10R-HA. pCDNA3-NRLuc plasmid was obtained by inserting the coding sequence corresponding to the N-terminal 1-229 residues from the green Renilla luciferase protein (RLuc; ThermoFisher Scientific), fused to a “GGGS” flexible linker, into pCDNA3 vector (1). From this plasmid were derived four expression vectors with respectively SUMO1 WT, SUMO1 T95R, SUMO2 WT or SUMO2 T91R fused in C-terminal of the 1-229 luciferase fragment. pCDNA3-CRLuc plasmid was obtained by inserting the coding sequence corresponding to the C-terminal 230-311 residues from the RLuc protein, fused to 3 “GGGS” flexible linkers, into pCDNA3 vector (1). From this plasmid were derived expression vectors for either a phosphorylation-mimic variant of Daxx SIM (KGGKTSVATQCDPEEIIVLDDDD) (1) or for PIAS2 SIM (KVDVIDLTIESSSDEEEDPPAKR) (2), fused in N-terminal of the 230-311 luciferase fragment. All generated constructs were verified by sequencing.



## **Antibodies**

Primary antibodies used for immunoblot analysis were the following: mouse anti-actin (R5441, Sigma-Aldrich) and anti-HA tag (#2367, Cell Signaling Technology); rabbit anti-RanGAP1 (#R0155, Sigma-Aldrich) and anti-SUMO1 (#4930, Cell Signaling Technology); home-made rabbit polyclonal antibodies raised against recombinant SUMO3 protein produced in *Escherichia coli* (R206). Anti-mouse and anti-rabbit HRP-conjugated antibodies (AbCys) were used as secondary antibodies.

## **Cell culture, SILAC labeling and transfections**

HeLa cells (ATCC, CCL-2) were cultured in MEM-glutamax medium (Invitrogen), supplemented with 10% fetal bovine serum, MEM non essential aminoacids (Invitrogen) and 1 mM sodium pyruvate (Invitrogen).

For SILAC labeling (3), cells were cultured in DMEM without L-Lysine, L-Arginine and L-Glutamine (Silantes GmbH) supplemented with 10 % dialyzed foetal bovine serum (Invitrogen), 2 mM GlutaMAX (Invitrogen) and either natural L-Arginine.HCl and L-Lysine.HCl (light, Sigma), D<sub>4</sub> L-Lysine.HCl and <sup>13</sup>C<sub>6</sub> L-Arginine.HCl (medium, Silantes GmbH) or <sup>13</sup>C<sub>6</sub> <sup>15</sup>N<sub>2</sub> L-Lysine.HCl and <sup>13</sup>C<sub>6</sub> <sup>15</sup>N<sub>4</sub> L-Arginine.HCl (heavy, Silantes GmbH). While L-Lysine.HCl was added at its normal concentration in DMEM medium (146 mg/L), the concentration of L-Arginine.HCl was reduced to 25 mg/L (30% of the normal concentration in DMEM medium) to prevent metabolic conversion of arginine to proline (4). Cells were kept for at least six population doublings to ensure complete incorporation of the labelled lysine and arginine.

For transfections, cells were seeded in 75 cm<sup>2</sup> flasks, or in 6- or 24-well plates at a density of 2.7x10<sup>6</sup> cells per flask, or 3x10<sup>5</sup> or 0.5 x10<sup>5</sup> cells per well respectively. Cells were transfected the day after with 20 µg per flask, or 3.5 µg or 0.75 µg of DNA per well

of 6- or 24-well plates respectively, using Lipofectamine LTX reagents (Invitrogen) during 48 hours.

For LLO treatment, cells were serum-starved for 2 h before direct addition of 3 nM of purified toxin (5) in the culture medium for 20 min. Cells were then lysed for further His pull down assays or immunoblot analysis.

### **Luciferase assays**

HeLa cells were transfected with different mixes of NRLuc and CRLuc-encoding plasmids (ratio 1:1). 48 hours after transfection, cells were harvested and luciferase activities were quantified on a Tristar LB491 luminometer (Berthold Technologies), using Renilla Luciferase Assay System (Promega).

### **His-pull down assays**

SUMOylated proteins were isolated from cell lysates as described in ref. (6). Briefly, cells were washed in PBS and lysed in Lysis buffer (6M Guanidium-HCl, 10 mM Tris, 100 mM sodium phosphate buffer pH 8.0, 5 mM  $\beta$ -mercaptoethanol, 1 mM imidazole). For mass spectrometry analysis,  $2 \times 10^7$  cells/SILAC condition were lysed in 40 mL of Lysis buffer without  $\beta$ -mercaptoethanol and imidazole. Equal volumes of each SILAC condition were mixed and protein were reduced and alkylated by addition of 5 mM tris(2-carboxyethyl)phosphine (TCEP) and 10 mM chloroacetamide. After incubation for 30 min at 37°C in the dark, excess chloroacetamide was quenched by addition of 20 mM dithiothreitol. 3 mL of packed NiNTA agarose beads (QIAGEN) pre-washed in Lysis buffer were then incubated with cell lysates overnight at 4°C. After incubation, beads were washed once in Lysis buffer, once in Wash buffer pH 8.0 (8 M Urea, 10 mM Tris, 100 mM

sodium phosphate buffer pH 8.0, 0.1% Triton X-100, 5 mM  $\beta$ -mercaptoethanol) and three times in Wash buffer pH 6.3 (8 M Urea, 10 mM Tris, 100 mM sodium phosphate buffer pH 6.3, 0.1% Triton X-100, 5 mM  $\beta$ -mercaptoethanol, 10 mM imidazole). SUMOylated proteins were then eluted from the beads using Elution buffer A (200 mM imidazole, 5% SDS, 150 mM Tris-HCl pH 6.7, 30% glycerol, 720 mM  $\beta$ -mercaptoethanol and 0.0025% bromophenol blue) for immunoblot analysis or Elution buffer B (100 mM sodium phosphate buffer pH 6.8, 200 mM imidazole) for mass spectrometry analysis. The latter eluates contained about 500  $\mu$ g of proteins in a volume of 1.5 mL for both SUMO1 and SUMO2 analysis.

### **Immunoblotting**

Cells lysed in Laemmli buffer (0.125 M Tris pH 6.8, 4% SDS, 20% glycerol, 100 mM DTT) and proteins eluted from His-pull down assays were separated on SDS-polyacrylamide gels. Proteins were transferred to PVDF membranes and incubated with primary and secondary antibodies. Proteins were revealed using Pierce ECL 2 Western Blotting Substrate (Fisher Scientific). All displayed immunoblots are representative of at least 2 independent experiments.

### **Immunocapture of GG-modified peptides**

Eluates from the His pull down were further diluted with 8.5 ml 50 mM ammoniumbicarbonate and proteins were digested with 20  $\mu$ g trypsin (Promega). Immunocapture of GG-modified peptides was then performed using the PTMScan® Ubiquitin Remnant Motif (K- $\epsilon$ -GG) Kit (Cell Signaling Technology) according to the manufacturer's instructions. Briefly, peptides were purified on Sep-Pak C18 cartridges (Waters), lyophilized for two days and re-dissolved in 1.4 ml 1x immunoprecipitation

buffer without detergent supplied with the kit. Note that at this point an aliquot corresponding to 4 µg of digested protein material was taken to analyze the input. Peptides were incubated with the antibody-bead slurry for 2 hours on a rotator at 4°C and after several wash steps, GG-modified peptides were eluted in 100 µl 0.15% TFA and desalted on reversed phase C18 OMIX tips (Agilent), all according to the manufacturer's protocol. Purified GG-modified peptides were dried under vacuum in HPLC inserts and stored at -20°C until LC-MS/MS analysis.

### **LC-MS/MS analysis**

Peptides were redissolved in 20 µl solvent A (0.1% formic acid in water/acetonitrile (98:2, v/v)) of which 6 µl was injected on an Ultimate 3000 HPLC system (Dionex) in line connected to an LTQ Orbitrap Velos mass spectrometer (Thermo Electron) operated as described before (7). Briefly, peptides were loaded onto a C18 reversed phase chromatography column and eluted with a linear gradient from 2 to 55% solvent B (0.08% formic acid in water/acetonitrile (2:8, v/v)) over 120 minutes at a constant flow rate of 300 nl/min. Separated peptides were ionized by electrospray ionization and measured in the mass spectrometer that was operated in data-dependent mode, automatically switching between MS and MS/MS acquisition for the 20 most abundant ion peaks per MS spectrum. Full-scan MS spectra (300-2000 m/z) were acquired at a resolution of 60,000 in the orbitrap analyzer after accumulation to a target value of 1000,000. The 20 most intense ions above a threshold value of 5000 were isolated for fragmentation by CID at a normalized collision energy of 35% in the linear ion trap (LTQ) after filling the trap at a target value of 5000 for maximum 50 ms. Peptides with

unassigned charge states, as well as with a charge state less than 2+ were excluded from fragmentation.

### **Data processing**

From the MS/MS data in each LC-run, Mascot generic files (mgf) were created using the Mascot Distiller software (version 2.4.3.3, Matrix Science Ltd.) as described before (7). Generated peak lists were then searched with Mascot using the Mascot Daemon interface (version 2.3.0, Matrix Science Ltd.) against the human proteins in the Swiss-Prot database (database release version of March 6, 2013 containing 20258 human protein sequences). Three independent searches were performed to identify light, medium and heavy labeled SILAC peptides. For all three searches variable modifications were set to oxidation of methionine residues and pyroglutamate formation of N-terminal glutamine residues. Carbamidomethyl formation of cysteine residues was set as fixed modification. Depending on the search, additional variable modifications included di-glycine modification of lysine residues (+114.042927 Da, light search), SILAC modification of lysine residues and di-glycine modification of SILAC labeled lysine residues (+4.025107 Da and +118.068034 Da, medium search; +8.014199 Da and +122.057126 Da, heavy search). SILAC modification of arginine residues was set as additional fixed modification for the medium (+6.020129 Da) and heavy (+10.008269 Da) search. For all searches mass tolerance of the precursor ions was set to 10 ppm and mass tolerance of the fragment ions was set to 0.5 Da. The peptide charge was set to 2+, 3+ and 4+, and up to three missed tryptic cleavage sites were allowed. Also, the C13 setting of Mascot was set to 1. To identify the phosphorylated peptides listed in Supplementary Table 3, the above searches were repeated with phosphorylation of

serine, threonine and tyrosine residues as additional variable modifications. Only peptides that were ranked first and scored above the threshold score set at 99% confidence were withheld. For processing of all MS data the ms\_lims software platform was used (version 7.7.7) (8). In total, 2016 and 3123 peptide spectrum matches (PSMs) were obtained for the SUMO1 and SUMO2 analysis, respectively, with a false discovery rate (FDR) < 0.3% (9). For GG-modified peptides peak intensities from the light, medium and heavy SILAC label were manually looked up in the MS spectra (a few peptides that were identified with modified lysine residues at their C-terminus were discarded for further analysis). Only peptides with no detectable light peak were annotated to report true SUMOylation sites (625 PSMs for SUMO1 and 324 PSMs for SUMO2). To calculate the degree of deSUMOylation upon LLO treatment, the ratio between the medium (M) and heavy (H) peptide envelope was normalized against the median M/H ratio from all non-GG-modified peptides that were quantified by the MaxQuant software (1427 for SUMO1 and 2954 for SUMO2). Indeed, initially raw data files were analyzed using the MaxQuant software (version 1.4.0.1) with similar search settings as described above and allowing a maximum FDR of 1%. However, we observed that specifically GG-modified peptides without any detectable light signal were not identified at the given confidence level, thus leading to very low numbers of identified SUMO-sites. Unlike the above Mascot workflow, in MaxQuant only a single search is performed to identify peptides derived from the three SILAC conditions. For peptides where three SILAC labels are expected, the complete lack of one of the labels presumably results in lower confidence about their identification. The M/H ratio for every SUMO site was calculated by averaging the M/H ratio of the different corresponding GG-modified peptides. Peptides that could not be precisely mapped in their cognate protein were excluded from analysis.

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium (<http://proteomecentral.proteomexchange.org>) via the PRIDE partner repository (10) with the dataset identifier PXD000459 (username: review32993 ; password: 2ppqHGjn).

### **Gene Ontology terms enrichment analysis**

GO terms enrichment analyses were performed using DAVID bioinformatics resources (11).

## Bacterial strains

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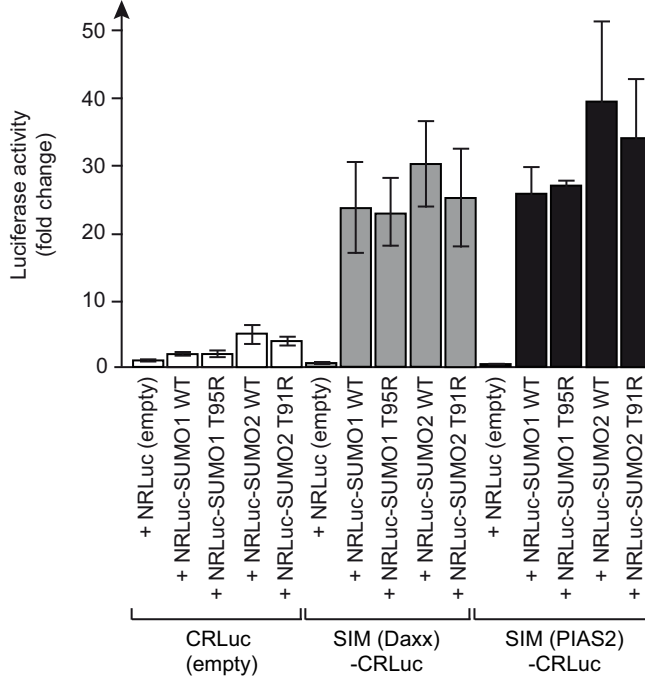
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BUG 3459	pSG5-His <sub>6</sub> SUMO1 T95R
BUG 3128	pSG5-His <sub>6</sub> SUMO2 WT
BUG 3460	pSG5-His <sub>6</sub> SUMO2 T91R
BUG 3509	pCDNA3-HA ZBTB20 WT
BUG 3510	pCDNA3-HA ZBTB20 K257R
BUG 3511	pCDNA3-HA HMBOX1 WT
BUG 3512	pCDNA3-HA HMBOX1 K413R
BUG 3513	pCDNA3-HA NACC1 WT
BUG 3514	pCDNA3-HA NACC1 K167R
BUG 3515	pCDNA3-HA MAP7 WT
BUG 3516	pCDNA3-HA MAP7 K406R
BUG 3517	pCDNA3-HA LMNB1 WT
BUG 3518	pCDNA3-HA LMNB1 K241R
BUG 3519	pCDNA3-TFAP2A WT-HA
BUG 3520	pCDNA3-TFAP2A K10R-HA
BUG 3623	pCDNA3-NRLuc
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BUG 3628	pCDNA3-NRLuc-SUMO2 T91R
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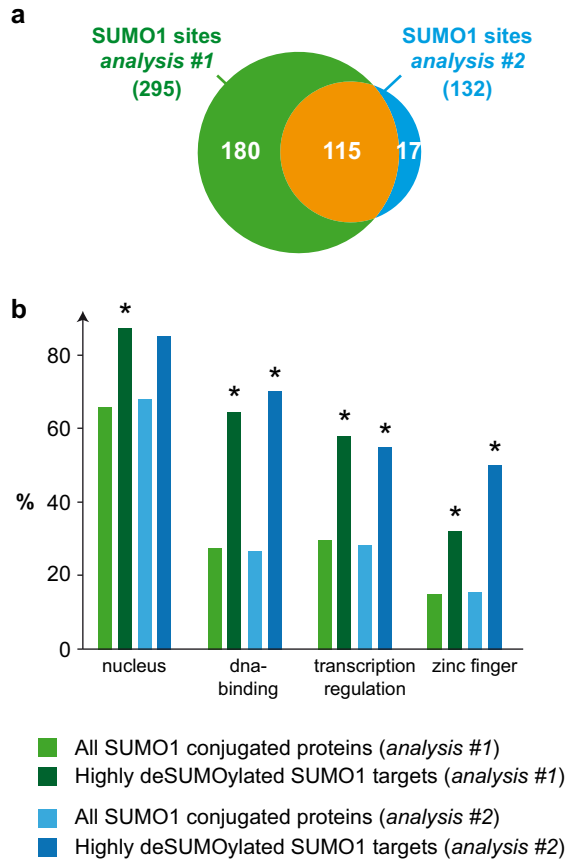


## Supplementary References

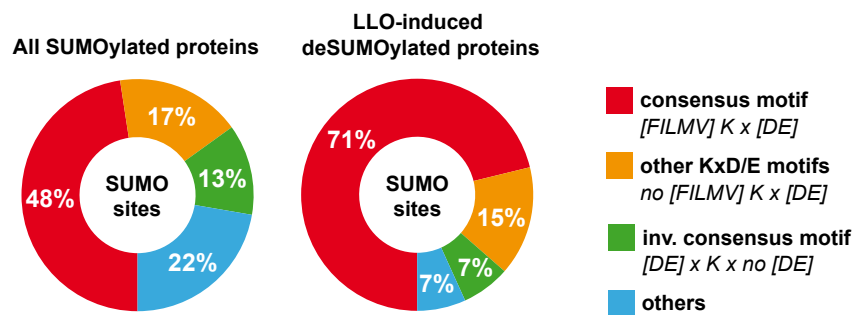
1. Hirohama M, *et al.* (2014) Assay methods for small ubiquitin-like modifier (SUMO)-SUMO-interacting motif (SIM) interactions in vivo and in vitro using a split-luciferase complementation system. *Anal Biochem* 448:92-94.
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**Fig. S1. Detection of SUMO-SIM interactions using split luciferase complementation assay.** In split luciferase complementation assays, N- and C-terminal fragments of Renilla luciferase are fused to potentially interacting proteins. If the proteins indeed interact, the two luciferase fragments are brought into proximity, reconstituting a functional luciferase protein that emits bioluminescence in presence of an adequate substrate. Here, we fused the N-terminal fragment of Renilla luciferase (NRLuc) to wild-type or variant SUMOs and the C-terminal fragment of Renilla luciferase (CRLuc) to Daxx or PIAS2 SIM domains. HeLa cells were transfected with the indicated pairs of plasmids and luciferase activities were quantified in cell lysates 48 h after transfection. Bars correspond to means  $\pm$  SD from 2 independent experiments. Split luciferase fragments alone have low affinity for each others, resulting in low luciferase activity. Both wild-type and SUMO variants, when co-expressed with Daxx or PIAS2 SIMs, are associated with a strong luciferase signal, indicating that these different SUMO forms are similarly interacting with the tested SIMs.



**Fig. S2. Evaluation of the reproducibility of the approach.** The large-scale analysis performed for SUMO1 (analysis #1) was repeated in a smaller scale (analysis #2). **a**, Overlap between SUMO1 sites identified in both experiments. 87% of sites identified in analysis #2 were also found in analysis #1, indicating a high degree of reproducibility of our approach. **b**, For each analysis, the functional enrichment of highly deSUMOylated proteins after LLO treatment compared to all identified SUMO-conjugated proteins is indicated. Bars correspond to the percentage of proteins annotated with each SP-PIR keyword (\*, groups with significant enrichment, modified fisher exact p-value<0.05). In both analyses, nuclear proteins involved in transcription regulation are enriched among highly deSUMOylated targets.



**Fig. S3. Analysis of SUMO sites highly deSUMOylated after LLO treatment.** The distribution of sites over different types of SUMOylation motifs in proteins highly deSUMOylated after LLO treatment, or in all identified SUMOylated proteins, is indicated.

**Table S1. List of identified SUMOylation sites for SUMO1 and SUMO2.** Peptides are ordered by protein name and increasing position of the SUMO-conjugated lysine residue. Columns from left to right contain the Swiss-Prot accession number, HGNC symbol, protein name, position of the SUMO-conjugated lysine residue, amino acid sequence surrounding the SUMO site (-15;+15), possible protein isoforms in which the same peptide sequence can be found, SUMO isoform specificity, type of SUMO site, previous report in mass spectrometry (MS) screens (Hsiao et al., 2009; Blomster et al., 2010; Matic et al., 2010; Galisson et al., 2011; Lamolatte et al., 2013; Schimmel et al., 2014), previous report of SUMOylation (S), acetylation (Ac) or Ubiquitylation (Ub) in PhosphoSite Plus database (Hornbeck et al., 2012). S1 only: site identified with SUMO1 only; S2 only: site identified with SUMO2 only; S1+S2: site identified both with SUMO1 and SUMO2; Cons.: SUMO consensus motif, Inv. Cons.: inverted consensus motif, PDSM: Phosphorylation-Dependent SUMO Motif, NDSM: Negatively charged amino acid-dependent SUMO motif, HCMSM: Hydrophobic Cluster SUMOylation Motif.

Swiss-Prot Acc.	HGNC Symbol	Protein name	Modified K	SUMO site	Isoforms	SUMO spec.	Type of site	MS screen	PhosphoDB (S)	PhosphoDB (Ac)	PhosphoDB (Ub)
Q15029	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component	64	DDDHFGMEVLIHEDKKYYPAREVYGPVEVET		S1 only	Inv. Cons.				
Q93932	PSMD12	26S proteasome non-ATPase regulatory subunit 12	92	AREWLLNENIMLLSKRRRSLQKQAVAKMVOQ		S1+S2		x	x		
Q43242	PSMD13	26S proteasome non-ATPase regulatory subunit 3	82	EQEPFPFPAQDVEKERRAALGGSTGADG		S1 only	Cons.				x
P08708	RPS17	40S ribosomal protein S17	103	VVALDQEIIEVDFPKMLKLLPGLQNLQ	POCW22	S1 only	Inv. Cons.				x
P15890	RPS2	40S ribosomal protein S2	275	VFTKSPVQIEFDHVKHTHTVYVQFTQAPAV		S1+S2				x	x
P63220	RPS21	40S ribosomal protein S21	41	AKDHASIQMNVAVYDVKVTRFNGQFKTYAIC		S2 only					x
P23396	RPS3	40S ribosomal protein S3	230	DEILIFPTPISLQGGKQFPFAMPQVPTA		S1+S2			x		x
P08195	SLC3A2	4F2 cell-surface antigen heavy chain	166	DEARAAAANKFTGLSKHELLKVGQSPQWRT		S2 only			x		x
P05388	RPLP0	60S acidic ribosomal protein P0	297	AAATTPAANAANAAPKVAEKBESEDEDEMG		S1+S2					x
P62906	RPL10A	60S ribosomal protein L10a	118	LAKKYDAFLASLILKQIPLIOPGLNKAKG		S1+S2				x	x
P26373	RPL13	60S ribosomal protein L13	174	NVYKKEKARVITTEENKFAFASLMMARANA		S1 only	Inv. Cons.			x	x
P84098	RPL19	60S ribosomal protein L19	181	TEARFRREERLQAKKEEIIKTLSEKEETK		S1 only					x
P39023	RPL3	60S ribosomal protein L3	294	EINKKIYKIQGGYLIKDGKLIKNNASTDYDL		S1 only				x	x
P36578	RPL4	60S ribosomal protein L4	364	LRVDKAAAALAAALQKSEKAAGAKPVVVG		S1 only					x
P46777	RPL5	60S ribosomal protein L5	220	ADYMYLMEDEEDAYKQFSQYKNSVTPDM		S1+S2				x	x
P11021	HSPA5	78 kDa glucose-regulated protein	352	TMKPVQKVLDESLLKKSDDIIEIVLGGSTR		S1+S2	Inv. Cons.	x		x	x
P11021	HSPA5	78 kDa glucose-regulated protein	353	TMKPVQKVLDESLLKKSDDIIEIVLGGSTRI		S1 only				x	
P60709	ACTB	Actin, cytoplasmic 1	61	GMGQKDSYVGDQAQKRGILILKYPIEHGIV	P62736, P63261, P63267, P68032, P68133	S1 only				x	x
P60709	ACTB	Actin, cytoplasmic 1	113	PEEHPVLLTRAPLNPKANREKMTQIMFETFN	P63261	S1+S2		x	x		x
P60709	ACTB	Actin, cytoplasmic 1	326	DRMQKEITALAPSTMKIKI IAPPERKYSVWI	P62736, P63261, P63267, P68032, P68133	S1+S2				x	x
P60709	ACTB	Actin, cytoplasmic 1	328	MQKEITALAPSTMKIKI IAPPERKYSVWIGG	P62736, P63261, P63267, P68032, P68133, Q562R1	S1 only				x	x
Q9NQW6	ANLN	Actin-binding protein anillin	254	SSASGASARINSSSVKQEAFCQRDGDASL		S1 only	Cons.				
P53999	SUB1	Activated RNA polymerase II transcriptional coactivator p15	68	KQSSSDNDMFPQIGMRYVSRDFKGLVLI		S1 only				x	x
O95433	AHSA1	Activator of 90 kDa heat shock protein ATPase homolog 1	182	TNGSEVDVPGQPALTEERKAKPAPSKTQA		S1 only	Cons. (HCMSM)				
P30566	ADSL	Adenylosuccinate lyase	415	HKIKRVLSSQAAASVQEGGNDLIERIQVD		S1 only	Cons.				x
Q01518	CAP1	Adenylyl cyclase-associated protein 1	348	NGENVNLVIEDTELQVAYIKVCVNTLQI		S1 only	Inv. Cons.				x
Q6IQ32	ADNP2	ADNP homeobox protein 2	1032	FKRQNESRTGPIVDEALGLALDLPKYE		S1 only	Cons. (HCMSM)				x
Q02952	AKAP12	A-kinase anchor protein 12	1051	ERTQVQLQAVAEKVVESQLPTGGPEDVL		S1 only	Cons.				x
Q02040	AKAP17A	A-kinase anchor protein 17A	118	LSGFSDDLKVAEAEKDFPFRHWDSPFRD		S1 only	Cons.				x
Q9Y2D5	AKAP2	A-kinase anchor protein 2	174	SKCSRRDSEFTLTLKKEAFELRAFHEKDK		S1 only	Cons. (NDSM)				x
Q12904	AIMP1	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	137	KAKKIKKKGKKEKQKQSIAGSADSKFIDV		S1 only	Inv. Cons.				x
P04083	ANXA1	Annexin A1	214	ADSDARALYBAGERKGTDMVFNLTITRS		S1 only					x
P04083	ANXA1	Annexin A1	332	KMYGISLQAI LDETQVDEKILVALCGGN		S1 only					x
P07355	ANXA2	Annexin A2	49	DAERDALNIBTAIKTGVDEVTIVNLNRS		S1 only			x		x
P07355	ANXA2	Annexin A2	324	KRYGSLYYIQQDTKGDYKALLVCGGDD		S1 only					x
P08758	ANXA5	Annexin A5	29	GFDERADATLRKAMKGLGTDEESILTLTS	A6NMY6	S1 only		x	x		x
P46013	MK167	Antigen KI-67	1093	PAARVTKMKWPRTPKREAAQSLDLAGFKEL		S1 only					x
P46013	MK167	Antigen KI-67	2009	SSKQRLKI SLGKGVKVEVLPVGLKQTSGK		S1 only	Cons. (HCMSM)				
P46013	MK167	Antigen KI-67	2492	SSKQRLKI PLVKVDMKEEPLAVSLKTRTSGE		S1 only	Cons.				
P46013	MK167	Antigen KI-67	2613	TSKRCPTTRPRKVEKBEELSAVERLQTSQG		S1 only	Cons.				
P46013	MK167	Antigen KI-67	2734	STRKHLRTKQKVEKVEEPAVKPTQTSGET		S1+S2	Cons.	x	x		
P46013	MK167	Antigen KI-67	2852	SKRRPRTKQKVEKVEEELAVGLKQTSQGE		S1 only	Cons.				
Q9UKV3	ACIN1	Apoptotic chromatin condensation inducer in the nucleus	268	ETPSNLRVADRNKLTSEEEEEEEEDD		S1+S2	Cons. (NDSM)				
Q9UKV3	ACIN1	Apoptotic chromatin condensation inducer in the nucleus	315	ILKEPKEGEEIPRVKPEEMDERPKTRSQE		S1 only	Cons. (NDSM)				
Q9UKV3	ACIN1	Apoptotic chromatin condensation inducer in the nucleus	532	DLEPESDRSAQPLFLKIEELALAGITBECL		S2 only	Cons. (HCMSM)	x	x		
Q7L4I2	RSRC2	Arginine/serine-rich coiled-coil protein 2	375	GMKDQNVKFRKLMGKISEEAGCSDVDEESY		S1 only	Cons.				
Q9N1U7	DDX19A	ATP-dependent RNA helicase DDX19A	26	DEQBAANVSMNLQIKREKVRADNIIKTS		S1+S2	Cons.				
Q95817	BAG3	BAG family molecular chaperone regulator 3	445	EYVQLQEQAVDNFEGKTKDKYLMIEEYLTK		S1 only	Inv. Cons.				
Q9NYF8	BCLAF1	Bcl-2-associated transcription factor 1	580	LTKDRLLASTLIVSVKVKDQEPFIFDHLKLP		S1+S2	Cons.				
Q9NYF8	BCLAF1	Bcl-2-associated transcription factor 1	831	NTQPNNGNTTTPQKPKHEWDEPFTPKSKYI		S1+S2		x	x		
Q5T5X7	BEND3	BEN domain-containing protein 3	20	EPTEDVEVLKSIIVKVEAEADAALDCSN		S1 only	Cons. (NDSM)	x			
P80723	BASP1	Brain acid soluble protein 1	143	APASAPAPAGEEPKKEGEPKTEAPAPAPA		S1 only					
P80723	BASP1	Brain acid soluble protein 1	163	PKTTEAPAPAPAGETSDGAPASDPSKPSSE		S2 only					x
Q5PSV4	BRMS1L	Breast cancer metastasis-suppressor 1-like protein	246	MATLGFHEVTEPFPVLEKHLHARSBEGRLL		S2 only	Cons. (HCMSM)				
Q9H6U6	BCAS3	Breast carcinoma-amplified sequence 3	215	VLQKIIAADSCTFKFKFVTVSCYCPGNM		S1+S2					
Q60885	BRD4	Bromodomain-containing protein 4	1111	LEASVYVQVQLVIVKREKIHSPRIIRSEPS		S1+S2	Cons. (HCMSM)	x		x	
Q9H0E9	BRD8	Bromodomain-containing protein 8	481	ERDKPVLPAPEMTVQRELDFTENKGIH		S1+S2	Cons. (NDSM)				
Q9NXV6	CDKN2AIP	CDKN2A-interacting protein	184	SAQCNSSCTIGSASIKSESGNSRSSGISQ		S1 only	Cons.				x
Q8IX12	CCAR1	Cell division cycle and apoptosis regulator protein 1	1012	EDMLGNLRLPTPTVYKQSKDVENVGLIVY		S1+S2	Cons. (NDSM)	x	x		
Q8IX12	CCAR1	Cell division cycle and apoptosis regulator protein 1	1067	EQKIQLEEKTEDEKTIINLLENKSLSGE		S2 only	Inv. Cons.				
Q13111	CHAF1A	Chromatin assembly factor 1 subunit A	182	DKLAPFGETLSDIPCKTEEEGGVCGGAGRRG		S1 only		x			
Q9HAF1	MEAF6	Chromatin modification-related protein MEAF6	113	AAVSALAGVQDLIEKREPGSTESDTPDF		S1+S2		x			
Q12873	CHD3	Chromodomain-helicase-DNA-binding protein 3	721	QDGPSSPFTNDPTVKYQPTPRTATGTL		S1 only	Cons.				
Q14839	CHD4	Chromodomain-helicase-DNA-binding protein 4	1304	EEMEGEVEVEREIKQESVDPDYWEKLR		S2 only	Cons.	x			x
O14503	BHLHE40	Class E basic helix-loop-helix protein 40	279	DHGRFRFMEEERIGAIKQESSEPTKKNRML		S1 only	Cons. (NDSM, HCMSM)		x		
Q9J6G6	CCDC132	Coiled-coil domain-containing protein 132	963	ARQKLLAAIDIDPKFR		S1+S2					
Q96MW1	CCDC43	Coiled-coil domain-containing protein 43	95	IYKNSWSETQNVTVKKEDEVQAIAFLIEKQ		S1 only	Cons.				
Q43175	PHGDH	D-3-phosphoglycerate dehydrogenase	21	LKVLISDLSLPCCRKILQDGGVQVEKQNL		S1+S2					x

P18887	XRCC1	DNA repair protein XRCC1	176	PSQKVTITLQGFVFKVEDESSANSLRPGALF		S1 only	Cons.					
P11387	TOP1	DNA topoisomerase 1	117	IKKKEKGFSSPPQIKDEPEDDGYVFPKED		S1+S2	Cons.			x	x	
P11388	TOP2A	DNA topoisomerase 2-alpha	1240	IMKAEAEKKNKKIKENETEGSPQEDGVEL		S1+S2	Cons. (PDSM, NDSM)			x	x	
O15446	CD3EAP	DNA-directed RNA polymerase I subunit RPA34	270	KPKGKETFPEDKTKVQEQINTEPLEDITVLS		S1 only	Cons. (PDSM, NDSM)			x	x	
O15446	CD3EAP	DNA-directed RNA polymerase I subunit RPA34	314	MBPEEGVTVSSQVQVKEPLEEALPLPFTK		S1 only	Cons. (NDSM)					
Q9NVUO	POLR3E	DNA-directed RNA polymerase III subunit RPC5	498	KBQLRVAVPPGVRIKKEPVSEGEDEBQE		S1+S2	Cons. (PDSM, NDSM)					
P04843	RPN1	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 1	538	HKALTSEIALQSLRKLTDGSLCDRVSEMQK		S2 only	Cons.					x
P55265	ADAR	Double-stranded RNA-specific adenosine deaminase	418	MVTTKLVNQGEPVTKLENRQEARPEPARLK		S1+S2	Cons. (NDSM, HCSM)			x	x	
P49792	RANBP2	E3 SUMO-protein ligase RanBP2	1414	TSPEVQDRFALVTPKKGHWDCSICLVNRE		S1 only	Cons.			x	x	
P49792	RANBP2	E3 SUMO-protein ligase RanBP2	2594	LSKNSDIEQSSDSKVNLFASFPTEESINY		S1 only	Cons.			x	x	
P49792	RANBP2	E3 SUMO-protein ligase RanBP2	2792	SVYTGTEVMVPSFKSEEDPDSITKSISSPS		S1+S2	Cons.					
Q9UPN9	TRIM33	E3 ubiquitin-protein ligase TRIM33	776	ABKTLSLFSDQVVKVQEPGTDEICSPFSGG		S1+S2	Cons. (NDSM)			x	x	x
Q9UPN9	TRIM33	E3 ubiquitin-protein ligase TRIM33	793	EPGTDEICSPFSGGVQKTKEDGRSSACMLS		S2 only	Cons. (HCSM)			x	x	
Q6PJG2	ELMSAN1	ELM2 and SANT domain-containing protein 1	590	IPGTDAQAQBDMNVKLGEGSPVSKPKQRPR		S1 only	Cons.					
P68104	EEF1A1	Elongation factor 1-alpha 1	392	EKIDRRGKLEDDGPKFLKSGDAIVDMVFG	Q5VTE0	S1 only	Inv. Cons.					x
P26641	EEF1G	Elongation factor 1-gamma	253	REBKQPKQAEKKEKAAAPAEPEEMDECBQ		S1 only	Inv. Cons.					x
P13639	EEF2	Elongation factor 2	239	TLKQFAMVYAKFAKGGQGLGPAERAKKVE		S1 only	Cons.					x
Q14244	MAP7	Ensoconsin	406	KVANEPLKGRAPLVKVEEATVEERTPAEPE		S1+S2	Cons. (NDSM, HCSM)					x
Q06265	EXOSC9	Exosome complex component RRP45	297	FGFAESIANQRITAFKMEKAPIDTSDVEEKA		S1 only	Cons.					x
Q01780	EXOSC10	Exosome component 10	583	EMHLILQQAEMPLLKSEVAAGVKSGLPS		S1 only	Cons. (HCSM)					x
Q92945	KHSRP	Fair upstream element-binding protein 2	121	GGQKQLLEDGQDPESEKSLASQDSISSGLGP		S1 only	Inv. Cons.					x
P49327	FASN	Fatty acid synthase	2449	TPKAKYHGNWMLLRKAGTGAYGEDLGDVYNL		S2 only	Cons.					x
Q90308	FGF2	Fibroblast growth factor 2	228	NRYLAMKEDGRLLASKVCYVDSFPFPERLESS		S1 only	Cons.					x
P21333	FLNA	Filamin-A	299	ARAYGPGIIEPTGNMVKRABPTVETSAQGG		S1+S2	Cons.			x	x	x
Q8N3X1	FBNP4	Formin-binding protein 4	301	VSSSKSPVIAKRWVKEKINQICQLSNSEB		S1 only	Cons.					x
Q8N3X1	FBNP4	Formin-binding protein 4	348	G1KBEERWRWYICKEBPVSEKSTFTVVE		S1+S2	Cons.			x	x	
Q8N3X1	FBNP4	Formin-binding protein 4	519	VESPEKIKVQTFVVEEQDLKFOIGELA		S1 only	Cons.					x
P15408	FOSL2	Fos-related antigen 2	222	QPRSGSGGIVAVVWQKPLEDSFSSSSNG		S1+S2	Cons. (PDSM, NDSM, HCSM)			x	x	
P04075	ALDOA	Fructose-bisphosphate aldolase A	42	QKGLLADESTGSLAKRLQIGTENTENRR		S1+S2	Cons.					x
Q16666	IFI16	Gamma-interferon-inducible protein 16	561	TFPSSSPLTLKPLKTEPEEVIIDSAQSD		S1 only	Cons. (NDSM)			x	x	x
Q9Y5B6	PAXBP1	GC-rich sequence DNA-binding factor 1	149	LLKXYKEDLEKSIKTELNSASBSEQLDK		S1 only	Cons. (NDSM)			x	x	
P78347	GTf2J	General transcription factor IIH	221	RSILSPGSGCP1KVKTEPTEDSGIILEMAA		S1+S2	Cons. (NDSM)					x
P78347	GTf2J	General transcription factor IIH	991	PATERIKETDGSQIQCEPDTW		S1+S2	Cons.			x	x	
Q9UHL9	GTf2IRD1	General transcription factor IIH repeat domain-containing protein 1	443	DERIPTNFKTKDTLKEPASPFDTSAEVS		S2 only	Cons.					x
Q9UKD1	GMEB2	Glucocorticoid modulatory element-binding protein 2	155	KDWKRAIRMGIMLRKIMDSGELDFYQHDKV		S1 only	Cons.					x
P04150	NR3C1	Glucocorticoid receptor	293	TEKEDFELCTPGVIKQKELTVYCCASFPG		S1+S2	Cons. (HCSM)			x	x	
Q9BV2	GNL3	Guanine nucleotide-binding protein-like 3	99	KELEKKELETNPDIKPSNVPEMRKEFLCK		S2 only	Inv. Cons.					x
Q9NVN8	GNL3L	Guanine nucleotide-binding protein-like 3-like protein	477	LLHSMPK1ADAIENKTYVIGIDLGYCTCN		S1 only	Inv. Cons.					x
Q9NX24	NHP2	H/ACA ribonucleoprotein complex subunit 2	5	MTKIKADPGPEAQAEACSG		S1+S2	Cons. (NDSM)			x	x	
O60832	DKC1	H/ACA ribonucleoprotein complex subunit 4	413	LDHKGKPTDSTPATWQEVYDVSBAKKEV		S1 only	Cons.					x
P11142	HSPA8	Heat shock cognate 71 kDa protein	512	KENKITTINDKGLSKEDIERMVAEKYKA		S1 only	Cons.					x
P07900	HSP90A1	Heat shock protein HSP 90-alpha	407	EDLPLNISREMLQSQKILKIRKNLVKKCLE	P08238, Q58FF7	S1 only	Cons.					x
P51858	HDGF	Hepatoma-derived growth factor	80	PYSESKEKFGPKNRKGFSEGLWIEINPTV		S1 only	Cons.			x	x	
Q14103	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0	197	KKIPVGLSDPTPEEKIREYFGGFEVESIE		S2 only	Inv. Cons.					x
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	34	FGKRAPEDMBEBAQAFKSRNTDMELRILL		S1+S2	Cons.					x
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	163	RLLIHQSLAGIIGVKGAKIKELRENTOTTI		S1 only	Cons.					x
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	422	GRR1KQIRHESGASIKIDEPLGESDR1ITI		S1+S2	Cons. (NDSM)			x	x	
P52272	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	698	DIKMENKSKGCVKFPESPEVAERACRMN		S1+S2	Cons. (NDSM, HCSM)			x	x	x
Q00839	HNRNPU	Heterogeneous nuclear ribonucleoprotein U	265	REHDGROYFYEIENKYSRAKSPQPPVEED		S1+S2	Inv. Cons.					x
Q9BUJ2	HNRNPUL1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	117	DNITRQNFYDVTQVIKQENESYERRPLEME		S1+S2	Cons. (NDSM)			x	x	x
Q9BUJ2	HNRNPUL1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	142	RFLMEQQAYRPEMTEMKQGAPTSFLPPE		S1 only	Cons.					x
P07910	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	229	LEK1EKEQSKAVEMKNDKSEEESSSVKVK		S2 only	Cons. (NDSM)			x	x	
P07910	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	232	IEKBEQSKAVEMKNDKSEEESSSVKVKDET		S1+S2	Cons.			x	x	x
P82970	HMGNS	High mobility group nucleosome-binding domain-containing protein 5	101	K1TEAPASKEIIVEKRENI EDATKGGKSK		S1+S2	Cons. (NDSM)			x	x	
Q9H9B1	EHMT1	Histone-lysine N-methyltransferase EHMT1	22	EAVPARGEPQDCCVKTLLGSETPMADEG		S1 only	Cons. (NDSM)					x
Q15047	SETDB1	Histone-lysine N-methyltransferase SETDB1	1032	SRMBAKASTSLGLIKDEGDIKQAKKEDTDD		S1 only	Cons. (HCSM)					x
Q6NT76	HMBOX1	Homeobox-containing protein 1	413	NHTTILALARQGANIKTEALDDD		S1+S2	Cons.					x
Q16543	CDC37	Hsp90 co-chaperone Cdc37	132	DTLSKDGFSKSMVNTPEKTEEDSEEVREKQ		S1 only	Cons.					x
P0492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	115	ILKSYCNDQSTGDIKVIQGDLSLTLGKNV		S1 only	Inv. Cons.					x
Q9NVR2	INTS10	Integrator complex subunit 10	464	RIFLTDMIYQQYKKAIALSLHLAALQGS1		S2 only	Cons.					x
Q96HW7	INTS4	Integrator complex subunit 4	791	FVDKLDLMPRLMTSKPAEVVKILQTLMLRQS		S1+S2	Cons.					x
P05556	ITGB1	Integrin beta-1	794	ENPIYKSAVTTVNNKYBKG		S1 only	Cons.					x
Q12906	ILF3	Interleukin enhancer-binding factor 3	348	VLGMDPLFSKMPKPKNENPVDYTVQIPFST		S1 only	Cons.					x
Q04695	KRT17	Keratin, type I cytoskeletal 17	15	MTTSIRQPTSSSSIKGSSGLGGSSRTSCR		S1+S2	Cons.					x
Q04695	KRT17	Keratin, type I cytoskeletal 17	399	YRLLLEGDAHLTYQKKEPVTTQVRTIIVEE		S1+S2	Cons.					x
Q04695	KRT17	Keratin, type I cytoskeletal 17	400	RRLLLEGDAHLTYQKKEPVTTQVRTIIVEE		S1 only	Cons.					x
Q04695	KRT17	Keratin, type I cytoskeletal 17	419	TTQVRTIIVEVQDQGVKISSREQVHQVTR		S1+S2	Inv. Cons.					x
P05783	KRT18	Keratin, type I cytoskeletal 18	426	RRIVDGVVSETNDTKVLRH		S1 only	Cons.					x
P78386	KRT85	Keratin, type II cuticular Hb5	229	EVALRATAENEFVVLKQDVCAYLRKSDLEA		S1 only	Cons. (HCSM)					x
P08729	KRT7	Keratin, type II cytoskeletal 7	130	QNKLETWTLLEQKSAKSSRLPDI FEAQI		S2 only	Inv. Cons.					x
P05787	KRT8	Keratin, type II cytoskeletal 8	101	AVRTQEKQIKTLNKKFASFDIKVRFLEQCN	Q95678, P02538, P04259, P08729, P12035, P13647, P35908, P48668, Q01546, Q5XKE5, Q9NSB2	S1+S2	Cons.				x	x
P05787	KRT8	Keratin, type II cytoskeletal 8	197	EINKRTMEMENFVLIKVDVEAYMNVKVELS		S1+S2	Cons. (NDSM, HCSM)					x
P05787	KRT8	Keratin, type II cytoskeletal 8	285	IANKRSRAEBSMYIKYBELQSLAGKHGDDL		S2 only	Cons.			x	x	
P05787	KRT8	Keratin, type II cytoskeletal 8	472	SRRAVVVKIKBTRDGLAESSDVLPK		S1+S2	Inv. Cons.					x
Q07666	KHDRBS1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	102	LPPSATASVKMPEKNYKLPFLMAKOSLDP		S1+S2	Inv. Cons.			x	x	



Q92766	RREB1	Ras-responsive element-binding protein 1	615	S1EALLPLLSMEAKIKQETTEGLKAFMTAP		S1+S2	Cons. (NDSM)		x	x			
Q96723	RSF1	Remodeling and spacing factor 1	277	LENSTANVLEETTVKKEDEKELVKLPLVI		S1+S2	Cons. (NDSM)		x	x			
Q96723	RSF1	Remodeling and spacing factor 1	294	EKEDKELVKLPLVIKLEKPLPENEKIKI		S1+S2	Cons. (NDSM, HCSM)		x	x			
Q96723	RSF1	Remodeling and spacing factor 1	456	LVNGVSDSERVAPNFKTEPIETKPYETBES		S1+S2	Cons. (NDSM)		x	x			
Q7Z5J4	RAI1	Retinoic acid-induced protein 1	819	ASLPGDFQGEVGGVKEAGGLQCEVAKA		S1 only	Cons. (HCSM)						
Q7Z5J4	RAI1	Retinoic acid-induced protein 1	901	GNQDPLSPKAPLICTEKEVEVLDSKAGWS		S1+S2			x				
P52565	ARHGDI	Rho GDP-dissociation inhibitor 1	138	VSMGYIQHTYRKGVIKDKTDYMGVSGPRA		S1+S2	Cons.			x			
P52565	ARHGDI	Rho GDP-dissociation inhibitor 1	141	MKYIQHTYRKGVIKDKTDYMGVSGPRAEY		S1+S2					x		x
Q14692	BMS1	Ribosome biogenesis protein BMS1 homolog	810	KSGPNTQNEDEKVEKKEEDLPEEESAKKKH		S1+S2	Cons. (NDSM)						
Q9GZL7	WDR12	Ribosome biogenesis protein WDR12	239	EDMEESTNRPRKQKTEBQLGLTRTPIVTL		S1 only							
Q9P2E9	RRBP1	Ribosome-binding protein 1	620	VQGRNTDVAQSPKAPQKAPAKKSGSKKGG		S1 only							
P38159	RBMX	RNA-binding motif protein, X chromosome	63	SRGFAPVTFESPADAKDAARNGKSLDGKA	Q96E39	S1 only	Inv. Cons.						x
Q5T8P6	RBM26	RNA-binding protein 26	106	GSLLKVFYFPHQEKDIKKEEITKEBEREKKFS		S1+S2	Cons. (NDSM)						
Q6PCB5	RSBN1L	Round spermatid basic protein 1-like protein	763	ELQIQHFEPIASVRIKKEPVNVIPEKTTAL		S2 only	Cons.						
Q5JTH9	RRP12	RRP12-like protein	71	VKLHNELGSGSLRLGKSEAPPTMPEEABLV		S1 only							x
Q9Y3B9	RRP15	RRP15-like protein	239	TASSRKKPKAKQTEVKSSEGPGWTLRDDFM		S1+S2	Cons.						x
Q9Y265	RUVBL1	RuvB-like 1	225	ATFPLDEABEYVPLPKGVDVHKKEIITQDVTL		S1 only				x			
Q8NSC6	SRBD1	S1 RNA-binding domain-containing protein 1	185	NDDPFFGQALKKIKTETYPQSQPVKFPAN		S1 only	Cons.						
Q15424	SABF	Scaffold attachment factor B1	381	PPAPKESSTSEADQKMSPEDESDTKRLSK		S1 only	Inv. Cons.						
Q15424	SABF	Scaffold attachment factor B1	578	TVVMKSGKVPVIVSVKTSKSKERASKSGDRK		S1 only							
Q14151	SABF2	Scaffold attachment factor B2	65	GKNSVLMERLAKKAVKEEEDQDDEIGILEEA		S1+S2	Cons. (NDSM)		x				
Q14151	SABF2	Scaffold attachment factor B2	225	EPNEKLLDLIGBTCKSEFVRESSELEQPF	Q15424	S1+S2			x	x			
Q14151	SABF2	Scaffold attachment factor B2	230	KILLDLGETCKSEFVRESSELEQPFQADTS	Q15424	S1+S2	Cons. (NDSM)		x	x			x
Q14151	SABF2	Scaffold attachment factor B2	252	EQPPAQDTSVGGPKLAEEDLFDSEHPPE	Q15424	S2 only	Inv. Cons.		x				
Q14151	SABF2	Scaffold attachment factor B2	293	ANAGSSKADSLAVKREPARQDSEPTDC	Q15424	S1+S2	Cons. (NDSM, HCSM)		x	x	x		x
Q14828	SCAMP3	Secretory carrier-associated membrane protein 3	313	KEIHSLVRRGTASFGAQGFPAQGVSNDAV		S1 only							x
Q8IYB3	SRRM1	Serine/arginine repetitive matrix protein 1	231	KEKTFPELPEPSVKKVRESVQRTSISLIX		S1 only							
Q13523	PRPF4B	Serine/threonine-protein kinase PRP4 homolog	117	DLALDLDEKQRALIKALDMLMBGKVGQS		S1 only	Cons. (NDSM, HCSM)						
Q76094	SRP72	Signal recognition particle 72 kDa protein	392	KLTMQAQLKISQGNISKALILRSIELKHKP		S1+S2							x
Q42224	STAT1	Signal transducer and activator of transcription 1-alpha/beta	703	PEPMELDGPKGTGVIKTELIISVSEVHPSRLQ		S1 only	Cons.			x			
Q8TAD8	SNIP1	Smad nuclear-interacting protein 1	30	RHRDDGVVLPACTYVQKREPLSPVAPPNRR		S1+S2	Cons. (PDSM, HCSM)		x	x			
P61956	SUMO2	Small ubiquitin-related modifier 2	11	MADEKPKGEVKTENNHNILNKVAGDD		S1 only	Cons.		x	x		x	x
P55854	SUMO3	Small ubiquitin-related modifier 3	11	MSEKPKGEVKTENNHNILNKVAGDDG		S2 only	Cons.		x	x		x	x
P63208	SKP1	S-phase kinase-associated protein 1	142	IKGKTFEEIRKTPNINKDPTREEBAVRKEN		S1 only	Cons. (NDSM)						x
Q75533	SF3B1	Splicing factor 3B subunit 1	413	PLSDEELDAMPPEGYVLPVPPAGYVPIPTFA		S1+S2			x	x			
Q13435	SF3B2	Splicing factor 3B subunit 2	280	VGPKIPQALEKILQLKESRQEMNSQSEERE		S1 only							x
Q14247	CTTN	Src substrate cortactin	144	MORVDQSAVGFYQGTKEKHSQKDYSSGPG		S1 only						x	
Q14247	CTTN	Src substrate cortactin	181	ARDVDSAVGFYQGTKEKHSQKDYSSGPG		S1 only					x		
P31948	STIP1	Stress-induced-phosphoprotein 1	123	LKEGLQMEARLAEKRFMNPFPNPNLYQKLE		S1 only	Inv. Cons.						x
P31948	STIP1	Stress-induced-phosphoprotein 1	210	EIATPFPFPPPEKKEKTEPEMDEELPENKQA		S1 only							
Q9UBT2	UBA2	SUMO-activating enzyme subunit 2	164	TTIKKGVTECYECPKPTQRTFFGCTIRNTP		S1+S2							
Q9UBT2	UBA2	SUMO-activating enzyme subunit 2	420	ILSGKIQDQCRITFLNKQPNRKKLLVFCALD		S1 only							x
P63279	UBE2I	SUMO-conjugating enzyme UBC9	49	GTMNLMWCAIPGKGTWPWEGGLFKLMLF		S1+S2			x	x			
Q9Y220	SUGT1	Suppressor of G2 allele of SKP1 homolog	295	SPPYTRMWDKLVGEIKKEEKNELGDAALN		S1 only	Cons. (NDSM)						
Q969G3	SMARCE1	subfamily E member 1	92	SRKVDQVKASNPDLKLEWIKGIIIGMWRDL		S1+S2	Inv. Cons.						x
Q92797	SYMPK	Symplekin	361	RKRPRDSDSTLKMMLKLEPNLGDDEDDKLE		S1+S2	Cons. (NDSM)		x	x			
Q92797	SYMPK	Symplekin	1239	EGPLPKETAAGGLTKEBERSPTLAPVGEDA		S1 only	Cons.						
P49368	CCT3	T-complex protein 1 subunit gamma	381	CHDKPACTILLGASKELISVEVERNLDQAMQ		S2 only							x
P50990	CCT8	T-complex protein 1 subunit theta	459	AFPAIPRALAENSQVKNVSIKLYAVHQEGB		S1 only							x
Q96FV9	THOC1	THO complex subunit 1	595	KLGEQWKILAPYLEMKDSEIRQICEDSEDMK		S1+S2	Inv. Cons.		x	x			
Q9Y2W1	THRAP3	Thyroid hormone receptor-associated protein 3	202	SRPSQAAGDNQGEAKBQTFSGQTSQDTKAS		S1 only	Inv. Cons.						
Q9Y2W1	THRAP3	Thyroid hormone receptor-associated protein 3	387	IKKESGSDTGLDGMKMSDSFAPKTSBEKP		S1 only	Inv. Cons.					x	
Q9Y2W1	THRAP3	Thyroid hormone receptor-associated protein 3	451	DKAKGRKESBFDEPKFMSKVIKANKQBE		S1+S2	Inv. Cons.						x
Q9UGU0	TCF20	Transcription factor 20	929	LVMSETKLKSQSGQIKBEDFQKSKQASFN		S1+S2	Cons.						
P05549	TFAP2A	Transcription factor AP-2-alpha	10	MLWKLTDNIIKYEDCEDRDHGTNSGT		S2 only	Cons.		x				
Q9UH73	EBF1	Transcription factor COE1	16	MFGIQESIQRSGSMKSEPELGSMMNAVITWM		S1+S2	Cons.						
P17275	JUNB	Transcription factor jun-B	240	GHAPQGLGRGASTFKKEEPTVPEARSADAT		S1+S2			x				x
Q15525	MAFG	Transcription factor MafG	14	MTPFNKGNKALKVKEPEGNGTSLTDEEL		S2 only	Cons.						
Q02447	SP3	Transcription factor Sp3	551	LHFGNENADSPADIRIKKEEEDPEEWQLSGDS		S1+S2	Cons. (NDSM)		x	x			x
Q15164	TRIM24	Transcription intermediary factor 1-alpha	723	STHKVPPVMLEPILIKQENSPPENYDFPVV		S1+S2	Cons.		x	x			
Q15164	TRIM24	Transcription intermediary factor 1-alpha	741	NSGPPENYDFPVVIVKQESDSESRPQNANYP		S1+S2	Cons. (PDSM, NDSM, HCSM)						
Q13263	TRIM28	Transcription intermediary factor 1-beta	377	LLSKLLIYFQLHRLAKMI VDPPEPHGEMKFO		S1 only						x	x
Q13263	TRIM28	Transcription intermediary factor 1-beta	469	GDDPYSSAEHPVSGVKRSRSGEBSVGLMRK		S1 only						x	x
Q13263	TRIM28	Transcription intermediary factor 1-beta	750	GDTLDTLIRARLQKLSPPYSSPQFADQDV		S1+S2			x	x			x
Q13263	TRIM28	Transcription intermediary factor 1-beta	779	DVGKMPKQFNKLTEDKADVQSIIGLQRFPE		S1+S2			x	x			x
P46100	ATRX	Transcriptional regulator ATRX	623	VQDQDGYKSGLNPKLCKGLQENSNDNH		S1+S2						x	
P46100	ATRX	Transcriptional regulator ATRX	1982	EGNVDTGNMNSVSLKLESKATSSNPFSSP		S1 only	Cons.						x
Q13428	TCOF1	Treacle protein	755	APVLPKGTGPTVTQVAKRKQEDSESESEED		S1+S2	Cons. (NDSM)		x	x			x
P60174	TPH1	Triosephosphate isomerase	179	C1GKLEDEBAGITEKVVFEQTKVIADNVKD		S1 only							x
Q9N9L9	TMOD3	Tropomodulin-3	169	GSSNGVDQEHFSNVKGEKILPVPDEPNPT		S1 only	Cons.						
P68363	TUBA1B	Tubulin alpha-1B chain	326	KYMAICLLYRGDVPVKDVAIAIATIKRRI	Q13748, Q6PEY2, Q71U36, Q9BQE3	S1 only					x		x
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	217	QYTRLSDDVANTAIKHEEQSNEIDIPEQS		S1+S2	Cons. (NDSM)				x		
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	868	PQTQKTSNLSLTRDSMANAKLSSDAEAQK		S1 only	Inv. Cons.						
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	1434	PLGIEDISPNLSPDDKSFSEVVRVPDSTR		S1+S2	Inv. Cons.		x				
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	1563	SDEYFSAGVGVGHRKESGELYYSIEKEGQR		S1+S2							
Q6IBS0	TWF2	Twinfilin-2	163	TSABRELQITRINEVKTEISVESKHQTLQGL		S1 only	Cons.						
Q9UGI0	BAZ1B	Tyrosine-protein kinase BAZ1B	826	VENGLGTDKREKIVKPEQVDTDEADMISA		S1+S2	Cons. (NDSM)		x				
Q43290	SART1	U4/U6.U5 tri-snRNP-associated protein 1	141	LRAKLGKPLEVNAIKKEAGTKBEPYTDVVI		S1+S2	Cons. (NDSM)		x	x			





**Table S2. List of identified GG-modified peptides reporting SUMO1 sites.** Peptides are ordered by protein name and increasing start position. Columns from left to right contain the Swiss-Prot accession number, sequence of the identified peptide (K<-> D<sub>1</sub> lysine; K<-> <sup>13</sup>C<sub>6</sub><sup>15</sup>N<sub>2</sub> lysine; K<-4GG>, GG-modified D<sub>1</sub> lysine; K<-8GG>, GG-modified <sup>13</sup>C<sub>6</sub><sup>15</sup>N<sub>2</sub> lysine; R<-6>, <sup>13</sup>C<sub>6</sub> arginine; R<-10>, <sup>13</sup>C<sub>6</sub><sup>15</sup>N<sub>2</sub> arginine; M<-ox>, methionine sulfoxide; C<-Cmm>, carbamidomethyl cysteine; Q<-Pyr>, pyrroglutamic acid, start and end position of the peptide in the protein sequence, m/z, charge (z), ppm, Mascot score and threshold by which the peptide was identified (99% confidence level), protein name, possible protein isoforms in which the same peptide sequence can be found and the normalized M/H ratio indicating the degree of deSUMOylation upon LO treatment.

Swiss-Prot Acc.	modified peptide sequence	start	end	m/z	z	ppm	score/threshold	Protein name	Isoforms	M/H ratio (fold change)
Q15029	K<4GG>YPTAEVYEPVEVTEQEDQPLTEPIIK<4>PVK<4>	64	98	1040.5486	4	-0.87	49/40	116 kDa U5 small nuclear ribonucleoprotein component		1.15
O00232	EVDLNLINIMLSK<4GG>R<6>	79	93	999.5392	2	-0.57	96/41	26S proteasome non-ATPase regulatory subunit 12		1.28
O43242	AK<4>PPPGGGEGEPPPPAPQDVEMK<4GG>EAAATGGSTGEADGK<4>	15	54	999.234	4	-0.46	50/38	26S proteasome non-ATPase regulatory subunit 3		1.02
P08708	R<10>DNVYVEVALDQIEIIVDPDK<8GG>EMLK<8>	81	107	822.6668	4	2.91	54/41	40S ribosomal protein S17	POCW22	1.01
P08708	R<6>DNVYVEVALDQIEIIVDPDK<4GG>EMLK<4>	81	107	819.4228	4	0.00	50/41	40S ribosomal protein S17	POCW22	1.01
P15880	SPVQFTDHLVK<4GG>YTHR<6>	264	279	695.025	3	0.14	51/40	40S ribosomal protein S2		1.09
P23396	GGK<8GG>PEPPAMPQPVFTA	228	243	848.432	2	-2.79	64/40	40S ribosomal protein S3		1.14
P23396	GGK<8GG>PEPPAMPQPVFTA	228	243	848.9327	2	-1.87	42/40	40S ribosomal protein S3		1.14
P05388	AFADPSAFVAAPAAATTAAPAAAAAPAK<4GG>VEAK<4>	267	301	1101.2721	3	-0.37	69/40	60S acidic ribosomal protein P0		1.24
P62906	K<4>YDFAFLASELTK<4GG>QIPR<6>	106	122	703.0741	3	-0.70	55/39	60S ribosomal protein L10a		0.93
P26373	VITEEEK<4GG>NFK<4>	168	177	679.8737	2	0.04	42/39	60S ribosomal protein L13		1.08
P84098	LQAK<4>K<4GG>EELIK<4>	177	186	663.436	2	8.04	40/34	60S ribosomal protein L19		0.93
P39023	IGQYLIK<4GG>DGG<4>	287	297	657.3868	2	-0.04	49/39	60S ribosomal protein L3		1.44
P36578	AAAAAALQAK<4GG>SDEK<4>	354	368	769.4242	2	-0.61	69/39	60S ribosomal protein L4		0.89
P46777	YLMEDEDAVK<8GG>K<8>	210	221	832.3766	2	-1.87	42/33	60S ribosomal protein L5		1.11
P46777	YLMEDEDAVK<4GG>K<4>	210	221	828.3887	2	-0.47	93/33	60S ribosomal protein L5		1.11
P46777	YLMEDEDAVK<4GG>K<4>	210	221	828.8903	2	1.50	61/34	60S ribosomal protein L5		1.11
P11021	VLESDLK<8GG>K<8>SDIDEIVLGGSTR<10>	345	367	876.8028	3	0.09	50/41	78 kDa glucose-regulated protein		1.31
P11021	VLESDLK<4>K<4GG>SDIDEIVLGGSTR<6>	345	367	872.8152	3	1.40	52/41	78 kDa glucose-regulated protein		1.31
P60709	DSYVGEAQS<8GG>R<10>	51	62	743.8478	2	-0.24	47/35	Actin, cytoplasmic 1	P62736, P63261, P63267, P68032, P68133	0.94
P60709	DSYVGEAQS<4GG>R<6>	51	62	740.3677	2	11.31	51/36	Actin, cytoplasmic 1	P62736, P63261, P63267, P68032, P68133	0.94
P60709	VAPEHPVLLTEAPLNK<8GG>ANR<10>	96	116	810.1086	3	0.20	71/41	Actin, cytoplasmic 1	P63261	1.17
P60709	VAPEHPVLLTEAPLNK<4GG>ANR<6>	96	116	807.1157	3	-0.52	54/41	Actin, cytoplasmic 1	P63261	1.17
P60709	VAPEHPVLLTEAPLNK<4GG>ANR<6>	96	116	1210.1703	2	-0.15	83/41	Actin, cytoplasmic 1	P63261	1.06
P60709	VAPEHPVLLTEAPLNK<4GG>ANR<6>	96	116	807.116	3	-0.07	60/41	Actin, cytoplasmic 1	P63261	1.17
P60709	VAPEHPVLLTEAPLNK<4GG>ANR<6>	96	116	807.453	3	4.44	44/40	Actin, cytoplasmic 1	P63261	1.17
P60709	EITALAPSTMK<8GG>IK<8>	316	328	766.9386	2	0.83	46/39	Actin, cytoplasmic 1	P62736, P63261, P63267, P68032, P68133	1.14
P60709	EITALAPSTMK<4GG>IK<4>	316	328	762.9488	2	-0.03	66/39	Actin, cytoplasmic 1	P62736, P63261, P63267, P68032, P68133	1.14
P60709	IK<4GG>IAPPER<6>K<4>	327	336	431.625	3	0.67	33/32	Actin, cytoplasmic 1	P62736, P63261, P63267, P68032, P68133, Q562R1	1.15
Q9NQW6	INSSSVK<4GG>QEATFC<Cmm>*SQR<6>	248	263	655.994	3	-0.93	42/37	Actin-binding protein anillin		1.30
P53999	Q<Pyr>SSSSR<6>DDNMFQIK<4GG>MR<6>	54	70	700.6694	3	-0.03	41/35	Activated RNA polymerase II transcriptional coactivator p15		2.06
P53999	DDNMFQIK<4GG>MR<6>	60	70	739.8595	2	-0.44	37/35	Activated RNA polymerase II transcriptional coactivator p15		2.02
Q95433	TEFTQMLPMTINGESVDPVGGPALK<4GG>TEER<6>	157	186	1133.8977	3	-0.57	57/40	Activator of 90 kDa heat shock protein ATPase homolog 1		1.42
P30566	VLSQQAASVVK<4GG>QEGGDNDLIER<6>	405	426	827.438	3	0.44	44/41	Adenylosuccinate lyase		2.06
Q01518	VENQENSVLVIDETLK<8GG>QVAYYK<8>	331	355	1023.528	3	-2.03	73/42	Adenyl cyclase-associated protein 1		1.02
Q01518	VENQENSVLVIDETLK<4GG>QVAYYK<4>	331	355	1020.8699	3	-0.76	80/41	Adenyl cyclase-associated protein 1		1.02
Q61Q32	TEGPVVK<4GG>DEALQLALDPAK<4>	1026	1044	725.0831	3	-0.70	43/40	ADNP homeobox protein 2		1.46
Q02952	VK<4GG>EESQLPGTGGPELVQVQR<6>	1050	1071	829.7741	3	-0.19	49/41	A-kinase anchor protein 12		1.08
Q02040	AAEFK<8GG>IDFPTR<10>	114	124	713.8775	2	2.35	51/39	A-kinase anchor protein 17A		1.02
Q02040	AAEFK<4GG>IDFPTR<6>	114	124	709.8852	2	-2.86	53/39	A-kinase anchor protein 17A		1.02
Q9Y2D5	DGEFTLLK<4GG>K<4>	165	175	687.8889	2	-0.75	49/39	A-kinase anchor protein 2		1.24
Q12904	K<4GG>QSIAGSADSK<4>PIDVSR<6>	137	154	672.3741	3	0.76	42/41	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1		0.75
P04083	R<6>K<4GG>GTDVNVFNLTILTR<6>	213	228	655.712	3	-0.15	47/40	Annexin A1		1.05
P04083	K<8GG>GTDVNVFNLTILTR<10>	214	228	905.9912	2	-1.45	94/41	Annexin A1		1.10
P04083	K<8GG>GTDVNVFNLTILTR<10>	214	228	604.3307	3	-0.07	50/41	Annexin A1		1.21
P04083	K<4GG>GTDVNVFNLTILTR<6>	214	228	902.0038	2	-0.06	123/40	Annexin A1		1.10
P04083	K<4GG>GTDVNVFNLTILTR<6>	214	228	601.672	3	0.49	62/40	Annexin A1		1.21
P04083	K<4GG>GTDVNVFNLTILTR<6>	214	228	602.0055	3	0.90	43/40	Annexin A1		1.21
P04083	MYGISLC<Cmm>*QAILDETK<8GG>GDYEK<8>	318	337	822.0609	3	-0.98	39/39	Annexin A1		1.42
P04083	MYGISLC<Cmm>*QAILDETK<4GG>GDYEK<4>	318	337	819.402	3	-0.39	48/38	Annexin A1		1.42
P04083	MYGISLC<Cmm>*QAILDETK<4GG>GDYEK<4>	318	337	819.7312	3	-5.39	77/37	Annexin A1		1.42
P07355	TK<4GG>GVDEVTIVNLTNR<6>	48	63	948.5437	2	0.36	74/40	Annexin A2	A6NMY6	1.07
P07355	SLYYYIQDQTK<4GG>GDYQK<4>	314	329	1068.0295	2	-0.63	72/38	Annexin A2	A6NMY6	0.88
P07355	SLYYYIQDQTK<4GG>GDYQK<4>	314	329	712.6909	3	2.32	43/39	Annexin A2	A6NMY6	0.91
P08758	AMK<4GG>GLGTDEESLTLSTR<6>	27	45	720.3914	3	-1.14	42/41	Annexin A5		1.05
P46013	TPK<4GG>EEAQSLEDLAGFK<4>	1091	1106	629.3298	3	-2.09	41/40	Antigen KI-67		2.97
P46013	VGVK<4GG>EELPVGK<4>	2006	2017	688.4233	2	-0.17	55/38	Antigen KI-67		3.10
P46013	VDMK<4GG>EELPLAVSK<4>	2489	2500	734.4022	2	0.58	58/39	Antigen KI-67		1.60
P46013	K<4>EVK<4GG>EELSAVER<6>	2610	2621	515.632	3	-0.59	44/40	Antigen KI-67		2.40
P46013	VGVK<4GG>EELSAVK<4>	2731	2741	665.3886	2	1.31	42/39	Antigen KI-67		1.69
P46013	VEVK<4GG>EELLAGVK<4>	2849	2860	718.4326	2	-1.82	60/38	Antigen KI-67		0.99
P46013	VEVK<4GG>EELLAGVK<4>	2849	2860	718.9385	2	6.43	53/38	Antigen KI-67		0.99
Q9UKV3	NLK<4GG>TEEEEEEEEEDEEEEGDDEGQK<4>	266	294	1208.139	3	-1.78	67/17	Apoptotic chromatin condensation inducer in the nucleus		1.45
Q9UKV3	NLK<4GG>TEEEEEEEEEDEEEEGDDEGQK<4>SR<6>	266	296	968.653	4	7.21	35/23	Apoptotic chromatin condensation inducer in the nucleus		2.33
Q9UKV3	VK<8GG>PEEMMDER<10>PK<8>	314	325	543.6039	3	-0.50	41/38	Apoptotic chromatin condensation inducer in the nucleus		1.37
Q7L4I2	K<4>LMGIK<4GG>SEDEAGC<Cmm>*SSVDEESYK<4>	370	391	863.749	3	3.14	43/37	Arginine/serine-rich coiled-coil protein 2		2.36
Q7L4I2	LMGIK<8GG>SEDEAGC<Cmm>*SSVDEESYK<8>	371	391	822.0315	3	-1.06	72/32	Arginine/serine-rich coiled-coil protein 2		0.98
Q7L4I2	LMGIK<4GG>SEDEAGC<Cmm>*SSVDEESYK<4>	371	391	819.3723	3	-0.72	115/32	Arginine/serine-rich coiled-coil protein 2		0.98
Q9NUU7	SMTNLQIK<8GG>EEK<8>	19	29	725.8808	2	0.10	63/39	ATP-dependent RNA helicase DDX19A		1.39
Q9NUU7	SMTNLQIK<4GG>EEK<4>	19	29	721.8913	2	-0.31	73/39	ATP-dependent RNA helicase DDX19A		1.39
Q95817	VGLLEQAVDNFEGK<8GG>K<8>	432	446	896.4644	2	0.48	93/40	BAG family molecular chaperone regulator 3		1.62
Q95817	VGLLEQAVDNFEGK<4GG>K<4>	432	446	892.4743	2	-0.60	96/40	BAG family molecular chaperone regulator 3		1.56
Q95817	VGLLEQAVDNFEGK<4GG>K<4>	432	446	595.319	2	0.03	50/40	BAG family molecular chaperone regulator 3		1.45
Q9NYF8	LILASTLWNSVK<4GG>PK<4>	570	581	709.4517	2	-1.05	78/25	Bcl-2-associated transcription factor 1		1.12
Q9NYF8	R<6>PK<4GG>EEDVPEYTPK<4>	829	842	644.5605	3	-0.55	45/39	Bcl-2-associated transcription factor 1		1.09
Q5T5X7	SITVK<4GG>VETEADALDC<Cmm>*SVNSR<6>	16	37	840.0823	3	-0.45	40/39	BEN domain-containing protein 3		1.20

P80723	AAEAAAAPASAPAAEFPK<8GG>EEGPK<8>	122	149	922.7719	3	-0.87	56/38	Brain acid soluble protein 1			1.08
Q9H6U6	IAAFDSC<Cmm>>TFTK<8GG>K<8>	205	216	759.8822	2	-1.30	41/38	Breast carcinoma-amplified sequence 3			1.15
Q9H6U6	IAAFDSC<Cmm>>TFTK<4GG>K<4>	205	216	755.8941	2	0.03	51/38	Breast carcinoma-amplified sequence 3			1.43
Q60885	AAVVQDPQLVVK<4GG>EEK<4>	1098	1114	972.074	2	-0.19	49/38	Bromodomain-containing protein 4			1.68
Q9H0E9	DK<8>PVLPAPEMTVK<8GG>QEK<10>	468	484	692.3773	3	0.51	56/41	Bromodomain-containing protein 8			1.62
Q9H0E9	DK<4>PVLPAPEMTVK<4GG>QEK<6>	468	484	688.3889	3	1.00	46/41	Bromodomain-containing protein 8			1.63
Q9NVX6	AGAGQENSTC<Cmm>>VSGSAIK<4GG>SESGNSAR<6>	168	192	888.7558	2	0.18	50/36	CDKN2A-interacting protein			1.35
Q8K12	LLLPTPTVK<8GG>QESK<8>	1004	1016	793.4699	2	-0.82	39/37	Cell division cycle and apoptosis regulator protein 1			1.33
Q8K12	LLLPTPTVK<4GG>QESK<4>	1004	1016	788.4808	2	-0.82	54/38	Cell division cycle and apoptosis regulator protein 1			1.32
Q13111	AIQNDK<4>LAFPGTSLDIPK<Cmm>>K<4GG>TEEGVGC<Cmm>>GGAGR<6>	163	195	901.9437	4	-0.70	40/39	Chromatin assembly factor 1 subunit A			2.54
Q13111	LAFPGTSLDIPK<Cmm>>K<4GG>TEEGVGC<Cmm>>GGAGR<6>	169	195	977.7999	3	-0.22	51/37	Chromatin assembly factor 1 subunit A			1.55
Q13111	LAFPGTSLDIPK<Cmm>>K<4GG>TEEGVGC<Cmm>>GGAGR<6>	169	195	978.1325	3	-0.95	40/37	Chromatin assembly factor 1 subunit A			1.55
Q9HAF1	SSVTSAAVSAALAGVQDLQIEK<8GG>R<10>	92	114	812.1137	3	8.34	46/40	Chromatin modification-related protein MEAF6			1.36
Q9HAF1	SSVTSAAVSAALAGVQDLQIEK<4GG>R<6>	92	114	809.4509	3	3.79	74/40	Chromatin modification-related protein MEAF6			1.36
Q12873	ELGGDGPSPPTNDPTVK<4GG>YETQPR<6>	704	727	913.1137	3	-1.55	60/39	Chromodomain-helicase-DNA-binding protein 3			1.02
Q14503	IGAIA<4GG>QESEFPPTK<4>K<4>	275	289	594.3451	3	0.85	41/40	Class E basic helix-loop-helix protein 40			4.54
Q9GJG5	LLAIDDDR<6>PK<4GG>R<6>	952	964	813.4872	2	-0.12	51/39	Coiled-coil domain-containing protein 132			1.09
Q96MW1	VK<8GG>K<8>EDEVQAIATLIEK<8>	94	109	651.3749	2	-1.19	42/39	Coiled-coil domain-containing protein 43			1.30
Q96MW1	VK<8GG>K<4>EDEVQAIATLIEK<4>	94	109	647.3872	3	0.89	49/38	Coiled-coil domain-containing protein 43			1.35
Q43175	K<4GG>LQDGGQLQVEK<4>	21	33	774.9624	2	-1.31	62/39	D-3-phosphoglycerate dehydrogenase			1.59
P18887	VK<4GG>EEDESANLIR<6>PGALFFSR<6>	175	194	596.3147	4	-0.87	53/41	DNA repair protein XRCC1			1.49
P11387	EK<4>ENGFSSPPQIK<4GG>DEPDDGVYVPPK<4>EDIK<4>PLK<4>	105	130	1025.8369	3	-0.30	52/39	DNA topoisomerase 1			3.57
P11387	ENGFSSPPQIK<4GG>DEPDDGVYVPPK<4>EDIK<4>PLK<4>	107	137	1215.9591	3	-0.61	49/41	DNA topoisomerase 1			2.95
P11388	IK<8GG>NENTEGSPQEDGVEGLK<8>	1239	1259	806.0644	3	-0.96	75/40	DNA topoisomerase 2-alpha			1.68
P11388	IK<4GG>NENTEGSPQEDGVEGLK<4>	1239	1259	803.4054	3	-0.45	86/40	DNA topoisomerase 2-alpha			1.68
P11388	IK<4GG>NENTEGSPQEDGVEGLK<4>	1239	1259	803.7399	3	1.06	48/40	DNA topoisomerase 2-alpha			1.68
O15446	TVK<4GG>QEIQINTEPLEDVLSPK<4>	268	288	831.4493	3	0.19	56/41	DNA-directed RNA polymerase I subunit RPA34			1.23
O15446	TVK<4GG>QEIQINTEPLEDVLSPK<4>	268	288	831.7847	3	2.60	61/41	DNA-directed RNA polymerase I subunit RPA34			1.22
O15446	Q<Pyr>K<8>GTGEMPEEGVTYESQPVK<8GG>VEPLEAIPPTK<8>	293	328	1341.3518	3	0.79	54/40	DNA-directed RNA polymerase I subunit RPA34			1.90
O15446	Q<Pyr>K<8>GTGEMPEEGVTYESQPVK<8GG>VEPLEAIPPTK<8>	293	328	1341.6854	3	0.99	64/40	DNA-directed RNA polymerase I subunit RPA34			1.90
O15446	GTEGMPEEGVTYESQPVK<8GG>VEPLEAIPPTK<4>	295	328	1256.6459	3	1.29	50/41	DNA-directed RNA polymerase I subunit RPA34			1.73
Q9NVX0	AGAGQENSTC<Cmm>>VSGSAIK<4GG>SESGNSAR<6>	497	529	852.3389	2	-1.48	58/39	DNA-directed RNA polymerase III subunit RPS3			1.77
P55265	NAEFLTC<Cmm>>NIPTSANSNMVTTEK<4>VENGEQPVK<4GG>LENR<6>	386	422	1073.2876	4	-0.61	64/40	Double-stranded RNA-specific adenosine deaminase			1.95
P55265	NAEFLTC<Cmm>>NIPTSANSNMVTTEK<4>VENGEQPVK<4GG>LENR<6>	386	422	1073.5373	4	-0.89	58/40	Double-stranded RNA-specific adenosine deaminase			1.95
P55265	VENGEQPVK<8GG>LENR<10>	409	422	586.3154	3	0.57	57/41	Double-stranded RNA-specific adenosine deaminase			1.75
P55265	VENGEQPVK<4GG>LENR<6>	409	422	874.9797	2	-0.74	70/40	Double-stranded RNA-specific adenosine deaminase			1.49
P49792	FALVTPK<4GG>K<4>	1408	1415	513.3328	2	-0.99	38/37	E3 SUMO-protein ligase RanBP2			0.95
P49792	SGFEGMFTK<4GG>K<4>	1597	1606	627.326	2	1.04	50/37	E3 SUMO-protein ligase RanBP2			0.89
P49792	SGFEGMFTK<4GG>K<4>	1597	1606	627.825	2	-0.58	39/37	E3 SUMO-protein ligase RanBP2			0.89
P49792	VK<4GG>NLFASPTTESSNYTFK<4>	2593	2612	815.4242	3	-0.11	44/41	E3 SUMO-protein ligase RanBP2			1.22
P49792	SQTEITSITVSQVTGTEVMVPSFC<Cmm>>K<8GG>SEEPSITK<8>	2766	2801	1357.6215	3	-1.28	91/35	E3 SUMO-protein ligase RanBP2			1.22
Q9UPN9	VK<8GG>QEPGTEDEIC<Cmm>>SFSGGVK<8>	775	793	1099.0233	2	-0.89	83/38	E3 ubiquitin-protein ligase TRIM33			1.48
Q9UPN9	VK<8GG>QEPGTEDEIC<Cmm>>SFSGGVK<8>	775	793	733.0182	3	-0.53	60/38	E3 ubiquitin-protein ligase TRIM33			1.51
Q9UPN9	VK<4GG>QEPGTEDEIC<Cmm>>SFSGGVK<4>	775	793	1095.0341	2	-0.98	96/37	E3 ubiquitin-protein ligase TRIM33			1.48
Q9UPN9	VK<4GG>QEPGTEDEIC<Cmm>>SFSGGVK<4>	775	793	730.3389	2	-0.47	74/37	E3 ubiquitin-protein ligase TRIM33			1.51
Q9UPN9	VK<4GG>QEPGTEDEIC<Cmm>>SFSGGVK<4>	775	793	730.6942	3	2.20	60/38	E3 ubiquitin-protein ligase TRIM33			1.51
Q9UPN9	VK<8GG>QEPGTEDEIC<Cmm>>SFSGGVK<8GG>QEK<8>	775	796	902.1025	3	-0.57	63/39	E3 ubiquitin-protein ligase TRIM33			1.96
Q9UPN9	VK<8GG>QEPGTEDEIC<Cmm>>SFSGGVK<8>QEK<8>	775	796	648.3183	4	-0.16	44/39	E3 ubiquitin-protein ligase TRIM33			1.59
Q9UPN9	VK<4GG>QEPGTEDEIC<Cmm>>SFSGGVK<4>QEK<4>	775	796	860.0991	3	-0.58	42/40	E3 ubiquitin-protein ligase TRIM33			1.48
Q9UPN9	VK<4GG>QEPGTEDEIC<Cmm>>SFSGGVK<4GG>QEK<4>	775	796	898.1136	3	-0.39	69/39	E3 ubiquitin-protein ligase TRIM33			1.96
Q9UPN9	VK<4GG>QEPGTEDEIC<Cmm>>SFSGGVK<4>QEK<4>	775	796	645.577	4	0.81	50/40	E3 ubiquitin-protein ligase TRIM33			1.59
Q6PJG2	IPGTDAAQAEADMMVK<4GG>LEGPSVVR<6>	575	598	894.1183	3	4.33	59/40	ELM2 and SANT domain-containing protein 1			2.04
P68104	K<4>LEDGPK<4GG>FLK<4>	386	395	650.9044	2	0.24	39/37	Elongation factor 1-alpha 1	Q5VTE0		1.11
P68104	K<4>LEDGPK<4GG>FLK<4>	386	395	651.4027	2	-2.41	40/38	Elongation factor 1-alpha 1	Q5VTE0		1.11
P26641	K<4GG>AAAPAEEMDECC<Cmm>>EQALAAEPK<4>	253	275	870.0761	3	-0.52	58/35	Elongation factor 1-gamma			0.94
P13839	FAAK<4GG>GEGQLQPAER<10>	236	249	777.9116	2	-1.35	52/39	Elongation factor 2			1.52
Q14244	APLVK<8GG>VEATVEER<10>	402	415	851.4596	2	-1.07	47/41	Exonuclease			0.80
Q06265	ITAFK<4GG>MEK<4>	293	300	545.3143	2	-0.03	48/38	Exosome complex component RRP45			1.09
Q01780	EMPLK<8GG>SEVAAGVK<8>	578	591	801.4485	2	-0.32	64/40	Exosome component 10			1.47
Q01780	EM<ox>PLK<8GG>SEVAAGVK<8>	578	591	809.4462	2	0.05	44/40	Exosome component 10			1.56
Q01780	EMPLK<8GG>SEVAAGVK<8>	578	591	801.4489	2	0.24	46/40	Exosome component 10			1.46
Q01780	EMPLK<4GG>SEVAAGVK<4>	578	591	797.4586	2	-1.28	68/40	Exosome component 10			1.50
Q01780	EM<ox>PLK<4GG>SEVAAGVK<4>	578	591	805.4568	2	-0.31	60/40	Exosome component 10			1.56
Q01780	EMPLK<4GG>SEVAAGVK<4>	578	591	797.4601	2	0.66	68/40	Exosome component 10			1.46
Q01780	EMPLK<4GG>SEVAAGVK<4>K<4>	578	592	863.5207	2	1.22	43/38	Exosome component 10			1.91
Q92945	Q<Pyr>LEDQPEPK<4GG>K<4>	111	122	739.8635	2	-0.82	41/35	Far upstream element-binding protein 2			0.38
P09038	LLASK<8GG><<Cmm>>VTDEC<Cmm>>FFFR<10>	224	239	718.675	3	-0.46	52/37	Fibroblast growth factor 2			1.47
P09038	LLASK<4GG><<Cmm>>VTDEC<Cmm>>FFFR<6>	224	239	716.0166	3	0.47	84/37	Fibroblast growth factor 2			1.48
P09038	LLASK<4GG><<Cmm>>VTDEC<Cmm>>FFFR<6>	224	239	1073.5226	2	1.75	44/38	Fibroblast growth factor 2			2.39
P21333	AVGPIEPTGNMVK<8GG>K<8>	286	300	846.4408	2	-0.76	75/40	Filamin-A			0.86
P21333	AVGPIEPTGNMVK<8GG>K<8>	286	300	846.4411	2	-0.44	62/40	Filamin-A			0.86
P21333	AVGPIEPTGNMVK<8GG>K<8>	286	300	564.6299	3	-0.18	47/40	Filamin-A			0.85
P21333	AVGPIEPTGNM<ox>VK<8GG>K<8>	286	300	854.439	2	0.15	63/40	Filamin-A			0.92
P21333	AVGPIEPTGNM<ox>VK<8GG>K<8>	286	300	570.298	3	5.14	42/40	Filamin-A			0.86
P21333	AVGPIEPTGNMVK<4GG>K<4>	286	300	842.4514	2	-1.12	64/40	Filamin-A			0.86
P21333	AVGPIEPTGNMVK<4GG>K<4>	286	300	842.4517	2	-0.68	57/40	Filamin-A			0.86
P21333	AVGPIEPTGNMVK<4GG>K<4>	286	300	842.4521	2	-0.30	70/40	Filamin-A			0.86
P21333	AVGPIEPTGNMVK<4GG>K<4>	286	300	561.9705	3	-0.29	46/40	Filamin-A			0.85
P21333	AVGPIEPTGNMVK<4GG>K<4>	286	300	561.9706	3	-0.09	48/40	Filamin-A			0.85
P21333	AVGPIEPTGNM<ox>VK<4GG>K<4>	286	300	567.3025	3	0.27	49/39	Filamin-A			0.84
P21333	AVGPIEPTGNMVK<8GG>K<8>R<10>	286	301	929.4959	2	-0.23	54/41	Filamin-A			0.97
P21333	AVGPIEPTGNMVK<4GG>K<4>K<6>	286	301	923.5136	2	-0.39	49/41	Filamin-A			0.97
Q8N3X1	EVK<4GG>K<4>EVNEGIAQLSSEEK<4>	399	318	796.4277	3	8.45	62/41	Formin-binding protein 4			1.13
Q8N3X1	VIC<Cmm>>K<8GG>EPPVSEVK<8>	345	356	773.9101	2	0.90	53/40	Formin-binding protein 4			1.58
Q8N3X1	VIC<Cmm>>K<4GG>EPPVSEVK<4>	345	356	769.9192	2	-1.46	46/40	Formin-binding protein 4			2.02
Q8N3X1	VQITPK<4GG>VEEQDLK<4>	514	527	883.4737	2	-0.92	57/40	Formin-binding protein 4			1.57
P15408	SGGSGVAVVK<8GG>QPLEDSSPSSSAGLDK<8>	211	240	1001.8285	3	-0.48	96/41	Fos-related antigen 2			2.42
P15408	SGGSGVAVVK<4GG>QPLEDSSPSSSAGLDK<4>	211	240	1498.25	2	-0.48	49/40	Fos-related antigen 2			2.36
P15408	SGGSGVAVVK<4GG>QPLEDSSPSSSAGLDK<4>	211	240	999.1698	3	0.25	91/40	Fos-related antigen 2			2.42
P04075	GILAADESTGIAK<8GG>R<10>	29	43	810.9372	2	0.14	84/41	Fructose-bisphosphate aldolase A			1.34
P04075	GILAADESTGIAK<4GG>R<6>	29	43	806.9417	2	-8.47	114/40	Fructose-bisphosphate aldolase A			1.34

P04075	GILAADESTGSIK<4GG>R<6>	29	43	806.947	2	-1.89	95/40	Fructose-bisphosphate aldolase A	1.40
P04075	GILAADESTGSIK<4GG>R<6>	29	43	538.301	3	-0.81	44/40	Fructose-bisphosphate aldolase A	1.30
Q16666	LK<4GG>TEFEVIEDSASDLK<4>	560	578	747.3846	3	0.62	60/40	Gamma-interferon-inducible protein 16	1.05
Q9Y586	IK<4GG>TELNSSAESEQLPLDK<4>	148	164	671.0193	3	0.28	42/40	GC-rich sequence DNA-binding factor 1	0.95
Q9Y586	IK<4GG>TELNSSAESEQLPLDK<4>	148	164	671.3496	3	-4.28	40/40	GC-rich sequence DNA-binding factor 1	0.95
P78347	VK<8GG>TEPTEDSGISLEMAAVTVK<8>	220	240	775.0726	3	0.10	44/41	General transcription factor II-I	1.33
P78347	VK<4GG>TEPTEDSGISLEMAAVTVK<4>	220	240	775.413	3	-0.20	55/41	General transcription factor II-I	1.34
P78347	ETDSSQIK<4GG>QEPDPTW	983	998	966.4479	2	0.82	56/33	General transcription factor II-I	4.12
Q9UKD1	K<4GG>IMDSGLDFQYHDK<4>	155	169	649.9817	3	-2.57	41/36	Glucocorticoid modulatory element-binding protein 2	0.90
P04150	TEK<8>EFDIELCCmm*>TPGVK<8GG>QEK<8>	278	296	801.417	3	1.28	45/41	Glucocorticoid receptor	1.01
Q9NVN8	IADAIENK<4GG>TYTVYK<4>	470	482	794.4439	2	-1.36	49/40	Guanine nucleotide-binding protein-like 3-like protein	1.52
Q9NX24	TK<8>IK<8GG>ADPDGPEAQAEAC<Cmm*>SGER<10>	2	22	791.0452	3	0.49	91/38	H/ACA ribonucleoprotein complex subunit 2	1.41
Q9NX24	TK<4>IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	2	22	786.7225	3	-0.36	96/38	H/ACA ribonucleoprotein complex subunit 2	1.47
Q9NX24	TK<4>IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	2	22	590.2939	4	0.09	47/38	H/ACA ribonucleoprotein complex subunit 2	1.44
Q9NX24	IK<8GG>ADPDGPEAQAEAC<Cmm*>SGER<10>	4	22	1066.9842	2	-0.96	61/34	H/ACA ribonucleoprotein complex subunit 2	1.29
Q9NX24	IK<8GG>ADPDGPEAQAEAC<Cmm*>SGER<10>	4	22	711.6587	3	-0.79	60/34	H/ACA ribonucleoprotein complex subunit 2	1.33
Q9NX24	IK<8GG>ADPDGPEAQAEAC<Cmm*>SGER<10>	4	22	711.6587	3	-0.78	51/34	H/ACA ribonucleoprotein complex subunit 2	1.33
Q9NX24	IK<8GG>ADPDGPEAQAEAC<Cmm*>SGER<10>	4	22	1066.9844	2	-0.77	85/34	H/ACA ribonucleoprotein complex subunit 2	1.32
Q9NX24	IK<8GG>ADPDGPEAQAEAC<Cmm*>SGER<10>	4	22	711.659	3	-0.30	67/34	H/ACA ribonucleoprotein complex subunit 2	1.33
Q9NX24	IK<8GG>ADPDGPEAQAEAC<Cmm*>SGER<10>	4	22	711.6592	3	-0.10	85/34	H/ACA ribonucleoprotein complex subunit 2	1.32
Q9NX24	IK<8GG>ADPDGPEAQAEAC<Cmm*>SGER<10>	4	22	711.9953	3	3.83	63/35	H/ACA ribonucleoprotein complex subunit 2	1.33
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	708.9981	3	-2.90	69/34	H/ACA ribonucleoprotein complex subunit 2	2.85
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	708.9993	3	-1.25	66/34	H/ACA ribonucleoprotein complex subunit 2	1.33
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	708.9997	3	-0.70	47/34	H/ACA ribonucleoprotein complex subunit 2	1.80
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	1062.9959	2	-0.68	64/34	H/ACA ribonucleoprotein complex subunit 2	1.32
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	708.9997	3	-0.60	40/34	H/ACA ribonucleoprotein complex subunit 2	1.83
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	708.9999	3	-0.33	75/34	H/ACA ribonucleoprotein complex subunit 2	1.33
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	1062.9969	2	0.26	112/34	H/ACA ribonucleoprotein complex subunit 2	1.29
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	709.0014	3	1.73	46/35	H/ACA ribonucleoprotein complex subunit 2	1.34
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	709.3297	3	-5.45	37/33	H/ACA ribonucleoprotein complex subunit 2	1.34
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	709.3341	3	0.76	58/34	H/ACA ribonucleoprotein complex subunit 2	2.85
Q9NX24	IK<4GG>ADPDGPEAQAEAC<Cmm*>SGER<6>	4	22	709.3341	3	4.21	46/35	H/ACA ribonucleoprotein complex subunit 2	2.85
O60832	HGK<8>PTDSTPATWK<8GG>QEYVDSSESAK<8>	401	424	716.5955	4	0.18	53/39	H/ACA ribonucleoprotein complex subunit 4	1.20
O60832	HGK<4>PTDSTPATWK<4GG>QEYVDSSESAK<4>	401	424	713.6041	4	0.86	56/39	H/ACA ribonucleoprotein complex subunit 4	1.17
O60832	HGK<4>PTDSTPATWK<4GG>QEYVDSSESAK<4>	401	424	713.8537	4	0.20	47/39	H/ACA ribonucleoprotein complex subunit 4	1.17
O60832	HGK<8>PTDSTPATWK<8GG>QEYVDSSESAK<8>K<8>	401	425	750.8708	4	-2.45	93/40	H/ACA ribonucleoprotein complex subunit 4	1.04
O60832	HGK<4>PTDSTPATWK<4GG>QEYVDSSESAK<4>K<4>	401	425	746.8838	4	0.42	50/41	H/ACA ribonucleoprotein complex subunit 4	1.04
P11142	LSK<4GG>EDIER<6>	510	517	557.3107	2	-0.23	46/38	Heat shock cognate 71 kDa protein	0.64
P07900	EM<ox>LQSK<8GG>ILK<8>	401	410	682.3824	2	-0.64	41/40	Heat shock protein HSP 90-alpha	1.25
P51858	K<8GG>GFSEGLWEIENNPTVK<8>	80	96	693.3554	3	-0.42	42/41	Hepatoma-derived growth factor	1.04
P61978	R<6>PAEDMEEEQAFK<4GG>R<6>	22	35	622.6425	3	-1.09	51/37	Heterogeneous nuclear ribonucleoprotein K	1.52
P61978	R<6>PAEDMEEEQAFK<4GG>R<6>	22	35	622.6427	3	-0.75	47/37	Heterogeneous nuclear ribonucleoprotein K	1.56
P61978	LHLSLQAGGIVGVK<4GG>GAK<4>	149	166	633.0667	3	1.28	42/32	Heterogeneous nuclear ribonucleoprotein K	1.22
P61978	HESGASIK<8GG>IDPLEGSEDR<10>	415	433	734.3531	3	0.51	60/38	Heterogeneous nuclear ribonucleoprotein K	1.43
P61978	HESGASIK<4GG>IDPLEGSEDR<6>	415	433	1097.0351	2	-1.53	94/37	Heterogeneous nuclear ribonucleoprotein K	2.07
P61978	HESGASIK<4GG>IDPLEGSEDR<6>	415	433	731.693	3	-0.79	72/37	Heterogeneous nuclear ribonucleoprotein K	1.47
P61978	HESGASIK<4GG>IDPLEGSEDR<6>	415	433	549.0224	4	0.61	51/38	Heterogeneous nuclear ribonucleoprotein K	1.42
P52272	SK<4>GC<Cmm*>GVVK<4GG>FESPEVAER<6>	693	707	502.5181	4	-0.33	43/40	Heterogeneous nuclear ribonucleoprotein M	1.44
P52272	GC<Cmm*>GVVK<8GG>FESPEVAER<10>	693	707	898.4406	2	-1.37	68/38	Heterogeneous nuclear ribonucleoprotein M	1.22
P52272	GC<Cmm*>GVVK<8GG>FESPEVAER<10>	693	707	599.2966	3	-0.66	49/38	Heterogeneous nuclear ribonucleoprotein M	1.21
P52272	GC<Cmm*>GVVK<8GG>FESPEVAER<10>	693	707	898.4414	2	-0.39	47/38	Heterogeneous nuclear ribonucleoprotein M	1.22
P52272	GC<Cmm*>GVVK<4GG>FESPEVAER<6>	693	707	596.6377	3	-0.32	46/38	Heterogeneous nuclear ribonucleoprotein M	1.21
P52272	GC<Cmm*>GVVK<4GG>FESPEVAER<6>	693	707	894.4532	2	0.09	91/38	Heterogeneous nuclear ribonucleoprotein M	1.22
P52272	GC<Cmm*>GVVK<4GG>FESPEVAER<6>	693	707	894.4535	2	0.37	83/38	Heterogeneous nuclear ribonucleoprotein M	1.22
P52272	GC<Cmm*>GVVK<4GG>FESPEVAER<6>	693	707	596.6382	3	0.65	53/38	Heterogeneous nuclear ribonucleoprotein M	1.21
Q00839	GVEFIEENK<8GG>YSR<10>	256	268	915.4272	2	0.68	53/36	Heterogeneous nuclear ribonucleoprotein U	0.89
Q00839	GVEFIEENK<4GG>YSR<6>	256	268	911.4302	2	1.37	41/36	Heterogeneous nuclear ribonucleoprotein U	0.89
Q9BUJ2	Q<Pyr>NQFYDTQVIK<8GG>QENESGYER<10>	107	126	864.3967	3	-0.26	49/25	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.68
Q9BUJ2	Q<Pyr>NQFYDTQVIK<8GG>QENESGYER<10>	107	126	1296.0916	2	-0.17	67/35	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.68
Q9BUJ2	QIQFYDTQVIK<8GG>QENESGYER<10>	107	126	870.0723	3	-0.16	53/36	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.59
Q9BUJ2	QIQFYDTQVIK<4GG>QENESGYER<6>	107	126	1300.6159	2	-0.44	83/36	Heterogeneous nuclear ribonucleoprotein U-like protein 1	2.30
Q9BUJ2	QIQFYDTQVIK<4GG>QENESGYER<6>	107	126	867.4132	3	-0.20	38/36	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.59
Q9BUJ2	Q<Pyr>NQFYDTQVIK<4GG>QENESGYER<6>	107	126	861.7378	3	-0.19	77/35	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.66
Q9BUJ2	Q<Pyr>NQFYDTQVIK<4GG>QENESGYER<6>	107	126	1292.1033	2	0.06	104/35	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.65
Q9BUJ2	QIQFYDTQVIK<4GG>QENESGYER<6>	107	126	867.4135	3	0.12	58/36	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.59
Q9BUJ2	R<10>PLEMEQQAYR<10>PEMK<8GG>TEMK<8>	127	146	669.0826	4	2.03	43/40	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.86
Q9BUJ2	R<6>PLEMEQQAYR<6>PEMK<4GG>TEMK<4>	127	146	665.0929	4	0.42	45/41	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.61
P07910	Q<Pyr>AVEMK<ox>K<8GG>NDK<8>SEEEQSSSVK<8>	224	243	793.0342	3	-0.26	41/36	Heterogeneous nuclear ribonucleoproteins C1/C2	0.71
P07910	Q<Pyr>AVEMK<8GG>NDK<8>SEEEQSSSVK<8>	224	243	787.7038	3	0.12	41/37	Heterogeneous nuclear ribonucleoproteins C1/C2	0.87
P07910	Q<Pyr>AVEMK<4>NDK<4GG>SEEEQSSSVK<4>	224	243	783.7123	3	-1.75	46/37	Heterogeneous nuclear ribonucleoproteins C1/C2	0.91
P82970	ITEAPASEK<8>EIVEVK<8GG>ENIEDATEK<8>	87	111	980.5039	3	6.03	47/41	High mobility group nucleosome-binding domain-containing protein 5	1.77
P82970	ITEAPASEK<8>EIVEVK<8GG>ENIEDATEK<8>	87	111	980.8315	3	0.27	52/41	High mobility group nucleosome-binding domain-containing protein 5	1.77
P82970	ITEAPASEK<4>EIVEVK<4GG>ENIEDATEK<4>	87	111	976.5084	3	-0.44	67/41	High mobility group nucleosome-binding domain-containing protein 5	1.78
Q9H981	GEPOQDC<Cmm*>C<Cmm*>VK<4GG>TELLGEETPMMADEGSAEK<4>	13	41	1101.163	3	-0.01	64/32	Histone-lysine N-methyltransferase EHMT1	1.60
Q15047	ASTSLGLIK<4GG>DEGDIK<4>	1024	1038	806.9349	2	-0.21	83/39	Histone-lysine N-methyltransferase SETDB1	1.39
Q6N176	QGANERK<4GG>TEALDD	407	420	818.8834	2	-0.23	83/33	Homeobox-containing protein 1	4.11
Q16543	SMVNTK<4GG>PEK<4>TEEDSEVR<6>	127	144	746.0375	3	1.51	39/38	Hsp90 co-chaperone Cdc37	1.46
P00492	SYC<Cmm*>NDQSTGDIK<4GG>VIGGGDLDLTKG<4>	104	128	923.1149	3	-1.32	78/38	Hypoxanthine-guanine phosphoribosyltransferase	1.67
Q96HW7	LMTSK<8GG>PAEVVK<8>	787	797	666.8796	2	-0.58	50/39	Integrator complex subunit 4	1.02
Q96HW7	LMTSK<4GG>PAEVVK<4>	787	797	662.8905	2	-0.54	48/39	Integrator complex subunit 4	1.02
P05556	SAVTVVNPK<8GG>YEGK<8>	785	798	541.6284	3	-0.70	43/40	Integrin beta-1	0.57
P05556	SAVTVVNPK<8GG>YEGK<8>	785	798	811.8195	3	-0.09	58/40	Integrin beta-1	0.45
P05556	SAVTVVNPK<4GG>YEGK<4>	785	798	807.9503	2	-0.17	60/40	Integrin beta-1	0.62
Q12906	K<4>PK<4GG>NENPVDYTYQIPPTTYAITPMK<4>	346	371	765.4131	4	-0.07	44/41	Interleukin enhancer-binding factor 3	0.95
Q12906	K<4>PK<4GG>NENPVDYTYQIPPTTYAITPMK<4>	346	371	1020.5494	3	0.97	42/41	Interleukin enhancer-binding factor 3	1.03
Q04695	Q<Pyr>FTSSSIK<8GG>GSSGLGGSSSR<10>	7	26	1001.4823	2	-0.93	71/38	Keratin, type I cytoskeletal 17	0.67
Q04695	QFTSSSIK<8GG>GSSGLGGSSSR<10>	7	26	1009.9962	2	-0.27	97/39	Keratin, type I cytoskeletal 17	0.95
Q04695	Q<Pyr>FTSSSIK<4GG>GSSGLGGSSSR<6>	7	26	997.4914	2	-3.20	101/37	Keratin, type I cytoskeletal 17	0.67
Q04695	QFTSSSIK<4GG>GSSGLGGSSSR<6>	7	26	1006.0077	2	-0.18	78/38	Keratin, type I cytoskeletal 17	0.95
Q04695	QFTSSSIK<4GG>GSSGLGGSSSR<6>	7	26	671.0077	3	0.08	52/38	Keratin, type I cytoskeletal 17	0.68
Q04695	LLEGDAHLTYK<8GG>K<8>	387	400	887.9632	2	-6.40	50/40	Keratin, type I cytoskeletal 17	0.64

Q04695	LLGEDAHLTQYK<4GG>K<4>	387	400	883.9793	2	-0.54	104/40	Keratin, type I cytoskeletal 17			0.64
Q04695	LLGEDAHLTQYK<4>K<4>4GG>EPVTR<6>	387	406	819.4492	3	0.11	43/41	Keratin, type I cytoskeletal 17			0.85
Q04695	TVEEVQDGK<4GG>VSSR<6>	410	424	892.4933	2	-0.06	76/40	Keratin, type I cytoskeletal 17			1.05
Q04695	TVEEVQDGK<4GG>VSSR<6>	410	424	595.3317	3	0.72	44/40	Keratin, type I cytoskeletal 17			0.71
Q04695	TVEEVQDGK<4GG>VSSR<6>	410	424	982.9892	2	-4.63	60/40	Keratin, type I cytoskeletal 17			1.01
P05783	VVSEINDTK<4GG>VLR<6>	418	429	742.9179	2	-1.83	51/40	Keratin, type II cytoskeletal 18			0.98
P78386	ATAENEFLVVK<8GG>K<8>	219	230	739.9131	2	0.38	72/40	Keratin, type II cuticular Hb5			0.75
P78386	ATAENEFLVVK<4GG>K<4>	219	230	735.9236	2	-0.23	69/40	Keratin, type II cuticular Hb5			0.81
P05787	TLNNK<8GG>FASFDIK<8>	97	108	764.4104	2	-0.14	67/40	Keratin, type II cytoskeletal 8	O95678, P02538, P04259, P08729, P12035, P13647, P35908, P48668, Q01546, Q5XKE5, Q9NS82		0.75
P05787	TLNNK<4GG>FASFDIK<4>	97	108	760.4218	2	0.61	63/40	Keratin, type II cytoskeletal 8	O95678, P02538, P04259, P08729, P12035, P13647, P35908, P48668, Q01546, Q5XKE5, Q9NS82		0.78
P05787	TEMENFVLK<8GG>K<8>	187	198	537.6192	3	0.20	41/40	Keratin, type II cytoskeletal 8			0.88
P05787	TEMENFVLK<4GG>K<4>	187	198	801.9359	2	-0.07	75/40	Keratin, type II cytoskeletal 8			0.87
P05787	DGK<8GG>LVSESSDLPK<8>	470	483	802.4279	2	-1.43	46/40	Keratin, type II cytoskeletal 8			0.61
P05787	DGK<4GG>LVSESSDLPK<4>	470	483	798.4422	2	2.76	62/40	Keratin, type II cytoskeletal 8			0.61
Q07666	MEPENK<8GG>YLPMLAEK<8>	97	111	976.4777	2	0.35	77/39	KH domain-containing, RNA-binding, signal transduction-associated protein 1			1.13
Q069R5	ASSPELVSNIK<4GG>QETDD	687	705	1088.5299	2	-1.31	64/38	Lethal(3)malignant brain tumor-like protein 2			1.25
Q32MZ4	ASEVEVK<4GG>NEIVAVGK<4>	299	314	905.0079	2	4.76	68/40	Leucine-rich repeat flightless-interacting protein 1			1.56
Q93052	NSDPTVYGGQHPNTWK<4GG>R<6>	311	328	742.3502	3	-0.13	40/35	Lipoma-preferred partner			1.83
O95232	ESDTK<8>NEVNGTSEDIK<8GG>SEGDTQSN	409	432	905.3986	3	-1.11	50/31	Luc7-like protein 3			1.29
O95232	ESDTK<4>NEVNGTSEDIK<4GG>SEGDTQSN	409	432	902.7401	3	-0.11	57/32	Luc7-like protein 3			1.29
O95232	ESDTK<4>NEVNGTSEDIK<4GG>SEGDTQSN	409	432	903.0762	3	2.95	52/32	Luc7-like protein 3			1.29
Q14676	K<4>SQLPAEDGAGNAEVAAVLKK<4GG>QER<6>	597	619	639.3447	4	2.28	50/41	Mediator of DNA damage checkpoint protein 1			2.74
Q14676	TPETLVTPAK<4GG>LEPSTDQDPTVPTPTQATK<6>	1402	1434	1167.6023	3	-2.21	50/41	Mediator of DNA damage checkpoint protein 1			2.74
O43513	VK<8GG>TEPMDADDNSNC<Cmm>TGQNEHOR<10>	184	205	893.381	3	-0.02	31/28	Mediator of RNA polymerase II transcription subunit 7			1.03
O43513	VK<4GG>TEPMDADDNSNC<Cmm>TGQNEHOR<6>	184	205	668.2932	4	-0.07	54/28	Mediator of RNA polymerase II transcription subunit 7			1.07
P27816	DMALATK<4GG>TEVALAK<4>	263	276	792.4493	2	0.08	87/40	Microtubule-associated protein 4			0.87
Q98YG3	Q<Pyr>PISCC<Cmm>>VK<8GG>EEIQETQTPHRS<10>	265	284	828.4025	3	-0.85	51/39	MKI67 FHA domain-interacting nuclear phosphoprotein			1.08
Q98YG3	QIPSC<Cmm>>VK<8GG>EEIQETQTPHRS<10>	265	284	834.0782	3	-0.59	51/40	MKI67 FHA domain-interacting nuclear phosphoprotein			1.11
Q98YG3	Q<Pyr>PISCC<Cmm>>VK<8GG>EEIQETQTPHRS<10>	265	284	828.7358	3	-0.81	40/39	MKI67 FHA domain-interacting nuclear phosphoprotein			1.08
Q98YG3	Q<Pyr>PISCC<Cmm>>VK<4GG>EEIQETQTPHRS<6>	265	284	826.0773	3	-0.21	54/39	MKI67 FHA domain-interacting nuclear phosphoprotein			1.08
Q98YG3	QIPSC<Cmm>>VK<4GG>EEIQETQTPHRS<6>	265	284	831.7552	3	2.71	42/40	MKI67 FHA domain-interacting nuclear phosphoprotein			1.11
Q9ULH7	HGSLGSSIK<8GG>DEALPDC<Cmm>SSSR<10>	620	640	774.6958	3	-0.68	43/36	MKL/myocardin-like protein 2			0.97
Q9ULH7	HGSLGSSIK<4GG>DEALPDC<Cmm>SSSR<6>	620	640	772.0375	3	0.28	64/36	MKL/myocardin-like protein 2			0.97
Q13765	SK<4GG>NILVPTK<4>PDVTK<4>	99	113	631.0531	3	0.32	42/37	Nascent polypeptide-associated complex subunit alpha	Q982K3		1.25
P18615	SGASAK<4GG>AETK<4>	71	82	649.3843	2	3.94	40/39	Negative elongation factor E			1.97
P48681	SLK<4GG>EESVAVK<4>	809	819	670.8786	2	-0.64	43/39	Nestin			1.05
Q09666	LK<8GG>SEDDVEGDLGETQSR<10>	133	149	651.3157	3	0.22	53/38	Neuroblast differentiation-associated protein AHNAK			1.09
Q09666	LK<4GG>SEDDVEGDLGETQSR<6>	133	149	648.6561	3	-0.71	43/38	Neuroblast differentiation-associated protein AHNAK			1.09
Q09666	LK<4GG>SEDDVEGDLGETQSR<6>	133	149	972.4805	2	-0.64	68/38	Neuroblast differentiation-associated protein AHNAK			1.01
Q09666	MPENNIK<4GG>APK<4>	936	945	640.8501	2	-0.98	48/38	Neuroblast differentiation-associated protein AHNAK			1.00
Q09666	VK<4GG>GYDVTMPK<4>	960	970	694.8701	2	0.01	45/39	Neuroblast differentiation-associated protein AHNAK			0.75
Q09666	VK<4GG>GDVYSLPK<4>	2131	2141	639.8798	2	1.56	46/39	Neuroblast differentiation-associated protein AHNAK			1.07
P30414	Q<Pyr>DMATEHPQAEVVK<4GG>QESSMSESK<4>	1164	1186	894.4131	3	-0.82	67/33	NK-tumor recognition protein			1.61
P30414	QDMATEHPQAEVVK<4GG>QESSMSESK<4>	1164	1186	900.089	3	-0.36	52/35	NK-tumor recognition protein			1.03
P49321	AK<4GG>QPEVNGGSDGADPVSNEVSENMEEAENQAESR<6>	735	770	1300.589	3	9.64	55/32	Nuclear autoantigenic sperm protein			1.84
Q16649	FQIHK<4GG>QEFMLESYTR<6>	215	230	712.7059	3	-0.28	51/40	Nuclear factor interleukin-3-regulated protein			2.95
Q94916	SHDQVPTTTPAAGALVNVVK<8GG>K<8>	533	557	924.1423	3	-0.25	69/41	Nuclear factor of activated T-cells 5			1.48
Q94916	SHDQVPTTTPAAGALVNVVK<4GG>K<4>	533	557	921.4825	3	-0.62	101/41	Nuclear factor of activated T-cells 5			1.48
Q6P488	DQAFCC<Cmm>>K<8GG>QENEISSDATTVPVR<10>	483	503	843.3741	3	-1.74	36/31	Nuclear factor related to kappa-B-binding protein			1.54
Q6P488	DQAFCC<Cmm>>K<4GG>QENEISSDATTVPVR<6>	483	503	840.7201	3	4.38	59/33	Nuclear factor related to kappa-B-binding protein			1.54
Q14980	LPPK<4GG>VESLESYFTTPAR<6>	1763	1781	761.4362	3	4.54	41/40	Nuclear mitotic apparatus protein 1			2.26
O75376	SATLPIVK<4GG>QEFSPR<6>	1099	1113	945.5015	2	-2.28	47/40	Nuclear receptor corepressor 1			1.37
Q14978	ITPVTVK<8GG>AQTK<8>	187	197	658.4	2	0.98	52/37	Nucleolar and coiled-body phosphoprotein 1			0.94
Q14978	Q<Pyr>PVGGGQK<8GG>LLTR<10>	408	419	684.8892	2	-0.11	49/40	Nucleolar and coiled-body phosphoprotein 1			0.92
Q14978	Q<Pyr>PVGGGQK<4GG>LLTR<6>	408	419	680.9003	2	-0.60	66/39	Nucleolar and coiled-body phosphoprotein 1			0.95
Q14978	NSEEEEEK<4>K<4>K<4>4GG>AAVVVK<4>	562	579	721.7326	3	0.07	54/41	Nucleolar and coiled-body phosphoprotein 1			1.14
Q14978	ANQVLK<4GG>FTK<4>	658	666	585.858	2	0.50	39/38	Nucleolar and coiled-body phosphoprotein 1			1.00
Q9Y2X3	IK<8>VK<8GG>VEEEEEK<8>VAEEETSVK<8>	464	485	684.8554	4	0.65	69/41	Nucleolar protein 58			1.16
Q9Y2X3	IK<8>VK<8GG>VEEEEEK<8>VAEEETSVK<8>	464	485	913.1391	3	1.78	71/41	Nucleolar protein 58			1.03
Q9Y2X3	IK<4>VK<4GG>VEEEEEK<4>VAEEETSVK<4>	464	485	907.4849	3	-0.48	78/41	Nucleolar protein 58			1.00
Q9Y2X3	IK<4>VK<4GG>VEEEEEK<4>VAEEETSVK<4>	464	485	681.1179	4	3.08	62/41	Nucleolar protein 58			1.16
Q9Y2X3	VK<8GG>VEEEEEK<8>VAEEETSVK<8>	466	485	829.7395	3	-0.28	50/40	Nucleolar protein 58			1.09
Q9Y2X3	VK<8GG>VEEEEEK<8>VAEEETSVK<8>	466	485	622.5565	4	-0.11	52/40	Nucleolar protein 58			1.13
Q9Y2X3	VK<8GG>VEEEEEK<8>VAEEETSVK<8>	466	485	1244.6185	2	10.11	44/41	Nucleolar protein 58			0.89
Q9Y2X3	VK<4GG>VEEEEEK<4>VAEEETSVK<4>	466	485	825.7478	3	-3.42	48/39	Nucleolar protein 58			1.18
Q9Y2X3	VK<4GG>VEEEEEK<4>VAEEETSVK<4>	466	485	1238.1207	2	-1.27	64/40	Nucleolar protein 58			0.89
Q9Y2X3	VK<4GG>VEEEEEK<4>VAEEETSVK<4>	466	485	619.5644	4	-0.58	57/40	Nucleolar protein 58			1.13
Q9Y2X3	VK<4GG>VEEEEEK<4>VAEEETSVK<4>	466	485	825.7502	3	-0.46	63/40	Nucleolar protein 58			1.09
Q9Y2X3	VK<4GG>VEEEEEK<4>VAEEETSVK<4>	466	485	619.8137	4	-1.80	79/40	Nucleolar protein 58			1.13
Q9Y2X3	VK<8GG>VEEEEEK<8>VAEEETSVK<8>	466	486	656.5834	4	-0.70	59/41	Nucleolar protein 58			1.08
Q9Y2X3	VK<4GG>VEEEEEK<4>VAEEETSVK<4>	466	486	869.7909	3	0.35	70/41	Nucleolar protein 58			1.09
Q9N830	K<4>VTK<4GG>NEEPEEEDAPK<4>PK<4>	113	131	765.7549	3	-0.55	68/41	Nucleolar RNA helicase 2			1.35
P19338	K<4>QK<4GG>VEGTEPTTANFLVGNLNFNK<8>	295	318	945.4099	3	-1.63	69/41	Nucleolin			1.20
P19338	K<4>QK<4GG>VEGTEPTTANFLVGNLNFNK<4>	295	318	941.5115	3	-0.93	112/41	Nucleolin			1.20
P19338	K<4>QK<4GG>VEGTEPTTANFLVGNLNFNK<4>	295	318	941.5115	3	-0.90	69/41	Nucleolin			1.21
P19338	SAPELK<4GG>TGISDVFVK<4>	319	333	842.9714	2	-0.05	60/40	Nucleolin			1.16
P19338	GLSEDTTEELK<4GG>ESFDGVR<6>	578	597	775.3766	3	0.86	44/37	Nucleolin			1.64
P06748	ADK<4>DYHFK<4GG>VDNDEHEQLSLR<6>	25	45	676.3348	4	0.93	48/39	Nucleophosmin			1.27
P06748	ADK<4>DYHFK<4GG>VDNDEHEQLSLR<6>	25	45	901.4449	3	2.00	59/39	Nucleophosmin			1.16
P06748	GPSSVEDIK<4GG>AK<4>	240	250	626.8536	2	1.25	61/39	Nucleophosmin			1.32
P06748	MQASIEK<4GG>GGLPK<4>	251	263	734.4056	2	-2.44	75/40	Nucleophosmin			1.36

P06748	VEAK<4GG>FINVVK<4>	264	273	666.8912	2	-0.87	47/39	Nucleophosmin		1.20
Q96RE7	VK<8GG>TEQQESDSVQC<Cmm*>MPVAK<8>	166	183	732.0194	3	-0.62	64/38	Nucleus accumbens-associated protein 1		1.71
Q96RE7	VK<4GG>TEQQESDSVQC<Cmm*>MPVAK<4>	166	183	1093.5363	2	-0.66	118/38	Nucleus accumbens-associated protein 1		2.24
Q96RE7	VK<4GG>TEQQESDSVQC<Cmm*>MPVAK<4>	166	183	729.3605	3	0.04	72/38	Nucleus accumbens-associated protein 1		1.71
Q96RE7	VK<4GG>TEQQESDSVQC<Cmm*>MPVAK<4>	166	183	729.6962	3	3.37	44/38	Nucleus accumbens-associated protein 1		1.70
Q9N774	ALVAMEIK<4GG>VEEK<4>	172	182	708.9041	2	0.32	62/39	Palmfelinin		1.06
Q96H41	ASAAPKRGSG<8>EPVIVQK<8>	84	97	516.9921	3	0.20	44/40	P02 and LIM domain protein 5		1.35
Q07290	AEASSGHPHTDEM<4GG>EEQK<4>	427	445	738.3351	3	-0.05	52/32	Peptidyl-prolyl cis-trans isomerase FKBP4		1.44
Q06664	VLAIDTK<4GG>ELVSK<4>	117	128	706.4159	2	0.16	71/39	Perilipin-3		1.19
Q06830	HGEVCC<Cmm*>PAGWK<4>PESDITK<4GG>PDVQK<4>	169	190	633.8312	4	-0.88	56/41	Peroxiredoxin-1		1.03
Q00541	VMAAGTLK<8GG>LEDK<8>	511	521	667.8692	2	-0.62	70/40	Pescadillo homolog		0.42
Q00541	VMAAGTLK<8GG>LEDK<8>	511	521	668.3675	2	-1.13	64/40	Pescadillo homolog		0.42
Q00541	VMAAGTLK<4GG>LEDK<4>	511	521	663.8801	2	-0.58	59/39	Pescadillo homolog		1.01
Q8WWQ0	ILK<8>PQLK<8GG>SESS5TAFSTPTR<10>	1464	1483	773.7581	3	1.53	53/40	PH-interacting protein		0.84
Q8WWQ0	ILK<4>PQLK<4GG>SESS5TAFSTPTR<6>	1464	1483	769.4345	3	-0.29	44/40	PH-interacting protein		0.90
P15259	HYGGLTGLNK<8GG>AETAAK<8>	91	106	587.6469	3	0.11	62/41	Phosphoglycerate mutase 2	P18669, Q8N0Y7	1.15
P15259	HYGGLTGLNK<4GG>AETAAK<4>	91	106	876.977	2	-0.60	63/40	Phosphoglycerate mutase 2	P18669, Q8N0Y7	1.52
P15259	HYGGLTGLNK<4GG>AETAAK<4>	91	106	584.9872	3	-0.44	47/40	Phosphoglycerate mutase 2	P18669, Q8N0Y7	1.16
P15259	HYGGLTGLNK<4GG>AETAAK<4>	91	106	585.3268	3	0.22	48/40	Phosphoglycerate mutase 2	P18669, Q8N0Y7	0.91
Q9H307	FK<8GG>QESTVATER<10>	156	166	714.366	2	0.27	44/39	Pinin		1.02
Q9H307	FK<4GG>QESTVATER<6>	156	166	710.3776	2	0.54	67/38	Pinin		1.00
Q9H307	FK<4GG>QESTVATER<6>	156	166	710.8827	2	7.70	51/39	Pinin		0.99
Q8NC51	EAGGGVGGPGAK<4GG>SAAQAAQTSNAAGK<4>	40	68	859.7655	3	-1.25	63/40	Plasminogen activator inhibitor 1 RNA-binding protein		1.49
Q8NC51	EAGGGVGGPGAK<4GG>SAAQAAQTSNAAGK<4>	40	68	860.0986	3	-1.56	42/40	Plasminogen activator inhibitor 1 RNA-binding protein		1.73
Q8NC51	GGSGSHNWGTVK<8GG>DELTEPK<8>	217	236	739.3565	3	0.01	46/38	Plasminogen activator inhibitor 1 RNA-binding protein		1.27
Q8NC51	GGSGSHNWGTVK<4GG>DELTEPK<4>	217	236	736.6968	3	-0.42	52/38	Plasminogen activator inhibitor 1 RNA-binding protein		1.27
Q8NC51	GGSGSHNWGTVK<4GG>DELTEPK<4>	217	236	737.0326	3	3.00	48/38	Plasminogen activator inhibitor 1 RNA-binding protein		1.27
P09874	QcPyr<1>PVGK<4GG>SEGK<4>	198	207	574.3315	2	0.04	51/38	Poly [ADP-ribose] polymerase 1		1.47
P09874	SIQELFLAHLSPWGAEVK<8GG>AEPVEVAPR<10>	468	496	830.2053	4	-0.53	51/39	Poly [ADP-ribose] polymerase 1		1.49
P09874	SIQELFLAHLSPWGAEVK<8GG>AEPVEVAPR<10>	468	496	1106.607	3	1.62	45/38	Poly [ADP-ribose] polymerase 1		1.58
P09874	SIQELFLAHLSPWGAEVK<4GG>AEPVEVAPR<6>	468	496	828.211	4	-0.50	53/39	Poly [ADP-ribose] polymerase 1		1.49
P09874	SIQELFLAHLSPWGAEVK<4GG>AEPVEVAPR<6>	468	496	1103.9466	3	0.41	68/39	Poly [ADP-ribose] polymerase 1		1.58
P09874	SIQELFLAHLSPWGAEVK<4GG>AEPVEVAPR<6>	468	496	1103.9466	3	0.41	55/39	Poly [ADP-ribose] polymerase 1		1.58
P09874	K<4GG>PPLLNADSVQAK<4>	748	761	808.9633	2	-0.82	62/40	Poly [ADP-ribose] polymerase 1		2.08
Q6N2I2	VMIYQDEVK<8GG>LPAK<8>	153	165	832.4504	2	-7.48	54/40	Polymerase I and transcript release factor		0.68
Q6N2I2	VMIYQDEVK<4GG>LPAK<4>	153	165	828.4665	2	-1.22	89/40	Polymerase I and transcript release factor		0.68
Q6N2I2	VM<ox>1YDEVK<4GG>LPAK<4>	153	165	557.9788	3	-0.49	42/40	Polymerase I and transcript release factor		0.62
Q15212	LLGPVLV<4GG>QELGEAR<6>	59	73	873.5355	2	6.86	65/37	Prefoldin subunit 6		3.29
P02545	TVLC<Cmm*>GTC<Cmm*>GQPADK<4GG>ASASGSAQVGPSSGSSAVTVTR<6>	585	624	1292.9605	3	-0.70	80/38	Prelamin-A/C		1.52
Q6UN15	TGAPQYGSYGTAPVNLNK<4GG>TGGR<6>	105	127	816.096	3	0.64	47/41	Pre-mRNA 3'-end-processing factor FIP1		1.52
Q92841	WDLSELPK<4GG>FEK<4>	122	132	757.4109	2	0.63	44/39	Probable ATP-dependent RNA helicase DDX17		1.23
P17844	WNLDSELPK<4GG>FEK<4>	46	56	770.9164	2	0.58	41/39	Probable ATP-dependent RNA helicase DDX5		1.91
Q72333	TK<4GG>EFESYLDMMITC<Cmm*>SQIVVNYNPK<4>	338	363	1086.8527	3	0.45	58/37	Probable helicase senataxin		1.84
Q5VW92	VK<4GG>HHEVSEETVFGGALGK<4>	1028	1056	688.7155	3	-0.21	57/43	Proteasome-associated protein ECM29 homolog		1.40
Q1E3D9	K<8>K<8GG>PVK<8>VEAPEVIPSDDPK<8>	245	263	767.0977	3	-2.77	41/39	Protein C16orf88		2.43
Q1E3D9	K<4>K<4>PVK<4GG>VEAPEVIPSDDPK<4>	245	263	761.7802	3	-1.06	67/38	Protein C16orf88		2.61
Q96E09	LHQIK<4GG>QEEGMDLNR<6>	85	99	650.0178	3	3.87	52/41	Protein FAM122A		0.76
Q96E09	LHQIK<4GG>QEEGMDLNR<6>	85	99	650.346	3	-4.05	46/40	Protein FAM122A		0.71
Q86U86	K<4GG>PVPQK<4>EPSPLEK<4>	1293	1307	915.0684	2	0.65	45/35	Protein polybromo-1		2.03
Q86U86	K<4GG>PVPQK<4>EPSPLEK<4>	1293	1307	915.5752	2	8.06	34/33	Protein polybromo-1		1.77
Q86U86	K<8GG>PVPQK<8>EPSPLEK<8>K<8>	1293	1308	495.0562	4	-1.06	39/31	Protein polybromo-1		1.30
Q86U86	K<8GG>PVPQK<8>EPSPLEK<8>K<8>	1293	1308	659.7393	3	-0.70	37/31	Protein polybromo-1		1.66
Q86U86	K<4GG>PVPQK<4>EPSPLEK<4>K<4>	1293	1308	654.4202	3	-1.18	46/29	Protein polybromo-1		1.66
Q14690	K<4GG>HTLSIGDMVTGTVK<4>	1030	1044	570.3215	3	-0.08	52/40	Protein RRP5 homolog		1.05
Q93590	NWLLNTR<4GG>LEK<4>	670	679	654.8895	2	-0.25	52/39	Protein SCF11		1.27
Q95785	AADLGEER<8>PLAAPPRTYK<4GG>AEHQRF<6>	1506	1529	858.7923	3	-1.48	45/41	Protein Wz		2.28
Q60361	VMLGETNPNADSK<4GG>PFTIR<6>	74	90	637.2389	3	-1.30	42/40	Putative nucleoside diphosphate kinase	P15531, P22392	1.44
Q60361	NHIGSDSVK<4GG>SAEK<4>	100	113	803.937	2	1.99	51/40	Putative nucleoside diphosphate kinase	P22392	1.76
P46087	FNSSIPQSQTGNETATPNVDLPQVPIK<8GG>SENSSQPAK<8>K<8>	587	625	1067.2905	4	0.44	57/40	Putative ribosomal RNA methyltransferase NOP2		1.26
P14618	NIC<Cmm*>K<4GG>VVEVSK<4>	163	173	677.887	2	5.09	66/39	Pyruvate kinase isozymes M1/M2		1.50
P46060	LLVHMGLL<8GG>SEDK<8>	516	528	806.9567	2	-0.06	93/40	Ran GTPase-activating protein 1		1.08
P46060	LLVHMGLL<8GG>SEDK<8>	516	528	538.307	3	0.11	43/40	Ran GTPase-activating protein 1		0.94
P46060	LLVHM<ox>GLL<8GG>SEDK<8>	516	528	814.9543	2	0.12	53/40	Ran GTPase-activating protein 1		1.01
P46060	LLVHMGLL<8GG>SEDK<8>	516	528	538.3071	3	0.34	42/40	Ran GTPase-activating protein 1		0.94
P46060	LLVHM<ox>GLL<4GG>SEDK<4>	516	528	810.9646	2	-0.54	51/40	Ran GTPase-activating protein 1		1.01
P46060	LLVHM<ox>GLL<4GG>SEDK<4>	516	528	540.979	3	-0.34	42/40	Ran GTPase-activating protein 1		1.16
P46060	LLVHMGLL<4GG>SEDK<4>	516	528	802.9674	2	-0.33	75/40	Ran GTPase-activating protein 1		1.08
P46060	LLVHMGLL<4GG>SEDK<4>	516	528	535.6474	3	-0.15	60/40	Ran GTPase-activating protein 1		0.94
P46060	LLVHMGLL<4GG>SEDK<4>	516	528	525.6475	3	0.04	46/40	Ran GTPase-activating protein 1		0.94
P46060	LLVHMGLL<4GG>SEDK<4>	516	528	802.9678	2	0.25	82/40	Ran GTPase-activating protein 1		1.08
P46060	LLVHMGLL<8GG>SEDK<8>VK<8>	516	530	924.5438	2	-1.91	66/37	Ran GTPase-activating protein 1		1.02
P46060	LLVHMGLL<8GG>SEDK<8>VK<8>	516	530	924.5443	2	-1.36	44/37	Ran GTPase-activating protein 1		1.02
P46060	LLVHMGLL<8GG>SEDK<8>VK<8>	516	530	616.6989	3	-0.95	47/37	Ran GTPase-activating protein 1		1.01
P46060	LLVHMGLL<8GG>SEDK<8>VK<8>	516	530	616.6994	3	-0.10	43/37	Ran GTPase-activating protein 1		1.01
P46060	LLVHMGLL<8GG>SEDK<8>VK<8>	516	530	924.5513	2	6.22	78/35	Ran GTPase-activating protein 1		1.02
P46060	LLVHMGLL<4GG>SEDK<4>VK<4>	516	530	918.5608	2	-1.19	88/36	Ran GTPase-activating protein 1		1.02
P46060	LLVHMGLL<4GG>SEDK<4>VK<4>	516	530	918.561	2	-0.99	77/36	Ran GTPase-activating protein 1		1.02
P46060	LLVHMGLL<4GG>SEDK<4>VK<4>	516	530	612.7098	3	-0.90	49/36	Ran GTPase-activating protein 1		1.01
P46060	LLVHMGLL<4GG>SEDK<4>VK<4>	516	530	612.7101	3	-0.38	39/36	Ran GTPase-activating protein 1		1.01
P46060	LLVHMGLL<4GG>SEDK<4>VK<4>	516	530	612.7103	3	-0.05	45/36	Ran GTPase-activating protein 1		1.01
P46060	LLVHMGLL<4GG>SEDK<4>VK<4>	516	530	612.7103	3	0.02	43/36	Ran GTPase-activating protein 1		1.01
P43487	LEALSIV<8GG>EETR<8>EDAEK<8>Q	184	201	738.7115	3	0.05	61/41	Ran-specific GTPase-activating protein		1.39
Q92766	IK<8GG>QETEGELK<8>	614	624	709.397	2	-0.04	49/40	Ras-responsive element-binding protein 1		1.60
Q92766	IK<4GG>QETEGELK<4>	614	624	705.4071	2	-1.24	53/39	Ras-responsive element-binding protein 1		1.80
Q96T23	STANVLETTVK<8GG>K<8>	266	278	775.4232	2	-0.76	64/40	Remodeling and spacing factor 1		1.31
Q96T23	STANVLETTVK<4GG>K<4>	266	278	771.4341	2	-0.77	62/40	Remodeling and spacing factor 1		1.31
Q96T23	STANVLETTVK<4GG>K<4>	266	278	771.4351	2	0.54	49/40	Remodeling and spacing factor 1		1.27
Q96T23	LPVIVK<4GG>LEK<4>PLPNEEK<4>	289	305	701.4272	3	0.77	39/35	Remodeling and spacing factor 1		0.92
Q96T23	VAPNFK<4GG>TEPIETK<4>	451	463	798.4465	2	-1.41	50/40	Remodeling and spacing factor 1		1.29
Q725J4	VASLPGDFK<4>QEEVGVK<4GG>EAAGLLQC<Cmm*>PEVAK<4>	803	833	1123.2579	3	-0.01	68/41	Retinoic acid-induced protein 1		1.59

Q725J4	APLIC<Cmm>*Tk<4GG>EVEEVLDSK<4>	895	911	695.0388	3	6.85	49/41	Retinoic acid-induced protein 1		1.78
P52565	K<4>GVK<4>DK<4GG>DMVMSYVGR<6>	135	152	716.0649	3	-0.44	57/41	Rho GDP-dissociation inhibitor 1		1.13
P52565	GVK<8GG>DK<8>TDYVMVSYVGR<10>	136	152	676.0135	3	-0.63	62/40	Rho GDP-dissociation inhibitor 1		1.33
P52565	GVK<4GG>DK<4>TDYVMVSYVGR<6>	136	152	1007.534	2	-0.13	90/40	Rho GDP-dissociation inhibitor 1		1.04
P52565	GVK<4GG>DK<4>TDYVMVSYVGR<6>	136	152	672.0264	3	1.87	47/41	Rho GDP-dissociation inhibitor 1		1.33
Q14692	SGPNTQNEDEK<8>EVK<8GG>EIIDPDEESAK<8>	796	822	1066.4935	3	-0.20	43/36	Ribosome biogenesis protein BMS1 homolog		1.45
Q14692	SGPNTQNEDEK<8>EVK<4GG>EIIDPDEESAK<4>	796	822	1066.4935	3	-1.74	47/36	Ribosome biogenesis protein BMS1 homolog		1.41
Q9GLZ7	Q<Pyr>K<4GG>TEQLGLTR<6>	238	247	640.8631	2	-1.09	60/39	Ribosome biogenesis protein WDR12		1.33
Q9P2E9	NTDVAQSPAPK<4GG>QEPAPK<4>	609	626	668.3479	3	0.66	43/40	Ribosome-binding protein 1		1.29
P38159	GFAPVTFSPADAK<4GG>DAAR<6>	50	67	675.3403	3	-2.64	43/38	RNA-binding motif protein, X chromosome	Q9639	1.16
P38159	GFAPVTFSPADAK<4GG>DAAR<6>	50	67	675.6769	3	2.13	47/39	RNA-binding motif protein, X chromosome	Q9639	1.16
Q5T8P6	DIK<4GG>K<4>EITK<4>EER<6>	104	116	593.6704	3	-0.74	42/40	RNA-binding protein 26		1.40
Q5JTH9	LQK<4GG>SEAPETPMEAEELVLEK<4>	69	90	851.7744	3	7.84	53/41	RRP15-like protein		1.05
Q9Y389	Q<Pyr>TEVK<8GG>SEEGPGWTLR<10>	235	250	972.9918	2	-0.88	76/40	RRP15-like protein		1.23
Q9Y389	QTEVK<8GG>SEEGPGWTLR<10>	235	250	654.6738	3	1.20	52/41	RRP15-like protein		1.14
Q9Y389	QTEVK<4GG>SEEGPGWTLR<6>	235	250	652.0138	3	-0.30	57/40	RRP15-like protein		1.21
Q9Y389	Q<Pyr>TEVK<4GG>SEEGPGWTLR<6>	235	250	969.0044	2	0.31	61/40	RRP15-like protein		1.19
Q9Y265	C<Cmm>*DITYATEFDLEAEVPLPK<8GG>GDVHK<8>	206	230	1019.4786	2	1.56	48/37	RuvB-like 1		1.66
Q9Y265	C<Cmm>*DITYATEFDLEAEVPLPK<4GG>GDVHK<4>	206	230	1012.1519	3	0.94	115/37	RuvB-like 1		1.66
Q8N5C6	IK<4GG>TETTRGQPVK<4>	184	196	805.9533	2	0.30	58/40	S1 RNA-binding domain-containing protein 1		1.86
Q15424	ESSTSAGADQ<8GG>MSPPEDDSTK<8>R<10>	371	393	876.3791	3	0.26	74/29	Scaffold attachment factor B1		2.06
Q15424	GVPSIVK<4GG>TSGSK<4>	571	583	690.9185	2	0.05	55/38	Scaffold attachment factor B1		0.95
Q14151	AVK<4GG>EEGQDPDEIELETSK<4>	63	83	794.069	3	-1.77	41/40	Scaffold attachment factor B2		0.78
Q14151	ILDLGETC<Cmm>*K<4GG>SEPVK<4>EESSELEQPFPAQDTSVSGPDR<6>	216	251	1374.0189	3	4.00	87/40	Scaffold attachment factor B2	Q15424	1.01
Q14151	SEPVK<8GG>EESSELEQPFPAQDTSVSGPDR<10>	226	251	994.4622	3	-1.74	75/37	Scaffold attachment factor B2	Q15424	1.40
Q14151	SEPVK<4GG>EESSELEQPFPAQDTSVSGPDR<6>	226	251	991.4717	3	0.14	88/37	Scaffold attachment factor B2	Q15424	1.40
Q14151	SEPVK<4GG>EESSELEQPFPAQDTSVSGPDR<6>	226	251	991.811	3	6.22	62/38	Scaffold attachment factor B2	Q15424	1.43
Q14151	SEPVK<4GG>EESSELEQPFPAQDTSVSGPDR<6>K<4>	226	252	1035.512	3	0.41	75/39	Scaffold attachment factor B2	Q15424	1.08
Q14151	SEPVK<4GG>EESSELEQPFPAQDTSVSGPDR<6>K<4>	226	252	1035.8546	3	9.36	81/40	Scaffold attachment factor B2	Q15424	1.08
Q14151	ADSLAVVK<8GG>R<10>	285	294	401.9106	3	-0.19	48/38	Scaffold attachment factor B2	Q15424	1.18
Q14151	ADSLAVVK<8GG>R<10>	285	294	602.3624	2	0.09	64/38	Scaffold attachment factor B2	Q15424	1.16
Q14151	ADSLAVVK<8GG>R<10>	285	294	602.3624	2	0.32	40/38	Scaffold attachment factor B2	Q15424	1.18
Q14151	ADSLAVVK<8GG>R<10>	285	294	401.9108	3	0.43	61/38	Scaffold attachment factor B2	Q15424	1.17
Q14151	ADSLAVVK<4GG>R<6>	285	294	598.3735	2	-0.40	58/38	Scaffold attachment factor B2	Q15424	1.16
Q14151	ADSLAVVK<4GG>R<6>	285	294	399.2515	3	-0.30	62/38	Scaffold attachment factor B2	Q15424	1.18
Q14151	ADSLAVVK<4GG>R<6>	285	294	598.3736	2	-0.28	56/38	Scaffold attachment factor B2	Q15424	1.18
Q14151	ADSLAVVK<4GG>R<6>	285	294	598.3736	2	-0.23	64/38	Scaffold attachment factor B2	Q15424	1.18
Q14151	ADSLAVVK<4GG>R<6>	285	294	399.252	3	0.96	52/38	Scaffold attachment factor B2	Q15424	1.17
Q14151	ADSLAVVK<4GG>R<6>EPAEOPGDGER<6>	285	305	789.758	3	-0.38	58/41	Scaffold attachment factor B2	Q15424	1.15
Q14151	ADSLAVVK<4GG>R<6>EPAEOPGDGER<6>	285	305	789.7581	3	-0.30	65/41	Scaffold attachment factor B2	Q15424	1.55
Q14151	ADSLAVVK<4GG>R<6>EPAEOPGDGER<6>	285	305	790.0937	3	2.59	49/41	Scaffold attachment factor B2	Q15424	1.55
Q14828	TGASFQK<4GG>AQQEFPAAGVFNPAVR<6>	307	329	846.1028	3	-1.75	43/40	Secretory carrier-associated membrane protein 3		1.23
Q8Y8B3	VK<4GG>EPVQEA1TS1SDLK<4>	230	246	652.0227	3	-2.20	59/40	Serine/arginine repetitive matrix protein 1		1.16
Q13523	ALIK<8GG>KELDELNLEWK<8>	114	128	602.3221	3	1.51	42/41	Serine/threonine-protein kinase PRP4 homolog		1.41
Q13523	ALIK<4GG>KELDELNLEWK<4>	114	128	602.4891	2	0.03	79/40	Serine/threonine-protein kinase PRP4 homolog		1.66
Q76094	ISQGNISK<8GG>AC<Cmm>*LILR<10>	384	397	568.9903	3	1.09	45/40	Signal recognition particle 72 kDa protein		1.23
Q76094	ISQGNISK<4GG>AC<Cmm>*LILR<6>	384	397	566.3304	3	-0.29	56/40	Signal recognition particle 72 kDa protein		1.23
Q76094	ISQGNISK<4GG>AC<Cmm>*LILR<6>	384	397	848.9926	2	0.39	69/40	Signal recognition particle 72 kDa protein		1.05
P42224	GTGYIK<4GG>TELSVSEVPSR<6>	698	717	733.0665	3	-0.29	60/41	Signal transducer and activator of transcription 1-alpha/beta		1.14
Q8TAD8	HR<10>DGDVLPAGVVK<8GG>QER<10>	16	33	529.7959	4	0.02	58/40	Smad nuclear-interacting protein 1		1.60
Q8TAD8	HR<6>DGDVLPAGVVK<4GG>QER<6>	16	33	526.8044	4	-0.14	51/40	Smad nuclear-interacting protein 1		1.57
Q8TAD8	HR<6>DGDVLPAGVVK<4GG>QER<6>	16	33	702.0703	3	0.11	68/40	Smad nuclear-interacting protein 1		1.58
Q8TAD8	HR<6>DGDVLPAGVVK<4GG>QER<6>	16	33	527.0545	4	-0.05	45/40	Smad nuclear-interacting protein 1		1.63
P61956	EGVK<4GG>TENNDHNLK<4>	8	21	866.9566	2	-0.28	41/39	Small ubiquitin-related modifier 2		1.02
P63208	TFNIK<4GG>NDFTEEEAQRV<6>	138	154	732.0264	3	-0.44	60/37	S-phase kinase-associated protein 1		1.21
Q75533	NR<10>PLSDELDAMFPEGYK<8GG>VLPPAGYVPIR<10>	396	425	1171.9399	3	4.97	82/41	Splicing factor 3B subunit 1		1.20
Q75533	NR<6>PLSDELDAMFPEGYK<4GG>VLPPAGYVPIR<6>	396	425	1169.9399	3	0.02	91/41	Splicing factor 3B subunit 1		1.20
Q75533	NR<6>PLSDELDAMFPEGYK<4GG>VLPPAGYVPIR<6>	396	425	879.9599	4	0.13	56/41	Splicing factor 3B subunit 1		1.15
Q75533	NR<6>PLSDELDAMFPEGYK<4GG>VLPPAGYVPIR<6>	396	425	875.9611	4	0.13	59/41	Splicing factor 3B subunit 1		1.28
Q75533	NR<6>PLSDELDAMFPEGYK<4GG>VLPPAGYVPIR<6>	396	425	875.9612	4	0.15	53/41	Splicing factor 3B subunit 1		1.28
Q75533	NR<6>PLSDELDAMFPEGYK<4GG>VLPPAGYVPIR<6>	396	425	1167.9467	3	0.93	79/41	Splicing factor 3B subunit 1		1.20
Q13435	ILQLK<4GG>ESR<6>	276	283	555.8478	2	0.80	39/38	Splicing factor 3B subunit 2		1.08
Q14247	VDQSAVGFYQGK<8GG>TEK<8>	132	147	639.3171	3	0.10	41/39	Src substrate cortactin		1.06
Q14247	VDQSAVGFYQGK<4GG>TEK<4>	132	147	636.658	3	0.45	47/39	Src substrate cortactin		1.20
Q14247	SAVFDYQGK<4GG>TEK<4>	172	184	776.3975	2	-0.81	69/38	Src substrate cortactin		1.31
Q14247	SAVGFYQGK<4GG>TEK<4>	209	221	783.4054	2	-0.62	57/38	Src substrate cortactin		1.30
P31948	K<8GG>FMFFNMPNLYQK<8>	123	136	951.472	2	-0.19	55/39	Stress-induced-phosphoprotein 1		1.56
P31948	K<8GG>FMFFNMPNLYQK<4>	123	136	631.9908	3	-0.53	41/39	Stress-induced-phosphoprotein 1		1.30
P31948	K<4GG>FMFFNMPNLYQK<4>	123	136	947.4931	2	-0.02	65/39	Stress-induced-phosphoprotein 1		1.56
P31948	K<4GG>FMFFNMPNLYQK<4>	123	136	947.9916	2	0.93	50/40	Stress-induced-phosphoprotein 1		1.56
P31948	K<4>ETK<4GG>PEPMEEDPENK<4>K<4>	207	223	725.0598	3	4.80	48/41	Stress-induced-phosphoprotein 1		1.43
Q9UBT2	GVTE<Cmm>*YEC<Cmm>*HPK<4GG>PTQR<6>	154	168	662.6453	3	0.59	40/34	SUMO-activating enzyme subunit 2		1.48
Q9UBT2	TIFLNK<4GG>QPNPR<6>	415	425	726.4212	2	-0.81	50/39	SUMO-activating enzyme subunit 2		1.99
P63279	K<8GG>GTPWEGGLFK<8>	49	59	675.3622	2	-0.84	46/39	SUMO-conjugating enzyme UBC9		1.07
P63279	K<4GG>GTPWEGGLFK<4>	49	59	671.3737	2	0.02	63/39	SUMO-conjugating enzyme UBC9		1.07
Q9Y220	LVGEIK<4GG>EEK<4>NEK<4>LEGDALNR<6>	290	311	872.8143	3	-1.50	48/41	Suppressor of G2 allele of SKP1 homolog		1.13
Q969G3	ASNPLK<8GG>LWEIGK<8>	86	98	800.9362	2	-0.76	69/40	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1		1.42
Q969G3	ASNPLK<8GG>LWEIGK<8>	86	98	534.2938	3	0.37	62/40	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1		1.26
Q969G3	ASNPLK<8GG>LWEIGK<8>	86	98	801.4311	2	-7.17	45/40	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1		1.42
Q969G3	ASNPLK<4GG>LWEIGK<4>	86	98	796.948	2	0.38	72/40	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1		1.42
Q92797	MK<4GG>LEPNLGEDDEK<4>DLEPGSGTSK<4>	360	384	943.1264	3	-1.51	46/38	Sumplekin		1.01
Q92797	TAAAGLTLK<4GG>EER<6>	1230	1242	749.8953	2	-4.48	75/39	Sumplekin		1.18
P50990	ALAENSQVK<4GG>ANVYSK<4>	451	466	876.49	2	-0.60	62/40	T-complex protein 1 subunit theta		1.03
Q96FV9	ILAPYLEMK<8GG>DSEIR<10>	587	600	905.4804	2	0.13	107/41	THO complex subunit 1		1.04
Q96FV9	ILAPYLEMK<4GG>DSEIR<6>	587	600	901.4914	2	-0.35	99/41	THO complex subunit 1		1.04
Q9Y2W1	DSR<10>PSQAAGDNQDDEAK<8GG>EQTFSGGTSQDTK<8>	186	215	814.1172	4	-0.38	59/33	Thyroid hormone receptor-associated protein 3		0.98
Q9Y2W1	DSR<6>PSQAAGDNQDDEAK<4GG>EQTFSGGTSQDTK<4>	186	215	1080.831	3	-1.06	38/33	Thyroid hormone receptor-associated protein 3		1.16
Q9Y2W1	DSR<6>PSQAAGDNQDDEAK<4GG>EQTFSGGTSQDTK<4>	186	215	810.8758	4	-0.13	64/34	Thyroid hormone receptor-associated protein 3		1.10
Q9Y2W1	DSR<6>PSQAAGDNQDDEAK<4GG>EQTFSGGTSQDTK<4>	186	215	1081.1632	3	-2.11	65/33	Thyroid hormone receptor-associated protein 3		1.16
Q9Y2W1	GFSFDTLGLDGK<4GG>MK<4>	376	389	761.3744	2	-2.60	57/36	Thyroid hormone receptor-associated protein 3		1.49
Q9Y2W1	ESEFDDEPK<4GG>FMSK<4>	443	455	855.8938	2	2.13	47/32	Thyroid hormone receptor-associated protein 3		1.10

Q9UGU0	LK<4>SQSGQIK<4GG>EEDFEQSK<4>	921	937	527.5317	4	-0.30	48/41	Transcription factor 20		1.44
Q9UGU0	SQSGQIK<4GG>EEDFEQSK<4>	923	937	931.4542	2	-0.14	70/37	Transcription factor 20		4.32
Q9UH73	SGSSMK<4GG>EPLGSGMNAVR<6>	11	28	654.3201	3	-0.18	63/37	Transcription factor COE1		3.99
P17275	GASTFK<8GG>EPEQTVPEAR<6>	235	250	626.9823	3	0.63	40/39	Transcription factor jun-B		2.47
P17275	GASTFK<4GG>EPEQTVPEAR<6>	235	250	624.3232	3	0.55	47/39	Transcription factor jun-B		2.47
P17275	GASTFK<4GG>EPEQTVPEAR<6>	235	250	935.9819	2	1.44	65/39	Transcription factor jun-B		1.73
QD2447	IK<8GG>EEEDPPEEWQLSGDSTLNTDLHLR<1D>	550	577	1133.5394	3	1.92	89/39	Transcription factor Sp3		1.98
QD2447	IK<8GG>EEEDPPEEWQLSGDSTLNTDLHLR<1D>	550	577	1133.8755	3	0.52	117/39	Transcription factor Sp3		1.98
QD2447	IK<4GG>EEEDPPEEWQLSGDSTLNTDLHLR<6>	550	577	1130.8824	3	-0.07	88/38	Transcription factor Sp3		1.98
QD2447	IK<4GG>EEEDPPEEWQLSGDSTLNTDLHLR<6>	550	577	848.4138	4	0.10	45/38	Transcription factor Sp3		2.11
O15164	IK<8GG>QENSGPPENYDFPVVVK<8>	722	741	801.7549	3	-1.00	54/41	Transcription intermediary factor 1-alpha		1.62
O15164	IK<8GG>QENSGPPENYDFPVVVK<8>	722	741	802.0906	3	1.92	44/41	Transcription intermediary factor 1-alpha		1.62
O15164	IK<4GG>QENSGPPENYDFPVVVK<4>	722	741	799.0965	3	0.20	54/41	Transcription intermediary factor 1-alpha		1.48
O15164	IK<8>QENSGPPENYDFPVVVK<8GG>QESDEESR<1D>PQNAVYPR<1D>	722	757	1082.0361	4	5.43	77/40	Transcription intermediary factor 1-alpha		1.47
Q13263	ALK<4GG>MIVDPVEPHGEMK<4>	375	390	639.3457	3	0.38	55/40	Transcription intermediary factor 1-beta		1.09
Q13263	QGSSSQPMEVQEGYFGSGDDPYSSAEPHVSQVVK<4GG>R<6>	435	470	960.1884	4	0.72	41/33	Transcription intermediary factor 1-beta		1.04
Q13263	LOEK<8GG>LSPYSSQEQEADQVGR<1D>	747	767	836.7544	3	0.08	80/41	Transcription intermediary factor 1-beta		1.35
Q13263	LOEK<8GG>LSPYSSQEQEADQVGR<1D>	747	767	857.0857	3	-2.34	77/41	Transcription intermediary factor 1-beta		1.35
Q13263	LOEK<4GG>LSPYSSQEQEADQVGR<6>	747	767	834.0952	3	-0.09	97/40	Transcription intermediary factor 1-beta		1.35
Q13263	LOEK<4GG>LSPYSSQEQEADQVGR<6>	747	767	1250.6395	2	0.22	95/40	Transcription intermediary factor 1-beta		0.82
Q13263	LOEK<4GG>LSPYSSQEQEADQVGR<6>	747	767	834.0958	3	0.64	68/40	Transcription intermediary factor 1-beta		1.37
Q13263	Q<Pyr>FNK<4>LTEDK<4GG>ADVQSIGLQR<6>	771	790	805.4449	3	-0.76	75/41	Transcription intermediary factor 1-beta		1.99
Q13263	QFNK<4>LTEDK<4GG>ADVQSIGLQR<6>	771	790	811.1205	3	-0.70	65/40	Transcription intermediary factor 1-beta		1.92
Q13263	LTEDE<8GG>ADVQSIGLQR<1D>	775	790	959.5204	2	-1.26	62/41	Transcription intermediary factor 1-beta		1.44
Q13263	LTEDE<8GG>ADVQSIGLQR<1D>	775	790	640.0164	3	-0.67	57/41	Transcription intermediary factor 1-beta		1.32
Q13263	LTEDE<8GG>ADVQSIGLQR<1D>	775	790	959.521	2	-0.61	92/41	Transcription intermediary factor 1-beta		1.44
Q13263	LTEDE<8GG>ADVQSIGLQR<1D>	775	790	640.3512	3	1.65	75/41	Transcription intermediary factor 1-beta		1.32
Q13263	LTEDE<4GG>ADVQSIGLQR<6>	775	790	955.5325	2	-0.52	94/40	Transcription intermediary factor 1-beta		1.44
Q13263	LTEDE<4GG>ADVQSIGLQR<6>	775	790	637.3574	3	-0.46	84/40	Transcription intermediary factor 1-beta		1.32
Q13263	LTEDE<4GG>ADVQSIGLQR<6>	775	790	955.5328	2	-0.19	91/40	Transcription intermediary factor 1-beta		1.42
Q13263	LTEDE<4GG>ADVQSIGLQR<6>	775	790	637.3578	3	0.12	42/40	Transcription intermediary factor 1-beta		1.32
P46100	SC<Cmm>*GLNPK<8GG>LEK<4>	617	626	638.3484	2	-0.10	50/39	Transcriptional regulator ATRX		0.79
P46100	SC<Cmm>*GLNPK<4GG>LEK<4>	617	626	624.3484	2	-1.46	44/38	Transcriptional regulator ATRX		0.79
P46100	GGGEGNVDETGNNPSVSLK<4GG>LEESK<4>	1964	1987	847.0837	3	0.25	84/38	Transcriptional regulator ATRX		1.30
P13428	TGPTVTQVK<4GG>AEK<4>	747	758	690.9001	2	-0.27	50/39	Treacle protein		1.15
P60174	EAGITEK<4GG>VVFQTK<4>	173	186	850.9687	2	-0.23	64/40	Triosephosphate isomerase		0.84
Q9NVL9	FC<Cmm>*NIMGSSNGVDQEHFSNVVK<4GG>GEEK<4>	149	172	702.3316	4	-4.46	39/35	Tropomodulin-3		2.40
P68363	GDVVPK<8GG>DVNAATIK<8>	321	336	580.9994	3	0.67	42/40	Tubulin alpha-1B chain	Q13748, Q6PEY2, Q71U36, Q98QE3	1.14
Q12888	LSDDVANTAIK<8GG>HEQSNEDIPAEQSSK<8>	207	234	1066.8494	3	-0.98	64/40	Tumor suppressor p53-binding protein 1		1.17
Q12888	LSDDVANTAIK<8GG>HEQSNEDIPAEQSSK<8>	207	234	1067.1855	3	1.62	91/40	Tumor suppressor p53-binding protein 1		1.11
Q12888	LSDDVANTAIK<4GG>HEQSNEDIPAEQSSK<4>	207	234	1064.1914	3	0.34	98/39	Tumor suppressor p53-binding protein 1		1.21
Q12888	LSDDVANTAIK<4GG>HEQSNEDIPAEQSSK<4>	207	234	1064.5228	3	-1.48	77/39	Tumor suppressor p53-binding protein 1		1.21
Q12888	TSNSLTEDSK<8GG>MANAK<8>	859	873	863.9172	2	1.37	70/37	Tumor suppressor p53-binding protein 1		1.61
Q12888	TSNSLTEDSK<4GG>MANAK<4>	859	873	859.9244	2	2.87	68/36	Tumor suppressor p53-binding protein 1		1.61
Q12888	TSNSLTEDSK<4GG>MANAK<4>	859	873	859.9261	2	-0.92	61/37	Tumor suppressor p53-binding protein 1		1.60
Q12888	TSNSLTEDSK<4GG>MANAK<4>	859	873	573.6202	3	-0.18	45/37	Tumor suppressor p53-binding protein 1		1.30
Q12888	ETAVPGPLGIEDISPLSPDDK<4GG>FSFR<6>	1413	1438	955.8215	3	-0.34	49/41	Tumor suppressor p53-binding protein 1		1.25
Q12888	K<4GG>ESGLYSEIK<4>	1563	1574	784.4102	2	2.61	47/38	Tumor suppressor p53-binding protein 1		1.21
Q61850	INEVK<8GG>TEISVESK<8>	159	171	803.4366	2	-0.38	63/40	Twinfilin-2		1.56
Q61850	INEVK<4GG>TEISVESK<4>	159	171	799.4475	2	-0.41	75/40	Twinfilin-2		1.51
Q61850	INEVK<4GG>TEISVESK<4>	159	171	533.6345	3	0.42	59/40	Twinfilin-2		1.30
Q9UIG0	EVK<8GG>FEPQVDEAEDMISAVK<8>	823	843	836.7543	3	-0.97	53/41	Tyrosine-protein kinase BAZ1B		1.30
Q9UIG0	EVK<4GG>FEPQVDEAEDMISAVK<4>	823	843	834.0959	3	0.13	67/40	Tyrosine-protein kinase BAZ1B		1.30
O43290	LGK<4>PLEVNAIK<4GG>K<4>	130	142	775.0131	2	-2.35	47/30	U4/U6.U5 tri-snRNP-associated protein 1		1.29
O43290	LGK<4>PLEVNAIK<4GG>K<4>	130	142	517.0132	3	1.64	29/28	U4/U6.U5 tri-snRNP-associated protein 1		1.11
P61086	EPK<4GG>EVK<4>SEFTK<4>	12	24	840.4544	2	1.51	80/40	Ubiquitin-conjugating enzyme E2 K		3.30
O43795	LGNIEFK<8GG>PESR<1D>	281	291	711.3793	2	0.77	48/40	Unconventional myosin-1b		1.04
O43795	LGNIEFK<4GG>PESR<6>	281	291	471.9288	3	-0.82	42/39	Unconventional myosin-1b		0.99
O43795	LGNIEFK<4GG>PESR<6>	281	291	707.3899	2	-0.36	61/39	Unconventional myosin-1b		1.04
O43795	LGNIEFK<4GG>PESR<6>	281	291	471.9293	3	0.31	40/39	Unconventional myosin-1b		0.99
O43795	LGNIEFK<4GG>PESR<6>	281	291	707.8851	2	-7.07	42/39	Unconventional myosin-1b		1.65
O95292	ISITASK<4GG>TETPIVSK<4>	140	155	899.5236	2	-0.47	74/39	Vesicle-associated membrane protein-associated protein B/C		0.92
P08670	TLIK<8GG>TVETR<1D>	441	450	653.3973	2	1.28	65/37	Vimentin		0.78
P08670	TLIK<4GG>TVETR<6>	441	450	649.4077	2	-0.16	69/37	Vimentin		0.78
O75717	LSAFAFK<4GG>QE	1121	1129	579.8085	2	0.49	49/38	WD repeat and HMG-box DNA-binding protein 1		2.79
Q15061	K<4GG>PLTNC<Cmm>*TIQATPK<4>	309	324	617.6788	3	-1.45	47/41	WD repeat-containing protein 43		2.01
Q15061	DISNC<Cmm>*WAPK<4GG>VETATK<4>	376	391	978.0098	2	-1.05	48/40	WD repeat-containing protein 43		2.01
O9ULM3	VK<8GG>TEFETPRGSC<Cmm>*SQEQTAVY<8>	1109	1130	825.0792	3	0.83	62/41	YEATS domain-containing protein 2		1.49
O9ULM3	VK<4GG>TEFETPRGSC<Cmm>*SQEQTAVY<4>	1109	1130	821.4187	4	-0.50	73/40	YEATS domain-containing protein 2		1.54
P49750	TGGMGEGTAVATSSLTADDFK<4GG>PVIGLPHSENNQDK<4>	767	803	960.2164	4	0.07	42/38	YLP motif-containing protein 1		1.49
P49750	GPLVK<4GG>QEDFR<6>	853	863	457.254	3	0.49	42/40	YLP motif-containing protein 1		1.46
O9HC78	IQTLVNIHK<4GG>QEMEDDYDYGQQR<6>	320	344	1060.8479	3	-0.26	87/38	Zinc finger and BTB domain-containing protein 20		1.50
O95365	HFK<4GG>DEDEDVAPSPDGLGR<6>	537	555	752.341	3	-0.42	38/31	Zinc finger and BTB domain-containing protein 7A		2.04
O96C00	IFYIK<4GG>QEPFEPK<4>EISGSGTQPGGAK<4>	282	307	741.8941	4	0.30	44/41	Zinc finger and BTB domain-containing protein 9		5.73
O96C00	IFYIK<4GG>QEPFEPK<4>EISGSGTQPGGAK<4>EETK<4>	282	311	1152.2735	3	-0.24	44/41	Zinc finger and BTB domain-containing protein 9		1.48
Q5VZL5	IK<8GG>EPLDDEYDK<8>	249	260	812.3893	2	-0.39	62/36	Zinc finger MYM-type protein 4		1.31
Q5VZL5	IK<8GG>EPLDDEYDK<8>	249	260	541.9296	3	1.54	38/37	Zinc finger MYM-type protein 4		1.34
Q5VZL5	IK<4GG>EPLDDEYDK<4>	249	260	808.3999	2	-0.75	58/36	Zinc finger MYM-type protein 4		1.33
Q5VZL5	IK<4GG>EPLDDEYDK<4>	249	260	808.9044	2	4.81	57/37	Zinc finger MYM-type protein 4		1.34
Q5VZL5	IK<8GG>EPLDDEYDK<8>AMAPQOGLDK<8>	249	271	925.1362	3	4.23	54/41	Zinc finger MYM-type protein 4		1.68
Q5VZL5	IK<4GG>EPLDDEYDK<4>AMAPQOGLDK<4>	249	271	925.1406	3	-0.20	54/41	Zinc finger MYM-type protein 4		1.68
Q5VZL5	IK<4GG>EPLDDEYDK<4>AMAPQOGLDK<4>	249	271	693.8595	4	0.45	64/41	Zinc finger MYM-type protein 4		1.53
Q5VZL5	IK<4GG>EPLDDEYDK<4>AMAPQOGLDK<4>	249	271	925.1445	3	1.50	50/41	Zinc finger MYM-type protein 4		1.69
Q9UQR1	VK<4GG>DEYMAEYAVEMPHSSVGGSHLEDASGEIHPK<4>	355	389	980.2185	4	-0.98	52/37	Zinc finger protein 148		1.79
P17028	VK<4GG>LEEDPDGEGSIPWNLHLPDFR<6>	26	52	1077.1937	3	-0.50	61/39	Zinc finger protein 24		2.26
O9ULJ3	LK<4>GQLC<Cmm>*DVLVIGDQK<4GG>FR<6>	25	42	558.3281	4	-0.88	51/39	Zinc finger protein 295		2.37
O9ULJ3	LK<4>GQLC<Cmm>*DVLVIGDQK<4GG>FR<6>	25	42	744.102	3	-0.36	51/39	Zinc finger protein 295		2.65
O9ULJ3	LK<4>GQLC<Cmm>*DVLVIGDQK<4GG>FR<6>	25	42	558.5801	4	2.74	40/38	Zinc finger protein 295		2.37
O9ULJ3	GQLC<Cmm>*DVLVIGDQK<4GG>FR<6>	27	42	993.0493	2	1.61	47/41	Zinc finger protein 295		1.36
O9ULJ3	IQVK<8GG>EPEVEAEAEFAEASTAPK<8>	876	898	880.7659	3	-0.90	62/40	Zinc finger protein 295		2.22



Q9ULJ3	IQVK<4GG>EPPVEEAEFAEASTAPK<4>	876	898	878.1064	3	-1.09	71/40	Zinc finger protein 295		2.23
P59923	LQTVK<4>K<4GG>EEDESYTPVQAAR<6>	23	42	817.0965	3	-0.09	51/41	Zinc finger protein 445		1.14
Q9Y4E5	TETSIK<4GG>TEDDFPVIETSNQLTC<Cmm*>GC<Cmm*>R<6>	701	725	1009.1416	3	-0.67	75/36	Zinc finger protein 451		1.46
Q96JM2	APSYEDLK<4GG>AHIQDVHTAFLQPTDVAEDNVNELK<6>	13	45	965.7334	4	-0.30	44/40	Zinc finger protein 462		1.39
Q9H582	VK<4GG>PESTDEDESVDFAFQLIWNPK<4>	345	369	753.6237	4	0.32	41/39	Zinc finger protein 644		1.86
Q9H582	VK<4GG>PESTDEDESVDFAFQLIWNPK<4>	345	369	753.8748	4	1.82	49/40	Zinc finger protein 644		1.72
Q2TB10	VK<4GG>VEPADSVESPPSITHSPONELK<4>	408	432	933.1532	3	-0.13	68/41	Zinc finger protein 800		1.50
Q2TB10	VK<4GG>VEPADSVESPPSITHSPONELK<4>	408	432	933.4883	3	1.76	57/41	Zinc finger protein 800		1.50
Q17R98	IK<4GG>EPPMEVDIQDSHVSSPSR<6>	672	692	631.0732	4	2.68	51/40	Zinc finger protein 827		2.40
Q9UHF7	MGEPPVSESVK<8GG>R<10>	756	767	483.921	3	0.04	59/39	Zinc finger transcription factor Trps1		2.61
Q9UHF7	M<α>GEPVSESVK<4GG>R<6>	756	767	486.5929	3	-1.39	57/39	Zinc finger transcription factor Trps1		0.84
Q9UHF7	MGEPPVSESVK<4GG>R<6>	756	767	481.262	3	0.06	51/39	Zinc finger transcription factor Trps1		2.65
Q9UHF7	MGEPPVSESVK<4GG>R<6>	756	767	721.3896	2	0.41	70/39	Zinc finger transcription factor Trps1		1.87
Q9UHF7	NEGPLNVVK<4GG>TEK<4>	1193	1204	725.4099	2	-1.44	61/40	Zinc finger transcription factor Trps1		1.73



P52272	SK<4>GC<Cmm*>GVVK<4GG>FESPEVAER<6>	691	707	1004.0295	2	0.32	75/40	Heterogeneous nuclear ribonucleoprotein M			2.72
P52272	GC<Cmm*>GVVK<8GG>FESPEVAER<1D>	693	707	898.4406	2	-1.27	76/38	Heterogeneous nuclear ribonucleoprotein M			1.90
P52272	GC<Cmm*>GVVK<4GG>FESPEVAER<6>	693	707	894.4524	2	-0.83	65/38	Heterogeneous nuclear ribonucleoprotein M			1.87
P52272	GC<Cmm*>GVVK<4GG>FESPEVAER<6>	693	707	596.6374	3	-0.79	53/38	Heterogeneous nuclear ribonucleoprotein M			1.95
P52272	GC<Cmm*>GVVK<4GG>FESPEVAER<6>	693	707	894.453	2	-0.15	92/38	Heterogeneous nuclear ribonucleoprotein M			1.90
Q08839	GFEFTEENK<4GG>TSR<6>	256	268	607.9611	3	0.02	41/36	Heterogeneous nuclear ribonucleoprotein U			2.47
Q98UJ2	Q<Pyr>NQFYDTQVIK<4GG>QENESGYER<6>	107	126	1292.102	2	-0.95	125/35	Heterogeneous nuclear ribonucleoprotein U-like protein 1			2.21
Q98UJ2	Q<Pyr>NQFYDTQVIK<4GG>QENESGYER<6>	107	126	867.4133	3	-0.17	76/36	Heterogeneous nuclear ribonucleoprotein U-like protein 1			2.81
Q98UJ2	Q<Pyr>NQFYDTQVIK<4GG>QENESGYER<6>	107	126	861.7388	3	1.02	58/35	Heterogeneous nuclear ribonucleoprotein U-like protein 1			1.75
Q98UJ2	Q<Pyr>NQFYDTQVIK<4GG>QENESGYER<6>	107	126	862.0712	3	-0.08	48/35	Heterogeneous nuclear ribonucleoprotein U-like protein 1			1.75
Q98UJ2	Q<Pyr>NQFYDTQVIK<4GG>QENESGYER<6>	107	126	867.7495	3	3.19	51/37	Heterogeneous nuclear ribonucleoprotein U-like protein 1			2.81
P07910	Q<Pyr>AVEMK<8>NDK<4>SEEQSSSVK<8>	224	243	787.7025	3	-0.32	42/37	Heterogeneous nuclear ribonucleoproteins C1/C2			0.87
P07910	Q<Pyr>AVEMK<8GG>NDK<8>SEEQSSSVK<8>	224	243	787.7026	3	-0.21	46/37	Heterogeneous nuclear ribonucleoproteins C1/C2			0.89
P07910	Q<Pyr>AVEMK<8>NDK<4>SEEQSSSVK<4>	224	243	789.7227	3	0.28	49/38	Heterogeneous nuclear ribonucleoproteins C1/C2			0.95
P82970	ITEAPASEK<4>EIVEVK<4GG>EENIEDATEK<4>	87	111	976.5085	3	-0.36	72/41	High mobility group nucleosome-binding domain-containing protein 5			4.45
P82970	ITEAPASEK<4>EIVEVK<4GG>EENIEDATEK<4>	87	111	976.8339	3	-8.46	76/41	High mobility group nucleosome-binding domain-containing protein 5			4.43
Q6NT76	QGMENEK<4GG>TEALDD	407	420	818.8847	2	1.37	88/33	Homeobox-containing protein 1			10.97
Q9NVR2	K<4GG>AIASLHLHALQGSISQPIQTGGTLEHQK<6>	464	494	854.4712	4	0.97	58/39	Integrator complex subunit 10			1.15
Q9NVR2	K<4GG>AIASLHLHALQGSISQPIQTGGTLEHQK<6>	464	494	854.7131	4	-8.52	47/40	Integrator complex subunit 10			2.29
Q96HW7	LMTSK<8GG>PAEVKK<4>	787	797	666.8908	2	1.19	42/39	Integrator complex subunit 4			1.43
Q96HW7	LMTSK<4GG>PAEVKK<4>	787	797	662.8908	2	-0.05	51/39	Integrator complex subunit 4			1.43
Q04695	QFTSSSIK<8GG>GSSGLGGSSR<1D>	7	26	1009.9958	2	-0.67	95/39	Keratin, type I cytoskeletal 17			1.87
Q04695	Q<Pyr>FTSSSIK<8GG>GSSGLGGSSR<1D>	7	26	1001.4832	2	-0.03	81/38	Keratin, type I cytoskeletal 17			1.97
Q04695	Q<Pyr>FTSSSIK<4GG>GSSGLGGSSR<6>	7	26	997.4938	2	-0.80	99/38	Keratin, type I cytoskeletal 17			1.97
Q04695	QFTSSSIK<4GG>GSSGLGGSSR<6>	7	26	1006.0072	2	-0.67	111/38	Keratin, type I cytoskeletal 17			1.87
Q04695	QFTSSSIK<4GG>GSSGLGGSSR<6>	7	26	1006.5106	2	2.71	76/39	Keratin, type I cytoskeletal 17			1.87
Q04695	LLGEDAHLTYK<4GG>K<4>	387	400	883.979	2	-0.83	80/40	Keratin, type I cytoskeletal 17			0.84
Q04695	LLGEDAHLTYK<8GG>K<8>EPVTR<1D>	387	406	823.4371	3	-0.85	54/41	Keratin, type I cytoskeletal 17			0.82
Q04695	LLGEDAHLTYK<4GG>K<4>EPVTR<6>	387	406	819.4489	3	-0.15	55/41	Keratin, type I cytoskeletal 17			0.82
Q04695	LLGEDAHLTYK<4GG>K<4>EPVTR<6>	387	406	819.7806	3	-2.16	55/41	Keratin, type I cytoskeletal 17			0.82
Q04695	TLVEEDGK<8GG>VISR<1D>	410	424	897.39	3	-0.61	42/41	Keratin, type I cytoskeletal 17			1.25
Q04695	TLVEEDGK<4GG>VISR<6>	410	424	892.482	2	-1.44	82/40	Keratin, type I cytoskeletal 17			0.66
P08729	WTLQEQK<4GG>SAK<4>	123	133	727.4162	2	0.23	47/40	Keratin, type II cytoskeletal 7			1.20
P05787	TLNKK<8GG>FASFDK<8>	97	108	764.4107	2	0.32	63/40	Keratin, type II cytoskeletal 8		Q95678, P02538, P04259, P08729, P12035, P13647, P35908, P48668, Q01546, Q5XKES, Q9NSB2	1.54
P05787	TLNKK<4GG>FASFDK<4>	97	108	760.4214	2	-0.01	65/40	Keratin, type II cytoskeletal 8		Q95678, P02538, P04259, P08729, P12035, P13647, P35908, P48668, Q01546, Q5XKES, Q9NSB2	1.54
P05787	TLNKK<4GG>FASFDK<4>	97	108	507.2835	3	0.21	41/40	Keratin, type II cytoskeletal 8		Q95678, P02538, P04259, P08729, P12035, P13647, P35908, P48668, Q01546, Q5XKES, Q9NSB2	1.28
P05787	TEMENFVLK<4GG>K<4>	187	198	801.9371	2	1.47	58/40	Keratin, type II cytoskeletal 8			1.01
P05787	SR<6>AEAESMYQIK<4GG>YEELQSLAGK<4>	274	295	665.5952	4	0.46	62/41	Keratin, type II cytoskeletal 8			1.98
P05787	AEAESMYQIK<8GG>YEELQSLAGK<8>	276	295	806.732	3	-0.55	57/40	Keratin, type II cytoskeletal 8			1.50
P05787	AEAESMYQIK<4GG>YEELQSLAGK<4>	276	295	804.0727	3	-0.45	57/40	Keratin, type II cytoskeletal 8			1.50
P05787	DKK<8GG>VSESSDLPK<8>	470	483	802.4322	2	3.96	43/40	Keratin, type II cytoskeletal 8			1.12
P05787	DKK<4GG>VSESSDLPK<4>	470	483	798.4399	2	-0.11	79/40	Keratin, type II cytoskeletal 8			1.12
Q07666	MEFENK<4GG>YPLMLAEK<4>	97	111	972.4879	2	-0.38	50/38	KH domain-containing, RNA-binding, signal transduction-associated protein 1			1.31
P20700	Q<Pyr>IYEVK<4GG>LAQALHEMR<6>	235	250	710.3628	3	0.47	55/39	Lamin-B1			1.18
Q43513	VK<8GG>TEPMDADDSNNC<Cmm*>TGQNEHQK<1D>	184	205	670.2878	4	0.33	32/28	Mediator of RNA polymerase II transcription subunit 7			1.58
Q14149	ILEMNDK<4>YVK<4GG>K<4>	731	741	753.9405	2	-0.07	41/39	MORC family CW-type zinc finger protein 3			1.55
Q13765	SK<4GG>NILEFVTK<4>PDVYK<4>	99	113	631.0526	3	-0.36	38/37	Nascent polypeptide-associated complex subunit alpha	Q9BZK3		2.94
P30414	K<4>TASQLSENK<4>PVK<4GG>TEPLR<6>	569	586	720.0934	3	-0.82	44/38	NK-tumor recognition protein			4.72
Q16649	FQIK<4GG>QEPMELESYTR<6>	215	230	712.7117	3	7.85	45/41	Nuclear factor interleukin-3-regulated protein			1.74
Q94916	SHDVQPTTPDPAAGALNNVVK<4GG>K<4>	533	557	921.4885	3	5.89	84/41	Nuclear factor of activated T-cells 5			1.74
Q6P4R8	DQAF<Cmm*>K<4GG>QENEDSDATTPVR<6>	483	503	840.383	3	-0.13	45/32	Nuclear factor related to kappa-B-binding protein			8.87
Q14980	LPPK<4GG>VESLESYFPIPAR<6>	1763	1781	1141.147	2	1.38	78/40	Nuclear mitotic apparatus protein 1			5.82
P49790	SGDITDFQK<4GG>R<6>	343	354	737.8981	2	-0.33	65/39	Nuclear pore complex protein Nup153			2.51
Q9Y2X3	IK<4>VK<8GG>VEEEEEK<8>VAEEETSVK<8>	464	485	912.8032	3	0.11	50/41	Nucleolar protein 58			1.44
Q9Y2X3	IK<4>VK<8GG>VEEEEEK<8>VAEEETSVK<8>	464	485	913.1384	3	0.98	61/41	Nucleolar protein 58			1.60
Q9Y2X3	IK<4>VK<4GG>VEEEEEK<4>VAEEETSVK<4>	464	485	680.8655	4	-0.54	76/41	Nucleolar protein 58			1.85
Q9Y2X3	IK<4GG>VK<4>VEEEEEK<4>VAEEETSVK<4>	464	485	907.485	3	-0.38	61/41	Nucleolar protein 58			1.65
Q9Y2X3	IK<4>VK<4GG>VEEEEEK<4>VAEEETSVK<4>	464	485	907.8214	3	3.01	55/41	Nucleolar protein 58			1.65
Q9Y2X3	IK<4>VK<4GG>VEEEEEK<4>VAEEETSVK<4>	464	485	681.1191	4	4.78	74/41	Nucleolar protein 58			1.86
Q9Y2X3	VK<8GG>VEEEEEK<8>VAEEETSVK<8>	466	485	622.5569	4	0.48	42/40	Nucleolar protein 58			1.83
Q9Y2X3	VK<8GG>VEEEEEK<8>VAEEETSVK<8>	466	485	829.7402	3	0.63	41/40	Nucleolar protein 58			1.47
Q9Y2X3	VK<4GG>VEEEEEK<4>VAEEETSVK<4>	466	485	619.5639	4	-1.34	73/40	Nucleolar protein 58			1.83
Q9Y2X3	VK<4GG>VEEEEEK<4>VAEEETSVK<4>	466	485	1238.123	2	0.59	110/40	Nucleolar protein 58			1.39
Q9Y2X3	VK<4GG>VEEEEEK<4>VAEEETSVK<4>K<4>	466	486	869.7905	3	-0.18	48/41	Nucleolar protein 58			1.91
Q9Y2X3	VK<4GG>VEEEEEK<4>VAEEETSVK<4>K<4>	466	486	870.1267	3	3.08	50/41	Nucleolar protein 58			1.97
P19338	K<4>K<4GG>VEGETPTAFNLFVGNLNFNK<4>	295	318	941.5125	3	0.14	73/41	Nucleolin			4.19
P19338	K<4>K<4GG>VEGETPTAFNLFVGNLNFNK<4>	295	318	941.338	3	8.59	47/40	Nucleolin			4.19
P06748	ADK<4>DYFK<4GG>VDNDEHQLSLR<6>	25	45	901.1092	3	-0.62	48/39	Nucleophosmin			1.35
P06748	GPSSVEDIK<4GG>AK<4>	240	250	626.8524	2	-0.66	50/39	Nucleophosmin			1.82
P06748	MQASIEK<4GG>GGLSPK<4>	251	263	734.4075	2	0.14	46/40	Nucleophosmin			2.34
Q96RE7	VK<8GG>TEQESDSVQC<Cmm*>MPVAK<8>	166	183	732.0194	3	-0.56	61/38	Nucleus accumbens-associated protein 1			3.90
Q96RE7	VK<4GG>TEQESDSVQC<Cmm*>M<4>M<4>MPVAK<4>	166	183	734.691	3	-1.53	50/37	Nucleus accumbens-associated protein 1			5.06
Q96RE7	VK<4GG>TEQESDSVQC<Cmm*>MPVAK<4>	166	183	1093.5361	2	-0.85	124/38	Nucleus accumbens-associated protein 1			6.05
Q96RE7	VK<4GG>TEQESDSVQC<Cmm*>MPVAK<4>	166	183	729.3601	3	-0.44	55/38	Nucleus accumbens-associated protein 1			3.90
O00541	VMAGLTK<4GG>LEDK<4>	511	521	663.8795	2	-1.43	55/39	Pescadillo homolog			2.12
QBWWQ0	ILK<4>PQLK<4GG>SESSASFSTR<6>	1464	1483	769.4349	3	0.15	71/40	PH-interacting protein			1.73

P15259	HYGGLTGLNK<8GG>AETAAK<8>	91	106	587.6464	3	-0.76	43/41	Phosphoglycerate mutase 2		P18669_Q8NOY7	1.79
P15259	HYGGLTGLNK<4GG>AETAAK<4>	91	106	876.9769	2	-0.74	79/40	Phosphoglycerate mutase 2		P18669_Q8NOY7	1.89
P15259	HYGGLTGLNK<4GG>AETAAK<4>	91	106	585.324	3	5.41	47/40	Phosphoglycerate mutase 2		P18669_Q8NOY7	1.79
Q9H307	FK<4GG>QESTVATER<6>	156	166	710.377	2	-0.37	44/38	Pinin			1.23
Q8NC51	GGSGSHNWTVK<4GG>DELTESTPR<4>	217	236	736.6972	3	0.16	44/38	Plasminogen activator inhibitor 1 RNA-binding protein			1.30
P09874	SLQEFLAHISPMVGEVAVK<4GG>AEPVVEVAPR<6>	468	496	828.2104	4	-1.20	40/39	poly [ADP-ribose] polymerase 1			4.35
Q6N212	VM<xxx>YQDEVK<8GG>LPAK<8>	153	165	849.9137	2	-0.40	55/41	Polymerase I and transcript release factor			0.73
Q6N212	VM<xxx>YQDEVK<8GG>LPAK<8>	153	165	832.4564	2	-0.16	85/40	Polymerase I and transcript release factor			0.70
Q6N212	VM<xxx>YQDEVK<8GG>LPAK<8>	153	165	560.6385	3	0.05	51/41	Polymerase I and transcript release factor			0.65
Q6N212	VM<xxx>YQDEVK<8GG>LPAK<8>	153	165	555.3069	3	0.07	43/40	Polymerase I and transcript release factor			0.70
Q6N212	VM<xxx>YQDEVK<4GG>LPAK<4>	153	165	557.9789	3	-0.31	44/40	Polymerase I and transcript release factor			0.65
Q6N212	VM<xxx>YQDEVK<4GG>LPAK<4>	153	165	836.4647	2	-0.31	65/40	Polymerase I and transcript release factor			0.73
Q6N212	VM<xxx>YQDEVK<4GG>LPAK<4>	153	165	828.4674	2	-0.08	85/40	Polymerase I and transcript release factor			0.70
Q6N212	LSISK<4GG>SLK<4>	166	173	499.3266	2	-3.26	39/36	Polymerase I and transcript release factor			0.54
P02545	LVEIDNGK<4GG>QR<6>	226	235	648.3693	2	0.19	41/39	Prelamin-A/C			1.30
P02545	TVLCC<Cmm*>GTC<Cmm*>GQPADK<4GG>ASASGSAQVGGPISGSSASSVTTR<6>	585	624	1292.9604	3	-0.78	82/38	Prelamin-A/C			1.77
P02545	TVLCC<Cmm*>GTC<Cmm*>GQPADK<4GG>ASASGSAQVGGPISGSSASSVTTR<6>	585	624	1293.2939	3	-0.65	85/38	Prelamin-A/C			1.77
P17844	WNLDLDPK<4GG>FEK<4>	46	56	770.9153	2	-0.81	41/39	Probable ATP-dependent RNA helicase DDX5			3.40
P12004	DLSHIGDAVVIC<Cmm*>AK<4GG>DGVK<4>	150	168	703.7082	3	0.03	63/41	Proliferating cell nuclear antigen			3.77
Q86U86	K<4GG>PIVPRQK<4>EPPSLEK<4>	1293	1307	458.0375	4	-0.05	36/25	protein polybromo-1			2.57
Q86U86	K<4GG>PIVPRQK<4>EPPSLEK<4>	1293	1307	915.0681	2	0.26	42/35	protein polybromo-1			3.18
Q86U86	K<4GG>PIVPRQK<8>EPPSLEK<8>K<8>	1293	1308	659.7394	3	-0.56	33/31	protein polybromo-1			2.19
Q86U86	K<4GG>PIVPRQK<4>EPPSLEK<4>K<4>	1293	1308	654.421	3	0.03	42/29	protein polybromo-1			2.19
Q86U86	K<4GG>PIVPRQK<4>EPPSLEK<4>K<4>	1293	1308	654.7563	3	3.07	42/27	protein polybromo-1			2.19
O95785	AADGGER<6>PLAASPTGVK<4GG>AEEHQER<6>	1506	1529	858.7831	3	-0.45	63/41	Protein Wiz			8.14
P46087	FSNSIPQSTGNSSETATPNVLDVPIVK<4GG>SENSQPAK<4>K<4>	587	625	1064.0476	4	-0.57	55/40	Putative ribosomal RNA methyltransferase NOP2			2.02
P46060	LVHMGLLK<8GG>SEDK<8>	516	528	806.9566	2	-0.21	85/40	Ran GTPase-activating protein 1			1.24
P46060	LVHMGLLK<8GG>SEDK<8>	516	528	538.307	3	0.08	42/40	Ran GTPase-activating protein 1			1.26
P46060	LVHMG<xxx>GLLK<8GG>SEDK<8>	516	528	814.9544	2	0.26	59/40	Ran GTPase-activating protein 1			1.16
P46060	LVHMG<xxx>GLLK<8GG>SEDK<8>	516	528	814.9548	2	0.72	53/40	Ran GTPase-activating protein 1			1.16
P46060	LVHMGLLK<4GG>SEDK<4>	516	528	802.9675	2	-0.19	82/40	Ran GTPase-activating protein 1			1.19
P46060	LVHMGLLK<4GG>SEDK<4>	516	528	538.307	4	-0.09	46/40	Ran GTPase-activating protein 1			1.26
P46060	LVHMGLLK<4GG>SEDK<4>	516	528	802.9678	2	0.28	67/40	Ran GTPase-activating protein 1			1.19
P46060	LVHMG<xxx>GLLK<4GG>SEDK<4>	516	528	810.9653	2	0.33	61/40	Ran GTPase-activating protein 1			1.19
P46060	LVHMGLLK<8GG>SEDK<8>VK<8>	516	530	616.6994	3	-0.05	43/37	Ran GTPase-activating protein 1			1.23
P46060	LVHMGLLK<8GG>SEDK<8>VK<8>	516	530	924.5462	2	0.71	82/37	Ran GTPase-activating protein 1			1.29
P46060	LVHMGLLK<4GG>SEDK<4>VK<4>	516	530	918.5611	2	-0.88	78/36	Ran GTPase-activating protein 1			1.32
P46060	LVHMGLLK<4GG>SEDK<4>VK<4>	516	530	612.71	3	-0.59	54/36	Ran GTPase-activating protein 1			1.23
P46060	LVHMGLLK<4GG>SEDK<4>VK<4>	516	530	918.5615	2	-0.45	63/36	Ran GTPase-activating protein 1			1.32
P46060	LVHMGLLK<4GG>SEDK<4>VK<4>	516	530	612.7101	3	-0.40	39/36	Ran GTPase-activating protein 1			1.23
P43487	LEALSVK<8GG>EETK<8>EAEAEK<8>Q	184	201	738.7115	3	0.12	50/41	Ran-specific GTPase-activating protein			1.60
Q92766	IK<4GG>QEITTEGELK<4>	614	624	705.4076	2	-0.42	49/39	Ras-responsive element-binding protein 1			3.66
Q96723	STANVLETTVK<8GG>K<8>	266	278	775.4228	2	-1.29	61/40	Remodeling and spacing factor 1			2.54
Q96723	STANVLETTVK<4GG>K<4>	266	278	771.4346	2	-0.09	85/40	Remodeling and spacing factor 1			2.54
Q96723	LVNIVK<4GG>LEK<4>PIEUNEK<4>	389	395	731.094	3	0.91	39/25	Remodeling and spacing factor 1			2.66
Q96723	VAPMFK<4GG>TEPETEK<4>	451	463	798.4477	2	0.19	46/40	Remodeling and spacing factor 1			7.62
Q725J4	APUC<Cmm*>TK<4GG>EVEEVLDSK<4>	895	911	1041.5442	2	-3.05	57/40	Retinoic acid-induced protein 1			4.73
Q725J4	APUC<Cmm*>TK<4GG>EVEEVLDSK<4>	895	911	694.7004	3	-0.41	64/40	Retinoic acid-induced protein 1			4.25
P52565	GVK<8GG>DK<8>TDYMVVSGPR<10>	136	152	676.0141	3	0.26	47/40	Rho GDP-dissociation inhibitor 1			1.30
P52565	GVK<4>DK<4>TDYMVVSGPR<6>	136	152	677.3564	3	-0.56	43/40	Rho GDP-dissociation inhibitor 1			1.37
P52565	GVK<4GG>DK<4>TDYMVVSGPR<6>	136	152	1007.5336	2	-0.52	95/40	Rho GDP-dissociation inhibitor 1			5.67
P52565	GVK<4GG>DK<4>TDYMVVSGPR<6>	136	152	672.0256	3	0.59	53/41	Rho GDP-dissociation inhibitor 1			1.31
Q14692	SGPNTQNEIEK<8>EVK<8GG>EIIDPDEESAK<8>	796	822	1066.4941	3	0.37	47/36	Ribosome biogenesis protein BMS1 homolog			1.14
Q14692	SGPNTQNEIEK<4>EVK<4GG>EIIDPDEESAK<4>	796	822	1062.5046	3	-0.01	39/36	Ribosome biogenesis protein BMS1 homolog			1.14
Q14692	SGPNTQNEIEK<4>EVK<4GG>EIIDPDEESAK<4>	796	822	1062.8392	3	1.18	46/37	Ribosome biogenesis protein BMS1 homolog			1.14
Q57896	DK<4GG>K<4>EITTK<4>EERK<4>	104	116	593.6703	3	-0.78	47/40	RNA-binding protein 26			2.37
Q6P683	IK<4GG>EPIVNIPIEK<4>	762	774	815.9664	2	0.27	52/40	Round spermatid basic protein 1-like protein			10.94
Q9Y389	Q<P>>TEVK<4GG>SEEGPGWTLR<6>	235	250	969.0044	2	0.29	68/40	RRP15-like protein			1.00
Q14151	AVK<4GG>EEGDDPEIGLEATSK<4>	63	83	794.0709	3	0.69	46/40	Scaffold attachment factor B2			1.80
Q14151	ILDILGETC<Cmm*>K<4GG>SEVPVK<4>EESSELEQPAQDTSVGPDR<6>	216	251	1373.6801	3	0.02	64/39	Scaffold attachment factor B2		Q15424	2.89
Q14151	SEPVK<8GG>EESSELEQPAQDTSVGPDR<10>	226	251	994.1296	3	-1.06	75/37	Scaffold attachment factor B2		Q15424	2.36
Q14151	SEPVK<4GG>EESSELEQPAQDTSVGPDR<6>	226	251	991.4721	3	0.56	52/37	Scaffold attachment factor B2		Q15424	2.31
Q14151	SEPVK<4GG>EESSELEQPAQDTSVGPDR<6>K<4>	226	252	1035.5111	3	-0.46	108/39	Scaffold attachment factor B2		Q15424	2.05
Q14151	K<4GG>LAEEELDFSAPHEGDLDALESTAHQSSK<4>	252	284	920.433	4	-0.70	39/36	Scaffold attachment factor B2		Q15424	2.66
Q14151	ADSLAVVK<8GG>R<10>	285	294	401.9108	3	0.28	49/38	Scaffold attachment factor B2		Q15424	2.33
Q14151	ADSLAVVK<8GG>R<10>	285	294	602.3626	2	0.39	63/38	Scaffold attachment factor B2		Q15424	2.27
Q14151	ADSLAVVK<4GG>R<6>	285	294	399.2516	3	0.03	60/38	Scaffold attachment factor B2		Q15424	2.33
Q14151	ADSLAVVK<4GG>R<6>	285	294	598.3738	2	0.12	62/38	Scaffold attachment factor B2		Q15424	2.27
Q14151	ADSLAVVK<4GG>R<6>	285	294	589.374	2	0.32	62/38	Scaffold attachment factor B2		Q15424	2.27
Q14151	ADSLAVVK<4GG>R<6>	285	294	396.2519	3	0.70	59/38	Scaffold attachment factor B2		Q15424	2.33
Q14151	ADSLAVVK<8GG>R<10>EPAEQDGER<10>	285	305	793.7465	3	-0.34	68/41	Scaffold attachment factor B2		Q15424	2.59
Q14151	ADSLAVVK<4GG>R<6>EPAEQDGER<6>	285	305	789.758	3	-0.46	78/41	Scaffold attachment factor B2		Q15424	2.59
O76094	ISQGNISK<4GG>AC<Cmm*>LILR<6>	384	397	566.3308	3	0.34	48/40	Signal recognition particle 72 kDa protein			2.04
Q8TAD8	HR<6>DGDVLPAGVVK<4GG>QER<6>	16	33	526.8042	4	-0.60	42/40	Smad nuclear-interacting protein 1			2.10
Q8TAD8	HR<6>DGDVLPAGVVK<4GG>QER<6>	16	33	702.0705	3	0.25	44/40	Smad nuclear-interacting protein 1			5.56
P55854	EGVK<4GG>TENDHNLK<4>	8	20	809.9357	2	0.36	53/40	Small ubiquitin-related modifier 3			10.47
O75533	NR<10>PLSDELDAMFPEGYK<8GG>VLPPPAGYVPIR<10>	396	425	878.9525	4	0.10	45/41	Splicing factor 3B subunit 1			1.78
O75533	NR<6>PLSDELDAMFPEGYK<4GG>VLPPPAGYVPIR<6>	396	425	1167.6114	3	-0.75	52/41	Splicing factor 3B subunit 1			1.71
O75533	NR<6>PLSDELDAM<xxx>FPEGYK<4GG>VLPPPAGYVPIR<6>	396	425	879.9597	4	-0.08	42/41	Splicing factor 3B subunit 1			1.57
O75533	NR<6>PLSDELDAMFPEGYK<4GG>VLPPPAGYVPIR<6>	396	425	1167.9391	3	-5.58	50/41	Splicing factor 3B subunit 1			1.71
Q9UB72	GVTE<Cmm*>NEC<Cmm*>HPK<8GG>PTQR<10>	154	168	665.6389	3	2.32	37/34	SUMO-activating enzyme subunit 2			1.35
P63279	K<4GG>GTFWFGFK<4>	49	59	447.9182	3	0.65	40/39	SUMO-conjugating enzyme UBC9			1.49
P63279	K<4GG>GTFWFGFK<4>	49	59	671.3728	2	0.17	67/39	SUMO-conjugating enzyme UBC9			1.51
Q969G3	ASNPDK<4GG>LWEIGK<4>	86	98	796.9475	2	-0.26	64/40	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1			5.21
Q969G3	ASNPDK<4GG>LWEIGK<4>	86	98	531.6348	3	1.03	42/40	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1			2.95
Q92797	MK<4GG>LEPNLGEDDEK<4>DLEPGPSGTS<4>	360	384	943.4628	3	1.66	60/39	Symplekin			4.44
P49368	GASK<8GG>EILSEVER<10>	378	389	725.3863	2	-0.67	51/40	T-complex protein 1 subunit gamma			0.72
P49368	GASK<4GG>EILSEVER<6>	378	389	721.3972	2	-1.23	45/39	T-complex protein 1 subunit gamma			0.72
Q96FV9	ILAPYLEM<K<8GG>DSEIR<10>	587	600	905.4804	2	0.10	81/41	THO complex subunit 1			1.09
Q96FV9	ILAPYLEM<K<4GG>DSEIR<6>	587	600	901.4912	2	-0.58	81/40	THO complex subunit 1			1.09
Q96FV9	ILAPYLEM<xxx>K<4GG>DSEIR<6>	587	600	909.4888	2	-0.37	82/40	THO complex subunit 1			0.86

Q9Y2W1	ESFFDDEPK<4GG>FMSK<4>	443	455	855.8915	2	-0.52	40/32	Thyroid hormone receptor-associated protein 3			0.92
Q9UGU0	SQSGQIK<4GG>EEDFEQSK<4>	923	937	931.4551	2	0.85	76/37	Transcription factor 20			3.49
P05549	LTDNIK<4GG>YEDC<Cmm>*EDR<6>HDGTSNGTAR<6>	5	27	933.434	3	3.30	35/34	Transcription factor AP-2-alpha			8.14
Q9UH73	SGSSMK<4GG>EPLGSGMNAVR<6>	11	28	654.6558	3	3.44	46/37	Transcription factor COE1			4.53
P17275	GASTFK<4GG>EFPQTVPEAR<6>	235	250	935.9804	2	-0.16	56/39	Transcription factor jun-B			9.50
Q15225	VK<4GG>RR<6>ERGENGTSITDEELVTVMSVR<6>	13	35	893.132	3	0.44	82/41	Transcription factor MafG			1.30
Q02447	IK<8GG>EEEPDREIVQLSGDSTLNTDNLHLR<10>	550	577	1133.3815	3	5.82	63/40	Transcription factor Sp3			5.05
Q15164	IK<4GG>QENSGPPENYDFPVVVK<4GG>	722	741	799.432	3	2.89	55/41	Transcription intermediary factor 1-alpha			3.90
Q15164	IK<4>QENSGPPENYDFPVVVK<4GG>QESDESR<6>PQNANYPYR<6>	722	757	1077.7912	4	-0.37	59/40	Transcription intermediary factor 1-alpha			3.82
Q15164	IK<4>QENSGPPENYDFPVVVK<4GG>QESDESR<6>PQNANYPYR<6>	722	757	1077.7912	4	-0.37	48/40	Transcription intermediary factor 1-alpha			3.86
Q15164	QENSGPPENYDFPVVVK<4GG>QESDESR<6>PQNANYPYR<6>	724	757	1016.4902	4	-0.37	57/38	Transcription intermediary factor 1-alpha			4.58
Q13263	AR<6>LQEK<4GG>LSPYSSPQEFADVGR<6>	745	767	911.8144	3	-0.30	85/41	Transcription intermediary factor 1-beta			1.99
Q13263	LQEK<8GG>LSPYSSPQEFADVGR<10>	747	767	836.7543	3	0.00	88/41	Transcription intermediary factor 1-beta			2.64
Q13263	LQEK<8GG>LSPYSSPQEFADVGR<10>	747	767	837.0906	3	3.51	43/41	Transcription intermediary factor 1-beta			2.64
Q13263	LQEK<8GG>LSPYSSPQEFADVGR<10>	747	767	1255.1344	2	5.24	54/41	Transcription intermediary factor 1-beta			2.89
Q13263	LQEK<4GG>LSPYSSPQEFADVGR<6>	747	767	834.0945	3	-0.86	45/40	Transcription intermediary factor 1-beta			5.47
Q13263	LQEK<4GG>LSPYSSPQEFADVGR<6>	747	767	1250.6389	2	-0.26	111/40	Transcription intermediary factor 1-beta			2.77
Q13263	LQEK<4GG>LSPYSSPQEFADVGR<6>	747	767	834.0953	3	0.04	85/40	Transcription intermediary factor 1-beta			2.63
Q13263	LQEK<4GG>LSPYSSPQEFADVGR<6>	747	767	834.4289	3	0.41	87/41	Transcription intermediary factor 1-beta			2.66
Q13263	QVY<P>PFIK<4>LTDK<4GG>ADVQSIGLQR<6>	771	790	805.78	3	1.45	66/41	Transcription intermediary factor 1-beta			4.42
Q13263	LTDK<8GG>ADVQSIGLQR<10>	775	790	959.5217	2	0.15	100/41	Transcription intermediary factor 1-beta			2.74
Q13263	LTDK<4GG>ADVQSIGLQR<6>	775	790	637.3578	3	0.06	70/40	Transcription intermediary factor 1-beta			2.85
Q13263	LTDK<4GG>ADVQSIGLQR<6>	775	790	637.3579	3	0.25	59/40	Transcription intermediary factor 1-beta			2.84
Q13263	LTDK<4GG>ADVQSIGLQR<6>	775	790	955.5332	2	0.29	92/40	Transcription intermediary factor 1-beta			2.74
Q13263	LTDK<4GG>ADVQSIGLQR<6>	775	790	955.5338	2	0.82	103/40	Transcription intermediary factor 1-beta			2.75
P46100	SC<Cmm>*GLNPK<4GG>LEK<4>	617	626	634.3494	2	-0.03	40/39	Transcriptional regulator ATRX			2.51
Q13428	TGPTVTQVK<8GG>AEK<8>	747	758	694.8895	2	0.24	48/40	Treacle protein			2.43
Q13428	TGPTVTQVK<4GG>AEK<4>	747	758	690.9003	2	-0.02	45/39	Treacle protein			2.52
Q12888	LSDDVANTAIK<4GG>HEGOSNEDIPIAESQSK<4>	207	234	1064.1906	3	-0.42	53/39	Tumor suppressor p53-binding protein 1			2.95
Q12888	ETAVPGLGLEDISPLSPDK<4GG>5FSR<6>	1413	1438	955.8216	3	-0.31	42/41	Tumor suppressor p53-binding protein 1			2.06
Q12888	K<4GG>ESGELYYSIEK<4>	1563	1574	784.4073	2	-1.09	45/38	Tumor suppressor p53-binding protein 1			3.09
Q9UIG0	K<4><4>EIK<4GG>FEPQVDTAEEDMISAVK<4>	821	843	922.176	3	0.28	59/40	Tyrosine protein kinase BAZ1B			3.54
Q9UIG0	EIVK<4GG>FEPQVDTAEEDMISAVK<4>	823	843	834.4307	3	1.95	55/41	Tyrosine protein kinase BAZ1B			4.14
Q43290	GLLK<4>PLEVNAIK<4GG><4>	130	142	775.0144	2	-0.58	51/29	U4/U6.U5 tri-snRNP-associated protein 1			2.45
Q43290	GLLK<4>PLEVNAIK<4GG><4>	130	142	517.0122	3	-0.33	37/29	U4/U6.U5 tri-snRNP-associated protein 1			2.15
Q93009	DLLQFFK<4GG>PR<6>	863	871	644.376	2	-0.48	40/39	Ubiquitin carboxyl-terminal hydrolase 7			2.51
Q43795	LGNIEFK<8GG>PESR<10>	281	291	474.5882	3	-0.11	42/40	Unconventional myosin-1b			1.22
Q43795	LGNIEFK<8GG>PESR<10>	281	291	711.3789	2	0.29	51/40	Unconventional myosin-1b			1.27
Q43795	LGNIEFK<4GG>PESR<6>	281	291	707.3899	2	-0.39	56/39	Unconventional myosin-1b			1.26
P08670	TLLIK<4GG>TVETR<6>	441	450	649.4075	2	-0.39	54/37	Vimentin			0.58
P13010	K<4>LK<4GG>TEQQGAHFSVSLAEGSVTSVSNPAENFR<6>	566	599	905.4721	4	-0.79	44/41	X-ray repair cross-complementing protein 5			1.01
P13010	K<4>LK<4GG>TEQQGAHFSVSLAEGSVTSVSNPAENFR<6>	566	599	1207.2889	3	-4.76	66/41	X-ray repair cross-complementing protein 5			0.90
Q9HC78	IQTLVGNIIHK<4GG>QJEMEDDYDYVQQQR<6>	320	344	1060.8474	3	-0.73	76/38	Zinc finger and BTB domain-containing protein 20			3.92
Q95365	HFK<4GG>DEDEDVAPSDGLGR<8>	537	555	752.3406	3	-0.95	59/31	Zinc finger and BTB domain-containing protein 7A			17.65
P37275	IIIIYSLQEQQLQVVPQNLK<4GG><4>	473	494	892.1844	3	0.37	55/37	Zinc finger C-box-binding homeobox 1			4.37
Q5VZL5	IK<8GG>EPELDDYDK<8>	249	260	812.3891	2	-0.64	55/36	Zinc finger MYM-type protein 4			2.10
Q5VZL5	IK<8GG>EPELDDYDK<8>AMAPQQLDK<8>	249	271	692.7983	3	-0.71	47/41	Zinc finger MYM-type protein 4			2.92
Q5VZL5	IK<8GG>EPELDDYDK<8>AMAPQQLDK<8>	249	271	696.8506	4	-0.50	42/41	Zinc finger MYM-type protein 4			3.41
Q5VZL5	IK<4GG>EPELDDYDK<4>AMAPQQLDK<4>	249	271	924.8094	3	-0.40	74/41	Zinc finger MYM-type protein 4			2.92
Q5VZL5	IK<4GG>EPELDDYDK<4>AMAPQQLDK<4>	249	271	697.8577	4	-0.37	61/41	Zinc finger MYM-type protein 4			2.59
Q5VZL5	IK<4GG>EPELDDYDK<4>AMAPQQLDK<4>	249	271	694.1102	4	1.55	89/41	Zinc finger MYM-type protein 4			3.41
Q5VZL5	IK<4GG>DEPDNAQEYSHGQQQK<4>	272	289	746.3598	3	-0.87	38/36	Zinc finger MYM-type protein 4			3.77
Q5VZL5	IK<4GG>DEPDNAQEYSHGQQQK<4>	272	289	1119.5334	2	-3.29	43/36	Zinc finger MYM-type protein 4			3.63
Q5VZL5	IK<4GG>DEPDNAQEYSHGQQQK<4>	272	289	560.2733	4	1.99	37/37	Zinc finger MYM-type protein 4			3.30
Q5VZL5	IK<4GG>DEPDNAQEYSHGQQQK<4>	272	289	746.6956	3	2.33	44/37	Zinc finger MYM-type protein 4			3.77
Q9H217	VK<4GG>GHNHVAIVNLIK<4>	1735	1751	662.3889	3	-0.48	49/39	Zinc finger protein 106			3.79
Q9UQR1	VK<4GG>DEYMAVAIVEMPHSSVGGSHLEDASGEIHPK<4>	355	389	980.2191	4	-0.33	52/37	Zinc finger protein 148			3.83
P17028	VK<4GG>LEEDPDGEGESSIPWHLPDFEIFR<6>	26	52	1077.1937	3	-0.50	58/39	Zinc finger protein 24			19.45
P17028	VK<4GG>LEEDPDGEGESSIPWHLPDFEIFR<6>	26	52	1077.5309	3	3.09	66/39	Zinc finger protein 24			19.45
Q9ULJ3	LK<4>GQLC<Cmm>*DVLIVGDK<4GG>FR<6>	25	42	744.102	3	-0.36	62/39	Zinc finger protein 295			3.18
Q9ULJ3	LK<4>GQLC<Cmm>*DVLIVGDK<4GG>FR<6>	25	42	558.5796	4	1.81	68/38	Zinc finger protein 295			2.06
Q9ULJ3	GQLC<Cmm>*DVLIVGDK<4GG>FR<6>	27	42	662.3677	3	0.17	45/41	Zinc finger protein 295			3.75
Q9ULJ3	IQVK<4GG>EPEVEEAEEFAEAPK<4>	876	898	878.1071	3	-0.31	65/40	Zinc finger protein 295			4.00
Q9ULJ3	IQVK<4GG>EPEVEEAEEFAEAPK<4>	876	898	878.4445	3	4.38	66/40	Zinc finger protein 295			3.91
Q9Y4E5	TETSIK<8GG>TEDDFPVIETSNQLTC<Cmm>*GC<Cmm>*R<10>	701	725	1012.1356	3	0.91	40/36	Zinc finger protein 451			1.84
Q9Y4E5	TETSIK<4GG>TEDDFPVIETSNQLTC<Cmm>*GC<Cmm>*R<6>	701	725	1009.1413	3	-0.97	90/36	Zinc finger protein 451			1.84
Q9Y4E5	TETSIK<4GG>TEDDFPVIETSNQLTC<Cmm>*GC<Cmm>*R<6>	701	725	1009.4805	3	4.85	64/37	Zinc finger protein 451			1.85
Q9H582	VK<4GG>PESTDELVSDAFQQLIYNPDK<4>	345	369	753.6235	4	0.01	47/39	Zinc finger protein 644			18.82
Q27810	EVIK<4GG>LEPIETNONAVSR<8>	128	149	931.5004	3	-0.15	79/41	Zinc finger protein 800			1.07
Q27810	VK<4GG>VEPADSVSSPSPSTHSPQNLK<4>	408	432	933.1532	3	-0.16	52/41	Zinc finger protein 800			4.40
Q17R98	IK<4GG>EPEMVEDIQDSHVSISSPR<6>	672	692	841.0941	3	1.29	62/40	Zinc finger protein 827			0.82
Q9UH7	MGEFVSESVK<4GG>R<6>	756	767	721.3888	2	-0.70	50/39	Zinc finger transcription factor Trps1			6.01
Q9UH7	MGEFVSESVK<4GG>R<6>	756	767	481.2623	3	0.81	45/39	Zinc finger transcription factor Trps1			4.90

**Table S3. List of identified phosphorylated/SUMOylated peptides.** Peptides are ordered by protein name. Columns from left to right contain the Swiss-Prot accession number, HGNC symbol, protein name, position of the SUMO-conjugated lysine residue, position and nature of the phosphorylated residue, type of SUMO/phosphorylation motif, amino acid sequence surrounding the SUMO site (-15:+20), maximum score/threshold of the corresponding identified peptides, detection of the corresponding unphosphorylated peptide, SUMO isoform specificity and previous report of phosphorylation. For peptides where the exact position of the phosphorylated residue was unresolved, the different possible positions are underlined. S1 only: site identified with SUMO1 only; S2 only: site identified with SUMO2 only; S1+S2: site identified both with SUMO1 and SUMO2.

Swiss-Prot Acc.	HGNC symbol	Protein name	Modified K	Phospho. aa	Motif	Modified sequence	max score/threshold	unmod. peptide	Isoform spec.	known
Q9UJX5	ANAPC4	Anaphase-promoting complex subunit 4	K772	S777	KXEX <sub>2</sub> SE	SSDEEBEASNKPVKIKEEVLS <sup>772</sup> ESEAENQQAGAAALA	82/46	absent	S2 only	X
P11388	TOP2A	DNA topoisomerase 2-alpha	K1240	S1247	KXEX <sub>4</sub> SP	IEMKABAEKKNKKIKNENTEGSPQEDGVLEGLKQ	64/46	detected	S1+S2	X
O15446	CD3EAP	DNA-directed RNA polymerase I subunit RPA34	K270	S285	KXEX <sub>12</sub> SP	KPKGKETFEPEDKTVKQEINTEPLEDTVLSPTKKR	61/46	detected	S1 only	
Q9NVU0	POLR3E	DNA-directed RNA polymerase III subunit RPC5	K498	S503	KXEX <sub>2</sub> SE	KEQLRVPAVPPGVRIKEEPVSEEGEEDDEEQEAEEEP	87/47	detected	S1+S2	
P15408	FOSL2	Fos-related antigen 2	K222	S(?)	nd	QPMRSGGGVGVAVVVKQEPLEEDSPSSSAGLDKAQ	89/47	detected	S1+S2	
Q00613	HSF1	Heat shock factor protein 1	K298	S303	KXEX <sub>4</sub> SP	SIDERPLSSSPLVRVKKEPPSPQSPRVEEASGRP	46/43	absent	S1 only	X
P56524	HDAC4	Histone deacetylase 4	K559	S565	KXEX <sub>3</sub> SD	LPGQKEAHAQAGVQVQKQEP <sup>559</sup> IESDEEEAEPPEVEPEPG	57/48	absent	S1+S2	
Q15596	NCOA2	Nuclear receptor coactivator 2	K731	S736	KXEX <sub>2</sub> SP	SQESSSTAPGSEVTIKQEPVSPKKENALLRYLLDK	53/47	absent	S1 only	
Q9Y2X3	NOP58	Nucleolar protein 58	K497	S502	KXEX <sub>2</sub> SE	TSVKKKKRGGKKKIKKEEPLSEEEPCSTAIASPEK	74/46	absent	S1+S2	X
Q8TAD8	SNIP1	Smad nuclear-interacting protein 1	K30	S35	KXEX <sub>2</sub> SP	RHRDGDVVLPAQVVVQKERLSEVAVAPPARRRDPHSG	118/43	detected	S1+S2	X
O15164	TRIM24	Transcription intermediary factor 1-alpha	K741	S(?)	nd	NSGPPENYDFPVVIVKQESDEESRPNQNYPRSLILT	51/48	detected	S1 only	
Q9ULJ3	ZBTB21	Zinc finger protein 295	K430	S(?)	nd	STDREGASPVTEVRIKTEPSSPLSDPDIIRVTVGD	60/44	absent	S1+S2	
Q2TB10	ZNF800	Zinc finger protein 800	K409	S(?)	nd	EKGPNNTANSSEIKVKEPADSVESSPPSITHSPQN	59/47	detected	S1 only	

**Table S4. Quantification of SUMOylation level of SUMO1-conjugated proteins in control versus LLO-treated cells.** Columns from left to right contain the Swiss-Prot accession number, HGNC symbol, protein name, position of the SUMO-conjugated lysine residue and normalized M/H ratio indicating the degree of deSUMOylation upon LLO treatment.

Swiss-Prot Acc.	HGNC symbol	Protein name	Modified K	M/H ratio (fold change)
O14503	BHLHE40	Class E basic helix-loop-helix protein 40	279	4.54
P78347	GTF2I	General transcription factor II-I	991	4.12
Q6NT76	HMBOX1	Homeobox-containing protein 1	413	4.11
Q9UH73	EBF1	Transcription factor COE1	16	3.99
Q96C00	ZBTB9	Zinc finger and BTB domain-containing protein 9	286	3.6
P61086	UBE2K	Ubiquitin-conjugating enzyme E2 K	14	3.3
O15212	PFDN6	Prefoldin subunit 6	66	3.29
P11387	TOP1	DNA topoisomerase 1	117	3.26
P46013	MKI67	Antigen KI-67	2009	3.1
P46013	MKI67	Antigen KI-67	1093	2.97
Q16649	NFIL3	Nuclear factor interleukin-3-regulated protein	219	2.95
Q9UGU0	TCF20	Transcription factor 20	929	2.88
O75717	WDHD1	WD repeat and HMG-box DNA-binding protein 1	1127	2.79
Q14676	MDC1	Mediator of DNA damage checkpoint protein 1	616	2.74
Q1ED39	KNOP1	Protein C16orf88	249	2.61
Q1ED39	KNOP1	Protein C16orf88	246	2.43
P46013	MKI67	Antigen KI-67	2613	2.4
Q17R98	ZNF827	Zinc finger protein 827	673	2.4
Q9NYL9	TMOD3	Tropomodulin-3	169	2.4
P15408	FOSL2	Fos-related antigen 2	222	2.39
Q95785	WIZ	Protein Wiz	1523	2.28
P17028	ZNF24	Zinc finger protein 24	27	2.26
Q14980	NUMA1	Nuclear mitotic apparatus protein 1	1766	2.26
Q9ULJ3	ZBTB21	Zinc finger protein 295	879	2.22
Q9ULJ3	ZBTB21	Zinc finger protein 295	40	2.13
P17275	JUNB	Transcription factor jun-B	240	2.1
P09874	PARP1	Poly [ADP-ribose] polymerase 1	748	2.08
P30566	ADSL	Adenylosuccinate lyase	415	2.06
Q15424	SAFB	Scaffold attachment factor B1	381	2.06
O95365	ZBTB7A	Zinc finger and BTB domain-containing protein 7A	539	2.04
P53999	SUB1	Activated RNA polymerase II transcriptional coactivator p15	68	2.04
Q02447	SP3	Transcription factor Sp3	551	2.04
Q13111	CHAF1A	Chromatin assembly factor 1 subunit A	182	2.04
Q6PJG2	ELMSAN1	ELM2 and SANT domain-containing protein 1	590	2.04
Q15061	WDR43	WD repeat-containing protein 43	384	2.01
Q9UBT2	UBA2	SUMO-activating enzyme subunit 2	420	1.99
Q9UHF7	TRPS1	Zinc finger transcription factor Trps1	766	1.99
P18615	NELFE	Negative elongation factor E	78	1.97
P17844	DDX5	Probable ATP-dependent RNA helicase DDX5	53	1.91
Q9UKV3	ACIN1	Apoptotic chromatin condensation inducer in the nucleus	268	1.89
Q96RE7	NACC1	Nucleus accumbens-associated protein 1	167	1.88
Q8N5C6	SRBD1	S1 RNA-binding domain-containing protein 1	185	1.86
P49321	NASP	Nuclear autoantigenic sperm protein	736	1.84
Q7Z333	SETX	Probable helicase senataxin	339	1.84
Q93052	LPP	Lipoma-preferred partner	327	1.83
O15446	CD3EAP	DNA-directed RNA polymerase I subunit RPA34	314	1.81

 = M/H ratio > 2.0

Q9H582	ZNF644	Zinc finger protein 644	346	1.79
Q9UQR1	ZNF148	Zinc finger protein 148	356	1.79
P09038	FGF2	Fibroblast growth factor 2	228	1.78
Q7Z5J4	RAI1	Retinoic acid-induced protein 1	901	1.78
P82970	HMG5	High mobility group nucleosome-binding domain-containing protein 5	101	1.77
Q8N3X1	FNBP4	Formin-binding protein 4	348	1.77
Q9NVU0	POLR3E	DNA-directed RNA polymerase III subunit RPC5	498	1.77
O60361	NME2P1	Putative nucleoside diphosphate kinase	109	1.76
Q9BUJ2	HNRNPUL1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	117	1.76
Q9BUJ2	HNRNPUL1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	142	1.74
P55265	ADAR	Double-stranded RNA-specific adenosine deaminase	418	1.73
Q9UHF7	TRPS1	Zinc finger transcription factor Trps1	1201	1.73
Q92766	RREB1	Ras-responsive element-binding protein 1	615	1.7
P46013	MKI67	Antigen KI-67	2734	1.69
Q86U86	PBRM1	Protein polybromo-1	1293	1.69
O60885	BRD4	Bromodomain-containing protein 4	1111	1.68
P11388	TOP2A	DNA topoisomerase 2-alpha	1240	1.68
P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	115	1.67
Q7L4I2	RSRC2	Arginine/serine-rich coiled-coil protein 2	375	1.67
Q9Y265	RUVBL1	RuvB-like 1	225	1.66
P19338	NCL	Nucleolin	589	1.64
Q14676	MDC1	Mediator of DNA damage checkpoint protein 1	1413	1.64
Q9H0E9	BRD8	Bromodomain-containing protein 8	481	1.62
Q8NC51	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	52	1.61
P46013	MKI67	Antigen KI-67	2492	1.6
Q9H9B1	EHMT1	Histone-lysine N-methyltransferase EHMT1	22	1.6
Q9UPN9	TRIM33	E3 ubiquitin-protein ligase TRIM33	776	1.6
O43175	PHGDH	D-3-phosphoglycerate dehydrogenase	21	1.59
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	422	1.59
Q13263	TRIM28	Transcription intermediary factor 1-beta	779	1.59
Q7Z5J4	RAI1	Retinoic acid-induced protein 1	819	1.59
Q8TAD8	SNIP1	Smad nuclear-interacting protein 1	30	1.59
Q9NX24	NHP2	H/ACA ribonucleoprotein complex subunit 2	5	1.58
Q8N3X1	FNBP4	Formin-binding protein 4	519	1.57
Q32MZ4	LRRFIP1	Leucine-rich repeat flightless-interacting protein 1	305	1.56
O15164	TRIM24	Transcription intermediary factor 1-alpha	723	1.55
O95817	BAG3	BAG family molecular chaperone regulator 3	445	1.54
P09874	PARP1	Poly [ADP-ribose] polymerase 1	486	1.54
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	34	1.54
Q6P4R8	NFRKB	Nuclear factor related to kappa-B-binding protein	488	1.54
Q13523	PRPF4B	Serine/threonine-protein kinase PRP4 homolog	117	1.53
P02545	LMNA	Prelamin-A/C	597	1.52
P13639	EEF2	Elongation factor 2	239	1.52
Q6UN15	FIP1L1	Pre-mRNA 3'-end-processing factor FIP1	123	1.52
Q9NVN8	GNL3L	Guanine nucleotide-binding protein-like 3-like protein	477	1.52
Q9ULM3	YEATS2	YEATS domain-containing protein 2	1110	1.52
P14618	PKM	Pyruvate kinase isozymes M1/M2	166	1.5
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	868	1.5
Q2TB10	ZNF800	Zinc finger protein 800	409	1.5
Q9HC78	ZBTB20	Zinc finger and BTB domain-containing protein 20	330	1.5
P18887	XRCC1	DNA repair protein XRCC1	176	1.49



P49750	YLPM1	YLP motif-containing protein 1	788	1.49
Q5VZL5	ZMYM4	Zinc finger MYM-type protein 4	250	1.49
Q9Y2W1	THRAP3	Thyroid hormone receptor-associated protein 3	387	1.49
O94916	NFAT5	Nuclear factor of activated T-cells 5	556	1.48
Q9UBT2	UBA2	SUMO-activating enzyme subunit 2	164	1.48
O15164	TRIM24	Transcription intermediary factor 1-alpha	741	1.47
P09874	PARP1	Poly [ADP-ribose] polymerase 1	203	1.47
P49750	YLPM1	YLP motif-containing protein 1	858	1.46
Q16543	CDC37	Hsp90 co-chaperone Cdc37	132	1.46
Q6IQ32	ADNP2	ADNP homeobox protein 2	1032	1.46
Q9Y4E5	ZNF451	Zinc finger protein 451	706	1.46
Q6IBS0	TWF2	Twinfilin-2	163	1.45
O60361	NME2P1	Putative nucleoside diphosphate kinase	85	1.44
P39023	RPL3	60S ribosomal protein L3	294	1.44
Q02790	FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4	441	1.44
P31948	STIP1	Stress-induced-phosphoprotein 1	123	1.43
P31948	STIP1	Stress-induced-phosphoprotein 1	210	1.43
Q14692	BMS1	Ribosome biogenesis protein BMS1 homolog	810	1.43
O95433	AHSA1	Activator of 90 kDa heat shock protein ATPase homolog 1	182	1.42
P04083	ANXA1	Annexin A1	332	1.42
Q01780	EXOSC10	Exosome component 10	583	1.41
Q5T8P6	RBM26	RNA-binding protein 26	106	1.4
Q5VYK3	KIAA0368	Proteasome-associated protein ECM29 homolog	1039	1.4
P43487	RANBP1	Ran-specific GTPase-activating protein	190	1.39
Q15047	SETDB1	Histone-lysine N-methyltransferase SETDB1	1032	1.39
Q96JM2	ZNF462	Zinc finger protein 462	20	1.39
Q9NUU7	DDX19A	ATP-dependent RNA helicase DDX19A	26	1.39
Q92945	KHSRP	Far upstream element-binding protein 2	121	1.38
O75376	NCOR1	Nuclear receptor corepressor 1	1106	1.37
Q9UKV3	ACIN1	Apoptotic chromatin condensation inducer in the nucleus	315	1.37
P06748	NPM1	Nucleophosmin	257	1.36
Q9HAF1	MEAF6	Chromatin modification-related protein MEAF6	113	1.36
P04075	ALDOA	Fructose-bisphosphate aldolase A	42	1.35
Q9NR30	DDX21	Nucleolar RNA helicase 2	116	1.35
Q9NXV6	CDKN2AIP	CDKN2A-interacting protein	184	1.35
P78347	GTF2I	General transcription factor II-I	221	1.34
Q969G3	SMARCE1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	92	1.34
Q96MW1	CCDC43	Coiled-coil domain-containing protein 43	95	1.33
Q9GZL7	WDR12	Ribosome biogenesis protein WDR12	239	1.33
P06748	NPM1	Nucleophosmin	248	1.32
P30414	NKTR	NK-tumor recognition protein	1177	1.32
Q8IX12	CCAR1	Cell division cycle and apoptosis regulator protein 1	1012	1.32
P11021	HSPA5	78 kDa glucose-regulated protein	352	1.31
P11021	HSPA5	78 kDa glucose-regulated protein	353	1.31
Q14247	CTTN	Src substrate cortactin	181	1.31
P46100	ATRX	Transcriptional regulator ATRX	1982	1.3
Q14151	SAFB2	Scaffold attachment factor B2	230	1.3
Q9NQW6	ANLN	Actin-binding protein anillin	254	1.3
Q9UIG0	BAZ1B	Tyrosine-protein kinase BAZ1B	826	1.3
O95232	LUC7L3	Luc7-like protein 3	424	1.29
Q96T23	RSF1	Remodeling and spacing factor 1	277	1.29


Q96T23	RSF1	Remodeling and spacing factor 1	456	1.29
Q9H6U6	BCAS3	Breast carcinoma-amplified sequence 3	215	1.29
Q9P2E9	RRBP1	Ribosome-binding protein 1	620	1.29
O00232	PSMD12	26S proteasome non-ATPase regulatory subunit 12	92	1.28
Q14151	SAFB2	Scaffold attachment factor B2	293	1.28
P52272	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	698	1.27
Q8NC51	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	228	1.27
Q99590	SCAF11	Protein SCAF11	676	1.27
P46087	NOP2	Putative ribosomal RNA methyltransferase NOP2	615	1.26
P07900	HSP90AA1	Heat shock protein HSP 90-alpha	407	1.25
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	1434	1.25
Q13765	NACA	Nascent polypeptide-associated complex subunit alpha	100	1.25
Q969R5	L3MBTL2	Lethal(3)malignant brain tumor-like protein 2	700	1.25
Q96HC4	PDLIM5	PDZ and LIM domain protein 5	89	1.25
P05388	RPLP0	60S acidic ribosomal protein P0	297	1.24
Q9Y2D5	AKAP2	A-kinase anchor protein 2	174	1.24
O14828	SCAMP3	Secretory carrier-associated membrane protein 3	313	1.23
O15446	CD3EAP	DNA-directed RNA polymerase I subunit RPA34	270	1.23
O43795	MYO1B	Unconventional myosin-Ib	287	1.23
Q92841	DDX17	Probable ATP-dependent RNA helicase DDX17	129	1.23
P06748	NPM1	Nucleophosmin	32	1.22
P49792	RANBP2	E3 SUMO-protein ligase RanBP2	2594	1.22
P49792	RANBP2	E3 SUMO-protein ligase RanBP2	2792	1.22
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	163	1.22
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	1563	1.22
O75533	SF3B1	Splicing factor 3B subunit 1	413	1.21
P19338	NCL	Nucleolin	297	1.21
P63208	SKP1	S-phase kinase-associated protein 1	142	1.21
O43290	SART1	U4/U6.U5 tri-snRNP-associated protein 1	141	1.2
P06748	NPM1	Nucleophosmin	267	1.2
Q5T5X7	BEND3	BEN domain-containing protein 3	20	1.2
O60664	PLIN3	Perilipin-3	122	1.19
P15259	PGAM2	Phosphoglycerate mutase 2	100	1.19
Q9Y3B9	RRP15	RRP15-like protein	239	1.19
P52565	ARHGDI1	Rho GDP-dissociation inhibitor 1	138	1.18
Q13263	TRIM28	Transcription intermediary factor 1-beta	750	1.18
Q8N3X1	FBNP4	Formin-binding protein 4	301	1.18
Q92797	SYMPK	Symplekin	1239	1.18
P19338	NCL	Nucleolin	324	1.16
P38159	RBMX	RNA-binding motif protein, X chromosome	63	1.16
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	217	1.16
Q8IYB3	SRRM1	Serine/arginine repetitive matrix protein 1	231	1.16
P60709	ACTB	Actin, cytoplasmic 1	326	1.15
Q13428	TCOF1	Treacle protein	755	1.15
Q15029	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component	64	1.15
O60832	DKC1	H/ACA ribonucleoprotein complex subunit 4	413	1.14
O76094	SRP72	Signal recognition particle 72 kDa protein	391	1.14
P23396	RPS3	40S ribosomal protein S3	230	1.14
P42224	STAT1	Signal transducer and activator of transcription 1-alpha/beta	703	1.14
P59923	ZNF445	Zinc finger protein 445	28	1.14
P60709	ACTB	Actin, cytoplasmic 1	328	1.14

P68363	TUBA1B	Tubulin alpha-1B chain	326	1.14
Q14978	NOLC1	Nucleolar and coiled-body phosphoprotein 1	572	1.14
P52565	ARHGDI1	Rho GDP-dissociation inhibitor 1	141	1.13
Q07666	KHDRBS1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	102	1.13
Q14247	CTTN	Src substrate cortactin	144	1.13
Q9Y220	SUGT1	Suppressor of G2 allele of SKP1 homolog	295	1.13
P04083	ANXA1	Annexin A1	214	1.12
P60709	ACTB	Actin, cytoplasmic 1	113	1.12
Q9NYF8	BCLAF1	Bcl-2-associated transcription factor 1	580	1.12
P46777	RPL5	60S ribosomal protein L5	220	1.11
P68104	EEF1A1	Elongation factor 1-alpha 1	392	1.11
Q9Y2W1	THRAP3	Thyroid hormone receptor-associated protein 3	451	1.1
P15880	RPS2	40S ribosomal protein S2	275	1.09
Q06265	EXOSC9	Exosome complex component RRP45	297	1.09
Q13263	TRIM28	Transcription intermediary factor 1-beta	377	1.09
Q96JG6	CCDC132	Coiled-coil domain-containing protein 132	963	1.09
Q9BYG3	MKI67IP	MKI67 FHA domain-interacting nucleolar phosphoprotein	271	1.09
Q9NYF8	BCLAF1	Bcl-2-associated transcription factor 1	831	1.09
P26373	RPL13	60S ribosomal protein L13	174	1.08
P80723	BASP1	Brain acid soluble protein 1	143	1.08
Q02952	AKAP12	A-kinase anchor protein 12	1051	1.08
Q13435	SF3B2	Splicing factor 3B subunit 2	280	1.08
Q9Y2W1	THRAP3	Thyroid hormone receptor-associated protein 3	202	1.08
P07355	ANXA2	Annexin A2	49	1.07
P63279	UBE2I	SUMO-conjugating enzyme UBC9	49	1.07
Q9Y2X3	NOP58	Nucleolar protein 58	467	1.07
Q9NP74	PALMD	Palmdelphin	179	1.06
O43513	MED7	Mediator of RNA polymerase II transcription subunit 7	185	1.05
P08758	ANXA5	Annexin A5	29	1.05
P48681	NES	Nestin	811	1.05
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	134	1.05
Q14690	PDCD11	Protein RRP5 homolog	1030	1.05
Q16666	IFI16	Gamma-interferon-inducible protein 16	561	1.05
Q5JTH9	RRP12	RRP12-like protein	71	1.05
P46060	RANGAP1	Ran GTPase-activating protein 1	524	1.04
P51858	HDGF	Hepatoma-derived growth factor	80	1.04
Q13263	TRIM28	Transcription intermediary factor 1-beta	469	1.04
Q96FV9	THOC1	THO complex subunit 1	595	1.04
P50990	CCT8	T-complex protein 1 subunit theta	459	1.03
Q06830	PRDX1	Peroxiredoxin-1	185	1.03
O43242	PSMD3	26S proteasome non-ATPase regulatory subunit 3	38	1.02
P61956	SUMO2	Small ubiquitin-related modifier 2	11	1.02
Q01518	CAP1	Adenylyl cyclase-associated protein 1	348	1.02
Q02040	AKAP17A	A-kinase anchor protein 17A	118	1.02
Q12873	CHD3	Chromodomain-helicase-DNA-binding protein 3	721	1.02
Q96HW7	INTS4	Integrator complex subunit 4	791	1.02
P04150	NR3C1	Glucocorticoid receptor	293	1.01
P08708	RPS17	40S ribosomal protein S17	103	1.01
Q14151	SAFB2	Scaffold attachment factor B2	225	1.01
Q92797	SYMPK	Symplekin	361	1.01
Q14978	NOLC1	Nucleolar and coiled-body phosphoprotein 1	663	1

Q9H307	PNN	Pinin	157	1
P46013	MKI67	Antigen KI-67	2852	0.99
Q12906	ILF3	Interleukin enhancer-binding factor 3	348	0.99
P05783	KRT18	Keratin, type I cytoskeletal 18	426	0.98
Q9ULH7	MKL2	MKL/myocardin-like protein 2	628	0.97
P49792	RANBP2	E3 SUMO-protein ligase RanBP2	1414	0.95
Q15424	SAFB	Scaffold attachment factor B1	578	0.95
Q9Y5B6	PAXBP1	GC-rich sequence DNA-binding factor 1	149	0.95
P26641	EEF1G	Elongation factor 1-gamma	253	0.94
P60709	ACTB	Actin, cytoplasmic 1	61	0.94
Q14978	NOLC1	Nucleolar and coiled-body phosphoprotein 1	193	0.94
Q14978	NOLC1	Nucleolar and coiled-body phosphoprotein 1	415	0.94
P62906	RPL10A	60S ribosomal protein L10a	118	0.93
P84098	RPL19	60S ribosomal protein L19	181	0.93
O95292	VAPB	Vesicle-associated membrane protein-associated protein B/C	147	0.92
Q04695	KRT17	Keratin, type I cytoskeletal 17	419	0.92
Q96T23	RSF1	Remodeling and spacing factor 1	294	0.92
P07355	ANXA2	Annexin A2	324	0.9
Q9UKD1	GMEB2	Glucocorticoid modulatory element-binding protein 2	155	0.9
P36578	RPL4	60S ribosomal protein L4	364	0.89
Q00839	HNRNPU	Heterogeneous nuclear ribonucleoprotein U	265	0.89
P05787	KRT8	Keratin, type II cytoskeletal 8	197	0.88
P21333	FLNA	Filamin-A	299	0.88
P27816	MAP4	Microtubule-associated protein 4	269	0.87
Q8WWQ0	PHIP	PH-interacting protein	1470	0.87
Q04695	KRT17	Keratin, type I cytoskeletal 17	400	0.85
P60174	TPI1	Triosephosphate isomerase	179	0.84
P07910	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	232	0.83
Q14244	MAP7	Ensconsin	406	0.8
P46100	ATRX	Transcriptional regulator ATRX	623	0.79
P08670	VIM	Vimentin	445	0.78
P78386	KRT85	Keratin, type II cuticular Hb5	229	0.78
Q14151	SAFB2	Scaffold attachment factor B2	65	0.78
P05787	KRT8	Keratin, type II cytoskeletal 8	101	0.77
Q04695	KRT17	Keratin, type I cytoskeletal 17	15	0.77
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	961	0.75
Q12904	AIMP1	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	137	0.75
Q96E09	FAM122A	Protein FAM122A	89	0.73
O00541	PES1	Pescadillo homolog	517	0.72
Q15061	WDR43	WD repeat-containing protein 43	309	0.71
Q6NZI2	PTRF	Polymerase I and transcript release factor	161	0.65
P11142	HSPA8	Heat shock cognate 71 kDa protein	512	0.64
Q04695	KRT17	Keratin, type I cytoskeletal 17	399	0.64
P05787	KRT8	Keratin, type II cytoskeletal 8	472	0.61
P05556	ITGB1	Integrin beta-1	794	0.55

**Table S4. Quantification of SUMOylation level of SUMO2-conjugated proteins in control versus LLO-treated cells.** Columns from left to right contain the Swiss-Prot accession number, HGNC symbol, protein name, position of the SUMO-conjugated lysine residue and normalized M/H ratio indicating the degree of deSUMOylation upon LLO treatment.

Swiss-Prot Acc.	HGNC symbol	Protein name	Modified K	M/H ratio (fold change)
P17028	ZNF24	Zinc finger protein 24	27	19.45
Q9H582	ZNF644	Zinc finger protein 644	346	18.82
O95365	ZBTB7A	Zinc finger and BTB domain-containing protein 7A	539	17.65
Q6NT76	HMBOX1	Homeobox-containing protein 1	413	10.97
Q6PCB5	RSBN1L	Round spermatid basic protein 1-like protein	763	10.94
P11388	TOP2A	DNA topoisomerase 2-alpha	1240	10.69
P55854	SUMO3	Small ubiquitin-related modifier 3	11	10.47
P11387	TOP1	DNA topoisomerase 1	117	10.09
P17275	JUNB	Transcription factor jun-B	240	9.5
Q6P4R8	NFRKB	Nuclear factor related to kappa-B-binding protein	488	8.87
Q9UHL9	GTF2IRD1	General transcription factor II-I repeat domain-containing protein 1	443	8.23
O95785	WIZ	Protein Wiz	1523	8.14
P05549	TFAP2A	Transcription factor AP-2-alpha	10	8.14
Q96T23	RSF1	Remodeling and spacing factor 1	456	7.62
O60885	BRD4	Bromodomain-containing protein 4	1111	6.47
Q8N3X1	FNBP4	Formin-binding protein 4	348	6.34
Q14980	NUMA1	Nuclear mitotic apparatus protein 1	1766	5.82
Q9UHF7	TRPS1	Zinc finger transcription factor Trps1	766	5.46
Q9UKV3	ACIN1	Apoptotic chromatin condensation inducer in the nucleus	268	5.33
Q02447	SP3	Transcription factor Sp3	551	5.05
P15408	FOSL2	Fos-related antigen 2	222	5.03
Q96RE7	NACC1	Nucleus accumbens-associated protein 1	167	5
P30414	NKTR	NK-tumor recognition protein	581	4.72
P09874	PARP1	Poly [ADP-ribose] polymerase 1	486	4.55
Q9UH73	EBF1	Transcription factor COE1	16	4.53
Q7Z5J4	RAI1	Retinoic acid-induced protein 1	901	4.49
P82970	HMG5	High mobility group nucleosome-binding domain-containing protein 5	101	4.44
Q92797	SYMPK	Symplekin	361	4.44
Q2TB10	ZNF800	Zinc finger protein 800	409	4.4
P37275	ZEB1	Zinc finger E-box-binding homeobox 1	493	4.37
Q9H0E9	BRD8	Bromodomain-containing protein 8	481	4.32
O43175	PHGDH	D-3-phosphoglycerate dehydrogenase	21	4.26
P19338	NCL	Nucleolin	297	4.19
O15164	TRIM24	Transcription intermediary factor 1-alpha	741	4.09
Q969G3	SMARCE1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	92	4.08
Q9ULJ3	ZBTB21	Zinc finger protein 295	879	3.95
Q9HC78	ZBTB20	Zinc finger and BTB domain-containing protein 20	330	3.92
O15164	TRIM24	Transcription intermediary factor 1-alpha	723	3.9
Q9UIG0	BAZ1B	Tyrosine-protein kinase BAZ1B	826	3.84
Q8TAD8	SNIP1	Smad nuclear-interacting protein 1	30	3.83
Q9UQR1	ZNF148	Zinc finger protein 148	356	3.83
P46013	MKI67	Antigen KI-67	2734	3.8
Q9H2Y7	ZNF106	Zinc finger protein 106	1737	3.79
P12004	PCNA	Proliferating cell nuclear antigen	164	3.77

 = M/H ratio > 4.0

Q8IX12	CCAR1	Cell division cycle and apoptosis regulator protein 1	1067	3.77
Q92766	RREB1	Ras-responsive element-binding protein 1	615	3.66
Q5VZL5	ZMYM4	Zinc finger MYM-type protein 4	273	3.57
Q14839	CHD4	Chromodomain-helicase-DNA-binding protein 4	1304	3.52
Q9UGU0	TCF20	Transcription factor 20	929	3.49
P78347	GTF2I	General transcription factor II-I	991	3.41
P17844	DDX5	Probable ATP-dependent RNA helicase DDX5	53	3.4
Q9UPN9	TRIM33	E3 ubiquitin-protein ligase TRIM33	776	3.28
Q9NX24	NHP2	H/ACA ribonucleoprotein complex subunit 2	5	3.18
Q13263	TRIM28	Transcription intermediary factor 1-beta	779	3.12
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	1563	3.09
Q13263	TRIM28	Transcription intermediary factor 1-beta	750	3.01
Q9ULJ3	ZBTB21	Zinc finger protein 295	40	3
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	217	2.95
Q13765	NACA	Nascent polypeptide-associated complex subunit alpha	100	2.94
Q14151	SAFB2	Scaffold attachment factor B2	225	2.89
P52565	ARHGDI1A	Rho GDP-dissociation inhibitor 1	138	2.76
Q5VZL5	ZMYM4	Zinc finger MYM-type protein 4	250	2.76
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	34	2.72
Q14151	SAFB2	Scaffold attachment factor B2	252	2.66
Q96T23	RSF1	Remodeling and spacing factor 1	294	2.66
Q86U86	PBRM1	Protein polybromo-1	1293	2.64
Q96T23	RSF1	Remodeling and spacing factor 1	277	2.54
Q8IX12	CCAR1	Cell division cycle and apoptosis regulator protein 1	1012	2.53
P46100	ATRX	Transcriptional regulator ATRX	623	2.51
P49790	NUP153	Nuclear pore complex protein Nup153	353	2.51
Q93009	USP7	Ubiquitin carboxyl-terminal hydrolase 7	869	2.51
Q00839	HNRNPU	Heterogeneous nuclear ribonucleoprotein U	265	2.47
Q13428	TCOF1	Treacle protein	755	2.47
P78347	GTF2I	General transcription factor II-I	221	2.41
P04150	NR3C1	Glucocorticoid receptor	293	2.39
Q5T8P6	RBM26	RNA-binding protein 26	106	2.37
Q14151	SAFB2	Scaffold attachment factor B2	293	2.36
P06748	NPM1	Nucleophosmin	257	2.34
Q9NVU0	POLR3E	DNA-directed RNA polymerase III subunit RPC5	498	2.33
O43290	SART1	U4/U6.U5 tri-snRNP-associated protein 1	141	2.3
Q9BUJ2	HNRNPUL1	Heterogeneous nuclear ribonucleoprotein U-like protein 1	117	2.26
Q14151	SAFB2	Scaffold attachment factor B2	230	2.24
P04843	RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	538	2.16
O00541	PES1	Pescadillo homolog	517	2.12
P52272	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	698	2.11
P55265	ADAR	Double-stranded RNA-specific adenosine deaminase	418	2.09
Q5PSV4	BRMS1L	Breast cancer metastasis-suppressor 1-like protein	246	2.08
Q12888	TP53BP1	Tumor suppressor p53-binding protein 1	1434	2.06
O76094	SRP72	Signal recognition particle 72 kDa protein	391	2.04
P46087	NOP2	Putative ribosomal RNA methyltransferase NOP2	615	2.02
Q9UPN9	TRIM33	E3 ubiquitin-protein ligase TRIM33	793	1.94
Q04695	KRT17	Keratin, type I cytoskeletal 17	15	1.92

P80723	BASP1	Brain acid soluble protein 1	163	1.89
P60709	ACTB	Actin, cytoplasmic 1	113	1.85
P04075	ALDOA	Fructose-bisphosphate aldolase A	42	1.84
P15259	PGAM2	Phosphoglycerate mutase 2	100	1.84
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	422	1.84
Q9Y4E5	ZNF451	Zinc finger protein 451	706	1.84
P06748	NPM1	Nucleophosmin	248	1.82
Q14151	SAFB2	Scaffold attachment factor B2	65	1.8
P02545	LMNA	Prelamin-A/C	597	1.77
O94916	NFAT5	Nuclear factor of activated T-cells 5	556	1.74
Q16649	NFIL3	Nuclear factor interleukin-3-regulated protein	219	1.74
Q8WWQ0	PHIP	PH-interacting protein	1470	1.73
Q9NVR2	INTS10	Integrator complex subunit 10	464	1.72
Q9Y2X3	NOP58	Nucleolar protein 58	467	1.7
O75533	SF3B1	Splicing factor 3B subunit 1	413	1.69
Q9Y2X3	NOP58	Nucleolar protein 58	465	1.65
P43487	RANBP1	Ran-specific GTPase-activating protein	190	1.6
Q9HAF1	MEAF6	Chromatin modification-related protein MEAF6	113	1.6
O43513	MED7	Mediator of RNA polymerase II transcription subunit 7	185	1.58
Q14149	MORC3	MORC family CW-type zinc finger protein 3	740	1.55
Q9NUU7	DDX19A	ATP-dependent RNA helicase DDX19A	26	1.54
P63279	UBE2I	SUMO-conjugating enzyme UBC9	49	1.5
Q9UKV3	ACIN1	Apoptotic chromatin condensation inducer in the nucleus	532	1.47
P05787	KRT8	Keratin, type II cytoskeletal 8	101	1.45
Q96HW7	INTS4	Integrator complex subunit 4	791	1.43
P05388	RPLP0	60S acidic ribosomal protein P0	297	1.42
Q96JG6	CCDC132	Coiled-coil domain-containing protein 132	963	1.42
P05787	KRT8	Keratin, type II cytoskeletal 8	285	1.41
Q9BVP2	GNL3	Guanine nucleotide-binding protein-like 3	99	1.41
P11021	HSPA5	78 kDa glucose-regulated protein	352	1.38
P52565	ARHGDI1	Rho GDP-dissociation inhibitor 1	141	1.37
P06748	NPM1	Nucleophosmin	32	1.35
Q9UBT2	UBA2	SUMO-activating enzyme subunit 2	164	1.35
Q9NYF8	BCLAF1	Bcl-2-associated transcription factor 1	580	1.34
Q07666	KHDRBS1	KH domain-containing, RNA-binding, signal transduction-associated protein 1	102	1.31
Q14103	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0	197	1.31
O15525	MAFG	Transcription factor MafG	14	1.3
P02545	LMNA	Prelamin-A/C	233	1.3
Q8NC51	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	228	1.3
P08195	SLC3A2	4F2 cell-surface antigen heavy chain	166	1.27
P21333	FLNA	Filamin-A	299	1.27
O43795	MYO1B	Unconventional myosin-Ib	287	1.25
P46060	RANGAP1	Ran GTPase-activating protein 1	524	1.24
Q9H307	PNN	Pinin	157	1.23
P15880	RPS2	40S ribosomal protein S2	275	1.22
Q9NYF8	BCLAF1	Bcl-2-associated transcription factor 1	831	1.22
P08729	KRT7	Keratin, type II cytoskeletal 7	130	1.2
P20700	LMNB1	Lamin-B1	241	1.18

P46777	RPL5	60S ribosomal protein L5	220	1.18
P60709	ACTB	Actin, cytoplasmic 1	326	1.18
Q14692	BMS1	Ribosome biogenesis protein BMS1 homolog	810	1.14
P05787	KRT8	Keratin, type II cytoskeletal 8	472	1.12
P62906	RPL10A	60S ribosomal protein L10a	118	1.12
Q2TB10	ZNF800	Zinc finger protein 800	132	1.07
P23396	RPS3	40S ribosomal protein S3	230	1.04
P05787	KRT8	Keratin, type II cytoskeletal 8	197	1.01
Q9Y3B9	RRP15	RRP15-like protein	239	1
Q96FV9	THOC1	THO complex subunit 1	595	0.98
P63220	RPS21	40S ribosomal protein S21	41	0.96
P13010	XRCC5	X-ray repair cross-complementing protein 5	568	0.95
Q04695	KRT17	Keratin, type I cytoskeletal 17	419	0.95
P07910	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	229	0.92
Q9Y2W1	THRAP3	Thyroid hormone receptor-associated protein 3	451	0.92
P49792	RANBP2	E3 SUMO-protein ligase RanBP2	2792	0.89
P07910	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	232	0.87
Q14244	MAP7	Ensconsin	406	0.87
O00232	PSMD12	26S proteasome non-ATPase regulatory subunit 12	92	0.86
Q04695	KRT17	Keratin, type I cytoskeletal 17	399	0.83
Q17R98	ZNF827	Zinc finger protein 827	673	0.82
P49368	CCT3	T-complex protein 1 subunit gamma	381	0.72
P49327	FASN	Fatty acid synthase	2449	0.71
Q6NZ12	PTRF	Polymerase I and transcript release factor	161	0.7
Q9H6U6	BCAS3	Breast carcinoma-amplified sequence 3	215	0.6
P08670	VIM	Vimentin	445	0.58
Q6NZ12	PTRF	Polymerase I and transcript release factor	170	0.54