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SILAC-based quantitative proteomic analysis of *Drosophila* gastrula stage embryos mutant for fibroblast growth factor signaling

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Abstract

Quantitative proteomic analyses in combination with genetics provide powerful tools in developmental cell signaling research. *Drosophila melanogaster* is one of the most widely used genetic models for studying development and disease. Here we combined quantitative proteomics with genetic selection to determine changes in the proteome upon depletion of Heartless (Htl) Fibroblast-Growth Factor (FGF) receptor signaling in *Drosophila* embryos at the gastrula stage. We present a robust, single generation SILAC (stable isotope labeling with amino acids in cell culture) protocol for labeling proteins in early embryos. For the selection of homozygously mutant embryos at the pre-gastrula stage we developed an independent genetic marker. Our analyses detected quantitative changes in the global proteome of *htl* mutant embryos during gastrulation. We identified distinct classes of downregulated and upregulated proteins, and network analyses indicate functionally related groups of proteins in each class. In addition, we identified changes in the abundance of phosphopeptides. In summary, our quantitative proteomic analysis reveals global changes in metabolic, nucleoplasmic, cytoskeletal and transport proteins in *htl* mutant embryos.

Introduction

Quantitative mass spectrometry-based proteomics have been implemented in studying levels of protein expression and protein modifications in various cell types, tissues and organisms for comparing diverse states, such as age, gender, drug treatments or various disease conditions. In 2002, the SILAC (stable isotope labeling with amino acids in cell culture) method was introduced as a tool for studying functional proteomics on a quantitative global scale[1]. SILAC-based mass spectrometry allows to directly compare populations of cells on the basis of differential signature labeling with stable isotopes. For example, one cell line grown on media containing the naturally predominant occurring amino acid is compared with cells grown on media containing a stable isotope-labeled form of that amino acid [2]. SILAC labeling has also proven successful for global quantitative proteomic comparisons of entire organisms including mammalian model systems[3]. Since then various multicellular model organisms were successfully labeled with stable, non-radioactive isotopes (SILAC or ^{15}N labeling) including the plant *Arabidopsis thaliana*, the nematode *Caenorhabditis elegans*, the insect *Drosophila melanogaster* and the mammal *Mus musculus*[4-13].

Drosophila melanogaster is one of the most widely studied genetically tractable model organism and has been employed for more than a century to advance our understanding in many areas in biology including genetics, developmental cell biology and signal transduction. Protocols for SILAC or ^{15}N labeling of *Drosophila* are based on feeding flies with yeast that has been labeled with stable isotopes[4, 9, 11]. Stable isotope labeling in flies has been used to determine sex-specific differences in the proteome of somatic cells[9], differences in the proteome during ageing[14], and differences in proteomes between adults, larvae and pupae[15, 16]. Recently, a quantitative proteomic study investigated the developmental profile of the *Drosophila* proteome throughout the life cycle using label-free approaches[15]. Proteome studies in embryos obtained from SILAC flies or using label-free methods also addressed proteome dynamics in early development like changes during the oocyte-to-egg transition (oocyte maturation), and the alterations that occur during the transition of the maternal to the zygotic transcriptional programs (maternal/zygotic transition)[8, 17, 18]. Despite the advances in quantitative proteomics and the plethora of mutations in developmental control genes, changes in the proteome of fly embryos homozygously mutant for a recessive developmental gene have not yet been performed due to technical difficulties in obtaining sufficient material.

In this study, we combined the power of *Drosophila* genetics with SILAC labeling to examine changes in the proteome when a major developmental signaling pathway is absent in the early embryo. The *Drosophila* gastrula stage embryo contains a relatively low cellular complexity, but the cells participate in major morphogenetic movements[19]. Most dramatically, the prospective mesoderm germ layer moves into the interior of the embryo, and undergoes an epithelial-to-mesenchymal transition (EMT), and collective cell migration. The latter two morphogenetic events are controlled by the activation of a fibroblast growth factor (FGF) receptor encoded by the *heartless* (*htl*) gene [20-26]. We employed *htl* loss-of-function mutations to investigate the effects of FGF receptor signaling in the context of an entire embryo. The response of mesoderm cells upon Htl receptor activation is rapid as the cells form protrusions and move towards the underlying ectoderm within the range of minutes [27]. Therefore, it has been suggested that initially the Htl signal affects posttranslational modifications and the turnover of proteins involved in cell movements rather than transcriptional responses [27, 28].

One major problem that has hampered the comparative analyses of proteomes from wild-type and mutant embryos was the selection of the homozygously mutant embryos, which make only 25% of the progeny from heterozygous parental animals. A possible solution to this problem would be provided by an independent phenotypic selection marker that can be readily dected early in development, ideally before the gene under investigation becomes active and its mutant phenotype becomes visible. Furthermore, the marker should not affect the viability of the embryo or the organism. In the present study, we used the *halo* mutation which allows the selection of homozygous mutant embryos in early developmental stages[29]. The *halo* mutation causes a readily visible defect in the transport of lipid droplets in early embryos, but does not affect viability and fertility of the organism [29, 30]. We present a protocol for efficient labeling of *Drosophila* embryos with stable non-radioactive isotopes in a single generation combined with genotyping and staging early embryos to discriminate between homozygous *htl* mutant embryos and *htl* heterozygous embryos. Quantitative global proteomic analysis of *htl* mutant embryos resulted in the discovery of protein networks that were down- or upregulated when compared to control embryos.

Methods

Drosophila strains

Fly stocks were kept under standard conditions. The stock containing the loss of function *halo*^{AJ} allele and a stock harboring a transgene with the *halo* genomic locus (*p[halo*$^{+}$*]*) were gifts of M.A. Welte (Univ. of Rochester, U.S.A.)[31, 32]. We used a chromosome harboring transposase *Δ2,3* under the control of a *hsp70* promoter to mobilize the *p[halo*$^{+}$*]* transposon insertion in the genome and isolated insertions on the autosomal balancer chromosomes TM3, TM6 and CyO. The loss-of-function *htl*^{AB42} allele was maintained over a TM6B, *Hu*, *Tb*, *e*, *p[halo*$^{+}$*]* balancer chromosome and crossed into a homozygous *halo*^{AJ} background.

SILAC labeling of *Saccharomyces cerevisiae*

Saccharomyces cerevisiae BY4742 colonies were allowed to grow for 2 days at 30°C. A single colony was inoculated into 5 ml DOA (Dropout) – no lysine media (synthetic complete) supplemented with 5 µl of heavy lysine (Lys-8; stock: 30 mg/ml) (L-lysine: 2HCl, U-$^{13}C_6$, 99%; U-$^{15}N_2$, 99%, Cambridge Isotope Laboratories, Inc.). The culture was incubated at 30°C for 24 hours. 5 µl of cell suspension was used to inoculate 5 ml of fresh media containing Lys-8 and was incubated for another 24 hours at 30°C in a shaking incubator. 1 ml of culture was used to inoculate 1 l of DOA media containing Lys-8. Incubation took place for another 24 hours at 30°C in a shaking incubator. 1 ml of the culture was saved for a label check and the remaining culture was pelleted by centrifugation. The yeast pellet was resuspended once in dH_2O and centrifuged; the supernatant was discarded and the Lys-8 – labeled yeast was stored at -80°C. Previous protocols used the lysine auxotrophic *S. cerevisiae* stock *SUB62* [9]. We found that the *SUB62* was insufficiently labeled in a Lys-8 containing medium with an average global SILAC ratio of 1.4 and below suggesting a maximum of 58.4 % Lys-8 label (Suppl. Mat. S1A,B). *SUB62* strain harbors the point mutation *lys2-801*, which was described as an amber mutation in the *lys2* gene and therefore is, in principle, revertible in particular when grown in large cultures. We found that in 1 l cultures the *SUB62* strain undergoes reversion to a lys prototrophic strain and that this effect appears to be enhanced in the presence of Lys-8 as a source (Suppl. Mat. S1). We therefore utilized the strain *BY4742* that carries the *lys2Δ0* mutation, which is a complete deletion of the *lys2* gene and does not undergo reversions[33]. The labeling effiency with *BY4742* was nearly complete exhibiting a global SILAC ratio of around 15 (Suppl. Mat. S1A,C).

SILAC labeling *of Drosophila melanogaster*

150 embryos were transferred onto a fresh apple juice agar plate supplemented with 300 µl of *BY4742* Lys-8 yeast and enclosed with a fly cage. Larvae were allowed to hatch and to feed on Lys-8 labeled yeast at 25°C. Once the larvae started to penetrate the apple juice agar dH_2O was supplemented according to humidity and evaporation to keep the apple juice agar/yeast mixture soft and moist. Pupae were gently transferred onto a fresh apple juice agar plate supplemented with a drop of *BY4742* Lys-8 yeast as food for the hatching SILAC flies. Control flies of the respective genotype were raised according to the same protocol except for using yeast grown on standard Lys-0 containing media.

Protein extraction from yeast

1 ml of Lys-8 *BY4742* culture was centrifuged, the supernatant was discarded and the yeast pellet was resuspended in 150 µl of 2 M NaOH, 1 M β-mercaptoethanol. 5 volumes of protein extract were supplemented with 1 volume of 20 % trichloracetic acid (TCA) and mixed by inversion. The mixture was incubated on ice for 10 minutes and subsequently centrifuged at 14000 rpm for 4 minutes at 4°C. The supernatant was removed, the pellet was washed with cold acetone and air dried. The pellet was resuspended in 8 M urea, 0.4 M ammonium bicarbonate and used for label check via mass spectrometry.

Embryo collection and protein lysis

The embryos were incubated on an agarose coated petri dish, covered with Halocarbon oil (27S; Sigma/Aldrich) and were staged under a dissection microscope in transmitted light. At the desired stages, embryos were dechorionated in 0.5% sodium hypochlorite solution and collected in microtubes (Protein LoBind tubes, Eppendorf), which were kept on dry ice. For lysis, RIPA buffer (50 mM Tris-HCl pH 8.0, 150 mM NaCl, 1 % NP40, 0.5 % Sodiumdesoxycholate, 0.1 % SDS) was supplemented with proteinase inhibitors (EDTA-free Protease Inhibitor Cocktail, cOmplete^{TM}, Roche) and phosphatase inhibitors (PhosSTOP, Roche). 100 µl of buffer was used for embryo lysis for each individual biological replicate. An equal number of embryos were homogenized with a bio-vortexer and incubated on ice for 20 minutes, followed by centrifugation at 14000 rpm for 10 minutes at 4°C. The supernatant was transferred into a fresh microtube and protein concentration was determined (Peptide and Protein Quantification Kit, LavaPep).

In-gel digestion

For each biological replicate, 40 µg of protein were run on SDS-PAGE (4-12% Bis Tris Nupage gels). Each lane was cut into 5 gel pieces for an in-gel digestion (Fig. 1C), and every individual piece was cut into smaller fragments that were rinsed with 100 µl 100 mM NH_4HCO_3 : 100% acetonitrile (ACN) for 10 minutes at room temperature in a shaking incubator. The solution was removed from the gel pieces and the washing step was repeated. 50 µl of 100% ACN were added until gel pieces formed an aggregate and turned white. 50 µl of 100 mM NH_4CO_3 were added and incubated at 37°C for 30 minutes, while shaking. The solution was removed, and gel pieces were dried in a vacuum centrifuge. 50 µl of 10 mM DTT were added and incubated at 55°C for 45 minutes. After removing DTT, 50 µl of 50 mM iodoacetamide solution was added and the gel pieces incubated for 30 minutes in the dark at room temperature. After removing the iodoacetamide solution, gel pieces were washed again twice with 100 µl 100 mM NH_4HCO_3 : 100% ACN for 10 minutes at room temperature in an shaking incubator. After removing the washing solution, gel pieces were dried in a vacuum centrifuge. In-gel digestion with the Lysyl endopeptidase (Lys-C) was performed overnight according to the manufacturers protocol (Lysyl Endopeptidase, Mass Spectrometry Grade, Fujifilm Wako Pure Chemical Corporation). After digestion, 20 µl of 0.1% trifluoroacetic acid (TFA) and 20 µl 100% ACN were added and the mixture sonicated in an ice water bath for 15 minutes. The supernatant was transferred into a new microtube and 100 µl 30% ACN : 0.1% were added to the gel pieces and sonicated in an ice water bath as before. The supernatant was transferred to previously collected supernatant, and 100 µl 50% ACN : 0.1% TFA were added to the gel pieces and handled as before. Pooled supernatant was finally vacuum centrifuged at 60°C to reduce the volume to approximately 100 µl. The peptides were further cleaned up with C18 columns using HPLC according to standard protocols (GRE support group University of Dundee, Scotland).

SCX chromatography

The peptide sample was reconstituted in 500 µl SCX loading/wash buffer (10 mM KH_2PO_4, 25% ACN, pH 3). SCX columns (Thermo Scientific Hypersep SCX; benzosulfonic acid, 25 mg/ml) were washed twice with 1 ml MilliQ water and were primed twice with 1 ml SCX priming/elution buffer (10 mM KH_2PO_4, 25% acetonitrile (ACN), 350 mM KCl, pH 3). The sample was loaded onto the column and pushed through slowly. Loaded columns were washed twice with 500 µl SCX wash buffer. Sample elution was achieved with 500 µl of SCX elution buffer and the eluate was cleaned up by reversed phase chromatography on a C18 column.

Phosphopeptide enrichment by TiO_2 binding

The unbound fraction of the SCX chromatography was subjected to phosphopeptide enrichment using affinity binding to TiO_2 beads. The TiO_2 beads were primed with 2x loading buffer (80% ACN, 2% TFA), 200 mg/ml 2,5-dihydroxy-benzoic acid, pH 2.0). the flow through of the SCX column was reduced to 100 µl by speed vacuum, resuspended in loading buffer and added to primed TiO_2 beads. After 1 h incubation at room temperature under agitation, beads were washed three times with 100 µl loading buffer, then washed three times with wash buffer (80% ACN, 2% TFA). Phosphopeptides were eluted from TiO_2 beads with 400 mM NH_4OH, pH 11.0. The eluate was purified by reversed phase chromatography on a C18 column before analysis by LC-MS/MS.

LC-MS/MS analysis

The peptide samples were run on a Thermo Fischer Orbitrap Velos Pro. They were separated on an Easy-Spray reversed chromatography C18 Column (ES803A, 75 μm, 500 mm). The LC temperature was 30° C, the LC conditions were from 2% B to 95% B over a 120 minute gradient (Solvent A: 0.1% Formic acid; Solvent B 80% ACN, 0.1% Formic acid). The flow rate was 200 nl/min. The fragmentation spectra were acquired at 2 Th precursor isolation width and a normalized collision energy of 35%. The resolution of the first MS run was 60,000 (scanning from 335-1800 m/z) and the top 15 ions selected for MS run 2 with a dynamic exclusion window of 30 seconds.

Data analysis

Raw MS data were analyzed with MaxQuant [34] version 1.5.2.8 and searched against the Uniprot *Drosophila* January 2016 database. The modifications used for L-lysine quantitations were: Lys-0: $^{12}C_6$, 99%; $^{14}N_2$, 99% (MW: 182.65); Lys-8: $^{13}C_6$, 99%; $^{15}N_2$, 99% (MW: 190.59). Default MaxQuant settings were used throughout with variable modifications set as Acetyl (Protein N-term); Oxidation (M); Deamidation (NQ); Gln->pyro-Glu; Phospho (STY) and fixed modifications set to Carbamidomethyl (C). Protein and peptide False Discovery Rate (FDR) cut offs were both set to 0.01, and a minimum peptide length was set to 7 amino acids. Only proteins with >1 peptide coverage were included in further analysis, with reversed and contaminant protein identifications removed. All quantified peptides were specified as the modified and unmodified versions. Statistical analysis was carried out with Perseus[35] and Microsoft Excel. Protein network analyses of down- and upregulated proteins were conducted with STRING version 10.5 (https://string-db.org/) [36]. The settings used for the STRING analyses were default settings including basic settings in which the network edges indicate the type of interaction evidence, and included text mining, experimental evidence, databases, co-expression, neighborhood, gene fusions or co-occurrence. The color code annotation for the edges is indicated in the figure legends. The minimum required interaction score was set on medium confidence (0.4) and the interactions were tested for the query proteins only. No clustering was applied and no enrichment analysis was performed.

Results

Generation of large quantities of SILAC flies

The aim of this study was to determine changes in the proteome of tightly staged gastrula embryos that are depleted of signaling through the FGF receptor Htl. The collection of tightly staged homozygous *htl* mutant embryos requires large quantities of heterozygous flies, because only a quarter of the embryos of this fly stock will be homozygous for the mutation. In addition, the time window for collecting the embryos at the gastrula stage only lasts about 15 min. The SILAC fly was described previously using protocols that reared flies on minimal media, e.g. Lys-8 labeled yeast on cotton wool with sucrose or low-melt agarose containing glucose for efficient labeling [9, 11]. In our hands, these procedures did not produce sufficient amounts of healthy flies; larvae developed initially normal and formed pupae, but many flies died before eclosion. In order to obtain healthy populations of SILAC flies that were required for collecting sufficient quantities of staged embryos, we set out to improve the labeling procedure (see methods). In particular, the substitution of low-melting agarose by apple juice agar did not compromise the labeling. This protocol produced large quantities of healthy Lys-8 labeled SILAC flies that produced embryos with >92% labeling efficiency (Fig. 1).

Identification of pre-gastrula stage *htl* mutant embryos

Before gastrulation commences, the *Drosophila* embryo consists of a monolayered epithelium, called blastoderm epithelium, that surrounds a central yolk cell [37, 38]. The mesoderm germ layer originates from the ventral domain of the blastoderm epithelium and is internalized in a process called mesoderm invagination. After invagination, the mesoderm cells spread out in mid gastrulation to form a single cell layer upon the basal surface of the neuroectoderm epithelium. This morphogenetic event, referred to as mesoderm spreading, is controlled by signaling through the FGF receptor Htl [20, 28]. Embryos heterozygously mutant for *htl* are viable, but homozygous *htl* mutant embryos exhibit severe mesoderm spreading defects and die during late embryogenesis [21-23]. To analyse changes in the proteome that are elicited by Htl FGF receptor signaling during mesoderm spreading, embryos mutant for *htl* should ideally be collected and compared to wild-type embryos at mid gastrula stages. However, it is impossible to discriminate *htl* homozygously mutant embryos from wild type embryos under the dissecting microscope at mid gastrulation, because the *htl* mutant phenotype cannot be identified at these stages. In order to overcome this problem, we made use of the *halo* mutation as an independent genetic selection marker.

Flies mutant for the zygotic locus *halo* are viable and fertile, but homozygous *halo* embryos exhibit a phenotype in the blastoderm embryo that can be readily scored under the dissecting microscope [30,32]. The *halo* gene is required for proper transport of lipid droplets from the periphery of the blastoderm embryo towards the central yolk cell leaving behind a rim of clear cytoplasm (Fig. 2A). In *halo* mutant embryos, clearing of the lipid droplets is blocked and the periphery of the embryo remains opaque due to persisting lipid droplets (Fig. 2B). The *halo* phenotype can be rescued by a transposon insertion containing the genomic *halo* sequence, called *p[halo$^+$]*[31]. We linked the *halo* rescue transgene *p[halo$^+$]* with the wild-type *htl* allele on balancer chromosomes. Balancer chromosomes are used to maintain recessive mutations in such a way that all inbred flies are heterozygous for the mutation and for the balancer chromosome. Thus, in a typical cross of heterozygous *htl* parents, one quarter of the embryos are homozygously mutant for the *htl* mutation and do not carry the balancer chromosome. In a *halo* mutant background, the *htl* mutant embryos will have lost the *p[halo$^+$]* balancer chromosome and therefore represent the only embryos that will show the *halo* phenotype (Fig. 2).

For each experiment, *halo* mutant embryos from the *halo^{AJ} ; htl^{AB42}* / TM6 *p[halo$^+$]* stock were first selected on the basis of their *halo* phenotype at the cellular blastoderm stage and then aged until mid gastrulation (stages 7/8; Fig.2). At mid gastrulation, the embryos were collected on dry ice to immediately stop development[39] (Fig. 2A',B'). We have chosen this developmental stage for the sampling, because we were interested to identify protein changes that are invovled in Htl-dependent mesoderm spreading [27]. Approximately 100 tightly staged embryos were collected this way to obtain 40 µg of total protein for each biological replicate. Because the *halo* mutation itself could have an effect on the global proteome, we labeled *halo^{AJ}* homozygous mutant embryos with Lys-8 as control sample for comparison with *halo^{AJ} ; htl^{AB42}* heterozygous embryos. Additionally, we compared Lys-8 labeled *halo^{AJ}* embryos with Lys-0 unlabeled *halo^{AJ}* embryos to identify false positive candidates, which might be caused by the stable-isotope labeling itself (see below).

SILAC-based quantitative proteomic analysis of *htl* mutants

Flies that were homozygously mutant for *halo^{AJ}* were labeled with Lys-8 as described in the methods section. We found that a single generation reared on Lys-8 labeled yeast was sufficient to produce isotope-labeled embryos. Such embryos showed robust incorporation of Lys-8 at a ratio of over 92% (Fig. 1D). The comparison of Lys-8 labeled embryos of *halo^{AJ}* mutants with Lys-0 unlabeled *halo* mutant embryos did not show any major changes in protein ratios indicating that the stable isotope labeling itself did not produce false positives (Fig. S2). For quantitative proteomic analysis, we collected late gastrula embryos from a Lys-8 labeled homozygous *halo^{AJ}*

; *htl*$^{+}$ stock and Lys-0 labeled homozygous *halo*^{AJ} ; *htl*^{AB42} embryos (Figs. 1,2). The protein lysates were mixed at equal protein concentrations such that 40 µg of total protein was size-separated on SDS-PAGE and digested by Lys C (Fig. 1). The resulting peptides were applied to SCX (strong cation exchange) chromatography for phospho-peptide enrichment. One aliquot in each biological replicate was kept as a reference for unenriched samples (see below). Both samples of each biological replicate were analysed by LC-MS/MS independently.

All experiments together detected a total number of 81.719 peptides including the comparison of the Lys-8 vs. Lys-0 labeled *halo*^{AJ} experiment. Using MaxQuant analysis these peptides were assigned to 2,131 proteins. All raw data and MaxQuant output tables are accessible in the Proteome Xchange repository PRIDE under accession number PXD016438. In between the three experimental replicates of the *htl*$^{\mathrm{AB42}}$ homozygous compared to wild-type control embryos 994 proteins were found in all three experiments and therefore were selected for further analysis. Single peptide protein identifications were excluded from our analyses. The average sequence coverage of these proteins was at 24.57% (STDEV: 15.92%). The overall changes in protein abundance was analyzed between embryos derived from *halo* control and *htl* mutant flies. The population histograms showed a positive correlation of the Lys-8 over Lys-0 labeled proteins, hereafter named (H, heavy)/(L, light) ratios, in all three bio replicates. This indicated that the majority of proteins did not significantly change in abundance between control and *htl* mutant embryos (Fig. 3A). The correlations of the three biological replicates with each other was tested in pairs by plotting the Log 2 ratios of heavy to light labeled proteins using Perseus [35]. Scatter plot analyses of the individual replicates to each other confirmed a positive relationship with Pearson correlation co-efficient values larger than 0.5, indicating a large correlation between the biological replicates (Fig. 3B).

Changes of protein abundance in *htl* mutant embryos

The positive correlation of the replicates provided a basis to determine changes in protein abundance that were consistent in all three experimental repeats. The median and standard deviations of the population distributions were calculated to determine the average cut-off values for up- and downregulated proteins within fold-change range of +/- 1.1. We found that 36 proteins were consistently downregulated in *htl* mutant embryos, whereas 25 proteins were consistently upregulated in all three biological replicates (Table 1, 2). We also detected six significant changes (two upregulated and four downregulated) in protein regulation when comparing Lys-8 labeled *halo* mutant embryos with Lys-0 unlabeled *halo* mutant embryos. These changes were scored to be false positives and were not considered in further analyses (Fig. S2B). The positive correlation between the three biological replicates allowed for the examination of statistically relevant changes in the protein abundances between control and htl^{AB42} mutant embryos. To consider both the degree of fold changes of proteins and the statistical significance (-logP value) of the change, we visualised the data using a Volcano plot (Fig. 4; Table 3).

To determine whether the up- or downregulated proteins shared any functional features, we performed STRING network analyses[36]. These analyses revealed that 31 of the downregulated proteins and 18 of the upregulated proteins were linked and belonged to networks for which STRING found independent evidence for interaction (see Material and Methods section for parameters and settings of STRING analyses). In *htl* mutant embryos the largest class of downregulated proteins was associated with chromatin (Fig. 5). Other downregulated proteins were found to occur in networks that included intracellular transport, mRNA binding/processing and translation. Interestingly, we found central components of the endomembrane transport machinery, including Clathrin heavy chain, Vps35, and the coatomer component COP1 alpha. In addition, we also found cytoskeletal components like Myosin heavy chain, Tubulin, the microtubule regulator Mini spindles and Dynein heavy chain 64C to be downregulated in *htl*^{AB42} mutant embryos (Table 1). To a smaller extent we detected downregulation of some metabolic and cytoskeletal components in *htl*^{AB42} embryos. In contrast to the downregulated proteins, the largest network detected to be upregulated in *htl*^{AB42} embryos is affecting metabolic pathways. Some proteins affecting chromatin and cytoskeletal networks were additionally found to be upregulated. A small number of proteins could not be assigned to particular networks (Figs. 5,6).

Analysis of Phosphopeptides

The responses of the mesoderm cells upon Htl FGF receptor activation involves the phosphoregulation of proteins in the cytoplasm (Muha and Muller, 2015). Therefore one aim of this study was to determine changes in the phosphorylation pattern of cellular proteins to further understand the mechanisms of how the Htl FGF receptor changes cell behaviors. In order to increase recovery of phosphopeptides we applied strong anion exchange chromatography (SCX) and in addition TiO_2 chromatography on the SCX unbound peptides. The SCX chromatography alone revealed a consistent enrichment of phosphopeptides and also exhibited highest level of consistency in between the different bioreplicates. 85% of all the multiply detected phosphopeptides in our experiments were enriched in the SCX fractions and only 3 additional phosphopeptides were detected in the SCX column-unbound fraction using TiO_2 affinity binding (Suppl. Mat. S3A,B). These results indicate that the SCX chromatography proved useful for enrichment of phosphopeptides in our experiments.

In total we identified 203 distinct phosphopeptides with phosphosites on Ser, Thr or Tyr in all bioreplicates, including the non-enriched samples (Suppl. Mat. S3A). 131 of these 203 phosphopeptides were single peptide detections and were therefore not considered any further. The remaining 72 phosphopeptides were detected more than once, with 42 phosphopeptides detected in at least two bioreplicates and 12 phosphopeptides detected in all 3 bioreplicates (Suppl. Mat. S3B). 7 of the 12 phosphopeptides that were found in all 3 bioreplicates were detected in the SCX-enriched samples, 3 were detected in the unenriched samples, while 2 were found in TiO_2 enriched fractions (Table 4). Among the 12 phosphopeptides found in all three bioreplicates, 9 phosphopeptides exhibited log2 values within a fold-change range of +/- 1.1. This analysis suggested that 8 phosphopeptides were downregulated and one phosphopeptide was upregulated in *htl* mutants (Table 4). The comparison to the heavy/light ratios levels of the respective proteins indicated that the changes in phosphopeptide levels were unlikely to be a consequence of changes in the overall protein levels (Table 4). Interestingly, three of the respective proteins, Garz, Spoon and Amun*,* are known to be involved in cell signaling[40-42]. One protein, ADF/cofilin encoded by the *twinstar* (*tsr*) gene, is a well characterized regulator of the actin cytoskeleton in cell migration[43]. Therefore we conclude that our experiments revealed candidates involved in Htl-dependent signaling events or might be the targets of such signaling events (Table 4).

Discussion

Although *Drosophila* is one of the most studied model organisms, it is somewhat surprising that quantitative proteomics have not been applied more extensively for the analyses of embryonic mutants [9, 11, 12]. One possible reason for this might relate to problems in growing healthy populations of flies that have incorporated stable non-radioactive isotopes. Furthermore, since *Drosophila* is routinely labeled with heavy L-lysine, peptides for mass spectrometric analysis are generated by lysyl-endopeptidase treatment. This endopeptidase is mandatory to ensure that all peptides contain at least one labeled amino acid. However, Lys8-labeled peptides are generally larger resulting in reduced sequence coverage compared to tryptic peptides, which arise from cleavage at lysine and arginine sites. Arginine is less useful for stable isotope labeling in *Drosophila*, because flies survive on an arginine deficient diet [44]. A further drawback in stable isotope labeling of amino acids in *Drosophila* is that both lysine and arginine can be metabolized into several other amino acids in the fly and this can affect the quantitation of the heavy and light ratios [16]. The use of lysine and arginine for stable isotope labeling could be improved by applying mutations that affect the metabolic pathways involved in arginine synthesis or pathways that convert lysine and arginine into other amino acids. Successful application of such mutants will allow the combined labeling of lysine and arginine and allow the use of trypsin which will improve the analyses and the quantitiation of the MS/MS data.

In this work, we were able to conduct a global proteomic analysis of embryos depleted for Htl FGF receptor signaling by combining genetics with a modified, more feasible and cost-efficient way of labeling *Drosophila* with stable non-radioactive heavy L-lysine. The SILAC fly was established previously, however unfortunately, we were not able to obtain large enough quantities of flies following these protocols confirming previous reports indicating growth retardation and low survival rates of larvae by replacing normal fly food with stable isotope labeled yeast [9, 11]. Here, we introduce a protocol that overcomes the decreased fitness of both larvae and flies, and that produces robustly labeled embryos in a single generation. We found that animals raised on apple juice agar supplied with the Lys-8 labeled yeast strain *BY4742,* were eclosing with expected ratios and appeared healthy. Our results suggest that low eclosing rates, as were observed using other protocols, might be due to the minimal food and lack of minerals and/or vitamins. We conclude that our protocol produces robustly labeled embryos while requiring only low amounts of labeled yeast, which together makes the SILAC fly an economically attractive approach.

Since we wanted to monitor the proteomic change in embryos depleted for FGF signaling during gastrulation stages, it was necessary to establish a reliable marker for the selection of embryos homozygous for the mutation in the FGF receptor Htl. Here we established a method using the *halo* mutation as a genetic marker, which is readily visible in transmitted light in living embryos [29]. Linking a transgenic *halo* rescue construct with a balancer chromosome allowed us to select *htl* homozygously mutant embryos before gastrulation by the presence of the *halo* phenotype. Other methods, like linking GFP to balancer chromosomes, do not provide a reliable signal-to-noise ratio for efficient selection in early embryos. *halo* has been previously used for early selection of homozygous mutations, but its use was restricted for genes located on the second chromosome [32]. The establishment of balancers containing the transgenic *p[halo$^+$]* in a *halo* mutant background opens the opportunity for the application of this technique to other experiments in order to genotype and select embryos homozygous for zygotic mutations before the actual phenotype occurs.

The *halo* linkage method was employed to collect tightly staged, homozygously *htl* mutant gastrula embryos for quantitative proteome analyses. By LC-MS/MS we compared unlabeled *htl* mutant embryos with stable isotope labeled *halo* embryos as control. Our data indicate that the lack of Htl FGF receptor signaling in the early embryo affects the abundance of proteins involved in the regulation of chromatin, nuclear transport, mRNA function, and endomembrane transport as well as the cytoskeleton. The majority of the upregulated proteins are related to various metabolic pathways including amino acid biosynthesis and carbohydrate metabolism.

As a classic receptor tyrosine kinase (RTK), the Htl FGF-receptor elicits its signaling activity by triggering phosphorylation cascades that transmit the signal by modifying other proteins, carbohydrates and lipids (Muha and Muller, 2015). The only protein previously known to be directly involved in RTK signaling and detected in our experiments was the *Drosophila* homolog of Importin 7, which is encoded by the gene *moleskin* (*msk*)[45]. Msk was previously shown to function in RTK signaling, including EGF signaling and FGF signaling[45], and found to mediate the nuclear transport of activated ERK in the EGF receptor pathway[46]. Our finding that depletion of Htl signaling causes a reduction in the level of Msk suggests that Htl signaling promotes the stabilisation of Msk protein levels. Interestingly, Msk has important functions beyond nuclear transport. A role of Msk in cell adhesion and in the activation of the small GTPase Rac has been reported and is particularly interesting in the light of our previous studies demonstrating a critical role for Rac GTPase signaling in Htl-dependent mesoderm spreading[45, 47, 48].

During gastrulation, Htl signaling is required for the control of the cell behavior in the mesoderm, but the molecular pathways that trigger these cellular changes are not well understood[28]. The proteins, which levels were reduced in embryos lacking Htl signaling may represent candidates for FGF-dependent signaling events involved in controlling these morphogenetic movements. These Htl-dependent cellular changes require the modification of cell interactions and the cytoskeleton. Consistent with this notion, we found that the levels of tubulin 67A, the microtubule plus-end-binding protein Mini spindles, the cytoplasmic dynein heavy chain 64C and non-muscle myosin heavy chain were all reduced in *htl* mutants. Another interesting group of candidates were proteins involved in intracellular transport including endomembrane transport (Clathrin heavy chain and COP1 alpha). These proteins are components of two distinct pathways. Clathrin mediates transport in the endosomal system, while COP1 alpha is involved in the secretory pathway and in the retrograde transport within the Golgi complex[49]. Binding of FGF ligands to their receptors stimulates Clathrin-dependent receptor endocytosis, which has been considered both as one mechanism of signal attenuation, but also as a mechanism of signal propagation[50]. COP1 alpha may also be indirectly involved in cell motility, as the assembly of the COP1 coatomer requires the small GTPase ARF1, which plays a role in protrusion formation during cell migration[51, 52].

A surprising finding was the reduction in *htl* mutants of proteins involved in nuclear transport (Moleskin, Artemis/Apollo1 [both RanGTP binding proteins], and Nup50). Nuclear transport of signaling proteins may play an important role in signal propagation during cell migration. A key factor in Htl-mediated mesoderm spreading is the Rho-guanine nucleotide exchange factor Pebble (Pbl)[25, 48, 53]. During interphase, Pbl is accumulated in the nucleus and a small amount of Pbl is localized at the cytocortex, where it is required to activate the small GTPase Rac for proper mesoderm spreading[25, 48]. We previously found that Pbl acts downstream of Htl, but the mechanism of this regulation by Htl is not understood[25]. One possibility would be that

Htl controls the nuclear transport or nuclear retainment of Pbl through components of the nuclear transport machinery. It will therefore be interesting to determine whether FGF signaling impacts on nuclear transport.

One initial aim of this study was to determine changes in the phosphorylation pattern of cellular proteins. However, the identification of phosphopeptides proved to be rather inefficient in our experimental setup, probably due to the low amount of peptides that could be applied to enrichment of phosphopeptides for SCX and TiO_2 chromatography. A single embryo only contains around 1 µg of protein, which requires to collect a large number of staged embryos for quantitative proteome analyses. To extend the global proteomic analysis of FGF receptor-depleted embryos towards the phosphoproteome will require the scaling up of each biological replicate by a factor of 20 in order to obtain enough material for enrichment of phosphopeptides using TiO_2 or Ti-IMAC [54, 55]. Alternatively, large-scale quantification of phosphorylated peptides can be also combined by the spike-in SILAC method [56, 57]. Nevertheless, the limited data of our phosphopeptide analyses suggested that in principle changes in interesting candidates in signaling events can be identified. Our detection of the reduced level of Serine 3 phosphorylation of Tsr, the *Drosophila* homolog of ADF/cofilin can be regarded as a proof of concept. Ser 3 phosphorylation of ADF/cofilin plays a evolutionary conserved role in the regulation of ADF/Cofilin during directional cell migration[58]. Strikingly, the phosphorylation of Ser 3 is dependent on Rac GTPase signaling downstream to PAK that phosphorylates LIM-Kinase, which in turn phosphorylates ADF/Cofilin on Ser 3 to promote F-actin remodelling [59]. Our discovery of changes in Tsr phosphorylation provides an excellent candidate pathway acting downstream of the Pbl/Rac GTPase activation downstream of the FGF receptor.

The discovery of changes in amounts of interesting proteins that fall into functionally related classes and changes in the levels of a limited number of phosphosites, represents a starting point for further functional analyses. The most important issue will be to determine the tissue-specificity of potential protein functions in Htl FGF receptor induced responses. *Drosophila* provides a rich resource to tackle this problem, for example by tissue-specific RNAi-mediated gene knock-down[60], expression of phosphosite mutant variants or tissue-specific protein knock-down[61].

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References

1. Ong, S. E.; Blagoev, B.; Kratchmarova, I.; Kristensen, D. B.; Steen, H.; Pandey, A.; Mann, M., Stable isotope labeling by amino acids in cell culture, SILAC, as a simple and accurate approach to expression proteomics. *Mol Cell Proteomics* **2002,** *1* (5), 376-86.
2. Chen, X.; Wei, S.; Ji, Y.; Guo, X.; Yang, F., Quantitative proteomics using SILAC: Principles, applications, and developments. *Proteomics* **2015,** *15* (18), 3175-92.
3. Zanivan, S.; Krueger, M.; Mann, M., In vivo quantitative proteomics: the SILAC mouse. *Methods Mol Biol* **2012,** *757*, 435-50.
4. Krijgsveld, J.; Ketting, R. F.; Mahmoudi, T.; Johansen, J.; Artal-Sanz, M.; Verrijzer, C. P.; Plasterk, R. H.; Heck, A. J., Metabolic labeling of C. elegans and D. melanogaster for quantitative proteomics. *Nat Biotechnol* **2003,** *21* (8), 927-31.
5. Larance, M.; Bailly, A. P.; Pourkarimi, E.; Hay, R. T.; Buchanan, G.; Coulthurst, S.; Xirodimas, D. P.; Gartner, A.; Lamond, A. I., Stable-isotope labeling with amino acids in nematodes. *Nat Methods* **2011,** *8* (10), 849-51.
6. Westman-Brinkmalm, A.; Abramsson, A.; Pannee, J.; Gang, C.; Gustavsson, M. K.; von Otter, M.; Blennow, K.; Brinkmalm, G.; Heumann, H.; Zetterberg, H., SILAC zebrafish for quantitative analysis of protein turnover and tissue regeneration. *J Proteomics* **2011,** *75* (2), 425-34.
7. Gouw, J. W.; Krijgsveld, J.; Heck, A. J., Quantitative proteomics by metabolic labeling of model organisms. *Mol Cell Proteomics* **2010,** *9* (1), 11-24.
8. Gouw, J. W.; Pinkse, M. W.; Vos, H. R.; Moshkin, Y.; Verrijzer, C. P.; Heck, A. J.; Krijgsveld, J., In vivo stable isotope labeling of fruit flies reveals post-transcriptional regulation in the maternal-to-zygotic transition. *Mol Cell Proteomics* **2009,** *8* (7), 1566-78.
9. Sury, M. D.; Chen, J. X.; Selbach, M., The SILAC fly allows for accurate protein quantification in vivo. *Mol Cell Proteomics* **2010,** *9* (10), 2173-83.
10. Sury, M. D.; Chen, J. X.; Selbach, M., In vivo stable isotope labeling by amino acids in Drosophila melanogaster. *Methods Mol Biol* **2014,** *1188*, 85-93.
11. Xu, P.; Tan, H.; Duong, D. M.; Yang, Y.; Kupsco, J.; Moberg, K. H.; Li, H.; Jin, P.; Peng, J., Stable isotope labeling with amino acids in Drosophila for quantifying proteins and modifications. *J Proteome Res* **2012,** *11* (9), 4403-12.
12. Sabino, D.; Gogendeau, D.; Gambarotto, D.; Nano, M.; Pennetier, C.; Dingli, F.; Arras, G.; Loew, D.; Basto, R., Moesin is a major regulator of centrosome behavior in epithelial cells with extra centrosomes. *Curr Biol* **2015,** *25* (7), 879-89.
13. Gruhler, A.; Schulze, W. X.; Matthiesen, R.; Mann, M.; Jensen, O. N., Stable isotope labeling of Arabidopsis thaliana cells and quantitative proteomics by mass spectrometry. *Mol Cell Proteomics* **2005,** *4* (11), 1697-709.
14. Xing, X.; Zhang, C.; Li, N.; Zhai, L.; Zhu, Y.; Yang, X.; Xu, P., Qualitative and quantitative analysis of the adult Drosophila melanogaster proteome. *Proteomics* **2014,** *14* (2-3), 286-90.
15. Casas-Vila, N.; Bluhm, A.; Sayols, S.; Dinges, N.; Dejung, M.; Altenhein, T.; Kappei, D.; Altenhein, B.; Roignant, J. Y.; Butter, F., The developmental proteome of Drosophila melanogaster. *Genome Res* **2017,** *27* (7), 1273-1285.
16. Chang, Y. C.; Tang, H. W.; Liang, S. Y.; Pu, T. H.; Meng, T. C.; Khoo, K. H.; Chen, G. C., Evaluation of Drosophila metabolic labeling strategies for in vivo quantitative proteomic analyses with applications to early pupa formation and amino acid starvation. *J Proteome Res* **2013,** *12* (5), 2138-50.
17. Fabre, B.; Korona, D.; Groen, A.; Vowinckel, J.; Gatto, L.; Deery, M. J.; Ralser, M.; Russell, S.; Lilley, K. S., Analysis of Drosophila melanogaster proteome dynamics during embryonic development by a combination of label-free proteomics approaches. *Proteomics* **2016,** *16* (15-16), 2068-80.
18. Kronja, I.; Whitfield, Z. J.; Yuan, B.; Dzeyk, K.; Kirkpatrick, J.; Krijgsveld, J.; Orr-Weaver, T. L., Quantitative proteomics reveals the dynamics of protein changes during Drosophila oocyte maturation and the oocyte-to-embryo transition. *Proc Natl Acad Sci U S A* **2014,** *111* (45), 16023-8.

19. Costa, M., Sweeton, D. Wieschaus, E. , Gastrulation in Drosophila: Cellular Mechanisms of Morphogenetic Movements. In *the Development of Drosophila melanogaster*, Bate, M., Martinez-Arias, A., Ed. Cold Spring Harbour Laboratory Press: United States, 1993; Vol. 1, pp 425-465.

20. Muha, V.; Muller, H. A., Functions and Mechanisms of Fibroblast Growth Factor (FGF) Signalling in Drosophila melanogaster. *Int J Mol Sci* **2013,** *14* (3), 5920-37.

21. Gisselbrecht, S.; Skeath, J. B.; Doe, C. Q.; Michelson, A. M., heartless encodes a fibroblast growth factor receptor (DFR1/DFGF-R2) involved in the directional migration of early mesodermal cells in the Drosophila embryo. *Genes Dev* **1996,** *10* (23), 3003-17.

22. Shishido, E.; Ono, N.; Kojima, T.; Saigo, K., Requirements of DFR1/Heartless, a mesoderm-specific Drosophila FGF-receptor, for the formation of heart, visceral and somatic muscles, and ensheathing of longitudinal axon tracts in CNS. *Development* **1997,** *124* (11), 2119-28.

23. Beiman, M.; Shilo, B. Z.; Volk, T., Heartless, a Drosophila FGF receptor homolog, is essential for cell migration and establishment of several mesodermal lineages. *Genes Dev* **1996,** *10* (23), 2993-3002.

24. Gryzik, T.; Muller, H. A., FGF8-like1 and FGF8-like2 encode putative ligands of the FGF receptor Htl and are required for mesoderm migration in the Drosophila gastrula. *Curr Biol* **2004,** *14* (8), 659-67.

25. Schumacher, S.; Gryzik, T.; Tannebaum, S.; Muller, H. A., The RhoGEF Pebble is required for cell shape changes during cell migration triggered by the Drosophila FGF receptor Heartless. *Development* **2004,** *131* (11), 2631-40.

26. Stathopoulos, A.; Tam, B.; Ronshaugen, M.; Frasch, M.; Levine, M., pyramus and thisbe: FGF genes that pattern the mesoderm of Drosophila embryos. *Genes Dev* **2004,** *18* (6), 687-99.

27. Clark, I. B.; Muha, V.; Klingseisen, A.; Leptin, M.; Muller, H. A., Fibroblast growth factor signalling controls successive cell behaviours during mesoderm layer formation in Drosophila. *Development* **2011,** *138* (13), 2705-15.

28. Winklbauer, R.; Muller, H. A., Mesoderm layer formation in Xenopus and Drosophila gastrulation. *Phys Biol* **2011,** *8* (4), 045001.

29. Gross, S. P.; Guo, Y.; Martinez, J. E.; Welte, M. A., A determinant for directionality of organelle transport in Drosophila embryos. *Curr Biol* **2003,** *13* (19), 1660-8.

30. Merrill, P. T.; Sweeton, D.; Wieschaus, E., Requirements for autosomal gene activity during precellular stages of Drosophila melanogaster. *Development* **1988,** *104* (3), 495-509.

31. Arora, G. K.; Tran, S. L.; Rizzo, N.; Jain, A.; Welte, M. A., Temporal control of bidirectional lipid-droplet motion in Drosophila depends on the ratio of kinesin-1 and its co-factor Halo. *J Cell Sci* **2016,** *129* (7), 1416-28.

32. Rembold, M.; Ciglar, L.; Yanez-Cuna, J. O.; Zinzen, R. P.; Girardot, C.; Jain, A.; Welte, M. A.; Stark, A.; Leptin, M.; Furlong, E. E., A conserved role for Snail as a potentiator of active transcription. *Genes Dev* **2014,** *28* (2), 167-81.

33. Brachmann, C. B.; Davies, A.; Cost, G. J.; Caputo, E.; Li, J.; Hieter, P.; Boeke, J. D., Designer deletion strains derived from Saccharomyces cerevisiae S288C: a useful set of strains and plasmids for PCR-mediated gene disruption and other applications. *Yeast* **1998,** *14* (2), 115-32.

34. Cox, J.; Mann, M., MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. *Nat Biotechnol* **2008,** *26* (12), 1367-72.

35. Tyanova, S.; Temu, T.; Sinitcyn, P.; Carlson, A.; Hein, M. Y.; Geiger, T.; Mann, M.; Cox, J., The Perseus computational platform for comprehensive analysis of (prote)omics data. *Nat Methods* **2016,** *13* (9), 731-40.

36. von Mering, C.; Huynen, M.; Jaeggi, D.; Schmidt, S.; Bork, P.; Snel, B., STRING: a database of predicted functional associations between proteins. *Nucleic Acids Res* **2003,** *31* (1), 258-61.

37. Muller, H. A., Of mice, frogs and flies: generation of membrane asymmetries in early development. *Dev Growth Differ* **2001,** *43* (4), 327-42.

38. Schmidt, A.; Grosshans, J., Dynamics of cortical domains in early Drosophila development. *J Cell Sci* **2018,** *131* (7).

39. Wieschaus, E.; Nüsslein-Volhard, C., Looking at Embryos. In *Drosophila: A Practical Approach*, 2nd Edition ed.; Roberts, D. B., Ed. Oxford University Press: United States, 1998; pp 179-213.

40. Shalaby, N. A.; Parks, A. L.; Morreale, E. J.; Osswalt, M. C.; Pfau, K. M.; Pierce, E. L.; Muskavitch, M. A., A screen for modifiers of notch signaling uncovers Amun, a protein with a critical role in sensory organ development. *Genetics* **2009,** *182* (4), 1061-76.

41. Szul, T.; Burgess, J.; Jeon, M.; Zinn, K.; Marques, G.; Brill, J. A.; Sztul, E., The Garz Sec7 domain guanine nucleotide exchange factor for Arf regulates salivary gland development in Drosophila. *Cell Logist* **2011,** *1* (2), 69-76.

42. Hadad, M.; Bresler-Musikant, T.; Neuman-Silberberg, F. S., Drosophila spoonbill encodes a dual-specificity A-kinase anchor protein essential for oogenesis. *Mech Dev* **2011,** *128* (7-10), 471-82.

43. Chen, J.; Godt, D.; Gunsalus, K.; Kiss, I.; Goldberg, M.; Laski, F. A., Cofilin/ADF is required for cell motility during Drosophila ovary development and oogenesis. *Nat Cell Biol* **2001,** *3* (2), 204-9.

44. Sang, J. H.; King, R. C., Nutritional requirements of axenically cultured Drosophila melanogaster adults. *J Exp Biol* **1961,** *38*, 793-809.

45. Lorenzen, J. A.; Baker, S. E.; Denhez, F.; Melnick, M. B.; Brower, D. L.; Perkins, L. A., Nuclear import of activated D-ERK by DIM-7, an importin family member encoded by the gene moleskin. *Development* **2001,** *128* (8), 1403-14.

46. Johnson Hamlet, M. R.; Perkins, L. A., Analysis of corkscrew signaling in the Drosophila epidermal growth factor receptor pathway during myogenesis. *Genetics* **2001,** *159* (3), 1073-87.

47. Liu, Z. C.; Odell, N.; Geisbrecht, E. R., Drosophila importin-7 functions upstream of the Elmo signaling module to mediate the formation and stability of muscle attachments. *J Cell Sci* **2013,** *126* (Pt 22), 5210-23.

48. van Impel, A.; Schumacher, S.; Draga, M.; Herz, H. M.; Grosshans, J.; Muller, H. A., Regulation of the Rac GTPase pathway by the multifunctional Rho GEF Pebble is essential for mesoderm migration in the Drosophila gastrula. *Development* **2009,** *136* (5), 813-22.

49. Nickel, W.; Brugger, B.; Wieland, F. T., Vesicular transport: the core machinery of COPI recruitment and budding. *J Cell Sci* **2002,** *115* (Pt 16), 3235-40.

50. Auciello, G.; Cunningham, D. L.; Tatar, T.; Heath, J. K.; Rappoport, J. Z., Regulation of fibroblast growth factor receptor signalling and trafficking by Src and Eps8. *J Cell Sci* **2013,** *126* (Pt 2), 613-24.

51. Humphreys, D.; Liu, T.; Davidson, A. C.; Hume, P. J.; Koronakis, V., The Drosophila Arf1 homologue Arf79F is essential for lamellipodium formation. *J Cell Sci* **2012,** *125* (Pt 23), 5630-5.

52. West, J. J.; Zulueta-Coarasa, T.; Maier, J. A.; Lee, D. M.; Bruce, A. E. E.; Fernandez-Gonzalez, R.; Harris, T. J. C., An Actomyosin-Arf-GEF Negative Feedback Loop for Tissue Elongation under Stress. *Curr Biol* **2017,** *27* (15), 2260-2270 e5.

53. Smallhorn, M.; Murray, M. J.; Saint, R., The epithelial-mesenchymal transition of the Drosophila mesoderm requires the Rho GTP exchange factor Pebble. *Development* **2004,** *131* (11), 2641-51.

54. Neville, D. C.; Rozanas, C. R.; Price, E. M.; Gruis, D. B.; Verkman, A. S.; Townsend, R. R., Evidence for phosphorylation of serine 753 in CFTR using a novel metal-ion affinity resin and matrix-assisted laser desorption mass spectrometry. *Protein Sci* **1997,** *6* (11), 2436-45.

55. Pinkse, M. W.; Uitto, P. M.; Hilhorst, M. J.; Ooms, B.; Heck, A. J., Selective isolation at the femtomole level of phosphopeptides from proteolytic digests using 2D-NanoLC-ESI-MS/MS and titanium oxide precolumns. *Anal Chem* **2004,** *76* (14), 3935-43.

56. Geiger, T.; Wisniewski, J. R.; Cox, J.; Zanivan, S.; Kruger, M.; Ishihama, Y.; Mann, M., Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. *Nat Protoc* **2011,** *6* (2), 147-57.

57. Monetti, M.; Nagaraj, N.; Sharma, K.; Mann, M., Large-scale phosphosite quantification in tissues by a spike-in SILAC method. *Nat Methods* **2011,** *8* (8), 655-8.

58. Zhang, L.; Luo, J.; Wan, P.; Wu, J.; Laski, F.; Chen, J., Regulation of cofilin phosphorylation and asymmetry in collective cell migration during morphogenesis. *Development* **2011,** *138* (3), 455-64.

59. Bamburg, J. R., Proteins of the ADF/cofilin family: essential regulators of actin dynamics. *Annu Rev Cell Dev Biol* **1999,** *15*, 185-230.

60. Kaya-Copur, A.; Schnorrer, F., A Guide to Genome-Wide In Vivo RNAi Applications in Drosophila. *Methods Mol Biol* **2016,** *1478*, 117-143.

61. Caussinus, E.; Affolter, M., deGradFP: A System to Knockdown GFP-Tagged Proteins. *Methods Mol Biol* **2016,** *1478*, 177-187.

Figures legends:

Figure 1: SILAC workflow using *Drosophila* embryos

(A) *Drosophila melanogaster* flies were grown on media containing Lys-0 or Lys-8 labeled yeast, respectively, and embryos were collected in microtubes on dry ice. After embryo lysis equal amounts of protein were mixed and separated via SDS-PAGE. Then ‘in-gel' digestions with Lys C endopeptidase were performed using 5 different SDS PAGE Gel slices per sample (indicated by red lines in C). The major fraction of the resulting peptides were applied to an SCX column. In addition, aliquots were kept before SCX enrichment as a reference. The SCX flow through was subjected to TiO_2 chromatography. The SCX fractions, TiO_2-bound peptides and the unenriched samples were run on a *LC-MS/MS Velo Orbitrap* instrument and data analyses were carried out using MaxQuant and Perseus. **(B)** *Drosophila* embryos were genotyped in cellular blastoderm stages as described below (see Fig. 2) and collected in mid-gastrula stages (early stage 8; anterior is left, dorsal up). **(C)** The 3 biological replicates (B1-B3) and a Lys-8 *halo*$^{AJ-/-}$ / Lys-0 *halo*$^{AJ-/-}$ comparison are shown after SDS-PAGE and Coomassie staining. Red lines indicate separation of the sample lines for further preparation. **(D)** Rearing *halo*^{AJ} embryos on Lys-8 containing yeast leads to heavy flies that produce embryos with a Lys-8 incorporation of > 92%.

Figure 2: *halo* as a selection marker for the identification of *htl* mutant embryos

Brightfield images of living embryos from the inbred line *w*^{1118} ; *halo*^{AJ}/*halo*^{AJ} ; *htl*^{AB42},*e*/*Tm6*,*e*,*Hu*,*Tb*, p[*halo*$^{+}$]. The *halo* gene is located on the second chromosome and the *htl* gene is located on the third chromosome. The genomic region containing the *halo* gene was inserted onto the Tm6 balancer chromosome. (**A**) Embryo at the cellular blastoderm stage exhibits a rim of clear cytoplasm due to clearing of lipid droplets. (**B**) Embryos mutant for *halo*^{AJ} develop an opaque ring in cellular blastoderm stages due to defect in clearing of lipid droplets. (**A**) The *halo*^{AJ} mutant phenotype is fully rescued by the TM6 *p[halo*$^{+}$*]* balancer chromosome. *htl*^{AB42} embryos were therefore identified by the *halo*^{AJ} phenotype, which indicates the absence of the balancer chromosome. The *halo* phenotype is only detectable during stage 5 of embryogenesis and disappears once gastrulation has started (**B'**). Homozygous *halo* mutant embryos were selected at cellular blastoderm stages and transferred to a fresh apple juice plate on which they were aged to mid gastrulation (stage 7/8) (A',B') and then frozen on dry ice.

Figure 3: Population statistics of *htl*^{AB42} embryos

(A) The distribution of the Lys-8 (H) over Lys-0 (L) protein ratios were found to be centered around 0 in all three biological replicates. The upper panel shows H/L ratios of unenriched sample sets (from aliquots taken before SCX enrichment) and the lower panel H/L ratios after the respective SCX chromatography. H/L protein ratios represent normalized values. **(B)** Scatter plots to indicate the correlation of the individual biological replicates to each other with Pearson correlation co-efficients larger than 0.5. The scatter plots on the left hand side represent the correlation of the unenriched data sets (before SCX chromatography); the right hand panels show the correlation between the bioreplicates after SCX enrichment. The fine lines within the scatter plots indicate the position of the perfect XY distribution of the two populations.

Figure 4: Changes in the proteome of Htl receptor deficient embryos

Vulcano plot depicting the quantification of proteome changes of *htl* mutant embryos during gastrulation. Relative fold changes are depicted as log2 averaged SILAC ratios of all three biological replicates and were plotted against the -log10 t-test p-value. Up- and downregulated proteins are indicated with cut-offs +/-1. One particular candidate (Q9VDT1, Arc42) was also identified as downregulated when comparing Lys-8 *halo* vs. Lys-0 *halo* mutants and thus considered as false positive.

Figure 5: String analysis of downregulated proteins

Summary view of the network of downregulated proteins in embryos lacking the Htl signaling pathway during gastrulation. The network analysis indicates the downregulation of proteins that are associated with chromatin, nuclear transport, the binding or processing of mRNA, and translation. Central components of the cytoskeleton, such as Myosin heavy chain, Tubulin, the microtubule regulating protein Mini spindles and Dynein heavy chain 64C, are also downregulated when Htl FGF signaling is depleted. A few downregulated components belong to metabolic and cytoskeletal pathways but could not be assigned to any particular network in *htl* mutant embryos. The connecting lines indicate the source of evidence for the interactions in the following color code: known interactions: turquoise - from curated databases, - magenta - experimentally determined; predicted interactions: green - gene neighborhood, red - gene fusions, blue - gene co-occurrence; others: yellow green - textmining, black - co-expression, purple - protein homology.

Figure 6: String analysis of upregulated proteins

Summary view depicting the network of upregulated proteins in embryos lacking Htl FGF signaling. Most of the identified upregulated proteins were assigned to metabolic pathways, whereas some proteins belong to chromatin and cytoskeletal networks. A few candidates were not assigned to any particular network. The connecting lines indicate the source of evidence for the interactions in the following color code: known interactions: turquoise - from curated databases, - magenta - experimentally determined; predicted interactions: green - gene neighborhood, red - gene fusions, blue - gene co-occurrence; others: yellow green - textmining, black - co-expression, purple - protein homology.

Supplemental Material:

Suppl. Mat. S1: Incorporation of Lys-8 in yeast *SUB62 vs. BY4742* strains

(**A,B**) Label check on *SUB62* grown in 1l Lys-8 containing culture. Global peptide ratios (**A**) and representative spectra (**B**) from *SUB62* grown to saturation in 1l Lys-8 culture. An average global SILAC ratio **(A)** of 0.980 indicates incomplete SILAC labeling of *SUB62*. (**B**) representative spectra of FALGQGVGVILCIGETLEEK peptide from Triosephosphate isomerase, with a calculated SILAC ratio of 1.110. (**A,C**) Label check on *BY4742* grown in 1l Lys-8 culture. Global peptide ratios (**A**) and representative spectra (**C**) from *BY4742* grown to saturation in 1l culture supplemented with Lys-8. An average global SILAC ratio **(A)** of 14.912 indicated complete SILAC labeling of *BY4742.* (**C**) Representative spectra of SRSGVAVADESLTAFNDLK peptide from COF1p, with a calculated SILAC ratio of 15.585. (**D**) Comparison of the growth rates of the *SUB62* and the *BY4742* strains. Growth of *SUB62* (**D'**) and *BY4742* (**D''**) strains on complete media plates (left panels, respectively) and complete media plates lacking lysine (right panels, respectively). **(D')** Growth of *SUB62* on plates lacking lysine was observed after growth in 1l culture, but not when plated from frozen stock. (**D''**) *BY4742* did not grow on plates lacking lysine when plated from either frozen stock or from 1l culture.

Suppl. Mat. S2: Comparison of Lys-8 labeled *halo*^{AJ} with Lys-0 unlabeled *halo*^{AJ} embryos. (A) The distribution of the Lys-8 (H) over Lys-0 (L) protein ratios were found to be centered around 0, when comparing Lys-8 vs. Lys-0 labeled *halo*^{AJ} mutants. The upper panel shows H/L ratios of unenriched sample sets (from aliquots drawn before SCX enrichment) and the lower panel H/L ratios after the respective SCX chromatography. H/L protein ratios represent log2 normalized values. (**B**) Proteins that were found downregulated or upregulated when comparing Lys-8 vs. Lys-0 labeled *halo*^{AJ} mutants. Note that all changes were under the cut-off of 1.1 log2 H/L ratios.

Suppl. Mat. S3: List of Phosphopeptides

(**A**) MaxQuant derived evidence file of all phosphopeptides detected in the experiments. (**B**) Extraction of the MaxQuant derived evidence file showing phosphopeptides that were detected in at least 2 biological replicates.

Table 1: Proteins downregulated in homozygous *htl* mutant embryos

proteins	H/L	STDEV
DNA topoisomerase 2	-2.15	0.76
Clathrin heavy chain	-2.04	0.71
Enhancer of mRNA-decapping protein 4 homolog	-1.86	0.50
Dynein heavy chain, cytoplasmic	-1.76	0.56
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A,DEAD/H box 1 homolog	-1.73	0.55
Myosin heavy chain, non-muscle	-1.73	0.50
CG8108	-1.70	0.36
Chromodomain-helicase-DNA-binding protein Mi-2 homolog	-1.62	0.42
Nuclear cap-binding protein subunit 1	-1.49	0.47
Polycomb protein l(1)G0020	-1.46	0.35
Coatomer subunit alpha	-1.42	0.49
Structural maintenance of chromosomes protein	-1.40	0.49
Probable ubiquitin carboxyl-terminal hydrolase FAF	-1.39	0.46
Cullin-associated NEDD8-dissociated protein 1	-1.38	0.45
Bifunctional glutamate/proline--tRNA ligase	-1.36	0.56
Eukaryotic translation initiation factor 3 subunit A	-1.34	0.25
ADP,ATP carrier protein	-1.30	0.27
Apollo; Artemis	-1.30	0.18
Isoleucyl-tRNA synthetase	-1.27	0.45
FACT complex subunit Ssrp1	-1.25	0.27
Mms19	-1.21	0.31
Nucleoporin 50kD	-1.21	0.36
Tailor	-1.21	0.46
Cullin homolog 1	-1.20	0.37
Tubulin alpha-4 chain	-1.18	0.49
Spenito	-1.17	0.28
NAT1	-1.17	0.33
mini spindles	-1.16	0.40
Probable glutamine--tRNA ligase	-1.16	0.19
Eukaryotic translation initiation factor 4G1	-1.14	0.19
Eukaryotic translation initiation factor 3 subunit L	-1.14	0.31
Eukaryotic translation initiation factor 3 subunit E	-1.12	0.44
Glutathione S-transferase 1-1	-1.04	0.08
Eukaryotic translation initiation factor 3 subunit B	-1.02	0.23
Probable 26S proteasome non-ATPase regulatory subunit 3	-0.99	0.24
Apolipophorins;Apolipophorin-2;Apolipophorin-1	-0.93	0.16

36 proteins were identified to be downregulated in *htl*^{AB42} embryos during late stage 7. Normalized H/L ratios are shown for each individual downregulated protein in average calculated from the values of the 3 individual biological replicates. The standard deviation denotes the variation value which was calculated from the individual H/L ratios between the biological replicates.

Table 2: Proteins upregulated in *htl* homozygous embryos

Upregulated proteins	H/L normalised	STDEV
Asparagine synthetase	1.61	0.05
Dipeptidase B	1.59	0.32
Peptidyl-prolyl cis-trans isomerase	1.29	0.09
Glutathione S-transferase S1	1.15	0.30
CG6084	1.12	0.11
Dihydropteridine reductase	1.00	0.15
Succinyl-CoA:3-ketoacid-coenzyme A transferase	0.94	0.15
Probable histone-binding protein Caf1	0.91	0.29
CTP synthase	0.78	0.25
CG2915	0.78	0.33
Maltase A5	0.78	0.21
Nucleoplasmin-like protein	0.78	0.22
Aldehyde dehydrogenase	0.73	0.19
Ecdysone-induced protein 55E	0.71	0.26
Glutathione S transferase E13	0.70	0.05
Microsomal glutathione S-transferase-like	0.68	0.11
CG4069	0.68	0.16
CG17337	0.67	0.26
CG9149	0.67	0.06
Aldehyde oxidase 1	0.67	0.23
vibrator	0.64	0.16
alphabet	0.62	0.12
Peptidyl-prolyl cis-trans isomerase	0.58	0.07
CG6028	0.58	0.10
CG6745	0.56	0.00

25 proteins were identified to be upregulated in *htl*^{AB42} embryos during late stage 7. Normalized H/L ratios are shown for each individual upregulated protein in average calculated from the values of the 3 individual biological replicates. The standard deviation denotes the variation value calculated from the individual H/L ratios between the biological replicates.

Table 3: Candidates of down- and upregulated proteins according to statistical evidence

Downregulated proteins	**T-Test Difference**
eIF2B-epsilon	-4.52
Glutathione S-transferase 1-1	-3.37
Lethal (2) 41Ab	-2.88
Splicing factor SRp54	-1.13
ATP-dependent RNA helicase p62	-1.02
Apolipophorins;Apolipophorin-2;Apolipophorin-1	-1.02
D-Importin 7/RanBP7	-0.88
Replication factor C subunit 1	-0.86

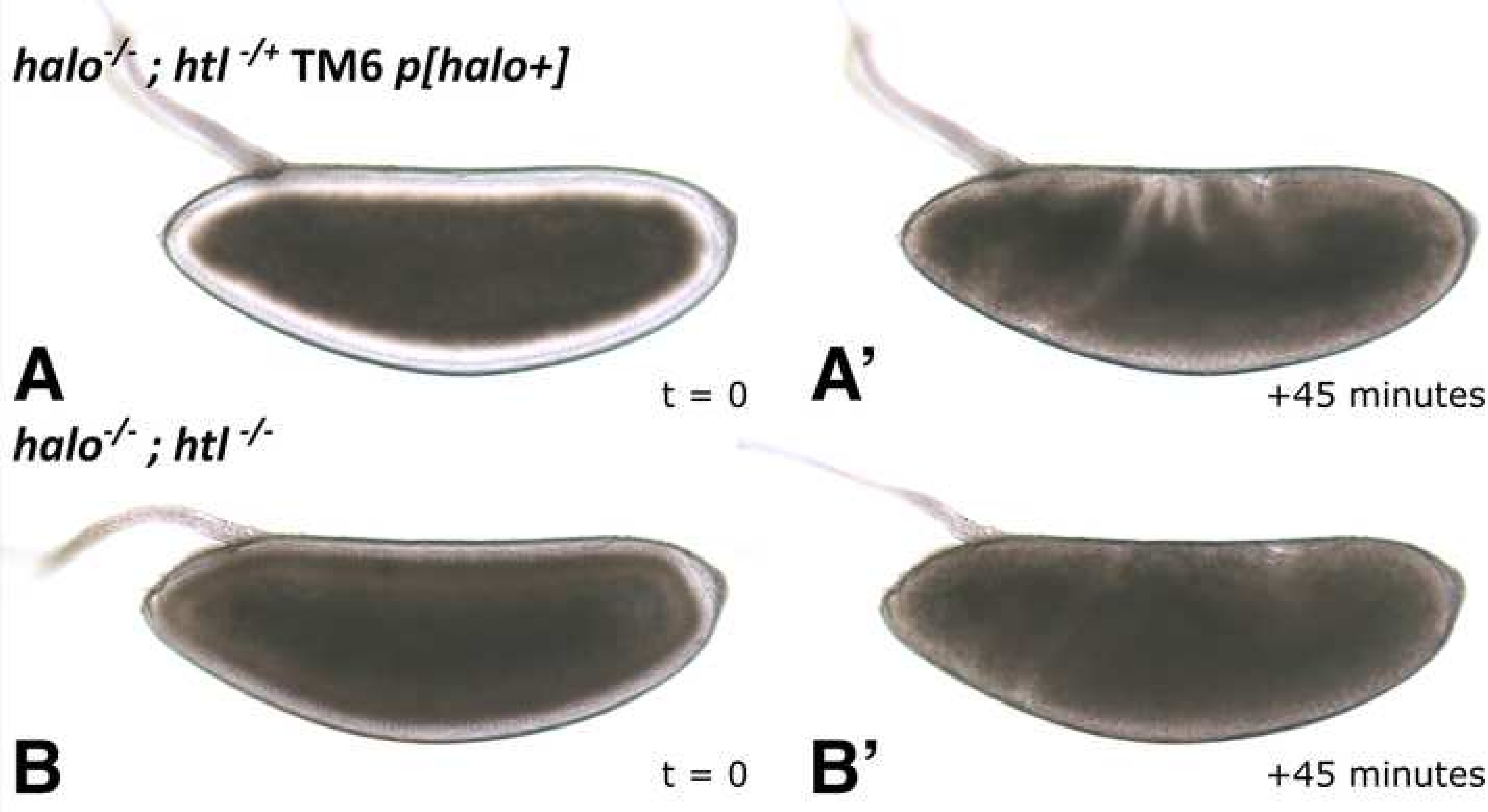
Upregulated proteins	**T-Test Difference**
Asparagine synthetase	1.61
Peptidyl-prolyl cis-trans isomerase	1.36
CG6084	1.07
Alpha-mannosidase	1.05
Dihydropteridine reductase	0.96

List of protein changes in *htl* mutant embryos, which were revealed by Volcano plot analysis. 5 proteins are found to be upregulated and 8 proteins are downregulated. Averaged normalized H/L ratios between the three biological replicates are shown. The standard deviation denotes the variation between the individual experimental replicates.

Table 4: Phosphopeptides detected in all 3 bioreplicates

phosphopeptide	H/L	STDEV	protein,gene	protein H/L	STDEV
[1]QISIGI**Y***ELLK	- 5.13	1.40	Garz, CG8487	-3.50**	0.09
[1]APATP....PVD**S***SGSPASPKK	- 2.90	0.45	TppII, CG3991	0.06	1.04
[1]DVDFGD**S***DNENEPDAYLARLK	-2.55	0.45	Ssrp1, CG4817	- 1.25	0.27
[1]ASAFQF**S***DDEEEVK	- 2.06	0.87	eIF3c, CG4954	- 0.71	0.61
[2]ASAFQF**S***DDEEEVK	- 1.61	1.24	eIF3c, CG4954	- 0.71	0.61
[3]V**T***ILWMGGSGSIVGKSVLL	- 1.14	0.14	Spoon, CG3249	- 0.16	0.89
[3]A**S***GVTVSDVCK	- 1.13	0.34	Tsr, CG4254	- 0.14	0.91
[1]NAGGVGVGVGEK**S***PDLK	- 1.12	0.18	Amun, CG2446	- 0.28	0.82
[1]RKKPEDPSSEAEALC**S***PAK	- 0.88	0.33	NASP, CG8223	0.12	1.09
[2]SAEAEAIVTTATADVS**S***PSK	- 0.80	0.21	NASP, CG8223	0.12	1.09
[3]SAEAEAIVTTATADVS**S***PSK	- 0.80	0.21	NASP, CG8223	0.12	1.09
[1]ALGGIVLTA**S***HNPGGPENDFGIK	1.10	1.75	Pgm1, CG5165	0.07	1.05

Phosphopeptides that were detected in all three SCX-enriched samples[1] or in all three TiO_2-enriched samples[2] or detected in all three unenriched bioreplicates[3]. The star (*) marks the phosphosite with the highest probability score for each peptide, respectively (see Suppl. File S3). The log2 ratios of the heavy/light populations (H/L) are indicated with their standard deviation (STDEV). The gene names encoding for the respective proteins are indicated with their CG number as annotated in FlyBase (www.Flybase.org). The overall H/L ratios of the respective proteins are indicated with their Standard deviation (STDEV). The full sequence of the phosphopeptide of TppII is APATPQAATSVTNPAAGDGISVQNDPPVD**S***SGSPASPKK. **Note that the sequence coverage of Garz in our data set was very low (1.8%), since only two distinct peptide species were identified for this protein. For all phosphopeptide data see Suppl. Mat. S3A.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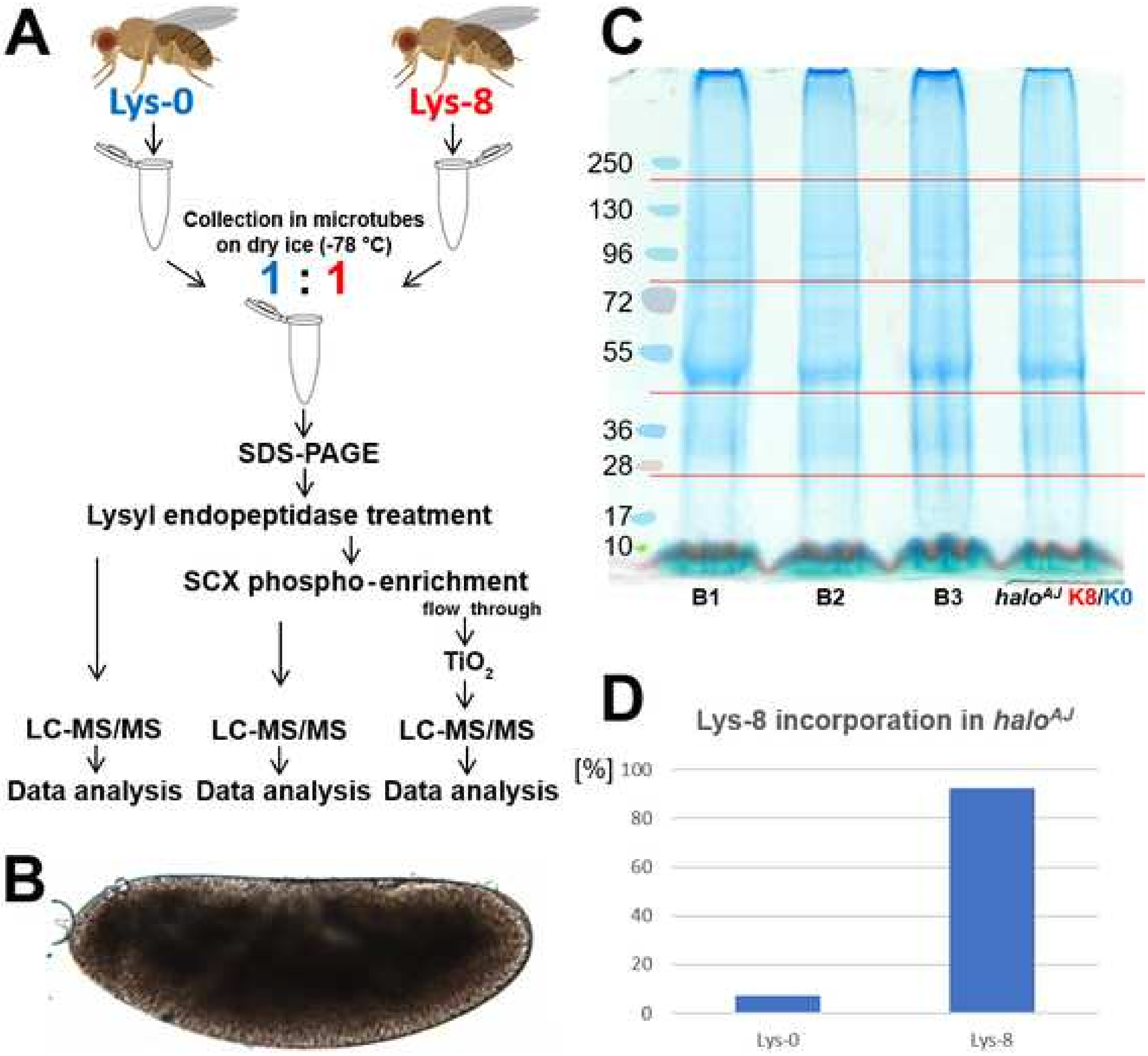
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Lys-8
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on dry ice (-78 °C)
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SDS-PAGE
Lysyl endopeptidase treatment
SCX phospho-enrichment
flow through
TiO2
LC-MS/MS
Data analysis
LC-MS/MS
Data analysis
LC-MS/MS
Data analysis
B
C
250
130
96
72
55
36
28
17
10
B1
B2
B3
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D
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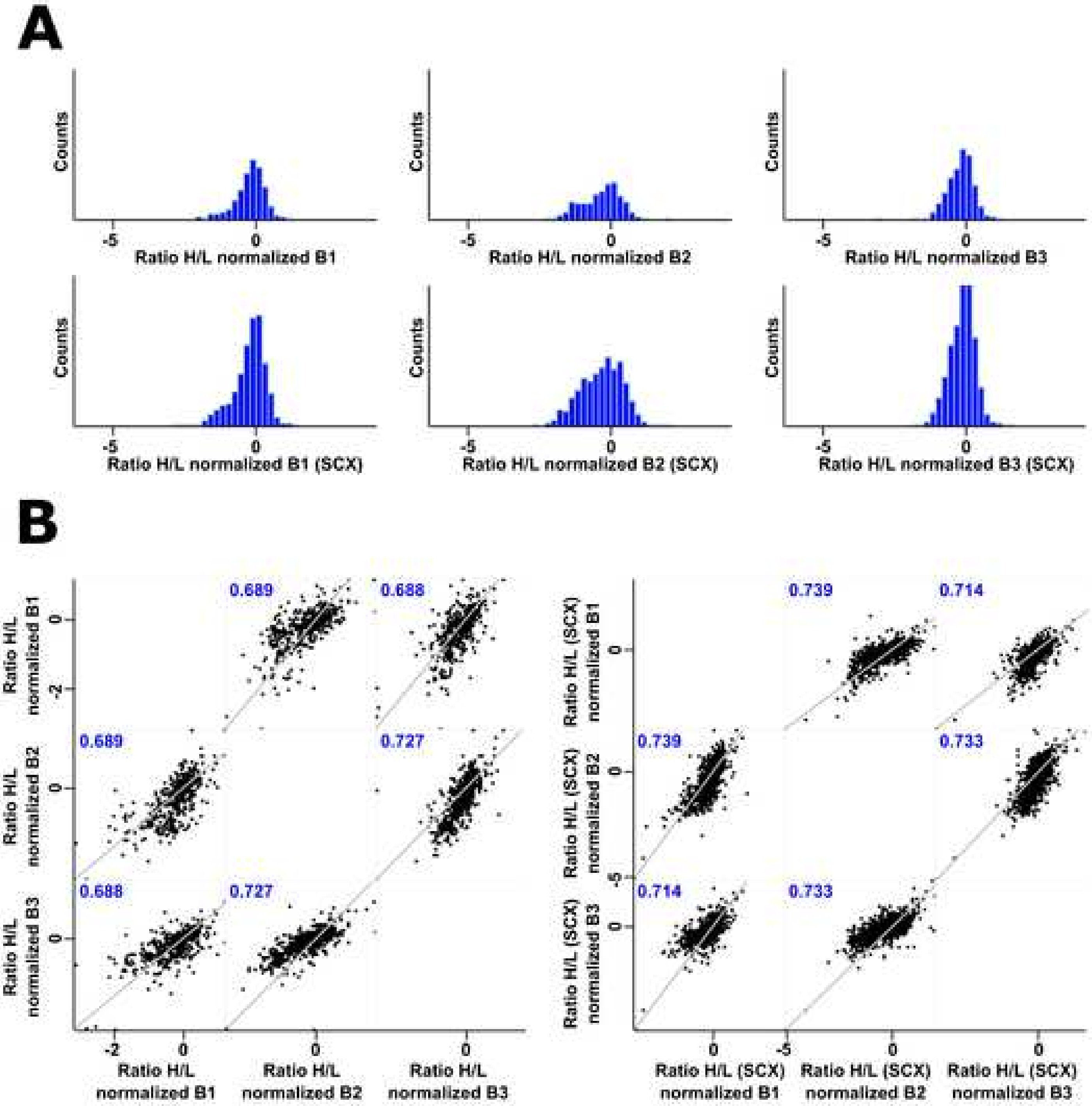
20
0
Lys-0
Lys-8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Counts
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0
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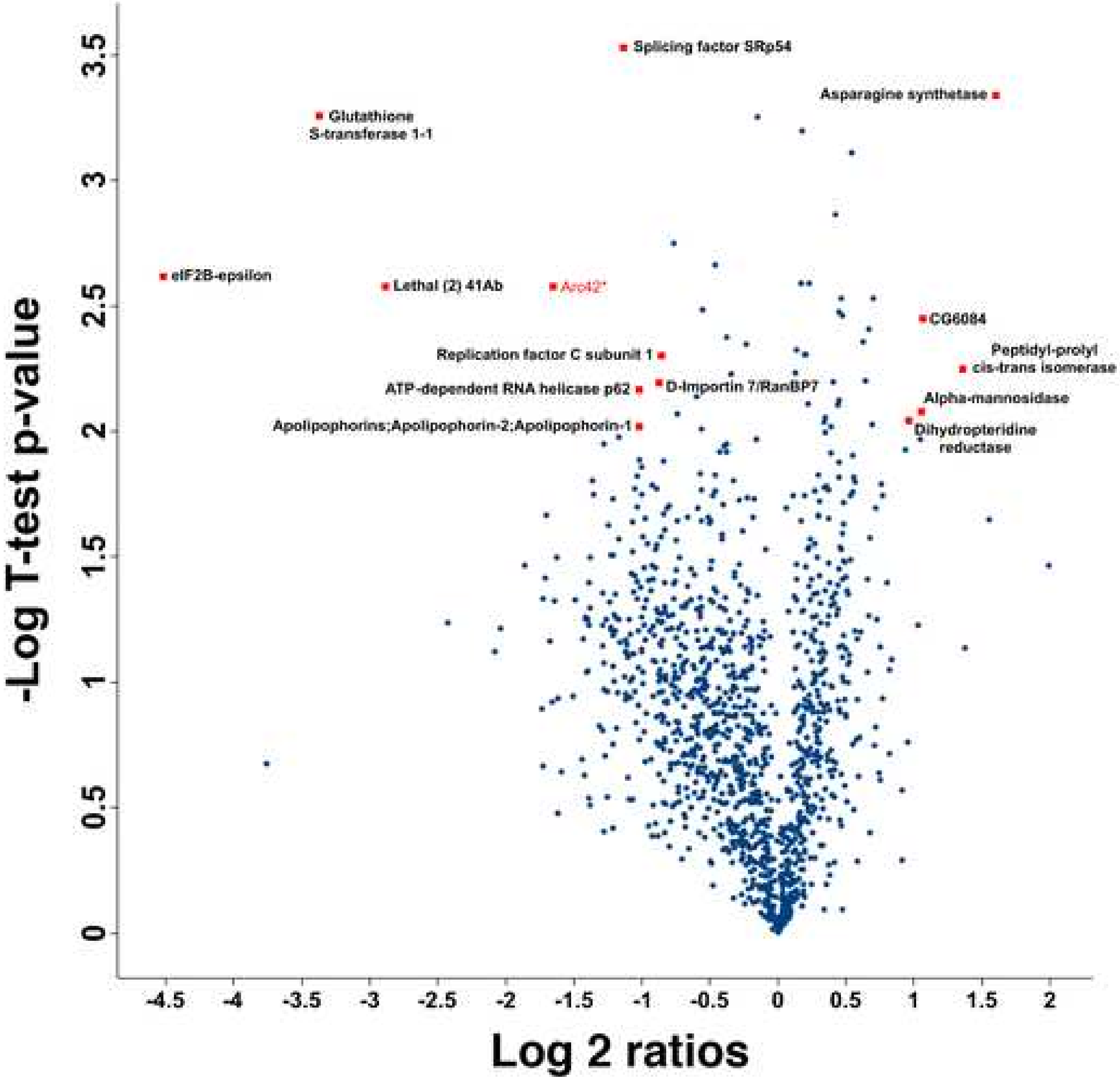
Ratio H/L normalized B2
Ratio H/L normalized B3
Ratio H/L normalized B1 (SCX)
Ratio H/L normalized B2 (SCX)
Ratio H/L normalized B3 (SCX)
B
0.689
0.688
0.727
0.739
0.714
0.733
Ratio H/L normalized B1
Ratio H/L normalized B2
Ratio H/L normalized B3
Ratio H/L (SCX) normalized B1
Ratio H/L (SCX) normalized B2
Ratio H/L (SCX) normalized B3
-2
0
-5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Asparagine synthetase
Glutathione S-transferase 1-1
elF2B-epsilon
Lethal (2) 41Ab
Arc42*
CG6084
Replication factor C subunit 1
Peptidyl-prolyl cis-trans isomerase
ATP-dependent RNA helicase p62
D-Importin 7/RanBP7
Alpha-mannosidase
Apolipophorins;Apolipophorin-2;Apolipophorin-1
Dihydropteridine reductase
-Log T-test p-value
0
0.5
1
1.5
2
2.5
3
3.5
-4.5
-4
-3.5
-3
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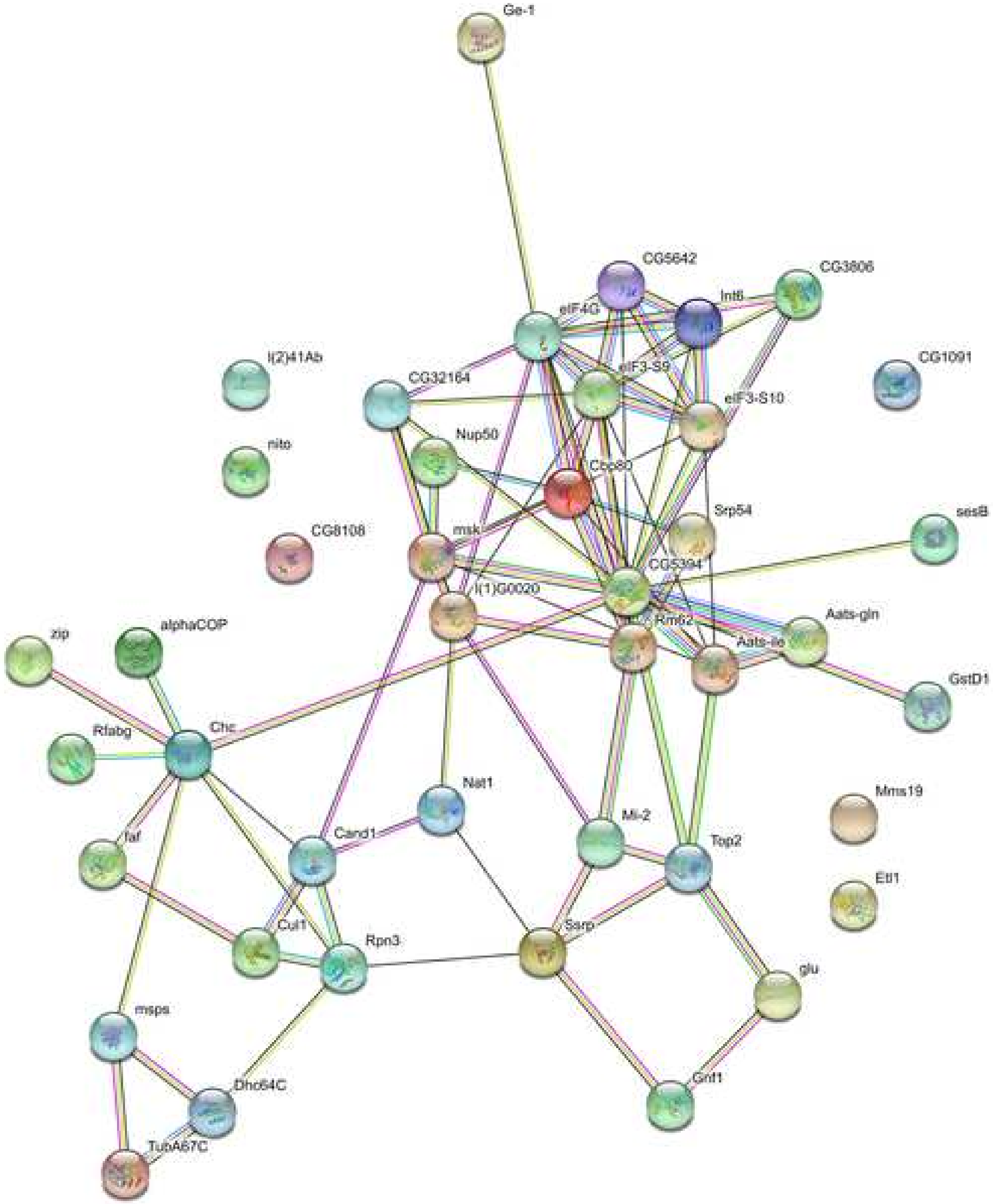
1
1.5
2
Log 2 ratios

Figure_5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nito
Cbp80
Srp54
sesB
CG8108
msk
CG5394
l(1)G0020
Rm62
Aats-gln
Aats-ile
GstD1
zip
alphaCOP
Chc
Rfabg
Nat1
Mms19
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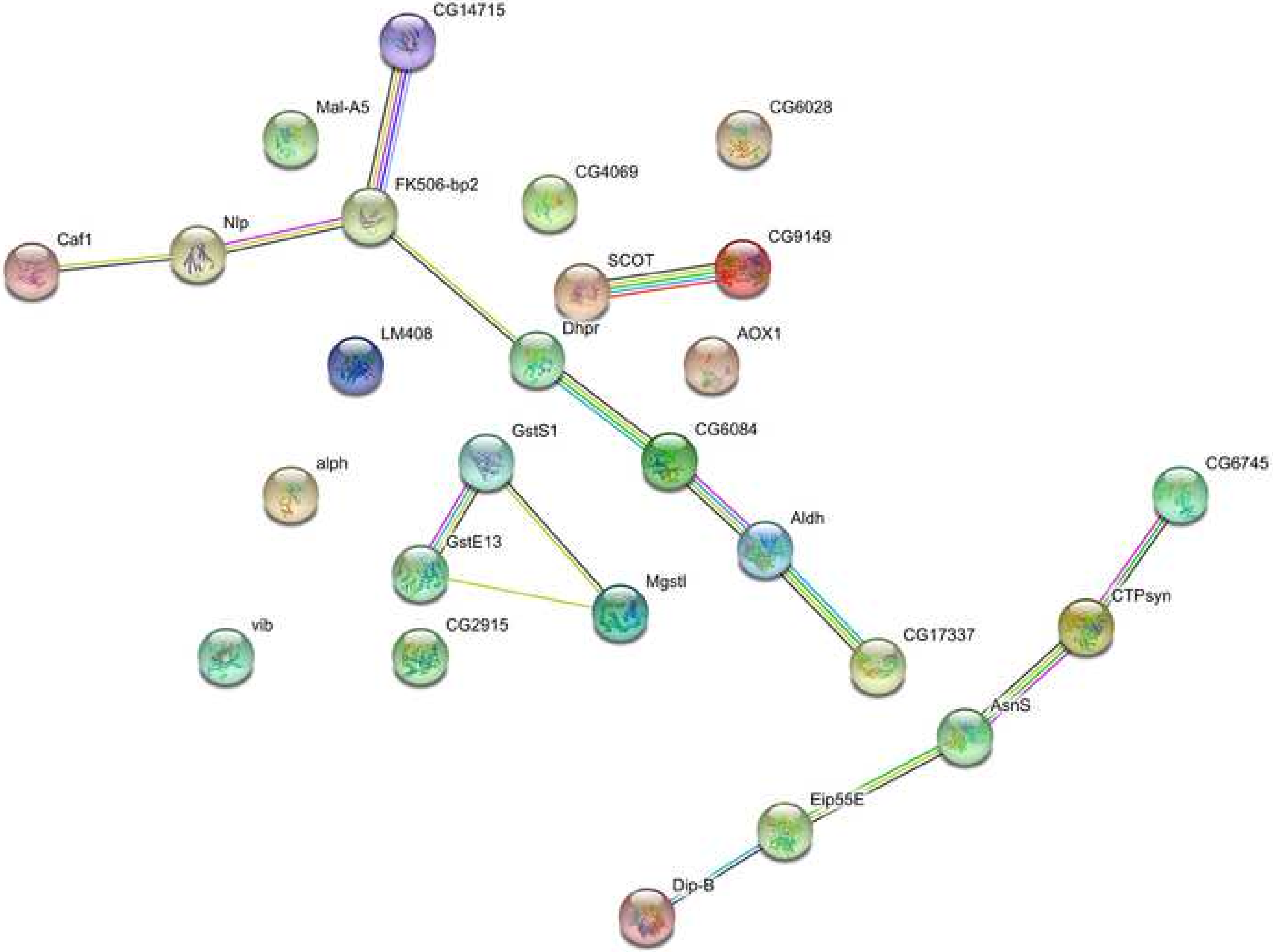
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CG6084
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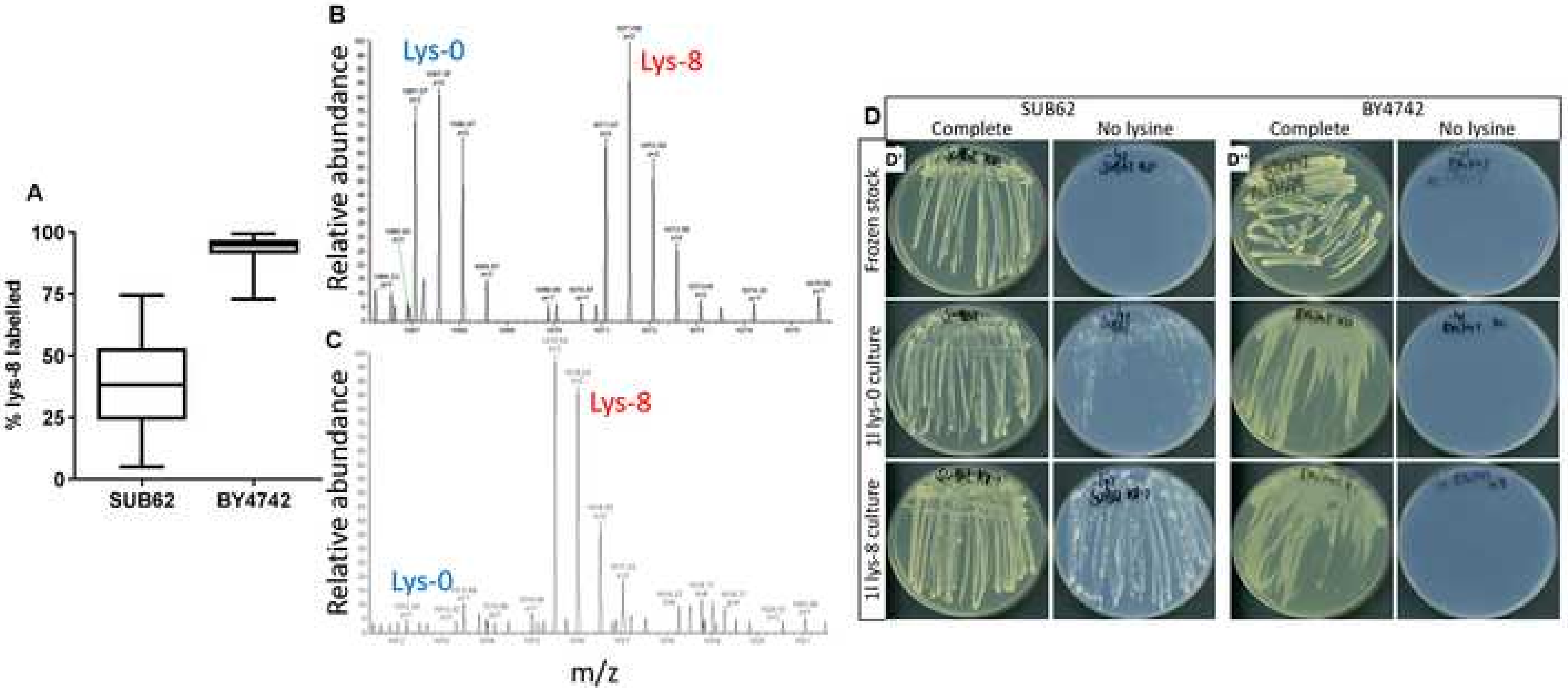
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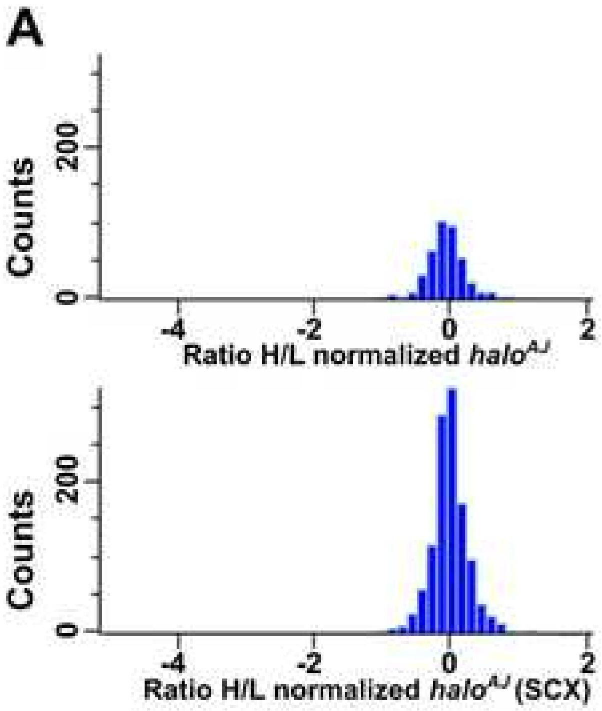
75
50
25
0
SUB62
BY4742
B
Relative abundance
Lys-0
Lys-8
C
Relative abundance
Lys-8
Lys-0
m/z
D
SUB62
BY4742
Complete
No lysine
Complete
No lysine
D'
D''
Frozen stock
1l lys-0 culture
1l lys-8 culture

A



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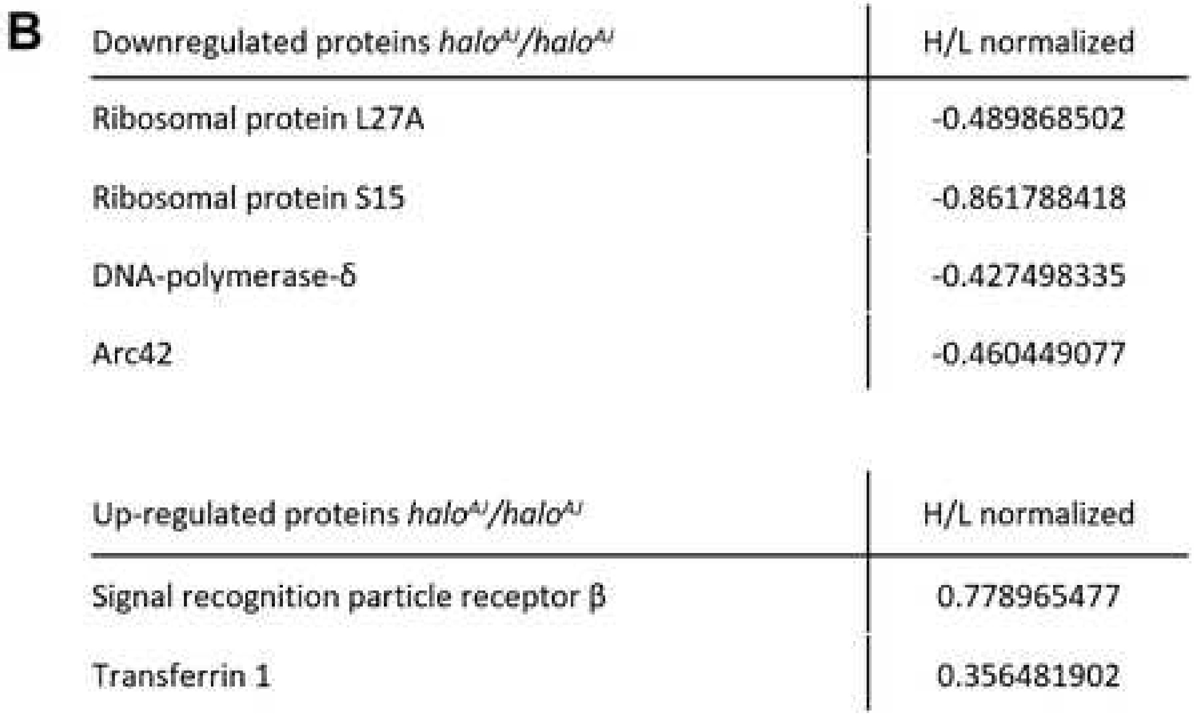

Downregulated proteins *halo*^{AJ}/*halo*^{AJ}	H/L normalized
Ribosomal protein L27A	-0.489868502
Ribosomal protein S15	-0.861788418
DNA-polymerase-δ	-0.427498335
Arc42	-0.460449077

Up-regulated proteins *halo*^{AJ}/*halo*^{AJ}	H/L normalized
Signal recognition particle receptor β	0.778965477
Transferrin 1	0.356481902

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Sequence	Length	K Count	Modification	Modified seq	Deamidation	Oxidation (M
AAAPAAVAS	25	1	2 Phospho (S	_AAAPAAVAS(ph)PAAAATSADASPS(ph)P		
AAAPAAVAS	25	1	2 Phospho (S	_AAAPAAVAS(ph)PAAAATSADASPS(ph)P		
AAAPAAVAS	25	1	Phospho (ST	_AAAPAAVASPAAAATSADASPS(ph)PAK_		
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AAAPAAVAS	26	2	Phospho (ST	_AAAPAAVASPAAAATSADASPS(ph)PAKK_		
AAAPAAVAS	26	2	2 Phospho (S	_AAAPAAVAS(ph)PAAAATSADASPS(ph)P		
AAAPAAVAS	26	2	2 Phospho (S	_AAAPAAVAS(ph)PAAAATSADAS(ph)PSP		
AASSAAAQA	23	1	Oxidation (M	_AASSAAAQAM(ox)LETS(p		AASSAAAQA
ACARGELYSL	15	1	Acetyl (Protei	_(ac)ACARGELY(ph)SLVLNTK_		
ADEKMVTDE	10	2	Oxidation (M	_ADEKM(ox)VT(ph)DEK_		ADEKM(1)VT
AIELSPGNAL	14	1	Phospho (ST	_AIELS(ph)PGNALFHAK_		
AIELSPGNAL	14	1	Phospho (ST	_AIELS(ph)PGNALFHAK_		
AKGEILDEVV	19	3	3 Phospho (S	_AKGEILDEVVT(ph)LS(ph)QIS(ph)AKK_		
ALDLLMSYRL	11	1	Oxidation (M	_ALDLLM(ox)S(ph)Y(ph)RL		ALDLLM(1)SY
ALDLLMSYRL	11	1	Oxidation (M	_ALDLLM(ox)S(ph)Y(ph)RL		ALDLLM(1)SY
ALELSHLKSFV	12	2	Phospho (ST	_ALELSHLKS(ph)FVK_		
ALGGIVLTAS	23	1	Phospho (ST	_ALGGIVLTAS(ph)HNPGGPENDFGIK_		
ALGGIVLTAS	23	1	Phospho (ST	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTAS	23	1	Phospho (ST	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTAS	23	1	Phospho (ST	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTAS	23	1	Phospho (ST	_ALGGIVLTAS(ph)HNPGGPENDFGIK_		
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ALGGIVLTAS	23	1	Phospho (ST	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTAS	23	1	Phospho (ST	_ALGGIVLT(p	ALGGIVLTASHN(0.529)PGG	
ALILNRTGAL	12	1	Phospho (ST	_ALILN(de)RT	ALILN(1)RTGALN(1)K	
ALQAVYPDY	19	1	Phospho (ST	_ALQAVYPDYVDELSLYGS(ph)K_		
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ALQAVYPDY	19	1	Phospho (ST	_ALQAVYPDYVDELSLYGS(ph)K_		
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ALQAVYPDY	19	1	Phospho (ST	_ALQAVYPDYVDELSLYGS(ph)K_		
ALQAVYPDY	19	1	2 Phospho (S	_ALQAVYPDYVDELS(ph)LYGS(ph)K_		
ALQAVYPDY	19	1	2 Phospho (S	_ALQAVYPDYVDELS(ph)LYGS(ph)K_		
APATPQAATS	39	2	Phospho (ST	_APATPQAATSVTNPAAGDGISVQNDPPVD		
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APATPQAATS	39	2	Phospho (STY	_APATPQAATSVTNPAAGDGISVQNDPPVD		
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AQDVVGRGA	17	1	Phospho (STY	_AQDVVGRGAT(ph)NILICNK_		
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AQNISPEQSG	18	1	Acetyl (Protei	_(ac)AQNIS(ph)PEQSGGAGGGGSK_		
ARLVFTEK	8	1	Acetyl (Protei	_(ac)ARLVFT(ph)EK_		
ARLVFTEK	8	1	Acetyl (Protei	_(ac)ARLVFT(ph)EK_		
ARSLSNSPLY	14	2	3 Phospho (S	_ARS(ph)LS(ph)NS(ph)PLYHRKK_		
ARSLSNSPLY	14	2	3 Phospho (S	_ARS(ph)LS(ph)NS(ph)PLYHRKK_		
ARSLSNSPLY	14	2	3 Phospho (S	_ARS(ph)LS(ph)NS(ph)PLYHRKK_		
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_		
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ASGVTSDVC	11	1	Acetyl (Protei	_(ac)AS(ph)GVTSDVCK_		
ASGVTSDVC	11	1	Acetyl (Protei	_(ac)ASGVT(ph)VSDVCK_		
ASRHNTASRA	18	1	2 Phospho (S	_AS(ph)RHN(	ASRHN(1)TASRAHVITRLVK	
CISAVNKQQR	20	2	2 Phospho (S	_CIS(ph)AVN	CISAVNKQ(0.001)Q(0.007)F	
CLPDYANKLK	10	2	Phospho (STY	_CLPDY(ph)ANKLK_		
CLPDYANKLK	10	2	Phospho (STY	_CLPDY(ph)ANKLK_		
DLEYFNNLK	9	1	Phospho (STY	_DLEY(ph)FN	DLEYFN(1)N(1)LK	
DLEYFNNLK	9	1	Phospho (STY	_DLEY(ph)FN	DLEYFN(1)N(1)LK	
DMRGTILRRK	10	1	Oxidation (M	_DM(ox)RGT(ph)ILRRK_		DM(1)RGTILR
DRQSLFTQVY	18	2	Phospho (STY	_DRQ(de)SLF	DRQ(0.991)SLFTQ(0.004)VY	
DVDFGDSDN	21	1	Phospho (STY	_DVDFGDS(ph)DNENEPDAYLARLK_		

DVDFGDSDN	21	1	Phospho (ST	_DVDFGDS(ph)DNENEPDAYLARLK_		
DVDFGDSDN	21	1	Phospho (ST	_DVDFGDS(ph)DNENEPDAYLARLK_		
DVDFGDSDN	21	1	Phospho (ST	_DVDFGDS(ph)DNENEPDAYLARLK_		
DVDFGDSDN	21	1	Phospho (ST	_DVDFGDS(ph)DNENEPDAYLARLK_		
DVDFGDSDN	21	1	Phospho (ST	_DVDFGDS(ph)DNENEPDAYLARLK_		
EAAAGEDITP	17	1	Phospho (ST	_EAAAGEDITPLADES(ph)IK_		
EAAQYGTVN	14	1	Phospho (ST	_EAAQY(ph)GTVNAVLPK_		
EAAQYGTVN	14	1	Phospho (ST	_EAAQY(ph)GTVNAVLPK_		
EANMLQSPV	15	1	2 Oxidation (	_EANM(ox)L	EAN(0.004)M	EANM(1)LQS
EASPVSMASP	25	2	Oxidation (M	_EASPVSM(ox)AS(ph)PAKD	EASPVSM(1)	
EASPVSMASP	25	2	Oxidation (M	_EASPVSM(ox)AS(ph)PAKD	EASPVSM(1)	
EASPVSMASP	25	2	Oxidation (M	_EASPVS(ph)M(ox)ASPAKD	EASPVSM(1)	
EFVFQLHGKM	18	3	Oxidation (M	_EFVFQLHGKM(ox)SNY(ph)		EFVFQLHGK
EKTDAMAKA	16	3	2 Phospho (S	_EKT(ph)DAMAKAQEFLRT(ph)K_		
ELGNAEPAPS	24	1	Phospho (ST	_ELGNAEPAPSVSSTTVSS(ph)PPAGVK_		
ELPDSDSLNV	27	1	Phospho (ST	_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK		
ELPDSDSLNV	27	1	Phospho (ST	_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK		
ELPDSDSLNV	27	1	Phospho (ST	_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK		
EMIKILQEQA	14	2	Phospho (ST	_EMIKILQ(de	EMIKILQ(0.503)EQ(0.503)A	
ENSPSNVAKK	13	3	2 Phospho (S	_ENS(ph)PS(	EN(0.039)SPSN(0.961)VAK	
ENTKNLVTGE	14	2	Phospho (ST	_EN(de)TKN(	EN(1)TKN(1)LVTGEPITK	
ESAQQLEAQT	11	1	2 Phospho (S	_ES(ph)AQ(d	ESAQ(0.854)Q(0.147)LEAQ	
ESTPLSASPKK	11	2	Phospho (ST	_ESTPLSAS(ph)PKK_		
ETELMQSKIQ	20	2	Phospho (ST	_ETELMQSKIQET(ph)LGLDPVDK_		
ETEQVAQPQ	20	1	Phospho (ST	_ETEQVAQP	ETEQ(0.085)VAQ(0.085)PQ	
ETIADIMRVKT	13	2	2 Phospho (S	_ET(ph)IADIMRVKT(ph)IK_		
EVCAQSLQD	23	2	Phospho (ST	_EVCAQS(ph)	EVCAQ(0.12)SLQ(0.116)DQ	
EVSDDEADDE	12	2	Phospho (ST	_EVS(ph)DDEADDEKK_		
FFDSGDYQM	11	1	Oxidation (M	_FFDS(ph)GDYQM(ox)AK_		FFDSGDYQM
FFDSGDYQM	11	1	Oxidation (M	_FFDS(ph)GDYQM(ox)AK_		FFDSGDYQM
FFDSGDYQM	11	1	Oxidation (M	_FFDS(ph)GDYQM(ox)AK_		FFDSGDYQM
FMSNKNPYSL	15	2	Oxidation (M	_FMSNKN(de	FMSN(0.008)	FMSNKNPYSL
FSSELFKEIIK	11	2	2 Phospho (S	_FS(ph)S(ph)ELFKEIIK_		
GEALTSKQRY	13	2	2 Phospho (S	_GEALT(ph)S	GEALTSKQ(0.991)RYQ(0.00	
GELQAGKSPF	11	2	Acetyl (Protei	_(ac)GELQAGKS(ph)PFK_		
GELQAGKSPF	11	2	Acetyl (Protei	_(ac)GELQAGKS(ph)PFK_		
GELQAGKSPF	11	2	Acetyl (Protei	_(ac)GELQAGKS(ph)PFK_		
GLGMTKINLI	12	2	Oxidation (M	_GLGM(ox)T(ph)KINLITK_		GLGM(1)TKIN
GPQLEDGKVT	15	3	Oxidation (M	_GPQ(de)LED	GPQ(1)LEDG	GPQLEDGKVT
GQPLVVLSA	11	1	Oxidation (M	_GQ(de)PLVV	GQ(1)PLVVLS	GQPLVVLSA
HNNSPNTNL	20	1	Phospho (ST	_HN(de)NSP	HN(0.468)N(0.468)SPN(0.0	
HNNSPNTNL	20	1	Phospho (ST	_HN(de)NSP	HN(0.371)N(0.371)SPN(0.1	
IGEGTYGVVY	11	1	Phospho (ST	_IGEGTY(ph)GVVYK_		

IITHPNFNGNT	20	1	Phospho (STY	_IITHPN(de)F	IITHPN(0.59)FN(0.205)GN(0	
IITHPNFNGNT	20	1	Phospho (STY	_IITHPN(de)F	IITHPN(0.65)FN(0.268)GN(0	
IKAEHEYRTSM	20	2	Oxidation (M	_IKAEHEYRTS	IKAEHEYRTSM	IKAEHEYRTSM
IKPILQATQTS	15	1	Oxidation (M	_IKPILQAT(ph	IKPILQ(0.026)	IKPILQATQTS
IKPILQATQTS	15	1	Oxidation (M	_IKPILQAT(ph	IKPILQ(0.005)	IKPILQATQTS
IKPILQATQTS	15	1	Oxidation (M	_IKPILQAT(ph)Q(de)TSQ(de)LFM(ox)_		
IKPILQATQTS	15	1	Oxidation (M	_IKPILQAT(ph)Q(de)TSQ(de)LFM(ox)_		
IKPILQATQTS	15	1	Oxidation (M	_IKPILQAT(ph)Q(de)TSQ(de)LFM(ox)_		
ILFVTESENQA	21	1	2 Phospho (S	_ILFVTESEN(c	ILFVTESEN(0.919)Q(0.08)AN	
ILFVTESENQA	21	1	2 Phospho (S	_ILFVTESEN(c	ILFVTESEN(0.919)Q(0.08)AN	
INQIQMKETN	14	2	Oxidation (M	_INQIQ(de)M	IN(0.033)Q(0.	INQIQM(1)KE
IQVQTKQIAQ	14	2	Oxidation (M	_IQVQTKQ(de	IQ(0.001)VQ(	IQVQTKQIAQ
IQVQTKQIAQ	14	2	Oxidation (M	_IQVQTKQ(de	IQ(0.011)VQ(	IQVQTKQIAQ
IQVQTKQIAQ	14	2	Phospho (STY	_IQ(de)VQTK	IQ(0.502)VQ(0.502)TKQ(0.0	
ISENTIAIISTEL	17	1	3 Phospho (S	_IS(ph)ENT(ph)IAIIST(ph)ELEIQK_		
ISMLKQVMSC	14	3	Oxidation (M	_IS(ph)M(ox)LKQVMS(ph)Q	ISM(0.818)LK	
KDFLPLAFQM	19	2	Oxidation (M	_KDFLPLAFQM(ox)QASTGIA	KDFLPLAFQM	
KDITNLSYKVV	12	3	Phospho (STY	_KDIT(ph)N(d	KDITN(1)LSYKVVK	
KEESESEDDDI	17	1	Oxidation (M	_KEESES(ph)EDDDM(ox)GFA	KEESESEDDDI	
KEESESEDDDI	17	1	Oxidation (M	_KEESES(ph)EDDDM(ox)GFA	KEESESEDDDI	
KEESESEDDDI	17	1	Oxidation (M	_KEESES(ph)EDDDM(ox)GFA	KEESESEDDDI	
KEPTPGEK	8	2	Phospho (STY	_KEPT(ph)PGEK_		
KIDNPESSAKV	25	3	Phospho (STY	_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_		
KIDNPESSAKV	25	3	Phospho (STY	_KIDNPESSAKVS(ph)DAEEEEEEYAVEK_		
KIDNPESSAKV	25	3	Phospho (STY	_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_		
KIDNPESSAKV	25	3	Phospho (STY	_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_		
KIEKFQSEEQQ	20	3	Phospho (STY	_KIEKFQS(ph)EEQQQTEDELQDK_		
KIEKFQSEEQQ	20	3	Phospho (STY	_KIEKFQS(ph)EEQQQTEDELQDK_		
KKEEESDQSD	19	2	Oxidation (M	_KKEEES(ph)DQS(ph)DDDM	KKEEESDQSD	
KKEEESDQSD	19	2	Oxidation (M	_KKEEES(ph)DQS(ph)DDDM	KKEEESDQSD	
KKEEESDQSD	19	2	Oxidation (M	_KKEEES(ph)DQS(ph)DDDM	KKEEESDQSD	
KKEEESDQSD	19	2	Oxidation (M	_KKEEESDQS(ph)DDDM(ox)	KKEEESDQSD	
KKQEESDEEFF	17	3	Phospho (STY	_KKQEES(ph)DEEFFDLDDIK_		
KLAFSDDESTP	19	2	Phospho (STY	_KLAFS(ph)DDESTPEEHQGQGK_		
KLIVNGASSNL	12	2	Phospho (STY	_KLIVN(de)GA	KLIVN(1)GASSN(1)LK	
KMEVLSVQNH	14	2	Phospho (STY	_KMEVLS(ph)	KMEVLSVQ(0.215)N(0.84)H	
KMKYDFGTLL	14	3	2 Phospho (S	_KMKY(ph)DFGT(ph)LLLLVK_		
KNKTNRQLSS	11	3	Acetyl (Protei	_(ac)KN(de)K	KN(0.97)KTN(0.029)RQ(0.00	
KPEDPSSEAEA	17	2	Phospho (STY	_KPEDPSSEAEALCS(ph)PAK_		
KPEDPSSEAEA	17	2	Phospho (STY	_KPEDPSSEAEALCS(ph)PAK_		
KPEDPSSEAEA	17	2	Phospho (STY	_KPEDPSSEAEALCS(ph)PAK_		
KPEDPSSEAEA	17	2	Phospho (STY	_KPEDPSSEAEALCS(ph)PAK_		
KPEDPSSEAEA	17	2	Phospho (STY	_KPEDPSSEAEALCS(ph)PAK_		

KPEDPSSEAE	17	2	Phospho (STY	_KPEDPSSEAEALCS(ph)PAK_		
KQEESDEEFF	16	2	Phospho (STY	_KQEES(ph)DEEFFDLDDIK_		
KSAPQSRQSC	18	2	Phospho (STY	_KS(ph)APQ(	KSAPQ(1)SRQ(1)SCFRSRPRL	
KSKPTAAVTP	13	3	2 Phospho (S	_KS(ph)KPT(p	KSKPTAAVTPIQ(1)K	
KVTTIGLNST	14	2	2 Phospho (S	_KVT(ph)T(ph)IGLNSTAATK_		
KVTWIGANG	15	2	Phospho (STY	_KVT(ph)WIG	KVTWIGAN(0.771)GDQ(0.2	
LDLTIVDLND	19	2	Phospho (STY	_LDLTIVDLND	LDLTIVDLN(0.079)DEVQ(0.	
LENLAYEKSE	24	2	Oxidation (M	_LENLAYEKS(ph)EDLLLT(ph)		LENLAYEKSE
LFEPPVTMRD	19	2	Phospho (STY	_LFEPPVTMRDMLKSLSRT(ph)K_		
LGIDIGDRLQ	15	1	2 Phospho (S	_LGIDIGDRLQAT(ph)S(ph)RK_		
LLDFNLLDTD	28	2	Phospho (STY	_LLDFNLLDT(ph)DDDDDEEGDEEDKEDTVT		
LNENFVTINI	12	1	Phospho (STY	_LN(de)EN(d	LN(0.913)EN(0.913)FVTIN(	
LRFDFNSKAA	24	3	2 Phospho (S	_LRFDFNS(ph	LRFDFN(0.002)SKAAMTIEQ	
LRTSPNEQQK	16	2	2 Phospho (S	_LRTS(ph)PN(	LRTSPN(1)EQ(1)Q(1)KDTLH	
LSVQSPPK	8	1	Phospho (STY	_LSVQS(ph)PPK_		
LTNGQRQME	16	1	Oxidation (M	_LT(ph)NGQR	LTN(0.008)G	LTNGQRQM(
LTNGQRQME	16	1	Oxidation (M	_LT(ph)NGQR	LTN(0.016)G	LTNGQRQM(
MESTTIVFVTL	19	1	Oxidation (M	_M(ox)ESTTI	MESTTIVFVTL	M(1)ESTTIVF
MFLTQQQL	13	1	Oxidation (M	_M(ox)FLT(p	MFLTQ(0.015	M(1)FLTQQQ
MFLTQQQL	13	1	Oxidation (M	_M(ox)FLT(p	MFLTQ(0.138	M(1)FLTQQQ
MGHLQLDFH	13	1	Acetyl (Protei	_(ac)M(ox)GHLQLDFHS(ph)		M(1)GHLQLD
MHKLIMRSVI	14	2	2 Oxidation (	_M(ox)HKLIM(ox)RS(ph)VI		M(1)HKLIM(1
MIRATSCALS	18	1	Oxidation (M	_M(ox)IRATSCALS(ph)TRPLI		M(1)IRATSCA
MLNRCLELVT	13	1	Oxidation (M	_M(ox)LN(de	MLN(1)RCLEL	M(1)LNRCLEL
MLNRCLELVT	13	1	Oxidation (M	_M(ox)LN(de)RCLELVT(ph)PFK_		
MLVRRLLQEL	18	1	Oxidation (M	_M(ox)LVRRL	MLVRRLLQ(1	M(1)LVRRLL
MNDSFGDFN	23	1	Acetyl (Protei	_(ac)M(ox)NDS(ph)FGDFN		M(1)NDSFGD
MPNLQSSIPH	13	2	Acetyl (Protei	_(ac)M(ox)PNLQS(ph)SIPHT		M(1)PNLQSSI
MPNLQSSIPH	13	2	Acetyl (Protei	_(ac)M(ox)PNLQS(ph)SIPHT		M(1)PNLQSSI
MPNLQSSIPH	13	2	Acetyl (Protei	_(ac)M(ox)PNLQS(ph)SIPHT		M(1)PNLQSSI
MPNLQSSIPH	13	2	Acetyl (Protei	_(ac)M(ox)PNLQS(ph)SIPHT		M(1)PNLQSSI
MQHSSMKV	15	2	Oxidation (M	_M(ox)Q(de)	MQ(1)HSSM	M(0.989)QHS
MQIFVKTLTG	11	2	Acetyl (Protei	_(ac)MQ(de)I	MQ(1)IFVKTLTGK	
MQLILSYLQS	14	1	Acetyl (Protei	_(ac)MQLILS(	MQ(0.212)LILSYLQ(0.848)S	
MQLILSYLQS	14	1	Acetyl (Protei	_(ac)MQLILS	MQ(0.007)LILSYLQ(0.996)S	
MQLILSYLQS	14	1	Acetyl (Protei	_(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_		
MQLILSYLQS	14	1	Acetyl (Protei	_(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_		
MQLILSYLQS	14	1	Oxidation (M	_M(ox)Q(de)I	MQ(0.844)LIL	M(1)QLILSYL
MQLILSYLQS	14	1	Oxidation (M	_M(ox)QLILS	MQ(0.066)LIL	M(1)QLILSYL
MQLILSYLQS	14	1	Oxidation (M	_M(ox)QLILSYLQ(de)S(ph)Q(de)QIK_		
MQLILSYLQS	14	1	Oxidation (M	_M(ox)Q(de)LILS(ph)YLQSQQ(de)IK_		
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)R	MRDKISQ(0.0	M(1)RDKISQL
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)R	MRDKISQ(0.0	M(1)RDKISQL

MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)RD	MRDKISQ(0.0	M(1)RDKISQL
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)RD	MRDKISQ(0.0	M(1)RDKISQL
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)RD	MRDKISQ(0.0	M(1)RDKISQL
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)RD	MRDKISQ(0.2	M(1)RDKISQL
MRFISQHNSS	12	1	Acetyl (Protei	_(ac)M(ox)RF	MRFISQ(0.53	M(1)RFISQHN
MSGALKSQQ	13	2	Acetyl (Protei	_(ac)M(ox)SG	MSGALKSQ(0	M(1)SGALKSC
MSLIHSFVTQ	13	1	2 Oxidation (I	_M(ox)S(ph)L	MSLIHSFVTQ	M(1)SLIHSFV
MSQGASEVPI	16	1	Acetyl (Protei	_(ac)MSQGASEVPLS(ph)ALRLK_		
MSTIVRK	7	1	2 Phospho (S	_MS(ph)T(ph)IVRK_		
MSTLLENIFAI	20	2	Oxidation (M	_M(ox)S(ph)T	MSTLLEN(0.9	M(1)STLLENIF
MTEIELPVES	26	1	Oxidation (M	_M(ox)TEIELPVESVPSASLS(		M(1)TEIELPVE
MTIFNLYIFDK	11	1	Oxidation (M	_M(ox)TIFNLY(ph)IFDK_		M(1)TIFNLYIF
MVEPSPETVG	24	1	Oxidation (M	_M(ox)VEPSPETVGDFQSVQ		M(1)VEPSPET
MVEPSPETVG	24	1	Oxidation (M	_M(ox)VEPSPETVGDFQSVQ		M(1)VEPSPET
MVEPSPETVG	24	1	Oxidation (M	_M(ox)VEPSPETVGDFQSVQ		M(1)VEPSPET
MYNIYVLKK	9	2	Phospho (STY	_MYN(de)IY(	MYN(1)IYVLKK	
MYNIYVLKK	9	2	Phospho (STY	_MY(ph)N(de	MYN(1)IYVLKK	
NAGGVGVGV	17	2	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLK_		
NAGGVGVGV	17	2	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLK_		
NAGGVGVGV	17	2	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLK_		
NAGGVGVGV	17	2	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLK_		
NAGGVGVGV	17	2	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLK_		
NAGGVGVGV	18	3	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLKK_		
NAGGVGVGV	18	3	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLKK_		
NGGILNYMIR	11	1	Oxidation (M	_N(de)GGILN	N(0.96)GGIL	NGGILNYM(1
NIWKDKTPNL	11	3	Phospho (STY	_N(de)IWKD	N(0.999)IWKDKTPN(0.001)	
NKEPLIQIAM	20	3	Oxidation (M	_N(de)KEPLIC	N(0.823)KEPL	NKEPLIQIAM(
NKLQKNHALI	23	3	Phospho (STY	_N(de)KLQ(d	N(0.999)KLQ(0.999)KN(0.9	
NLKLQMASTF	12	2	Oxidation (M	_N(de)LKLQ	N(0.938)LKLC	NLKLQM(1)A
NNIKLKCLIDT	20	3	Acetyl (Protei	_(ac)NNIKLKC	N(0.023)N(0.023)IKLKCLIDT	
NSQYERESLL	11	1	Phospho (STY	_NSQY(ph)ERESLLK_		
NSQYERESLL	11	1	Phospho (STY	_NSQY(ph)ERESLLK_		
NVGIFIKDDSD	19	3	Phospho (STY	_NVGIFIKDDS(ph)DEEDVDDKK_		
NVGIFIKDDSD	19	3	Phospho (STY	_NVGIFIKDDS(ph)DEEDVDDKK_		
NVGIFIKDDSD	19	3	Phospho (STY	_NVGIFIKDDS(ph)DEEDVDDKK_		
NYPFNIEF	8	0	Phospho (STY	_N(de)Y(ph)P	N(1)YPFN(1)IEF	
PCNLYQTAQE	13	1	Phospho (STY	_PCNLY(ph)QTAQEQLK_		
PCNLYQTAQE	13	1	Phospho (STY	_PCN(de)LY(	PCN(0.992)LYQ(0.004)TAQ(	
PLMQLIIQDT	16	1	2 Oxidation (I	_PLM(ox)QLIIQDTGIGM(ox)		PLM(1)QLIIQD
PLPSGRIPQIT	17	1	2 Phospho (S	_PLPS(ph)GRIPQIT(ph)PPASPK_		
PLPSGRIPQIT	17	1	2 Phospho (S	_PLPS(ph)GRIPQIT(ph)PPASPK_		
PTVAAAAKPA	34	2	Phospho (STY	_PTVAAAAKPAADDDDDVDLFGS(ph)DDEE		
QELLQSYMK	9	1	Oxidation (M	_(gl)Q(de)ELL	Q(1)ELLQ(1)S	QELLQSYM(1)

QELLQSYMK	9	1	Oxidation (M	_(gl)Q(de)ELL	Q(1)ELLQ(1)S	QELLQSYM(1
QELLQSYMK	9	1	Phospho (STY	_(gl)Q(de)ELL	Q(1)ELLQ(1)SYMK	
QHSFTSSSAL	11	1	Phospho (STY	_Q(de)HSFTS	Q(1)HSFTSSSALK	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISVRGIAEV	17	1	Phospho (STY	_(gl)QIS(ph)VRGIAEVGNVTEVK_		
QISVRGIAEV	17	1	Phospho (STY	_(gl)QIS(ph)VRGIAEVGNVTEVK_		
QISVRGIAEV	18	2	Phospho (STY	_(gl)QIS(ph)VRGIAEVGNVTEVKK_		
QISVRGIAEV	18	2	Phospho (STY	_(gl)QIS(ph)VRGIAEVGNVTEVKK_		
QIVPLLNYK	9	1	Phospho (STY	_Q(de)IVPLL	Q(1)IVPLLN(1)YK	
QKESGEFPEV	12	2	Phospho (STY	_QKES(ph)GEFPEVGK_		
QKFITTEDVNI	19	2	Oxidation (M	_Q(de)KFIT(p	Q(0.941)KFIT	QKFITTEDVNI
QLRDLETELD	14	1	Phospho (STY	_(gl)QLRDLET(ph)ELDEERK_		
QLRDLETELD	14	1	Phospho (STY	_(gl)QLRDLET(ph)ELDEERK_		
QLSIIRQKSLK	11	2	Phospho (STY	_(gl)Q(de)LSII	Q(0.999)LSIIRQ(0.001)KSLK	
QMPDVETTE	16	1	Oxidation (M	_Q(de)M(ox)	Q(1)MPDVET	QM(1)PDVET
QNDLIHDRSL	13	1	Phospho (STY	_(gl)QNDLIHDRS(ph)LINK_		
QNDLIHDRSL	13	1	Phospho (STY	_(gl)QNDLIHDRS(ph)LINK_		
QNDLIHDRSL	13	1	Phospho (STY	_(gl)QNDLIHDRS(ph)LINK_		
QRDLPAPRES	15	1	Phospho (STY	_(gl)QRDLPAPRES(ph)QSRSK_		
QSLIMYFNK	9	1	Oxidation (M	_Q(de)SLIM(	Q(0.998)SLIM	QSLIM(1)YFN
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_		
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_		
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_		
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_		
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_		
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_		

QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_		
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_		
QSVPQLANLT	16	1	Phospho (STY	_Q(de)SVPQ(	Q(0.987)SVPQ(0.987)LAN(0	
QSVPQLANLT	16	1	Phospho (STY	_Q(de)SVPQ(	Q(0.962)SVPQ(0.972)LAN(0	
QSVPQLANLT	16	1	Phospho (STY	_Q(de)SVPQ(	Q(0.942)SVPQ(0.985)LAN(0	
QSVPQLANLT	16	1	Phospho (STY	_Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_		
QSVPQLANLT	16	1	Phospho (STY	_Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_		
QVEPRQLVR	22	1	Oxidation (M	_QVEPRQLVR	Q(0.001)VEP	QVEPRQLVR
QVRTNLQEIQ	11	1	Phospho (STY	_(gl)Q(de)VR	Q(0.334)VRTN(0.334)LQ(0.	
QVRTNLQEIQ	11	1	Phospho (STY	_(gl)Q(de)VRT(ph)NLQEIQ(de)K_		
REEENAAAAE	31	1	Phospho (STY	_REEENAAAAEEEAGEISATGGATS(ph)PEP		
REEENAAAAE	31	1	Phospho (STY	_REEENAAAAEEEAGEISATGGAT(ph)SPEP		
REEENAAAAE	31	1	Phospho (STY	_REEENAAAAEEEAGEISATGGAT(ph)SPEP		
RGCQILGLNK	18	2	Phospho (STY	_RGCQ(de)IL	RGCQ(0.965)ILGLN(0.024)K	
RGCQILGLNK	18	2	Phospho (STY	_RGCQ(de)IL	RGCQ(0.838)ILGLN(0.155)K	
RGCQILGLNK	18	2	Phospho (STY	_RGCQ(de)IL	RGCQ(0.999)ILGLNKYGIQQ	
RGPPPPPTAS	17	1	2 Phospho (S	_RGPPPPPTA	RGPPPPPTASESTRRN(1)K	
RGPPPPPTAS	17	1	2 Phospho (S	_RGPPPPPTASES(ph)T(ph)RRN(de)K_		
RGPPPPPTAS	17	1	2 Phospho (S	_RGPPPPPTASES(ph)T(ph)RRN(de)K_		
RIASFKNYISK	11	2	Phospho (STY	_RIASFKNY(ph)ISK_		
RIQEVYLQK	9	1	Phospho (STY	_RIQEVY(ph)	RIQ(0.049)EVYLQ(0.951)K	
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_		
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_		
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_		
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_		
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_		
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_		
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_		
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_		
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_		
RMASSEQPT	17	1	Oxidation (M	_RM(ox)ASSE	RMASSEQ(0.	RM(1)ASSEQ
RPLMLQGHE	16	1	Acetyl (Protei	_(ac)RPLMLQ	RPLMLQ(1)GHERSITQ(1)IK	
RPLMLQGHE	16	1	Acetyl (Protei	_(ac)RPLMLQ(de)GHERS(ph)ITQ(de)IK_		
SAAVAEGGD	23	2	Phospho (STY	_SAAVAEGGDAVAET(ph)AKGEEGSPK_		
SAAVAEGGD	23	2	Phospho (STY	_SAAVAEGGDAVAET(ph)AKGEEGSPK_		
SAAVAEGGD	23	2	Phospho (STY	_SAAVAEGGDAVAET(ph)AKGEEGSPK_		
SAAVAEGGD	23	2	Phospho (STY	_SAAVAEGGDAVAET(ph)AKGEEGSPK_		
SAAVAEGGD	23	2	Phospho (STY	_SAAVAEGGDAVAETAKGEEGS(ph)PK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		

SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVS(ph)SPSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSSPS(ph)K_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSSPS(ph)K_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVS(ph)SPSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSSPS(ph)K_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSSPS(ph)K_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_		
SASIRILNLINS	17	1	Oxidation (M	_SASIRILNLIN	SASIRILN(0.0	SASIRILNLINS
SDSAVATSASI	21	1	Acetyl (Protei	_(ac)SDSAVAT(ph)SASPVAAPPATVEK_		
SDSAVATSASI	21	1	Acetyl (Protei	_(ac)SDSAVATS(ph)ASPVAAPPATVEK_		
SDSAVATSASI	21	1	Acetyl (Protei	_(ac)SDSAVAT(ph)SASPVAAPPATVEK_		
SETVDSTEVK	10	1	Acetyl (Protei	_(ac)S(ph)ET(ph)VDS(ph)T(ph)EVK_		
SHSPPPASNC	18	1	Acetyl (Protei	_(ac)S(ph)HSPPPASNCEEALIQLK_		
SIQNLNTRDPI	16	1	Acetyl (Protei	_(ac)S(ph)IQNLNTRDPFADAIK_		
SIQNLNTRDPI	16	1	Acetyl (Protei	_(ac)S(ph)IQNLNTRDPFADAIK_		
SISEFVDLEAEI	15	1	Phospho (STY	_S(ph)ISEFVDLEAEDAGK_		
SISEFVDLEAEI	15	1	Phospho (STY	_S(ph)ISEFVDLEAEDAGK_		
SITMSTISLPAI	21	2	Oxidation (M	_SIT(ph)MS(ph)TISLPAM(o	SITM(0.078)S	
SITMSTISLPAI	21	2	2 Oxidation (I	_SITM(ox)S(ph)T(ph)ISLPAM	SITM(1)STISLI	
SITMSTISLPAI	21	2	2 Oxidation (I	_SITM(ox)S(ph)T(ph)ISLPAM(ox)LSGVNLK		
SKKSWQARH	13	3	2 Phospho (S	_S(ph)KKSWC	SKKSWQ(1)ARHTGIK	
SLSRLNTLMK	10	1	Acetyl (Protei	_(ac)S(ph)LSR	SLSRLN(1)TLN	SLSRLNTLM(1
SLYRISARK	9	1	Acetyl (Protei	_(ac)S(ph)LYRISARK_		
SPIVFELTQPSI	14	1	Phospho (STY	_SPIVFELTQPS(ph)PEK_		
SPIVFELTQPSI	14	1	Phospho (STY	_SPIVFELTQPS(ph)PEK_		
SPIVFELTQPSI	14	1	Phospho (STY	_SPIVFELTQPS(ph)PEK_		
SPIVFELTQPSI	14	1	Phospho (STY	_SPIVFELTQPS(ph)PEK_		

SPIVFELTQPS	14	1	Phospho (STY	_SPIVFELTQPS(ph)PEK_		
SPIVFELTQPS	14	1	2 Phospho (S	_S(ph)PIVFELTQPS(ph)PEK_		
SRASFLAQNS	15	1	2 Phospho (S	_S(ph)RASFL	SRASFLAQ(0.715)N(0.27)SS	
SRKHKENLLK	10	3	Phospho (STY	_S(ph)RKHKE	SRKHKEN(1)LLK	
SSENSEYYSD	11	1	Acetyl (Protei	_(ac)S(ph)SENSEYYS(ph)DK_		
SSLSVKPNYTL	12	2	2 Phospho (S	_S(ph)SLS(ph	SSLSVKPN(1)YTLK	
STGQLQQLSA	17	1	Phospho (STY	_STGQLQQLS	STGQ(0.007)LQ(0.107)Q(0.	
SVFAEAYDPE	24	1	Phospho (STY	_S(ph)VFAEAYDPEADDDDDGATAVFPK_		
SVHSPNPGLIL	14	1	Acetyl (Protei	_(ac)SVHS(ph)PNPGLILQSK_		
SVHSPNPGLIL	14	1	Acetyl (Protei	_(ac)SVHS(ph)PNPGLILQSK_		
SVHSPNPGLIL	14	1	Acetyl (Protei	_(ac)SVHS(ph)PNPGLILQSK_		
SVHSPNPGLIL	14	1	Acetyl (Protei	_(ac)SVHS(ph)PNPGLILQSK_		
TELAAKLASSL	26	3	2 Phospho (S	_TELAAKLAS(	TELAAKLASSLVSQ(0.165)GK	
TIKYLKRVK	9	3	Phospho (STY	_TIKY(ph)LKRVK_		
TKIKIHYIEMT	16	3	2 Phospho (S	_T(ph)KIKIHYIEMT(ph)NVHAK_		
TLLNTSPNLLP	23	1	Phospho (STY	_TLLNTS(ph)PNLLPITTATDTFNNLK_		
TLPRNYIHREL	26	1	3 Phospho (S	_TLPRNY(ph)IHRELPS(ph)NLT(ph)RAMPS		
TNISRLGNYF	11	1	Acetyl (Protei	_(ac)TNIS(ph)RLGNYFK_		
TRRFDEVQMI	14	1	Oxidation (M	_T(ph)RRFDE	TRRFDEVQ(1)	TRRFDEVQM(
TSKKIIVANSG	13	2	2 Phospho (S	_T(ph)SKKIIVANS(ph)GSL_		
TSPKPTKPAS	12	3	Phospho (STY	_TSPKPTKPAS(ph)PK_		
TSPKPTKPAS	12	3	Phospho (STY	_TSPKPTKPAS(ph)PK_		
TSWIANPSAV	26	2	2 Phospho (S	_T(ph)SWIAN	TSWIAN(0.999)PSAVDKLLT	
TVNRLSFEKK	10	2	Phospho (STY	_T(ph)VN(de)	TVN(1)RLSFEKK	
VDRSDNAAES	25	1	Acetyl (Protei	_(ac)VDRSDNAAES(ph)FDDAVEERVINEEY		
VDRSDNAAES	25	1	Acetyl (Protei	_(ac)VDRSDNAAES(ph)FDDAVEERVINEEY		
VDRSDNAAES	25	1	Acetyl (Protei	_(ac)VDRSDNAAES(ph)FDDAVEERVINEEY		
VNSLIVLESDE	33	1	Phospho (STY	_VNSLIVLES(ph)DEEEDEQLVQAADLVEQE		
VNSLIVLESDE	33	1	Phospho (STY	_VNSLIVLES(ph)DEEEDEQLVQAADLVEQE		
VNSLIVLESDE	33	1	Phospho (STY	_VNSLIVLES(ph)DEEEDEQLVQAADLVEQE		
VQEEETVVPQ	15	2	Phospho (STY	_VQEEETVVPQS(ph)PSKK_		
VTDRSHYSPL	16	1	Phospho (STY	_VTDRSHYS(ph)PLVSEIAK_		
VTDRSHYSPL	16	1	Phospho (STY	_VTDRSHYS(ph)PLVSEIAK_		
VTILWMGGS	19	1	Oxidation (M	_VT(ph)ILWM(ox)GGSGSIV	VTILWM(1)G	
VTILWMGGS	19	1	Oxidation (M	_VT(ph)ILWM(ox)GGSGSIV	VTILWM(1)G	
VTILWMGGS	19	1	Oxidation (M	_VT(ph)ILWM(ox)GGSGSIV	VTILWM(1)G	
VTKSSSSK	8	2	Phospho (STY	_VT(ph)KSSSSK_		
VTRSTSENIIK	16	2	Oxidation (M	_VTRSTSENIIKM(ox)SGT(ph	VTRSTSENIIK	
VTSKPTLELLS	20	3	2 Phospho (S	_VTSKPTLELLS(ph)PIKPSS(ph)PIK_		
VTSKPTLELLS	20	3	2 Phospho (S	_VTSKPTLELLS(ph)PIKPSS(ph)PIK_		
VVDTLYQKAK	10	2	Phospho (STY	_VVDTLY(ph)	VVDTLYQ(1)KAK	
WEEPFYGGS	13	1	Phospho (STY	_WEEPFYGGS(ph)SPAK_		
WEEPFYGGS	13	1	Phospho (STY	_WEEPFYGGSS(ph)PAK_		

YFIESPHPEVL	13	1	2 Phospho (S	_Y(ph)FIES(p	YFIESPHPEVLQ(1)K	
YKVPQLEIVP	21	2	Oxidation (M	_YKVPQLEIVPNSAEERLHS(p		YKVPQLEIVP
YKVPQLEIVP	21	2	Oxidation (M	_YKVPQLEIVPNSAEERLHS(p		YKVPQLEIVP
YLAVGLLDAT	12	1	Phospho (STY	_Y(ph)LAVGLLDATVK_		
YLAVGLLDAT	12	1	Phospho (STY	_Y(ph)LAVGLLDATVK_		
YLNQWLHNLI	10	1	Phospho (STY	_Y(ph)LNQW	YLN(0.001)Q(0.151)WLHN(	
YLTVLLSLKTK	11	2	2 Phospho (S	_Y(ph)LTVLLS(ph)LKTK_		
YMKLTQEILQ	11	2	Phospho (STY	_Y(ph)MKLT	YMKLTQ(1)EILQ(1)K	
YNLKTPEAP	9	1	Phospho (STY	_YN(de)LKT(	YN(1)LKTPEAP	
YQGQQNDYIL	17	1	Phospho (STY	_YQ(de)GQQ	YQ(0.25)GQ(0.25)Q(0.25)N	
YRLLSANRAA	14	1	Phospho (STY	_Y(ph)RLLSA	YRLLSAN(1)RAAAVQ(1)K	
YRQAKMRHI	22	2	Oxidation (M	_YRQ(de)AK	YRQ(1)AKMR	YRQAKMRHI

Phospho (STY	Deamidation	Oxidation (M	Phospho (STY	Acetyl (Protei	Deamidation	Gln->pyro-Glu
AAAPAAVAS(0.997)PAAAAT(0.005)S(0.00			AAAPAAVAS(	0	0	0
AAAPAAVAS(0.995)PAAAAT(0.003)S(0.00			AAAPAAVAS(	0	0	0
AAAPAAVASPAAAAT(0.005)S(0.034)ADAS			AAAPAAVAS(	0	0	0
AAAPAAVASPAAAAT(0.006)S(0.042)ADAS			AAAPAAVAS(	0	0	0
AAAPAAVAS(0.078)PAAAAT(0.34)S(0.427			AAAPAAVAS(	0	0	0
AAAPAAVAS(0.004)PAAAAT(0.062)S(0.28			AAAPAAVAS(	0	0	0
AAAPAAVAS(0.993)PAAAAT(0.03)S(0.03)			AAAPAAVAS(	0	0	0
AAAPAAVAS(0.985)PAAAAT(0.077)S(0.08			AAAPAAVAS(	0	0	0
AAS(0.001)S(0.001)AAAQAI	AASSAAAQA		AAS(-27.34)S(	0	0	0
ACARGELY(0.814)S(0.183)LVLNT(0.003)K			ACARGELY(6.	1	0	0
ADEKMVT(1)DEK		ADEKM(80.6	ADEKMVT(80	0	0	0
AIELS(1)PGNALFHAK			AIELS(73.36)	0	0	0
AIELS(1)PGNALFHAK			AIELS(80.6)P	0	0	0
AKGEILDEVVT(1)LS(1)QIS(1)AKK			AKGEILDEVV	0	0	0
ALDLLMS(1)Y(1)RLK		ALDLLM(45.4	ALDLLMS(45.	0	0	0
ALDLLMS(1)Y(1)RLK		ALDLLM(57.1	ALDLLMS(57.	0	0	0
ALELS(0.008)HLKS(0.992)FVK			ALELS(-21.07	0	0	0
ALGGIVLT(0.066)AS(0.934)HNPGGPENDF			ALGGIVLT(-11	0	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK			ALGGIVLT(0)	0	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK			ALGGIVLT(0)	0	0	0
ALGGIVLT(0.784)AS(0.216)HNPGGPENDF			ALGGIVLT(5.6	0	0	0
ALGGIVLT(0.121)AS(0.879)HNPGGPENDF			ALGGIVLT(-8.	0	0	0
ALGGIVLT(0.098)AS(0.902)HNPGGPENDF			ALGGIVLT(-9.	0	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK			ALGGIVLT(0)	0	0	0
ALGGIVLT(0.204)AS(0.796)HNPGGPENDF			ALGGIVLT(-5.	0	0	0
				0	0	0
				0	0	0
				0	0	0
ALGGIVLT(0.5	ALGGIVLTASHN(-0.65)PGG		ALGGIVLT(0.6	0	1	0
ALILNRT(1)G	ALILN(44.61)RTGALN(44.61		ALILNRT(44.6	0	2	0
ALQAVYPDYVDELS(0.161)LY(0.135)GS(0.7			ALQAVY(-67.	0	0	0
ALQAVYPDYVDELS(0.021)LY(0.015)GS(0.			ALQAVY(-63.	0	0	0
ALQAVYPDYVDELS(0.001)LY(0.057)GS(0.			ALQAVY(-81.	0	0	0
ALQAVYPDYVDELS(0.001)LY(0.016)GS(0.			ALQAVY(-70.	0	0	0
ALQAVYPDY(0.002)VDELS(0.04)LY(0.004)			ALQAVY(-51.	0	0	0
				0	0	0
ALQAVYPDYVDELS(0.996)LY(0.009)GS(0.			ALQAVY(-75.	0	0	0
ALQAVY(0.084)PDY(0.078)VDELS(0.605)L			ALQAVY(-10.	0	0	0
APATPQAATSVTNPAAGDGIS(0.001)VQN			APAT(-56.02)	0	0	0
APATPQAATSVTNPAAGDGIS(0.001)VQN			APAT(-50.33)	0	0	0
APATPQAATSVTNPAAGDGIS(0.002)VQN			APAT(-39.76)	0	0	0
APATPQAATSVTNPAAGDGIS(0.004)VQN			APAT(-40.05)	0	0	0

APATPQAATSVTNPAAGDGIS(0.004)VQND			APAT(-44.28)	0	0	0
APS(0.997)LH	APSLHPPHME	APSLHPPHM(	APS(26.22)LH	0	1	0
AQDVVGRGAT(1)NILICNK			AQDVVGRGA	0	0	0
AQDVVGRGAT(1)NILICNK			AQDVVGRGA	0	0	0
				0	0	0
AQNIS(0.997)PEQS(0.003)GGAGGGGSK			AQNIS(24.87)	1	0	0
ARLVFT(1)EK			ARLVFT(64.82	1	0	0
ARLVFT(1)EK			ARLVFT(106.2	1	0	0
ARS(0.999)LS(0.999)NS(0.964)PLY(0.038)			ARS(32.82)LS	0	0	0
ARS(1)LS(0.989)NS(0.852)PLY(0.16)HRKK			ARS(33.29)LS	0	0	0
ARS(1)LS(1)NS(0.998)PLY(0.003)HRKK			ARS(46.06)LS	0	0	0
ASAFQFS(1)DDEEEVK			AS(-64.04)AF	0	0	0
ASAFQFS(1)DDEEEVK			AS(-48.64)AF	0	0	0
ASAFQFS(1)DDEEEVK			AS(-75.24)AF	0	0	0
ASAFQFS(1)DDEEEVK			AS(-54.82)AF	0	0	0
ASAFQFS(1)DDEEEVK			AS(-61.47)AF	0	0	0
ASAFQFS(1)DDEEEVK			AS(-59.12)AF	0	0	0
ASAFQFS(1)DDEEEVK			AS(-56.8)AFQ	0	0	0
ASAFQFS(1)DDEEEVK			AS(-42.65)AF	0	0	0
ASAFQFS(1)DDEEEVK			AS(-66.2)AFQ	0	0	0
ASAFQFS(1)DDEEEVK			AS(-67.24)AF	0	0	0
ASAFQFS(1)DDEEEVK			AS(-96.36)AF	0	0	0
				0	0	0
AS(1)GVTVSDVCK			AS(39.82)GV	1	0	0
AS(1)GVTVSDVCK			AS(38.57)GV	1	0	0
AS(1)GVTVSDVCK			AS(40.23)GV	1	0	0
AS(1)GVTVSDVCK			AS(38.02)GV	1	0	0
AS(0.977)GVT(0.022)VSDVCK			AS(16.42)GV	1	0	0
AS(0.997)GVT(0.003)VSDVCK			AS(25.59)GV	1	0	0
AS(0.42)GVT(0.568)VS(0.012)DVCK			AS(-1.31)GVT	1	0	0
AS(0.998)GVT(0.002)VSDVCK			AS(26.02)GV	1	0	0
AS(1)GVTVSDVCK			AS(35.02)GV	1	0	0
AS(0.976)GVT(0.023)VS(0.001)DVCK			AS(16.37)GV	1	0	0
				1	0	0
AS(0.748)RH	ASRHN(47.22)TASRAHVITRI		AS(5.52)RHN	0	1	0
CIS(1)AVNKQ	CISAVN(-36.09)KQ(-29.43)		CIS(58.63)AV	0	1	0
CLPDY(1)ANKLK			CLPDY(43.63)	0	0	0
				0	0	0
DLEY(1)FNNL	DLEYFN(65.22)N(65.22)LK		DLEY(65.22)F	0	2	0
DLEY(1)FNNL	DLEYFN(54.07)N(54.07)LK		DLEY(54.07)F	0	2	0
DMRGT(1)ILRRK		DM(57.55)RG	DMRGT(57.5	0	0	0
DRQSLFT(0.0	DRQ(24.42)SLFTQ(-24.42)V		DRQS(-44.49)	0	1	0
DVDFGDS(1)DNENEPDAYLARLK			DVDFGDS(53.	0	0	0

DVDFGDS(1)DNENEPDAYLARLK			DVDFGDS(67.	0	0	0
DVDFGDS(1)DNENEPDAYLARLK			DVDFGDS(43.	0	0	0
DVDFGDS(1)DNENEPDAYLARLK			DVDFGDS(56.	0	0	0
DVDFGDS(0.994)DNENEPDAY(0.006)LARL			DVDFGDS(22.	0	0	0
DVDFGDS(0.999)DNENEPDAY(0.001)LARL			DVDFGDS(31.	0	0	0
EAAAGEDIT(0.001)PLADES(0.999)IK			EAAAGEDIT(-	0	0	0
EAAQY(0.933)GT(0.067)VNAVLPK			EAAQY(11.44	0	0	0
EAAQY(0.799)GT(0.201)VNAVLPK			EAAQY(6)GT(	0	0	0
EANMLQS(1)I	EAN(-24.31)M	EANM(56.46)	EANMLQS(56	0	1	0
EAS(0.012)PVS(0.157)MAS(		EASPVSM(53.	EAS(-18.36)P	0	0	0
EAS(0.014)PVS(0.221)MAS(		EASPVSM(53.	EAS(-17.37)P	0	0	0
EAS(0.127)PVS(0.465)MAS(		EASPVSM(40.	EAS(-5.65)PV	0	0	0
EFVFQLHGKMS(0.255)NY(0		EFVFQLHGKM	EFVFQLHGKM	0	0	0
EKT(1)DAMAKAQEFLRT(1)K			EKT(46.68)DA	0	0	0
ELGNAEPAPSVSSTTVS(0.286)S(0.713)PPA			ELGNAEPAPS	0	0	0
ELPDSDSLNVAPPEGFS(1)DEEPEERQCK			ELPDS(-46.35	0	0	0
ELPDSDSLNVAPPEGFS(1)DEEPEERQCK			ELPDS(-49.23	0	0	0
ELPDSDS(0.001)LNVAPPEGFS(0.999)DEEF			ELPDS(-38.75	0	0	0
EMIKILQEQAI	EMIKILQ(0)EQ(0)ALN(19.11		EMIKILQEQAL	0	2	0
ENS(1)PS(1)N	EN(-13.93)SPSN(13.93)VAK		ENS(49.45)PS	0	1	0
ENTKNLVT(0.	EN(40.01)TKN(40.01)LVTGE		ENT(-37.23)K	0	2	0
ES(1)AQQLEA	ESAQ(7.67)Q(-7.67)LEAQ(2		ES(40.73)AQQ	0	2	0
ESTPLS(0.351)AS(0.649)PKK			ES(-36.54)T(-	0	0	0
ETELMQS(0.001)KIQET(0.999)LGLDPVDK			ET(-43.05)ELM	0	0	0
ETEQVAQPQI	ETEQ(-11.49)VAQ(-11.49)P		ET(-42.33)EQ	0	2	0
ET(1)IADIMRVKT(1)IK			ET(47.55)IADI	0	0	0
EVCAQS(0.88	EVCAQ(-12.82)SLQ(-12.82)I		EVCAQS(12.8	0	2	0
EVS(1)DDEADDEKK			EVS(51.07)DD	0	0	0
FFDS(1)GDYQMAK		FFDSGDYQM(	FFDS(40.97)G	0	0	0
FFDS(0.994)GDY(0.006)QM		FFDSGDYQM(	FFDS(22.15)G	0	0	0
FFDS(1)GDYQMAK		FFDSGDYQM(	FFDS(36.09)G	0	0	0
FMSNKNPY(0	FMSN(-21.26)	FM(-38.75)SN	FMS(-39.87)N	0	1	0
FS(1)S(1)ELFKEIIK			FS(42.43)S(42	0	0	0
GEALT(0.8)S(	GEALTSKQ(20.61)RYQ(-20.6		GEALT(5.85)S	0	1	0
GELQAGKS(1)PFK			GELQAGKS(61	1	0	0
GELQAGKS(1)PFK			GELQAGKS(60	1	0	0
GELQAGKS(1)PFK			GELQAGKS(60	1	0	0
GLGMT(0.906)KINLIT(0.094		GLGM(45.65)	GLGMT(9.84)	0	0	0
GPQLEDGKVT	GPQ(67.17)LE	GPQLEDGKVT	GPQLEDGKVT	0	1	0
GQPLVVLS(1)	GQ(40.62)PLV	GQPLVVLSAM	GQPLVVLS(40	0	1	0
HNNSPNTNLA	HN(0)N(0)SPN(-9.76)TN(-15		HNNS(-46.33)	0	1	0
HNNSPNTNLA	HN(0)N(0)SPN(-4.61)TN(-4.		HNNS(-52.12)	0	1	0
IGEGT(0.186)Y(0.809)GVVY(0.006)K			IGEGT(-6.39)Y	0	0	0

IIT(0.001)HPN	IITHPN(4.6)FN(-4.6)GN(-4.6		IIT(-32.2)HPN	0	2	0
IITHPNFNGNT	IITHPN(3.85)FN(-3.85)GN(-8		IIT(-38.2)HPN	0	2	0
IKAEHEYRTS(	IKAEHEYRTSM	IKAEHEYRTSM	IKAEHEY(-42.5	0	1	0
IKPILQAT(0.45	IKPILQ(-16.83	IKPILQATQTS(	IKPILQAT(0)Q	0	2	0
IKPILQAT(0.37	IKPILQ(-23.57	IKPILQATQTS(	IKPILQAT(0)Q	0	2	0
				0	2	0
				0	2	0
				0	2	0
ILFVTESENQA	ILFVTESEN(10.6)Q(-10.6)AN		ILFVT(-51.46)	0	1	0
ILFVTESENQA	ILFVTESEN(10.6)Q(-10.6)AN		ILFVT(-51.46)	0	1	0
INQIQMKET(1	IN(-12.2)Q(-1	INQIQM(54.2	INQIQMKET(5	0	2	0
IQVQTKQIAQ	IQ(-30.74)VQ	IQVQTKQIAQ	IQVQT(-61.06	0	2	0
IQVQTKQIAQ	IQ(-21.7)VQ(-	IQVQTKQIAQ	IQVQT(-54.25	0	2	0
IQVQTKQIAQ	IQ(0)VQ(0)TKQ(-12.69)IAQ(		IQVQT(-41.78	0	2	0
IS(1)ENT(0.999)IAIIS(0.061)T(0.94)ELEIQK			IS(34.56)ENT(	0	0	0
IS(1)MLKQVMS(1)QLIKK		ISM(6.54)LKQ	IS(57.43)MLK	0	0	0
KDFLPLAFQMQAS(0.227)T(		KDFLPLAFQM	KDFLPLAFQM	0	0	0
KDIT(0.837)N	KDITN(56.04)LSYKVVK		KDIT(9.69)NLS	0	1	0
KEES(0.181)ES(0.819)EDDD		KEESESEDDDI	KEES(-6.55)ES	0	0	0
KEES(0.209)ES(0.791)EDDD		KEESESEDDDI	KEES(-5.78)ES	0	0	0
KEES(0.074)ES(0.926)EDDD		KEESESEDDDI	KEES(-10.98)E	0	0	0
KEPT(1)PGEK			KEPT(41.43)P	0	0	0
KIDNPES(0.333)S(0.333)AKVS(0.333)DAEE			KIDNPES(0)S(	0	0	0
KIDNPES(0.012)S(0.022)AKVS(0.966)DAEE			KIDNPES(-19.	0	0	0
KIDNPES(0.489)S(0.489)AKVS(0.022)DAEE			KIDNPES(0)S(	0	0	0
KIDNPES(0.567)S(0.41)AKVS(0.023)DAEEE			KIDNPES(1.41	0	0	0
KIEKFQS(1)EEQQQTEDELQDK			KIEKFQS(34.8	0	0	0
KIEKFQS(1)EEQQQTEDELQDK			KIEKFQS(54.1	0	0	0
KKEEES(1)DQS(1)DDDMGF(		KKEEESDQSD	KKEEES(46.14	0	0	0
KKEEES(1)DQS(1)DDDMGF(		KKEEESDQSD	KKEEES(46.7)	0	0	0
KKEEES(1)DQS(1)DDDMGF(		KKEEESDQSD	KKEEES(42.09	0	0	0
KKEEES(0.035)DQS(0.965)D		KKEEESDQSD	KKEEES(-14.3	0	0	0
KKQEES(1)DEEFFDLDDIK			KKQEES(93.2)	0	0	0
KLAFS(0.939)DDES(0.054)T(0.007)PEEHQ			KLAFS(12.41)	0	0	0
KLIVNGAS(0.9	KLIVN(62.53)GASSN(62.53)		KLIVNGAS(31	0	2	0
KMEVLS(1)VQ	KMEVLSVQ(-6.9)N(6.9)HIQ(		KMEVLS(44.5	0	2	0
KMKY(1)DFGT(1)LLLLVK			KMKY(58.46)	0	0	0
KNKT(0.997)N	KN(15.36)KTN(-15.36)RQ(-3		KNKT(30.06)N	1	1	0
KPEDPSSEAEALCS(1)PAK			KPEDPS(-47.0	0	0	0
KPEDPSSEAEALCS(1)PAK			KPEDPS(-37.5	0	0	0
KPEDPSSEAEALCS(1)PAK			KPEDPS(-41.9	0	0	0
KPEDPSSEAEALCS(1)PAK			KPEDPS(-51.7	0	0	0
KPEDPSSEAEALCS(1)PAK			KPEDPS(-69.7	0	0	0

KPEDPSSEAEALCS(1)PAK			KPEDPS(-49.5	0	0	0
KQEES(1)DEEFFDLDDIK			KQEES(130.52	0	0	0
KS(0.928)APC	KSAPQ(47.92)SRQ(47.92)SC		KS(13.71)APC	0	2	0
KS(1)KPT(0.99	KSKPTAAVTPIQ(46.34)K		KS(43.28)KPT	0	1	0
KVT(1)T(0.997)IGLNS(0.003)TAATK			KVT(37.94)T(2	0	0	0
KVT(1)WIGAN	KVTWIGAN(5.27)GDQ(-5.27		KVT(40.09)W	0	1	0
LDLT(0.002)IV	LDLTIVDLN(-9.21)DEVQ(-3.8		LDLT(-26.77)I	0	1	0
LENLAY(0.472)EKS(0.53)EDI		LENLAYEKSED	LENLAY(-0.55	0	0	0
LFEPPVT(0.001)MRDMLKS(0.016)LS(0.20			LFEPPVT(-31.	0	0	0
LGIDIGDRLQAT(1)S(1)RK			LGIDIGDRLQA	0	0	0
LLDFNLLDT(0.999)DDDDDEEGDEEDKEDTV			LLDFNLLDT(3	0	0	0
LNENFVT(1)IN	LN(9)EN(9)FVTIN(-7.29)IQ(7		LNENFVT(41.	0	3	0
LRFDFNS(0.98	LRFDFN(-32.02)SKAAMTIEC		LRFDFNS(20.3	0	1	0
LRT(0.242)S(0	LRTSPN(50.04)EQ(50.04)Q(		LRT(-4.96)S(4	0	3	0
LSVQS(1)PPK			LS(-82.61)VQS	0	0	0
LT(1)NGQRQI	LTN(-22.9)GC	LTNGQRQM(5	LT(53.12)NGC	0	2	0
LT(0.999)NGC	LTN(-20.27)G	LTNGQRQM(4	LT(40.05)NGC	0	2	0
MESTTIVFVTL	MESTTIVFVTL	M(54.95)ESTT	MES(-53.59)T	0	1	0
MFLT(1)QQQ	MFLTQ(-17.64	M(49.63)FLTC	MFLT(49.63)C	0	2	0
MFLT(1)QQQ	MFLTQ(-8.51)	M(68.68)FLTC	MFLT(68.68)C	0	2	0
MGHLQLDFHS(1)IPK		M(44.69)GHL	MGHLQLDFHS	1	0	0
MHKLIMRS(1)VINNLK		M(59.98)HKLI	MHKLIMRS(59	0	0	0
MIRAT(0.001)S(0.001)CALS		M(42.82)IRAT	MIRAT(-36.1)	0	0	0
MLNRCLELVT	MLN(55.75)R	M(55.75)LNR	MLNRCLELVT	0	1	0
				0	1	0
MLVRRLLQEL	MLVRRLLQ(4	M(41.42)LVRI	MLVRRLLQEL	0	2	0
MNDS(0.993)FGDFNAT(0.0		M(76.82)NDS	MNDS(22.16)	1	0	0
MPNLQS(0.857)S(0.121)IPH		M(56.2)PNLQ	MPNLQS(8.49	1	0	0
MPNLQS(0.492)S(0.492)IPH		M(40.24)PNL	MPNLQS(0)S(	1	0	0
MPNLQS(0.778)S(0.175)IPH		M(47.71)PNL	MPNLQS(6.47	1	0	0
MPNLQS(0.497)S(0.497)IPH		M(58.89)PNL	MPNLQS(0)S(	1	0	0
MQHS(0.5)S(0	MQ(38.01)HS	M(19.78)QHS	MQHS(0)S(0)I	0	1	0
MQIFVKT(0.5	MQ(42.8)IFVKTLTGK		MQIFVKT(0)L	1	1	0
MQLILS(0.695	MQ(-7.66)LILSYLQ(7.66)SQ(		MQLILS(7.66)	1	3	0
MQLILS(0.245	MQ(-25.8)LILSYLQ(25.8)SQ(		MQLILS(-4.01	1	3	0
				1	3	0
				1	3	0
MQLILS(0.974	MQ(7.74)LILS	M(44.25)QLIL	MQLILS(19.37	0	2	0
MQLILS(0.201	MQ(-13.61)LI	M(43.69)QLIL	MQLILS(-5.35	0	2	0
				0	2	0
				0	2	0
MRDKIS(1)QL	MRDKISQ(-15	M(62.09)RDK	MRDKIS(62.09	1	1	0
MRDKIS(1)QL	MRDKISQ(-15	M(54.34)RDK	MRDKIS(54.34	1	1	0

MRDKIS(1)QL	MRDKISQ(-10	M(56.2)RDKIS	MRDKIS(56.2	1	1	0
MRDKIS(1)QL	MRDKISQ(-17	M(51.13)RDK	MRDKIS(51.1	1	1	0
MRDKIS(1)QL	MRDKISQ(-12	M(51.46)RDK	MRDKIS(51.4	1	1	0
MRDKIS(1)QL	MRDKISQ(-4.	M(43.8)RDKIS	MRDKIS(43.8	1	1	0
MRFIS(0.025)	MRFISQ(0.64	M(45.21)RFIS	MRFIS(-15.4)	1	1	0
MSGALKS(0.7	MSGALKSQ(-	M(50.15)SGA	MS(-33.15)GA	1	1	0
MS(0.417)LIH	MSLIHSFVTQ(	M(54.77)SLIH	MS(0)LIHS(0)	0	1	0
MS(0.002)QGAS(0.01)EVPLS(0.988)ALRLK			MS(-26.68)Q	1	0	0
MS(1)T(1)IVRK			MS(44.98)T(4	0	0	0
MS(0.5)T(0.5	MSTLLEN(7.5	M(43.21)STLL	MS(0)T(0)LLE	0	2	0
MTEIELPVESVPS(0.051)AS(		M(60.73)TEIE	MT(-56.15)EI	0	0	0
MTIFNLY(1)IFDK		M(46.88)TIFN	MT(-34.52)IFI	0	0	0
MVEPSPETVGDFQSVQEEVE		M(86.56)VEPS	MVEPS(-69.6	0	0	0
MVEPSPETVGDFQS(0.245)V		M(50.26)VEP	MVEPS(-41.7	0	0	0
MVEPSPETVGDFQS(0.001)V		M(50.32)VEP	MVEPS(-37.1	0	0	0
MY(0.401)NI	MYN(63.42)IYVLKK		MY(-1.74)NIY	0	1	0
MY(0.636)NI	MYN(53.77)IYVLKK		MY(2.43)NIY(	0	1	0
NAGGVGVGVGEKS(1)PDLK			NAGGVGVGV	0	0	0
NAGGVGVGVGEKS(1)PDLK			NAGGVGVGV	0	0	0
NAGGVGVGVGEKS(1)PDLK			NAGGVGVGV	0	0	0
NAGGVGVGVGEKS(1)PDLK			NAGGVGVGV	0	0	0
				0	0	0
NAGGVGVGVGEKS(1)PDLKK			NAGGVGVGV	0	0	0
NAGGVGVGVGEKS(1)PDLKK			NAGGVGVGV	0	0	0
NGGILNY(1)M	N(13.8)GGILN	NGGILNYM(4	NGGILNY(49.	0	1	0
NIWKDKT(1)P	N(31.96)IWKDKTPN(-31.96)		NIWKDKT(52.	0	1	0
NKEPLIQIAM	N(8)KEPLIQ(-	NKEPLIQIAM(	NKEPLIQIAM	0	1	0
NKLQKNHALI	N(32.5)KLQ(32.5)KN(32.5)H		NKLQKNHALI	0	4	0
NLKLQMAS(1	N(12.81)LKL	NLKLQM(41.	NLKLQMAS(4	0	1	0
NNIKLKCLIDT	N(-18.42)N(-18.42)IKLKCLID		NNIKLKCLIDT	1	1	0
NS(0.002)QY(0.97)ERES(0.029)LLK			NS(-27.81)QY	0	0	0
				0	0	0
NVGIFIKDDS(1)DEEDVDDKK			NVGIFIKDDS(	0	0	0
NVGIFIKDDS(1)DEEDVDDKK			NVGIFIKDDS(	0	0	0
NVGIFIKDDS(1)DEEDVDDKK			NVGIFIKDDS(	0	0	0
NY(1)PFNIEF	N(41.43)YPFN(41.43)IEF		NY(41.43)PFN	0	2	0
PCNLY(0.854)QT(0.146)AQEQLK			PCNLY(7.67)	0	0	0
PCNLY(0.962)	PCN(24.93)LYQ(-24.93)TAQ		PCNLY(14.07)	0	1	0
PLMQLIIQDTGIGMT(1)K		PLM(40.86)Q	PLMQLIIQDT(	0	0	0
PLPS(1)GRIPQIT(0.999)PPAS(0.001)PK			PLPS(41.55)G	0	0	0
PLPS(1)GRIPQIT(0.997)PPAS(0.004)PK			PLPS(33.2)GR	0	0	0
PTVAAAAKPAADDDDDVDLFGS(1)DDEEDE			PT(-35.3)VAA	0	0	0
QELLQS(0.87	Q(51.95)ELL	QELLQSYM(5	QELLQS(8.31)	0	2	1

QELLQS(0.84	Q(41.43)ELLC	QELLQSYM(4	QELLQS(7.5)Y	0	2	1
QELLQS(0.24	Q(45.02)ELLQ(45.02)SYMK		QELLQS(-4.96	0	2	1
QHS(0.009)F	Q(50.79)HSFTSSSALK		QHS(-16.7)FT	0	1	0
QISIGIY(1)ELLK			QIS(-47.73)IG	0	0	0
QISIGIY(1)ELLK			QIS(-48.31)IG	0	0	0
QISIGIY(1)ELLK			QIS(-46.94)IG	0	0	0
QIS(0.001)IGIY(0.999)ELLK			QIS(-32.34)IG	0	0	0
QISIGIY(1)ELLK			QIS(-55.01)IG	0	0	0
QISIGIY(1)ELLK			QIS(-38.47)IG	0	0	0
QISIGIY(1)ELLK			QIS(-43.94)IG	0	0	0
QISIGIY(1)ELLK			QIS(-39.86)IG	0	0	0
QISIGIY(1)ELLK			QIS(-57.55)IG	0	0	0
QISIGIY(1)ELLK			QIS(-35.76)IG	0	0	0
QISIGIY(1)ELLK			QIS(-50.69)IG	0	0	0
QISIGIY(1)ELLK			QIS(-47.93)IG	0	0	0
QISIGIY(1)ELLK			QIS(-49.83)IG	0	0	0
QISIGIY(1)ELLK			QIS(-53)IGIY(	0	0	0
QISIGIY(1)ELLK			QIS(-39.44)IG	0	0	0
QISIGIY(1)ELLK			QIS(-55.72)IG	0	0	0
QISIGIY(1)ELLK			QIS(-52.88)IG	0	0	0
QISIGIY(1)ELLK			QIS(-36.23)IG	0	0	0
QIS(1)VRGIAEVGNVTEVK			QIS(75.86)VR	0	0	1
QIS(1)VRGIAEVGNVTEVK			QIS(45.62)VR	0	0	1
QIS(1)VRGIAEVGNVTEVKK			QIS(87.21)VR	0	0	1
				0	0	1
QIVPLLNY(1)	Q(75.74)IVPLLN(75.74)YK		QIVPLLNY(75.	0	2	0
QKES(1)GEFPEVGK			QKES(64.64)	0	0	0
QKFIT(0.5)T(	Q(12.07)KFIT	QKFITTEDVN	QKFIT(0)T(0)E	0	1	0
QLRDLET(1)ELDEERK			QLRDLET(50.	0	0	1
QLRDLET(1)ELDEERK			QLRDLET(46.	0	0	1
QLSIIRQKS(1)	Q(28.76)LSIIRQ(-28.76)KSL		QLS(-42.53)II	0	1	1
QMPDVETTE	Q(47.51)MPD	QM(47.51)PD	QMPDVET(-3	0	1	0
QNDLIHDRS(1)LINK			QNDLIHDRS(	0	0	1
QNDLIHDRS(1)LINK			QNDLIHDRS(	0	0	1
QNDLIHDRS(1)LINK			QNDLIHDRS(	0	0	1
QRDLPAPRES(0.569)QS(0.42)RS(0.011)K			QRDLPAPRES	0	0	1
QS(0.023)LIM	Q(28.35)SLIM	QSLIM(45.37)	QS(-16.46)LIM	0	1	0
QSSYHGVHQAWNT(0.042)NQDS(0.957)K			QS(-41.5)S(-4	0	0	1
QSSYHGVHQAWNT(0.028)NQDS(0.972)K			QS(-47.65)S(	0	0	1
QSSYHGVHQAWNT(0.042)NQDS(0.958)K			QS(-80.23)S(	0	0	1
QSSYHGVHQAWNT(0.001)NQDS(0.999)K			QS(-87.48)S(	0	0	1
QSSYHGVHQAWNT(0.01)NQDS(0.99)K			QS(-52.27)S(	0	0	1
QSSYHGVHQAWNT(0.025)NQDS(0.975)K			QS(-60.4)S(-6	0	0	1

QSSYHGVHQAWNT(0.005)NQDS(0.995)K			QS(-73.94)S(-	0	0	1
QSSYHGVHQAWNT(0.128)NQDS(0.872)K			QS(-48.42)S(-	0	0	1
QS(0.014)VP	Q(21.8)SVPQ(21.8)LAN(20.		QS(-21.8)VPC	0	3	0
QS(0.005)VP	Q(13.41)SVPQ(14.75)LAN(5		QS(-25.08)VP	0	3	0
QS(0.006)VP	Q(11.59)SVPQ(18.04)LAN(6		QS(-24.64)VP	0	3	0
				0	3	0
				0	3	0
QVEPRQLVR	Q(-32.88)VEP	QVEPRQLVR	QVEPRQLVR	0	1	0
QVRT(1)NLQ	Q(0)VRTN(0)LQ(0)EIQ(30.0		QVRT(64.82)	0	2	1
				0	2	1
REEENAAAAEEEAGEISAT(0.01)GGAT(0.21			REEENAAAAE	0	0	0
REEENAAAAEEEAGEISAT(0.001)GGAT(0.4			REEENAAAAE	0	0	0
REEENAAAAEEEAGEIS(0.005)AT(0.02)GG			REEENAAAAE	0	0	0
RGCQILGLNK	RGCQ(16.13)ILGLN(-16.13)		RGCQILGLNK	0	1	0
RGCQILGLNK	RGCQ(7.33)ILGLN(-7.33)KY		RGCQILGLNK	0	1	0
RGCQILGLNK	RGCQ(33.24)ILGLN(-33.24)		RGCQILGLNK	0	1	0
RGPPPPPT(0.	RGPPPPPTASESTRRN(43.11		RGPPPPPT(-2	0	1	0
				0	1	0
				0	1	0
RIAS(0.064)FKNY(0.898)IS(0.037)K			RIAS(-11.45)F	0	0	0
RIQEVY(1)LQ	RIQ(-12.87)EVYLQ(12.87)K		RIQEVY(55.06	0	1	0
RKKPEDPSSEAEALCS(1)PAK			RKKPEDPS(-5	0	0	0
RKKPEDPSSEAEALCS(1)PAK			RKKPEDPS(-4	0	0	0
RKKPEDPSSEAEALCS(1)PAK			RKKPEDPS(-4	0	0	0
RKKPEDPSSEAEALCS(1)PAK			RKKPEDPS(-3	0	0	0
RKKPEDPSSEAEALCS(1)PAK			RKKPEDPS(-4	0	0	0
RKKPEDPSSEAEALCS(1)PAK			RKKPEDPS(-3	0	0	0
RKKPEDPSSEAEALCS(1)PAK			RKKPEDPS(-4	0	0	0
RKKPEDPSSEAEALCS(1)PAK			RKKPEDPS(-4	0	0	0
RKKPEDPSSEAEALCS(1)PAK			RKKPEDPS(-5	0	0	0
RMASSEQPT(	RMASSEQ(0)	RM(67.65)AS	RMAS(-37.42	0	1	0
RPLMLQGHE	RPLMLQ(40.43)GHERSITQ(		RPLMLQGHE	1	2	0
				1	2	0
SAAVAEGGDAVAET(0.733)AKGEEGS(0.26			S(-42.23)AAV	0	0	0
SAAVAEGGDAVAET(0.901)AKGEEGS(0.09			S(-58.47)AAV	0	0	0
SAAVAEGGDAVAET(0.614)AKGEEGS(0.38			S(-39.38)AAV	0	0	0
S(0.001)AAVAEGGDAVAET(0.702)AKGEE			S(-28.94)AAV	0	0	0
SAAVAEGGDAVAET(0.209)AKGEEGS(0.79			S(-48.44)AAV	0	0	0
SAEAEAIVTTATADVS(0.307)S(0.514)PS(0.			S(-107.65)AE	1	0	0
SAEAEAIVTTATADVS(0.034)S(0.483)PS(0.			S(-78.78)AEA	1	0	0
SAEAEAIVTTATADVS(0.051)S(0.77)PS(0.1			S(-102.74)AE	1	0	0
SAEAEAIVTTATADVS(0.007)S(0.496)PS(0.			S(-76.49)AEA	1	0	0
SAEAEAIVT(0.022)T(0.02)AT(0.067)ADVS			S(-61.37)AEA	1	0	0

SAEAEAIVTTATADVS(0.01)S(0.495)PS(0.4			S(-54.67)AEA	1	0	0
SAEAEAIVTT(0.001)AT(0.004)ADVS(0.046			S(-61.79)AEA	1	0	0
SAEAEAIVTTATADVS(0.019)S(0.957)PS(0.			S(-108.85)AE	1	0	0
SAEAEAIVTTATADVS(0.041)S(0.479)PS(0.			S(-81.76)AEA	1	0	0
SAEAEAIVTTATADVS(0.047)S(0.743)PS(0.			S(-102.8)AEA	1	0	0
SAEAEAIVTTATADVS(0.48)S(0.329)PS(0.1			S(-50.28)AEA	1	0	0
SAEAEAIVTTATADVS(0.045)S(0.421)PS(0.			S(-119.63)AE	1	0	0
SAEAEAIVTTAT(0.001)ADVS(0.035)S(0.37			S(-66.49)AEA	1	0	0
SAEAEAIVTTATADVS(0.007)S(0.783)PS(0.			S(-112.12)AE	1	0	0
SAEAEAIVTTATADVS(0.052)S(0.762)PS(0.			S(-82.71)AEA	1	0	0
SAEAEAIVT(0.01)T(0.012)AT(0.04)ADVS(			S(-39.1)AEAE	1	0	0
SAEAEAIVTTATADVS(0.067)S(0.467)PS(0.			S(-77.93)AEA	1	0	0
SAEAEAIVTTATADVS(0.021)S(0.489)PS(0.			S(-77.91)AEA	1	0	0
SAEAEAIVTT(0.002)AT(0.006)ADVS(0.174			S(-40.69)AEA	1	0	0
SAEAEAIVTTATADVS(0.035)S(0.71)PS(0.2			S(-81.87)AEA	1	0	0
SAEAEAIVTTATADVS(0.175)S(0.771)PS(0.			S(-108.29)AE	1	0	0
SAEAEAIVTTATADVS(0.035)S(0.813)PS(0.			S(-91.77)AEA	1	0	0
SAEAEAIVTTATADVS(0.008)S(0.158)PS(0.			S(-76.74)AEA	1	0	0
SAEAEAIVTTATADVS(0.066)S(0.717)PS(0.			S(-108.3)AEA	1	0	0
SAEAEAIVTTATADVS(0.185)S(0.408)PS(0.			S(-80.53)AEA	1	0	0
SAEAEAIVTTATADVS(0.018)S(0.396)PS(0.			S(-55.82)AEA	1	0	0
SAEAEAIVTTATADVS(0.068)S(0.878)PS(0.			S(-89.55)AEA	1	0	0
				1	0	0
SASIRILNLINS	SASIRILN(-15.	SASIRILNLINS	S(-45.57)AS(-	0	1	0
S(0.015)DS(0.015)AVAT(0.71)S(0.194)AS(			S(-16.63)DS(-	1	0	0
S(0.01)DS(0.01)AVAT(0.112)S(0.693)AS(0			S(-18.26)DS(-	1	0	0
SDSAVAT(0.333)S(0.333)AS(0.333)PVAAP			S(-34.71)DS(-	1	0	0
S(1)ET(1)VDS(1)T(1)EVK			S(47.19)ET(4	1	0	0
S(0.55)HS(0.449)PPPAS(0.001)NCEEALIQ			S(0.88)HS(-0.	1	0	0
S(0.984)IQNLNT(0.016)RDPFADAIK			S(17.92)IQNL	1	0	0
S(0.955)IQNLNT(0.045)RDPFADAIK			S(13.27)IQNL	1	0	0
S(0.89)IS(0.11)EFVDLEAEDAGK			S(9.1)IS(-9.1)	0	0	0
				0	0	0
S(0.193)IT(0.578)MS(0.578		SITM(-11.71)	S(-6.05)IT(0)	0	0	0
S(0.239)IT(0.275)MS(0.533		SITM(40.18)S	S(-4.82)IT(-4.	0	0	0
SK_				0	0	0
S(0.5)KKS(0.5	SKKSWQ(45.36)ARHTGIK		S(0)KKS(0)W	0	1	0
S(0.5)LS(0.5)	SLSRLN(52.5	SLSRLNTLM(5	S(0)LS(0)RLN	1	1	0
S(0.889)LY(0.111)RISARK			S(9.03)LY(-9.	1	0	0
SPIVFELT(0.001)QPS(0.999)PEK			S(-54.97)PIVF	0	0	0
SPIVFELT(0.001)QPS(0.999)PEK			S(-67.16)PIVF	0	0	0
SPIVFELT(0.001)QPS(0.999)PEK			S(-63.62)PIVF	0	0	0
SPIVFELTQPS(1)PEK			S(-86.11)PIVF	0	0	0

SPIVFELTQPS(1)PEK			S(-70.03)PIVF	0	0	0
S(1)PIVFELT(0.009)QPS(0.991)PEK			S(40.41)PIVF	0	0	0
S(0.773)RAS(	SRASFLAQ(4.71)N(-4.71)SS(		S(6.47)RAS(-6	0	1	0
S(1)RKHKENL	SRKHKEN(58.59)LLK		S(58.59)RKHK	0	1	0
S(0.397)S(0.397)ENS(0.206)EY(0.038)Y(0.			S(0)S(0)ENS(-	1	0	0
S(0.51)S(0.51	SSLSVKPN(46.89)YTLK		S(0)S(0)LS(9.2	0	1	0
STGQLQQLS(	STGQ(-23.59)LQ(-11.38)Q(-		S(-72.86)T(-7	0	3	0
S(0.997)VFAEAY(0.003)DPEADDDDDGAT			S(24.92)VFAE	0	0	0
S(0.06)VHS(0.94)PNPGLILQSK			S(-11.98)VHS	1	0	0
S(0.003)VHS(0.997)PNPGLILQSK			S(-25.47)VHS	1	0	0
S(0.002)VHS(0.998)PNPGLILQSK			S(-27.48)VHS	1	0	0
S(0.008)VHS(0.992)PNPGLILQSK			S(-21.15)VHS	1	0	0
T(0.001)ELAA	TELAAKLASSLVSQ(-4.24)GK		T(-28.81)ELA	0	1	0
T(0.016)IKY(0.984)LKRVK			T(-17.9)IKY(1	0	0	0
T(1)KIKIHYIEMT(1)NVHAK			T(39.99)KIKIH	0	0	0
T(0.232)LLNT(0.322)S(0.426)PNLLPIT(0.0			T(-2.64)LLNT(	0	0	0
T(0.235)LPRNY(0.765)IHRELPS(0.839)NLT			T(-5.33)LPRN	0	0	0
T(0.032)NIS(0.963)RLGNY(0.005)FK			T(-14.81)NIS(	1	0	0
T(1)RRFDEVQ	TRRFDEVQ(6	TRRFDEVQM(	T(56.33)RRFD	0	2	0
T(0.971)S(0.03)KKIIVANS(0.992)GS(0.006			T(15.33)S(-15	0	0	0
TSPKPT(0.028)KPAS(0.972)PK			T(-33.19)S(-3	0	0	0
TSPKPT(0.079)KPAS(0.921)PK			T(-51.25)S(-4	0	0	0
T(0.432)S(0.4	TSWIAN(33.19)PSAVDKLLTI		T(0)S(0)WIAN	0	1	0
T(0.98)VNRLS	TVN(61.16)RLSFEKK		T(16.84)VNRL	0	1	0
VDRS(0.006)DNAAES(0.994)FDDAVEERVI			VDRS(-22.51)	1	0	0
VDRS(0.003)DNAAES(0.997)FDDAVEERVI			VDRS(-24.86)	1	0	0
VDRS(0.007)DNAAES(0.993)FDDAVEERVI			VDRS(-21.63)	1	0	0
VNS(0.002)LIVLES(0.998)DEEEDEQLVQAA			VNS(-28.14)L	0	0	0
VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA			VNS(-29.34)L	0	0	0
VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA			VNS(-31.63)L	0	0	0
VQEEET(0.008)VVPQS(0.566)PS(0.426)KK			VQEEET(-18.4	0	0	0
VTDRS(0.002)HY(0.002)S(0.996)PLVSEIAK			VT(-36.61)DR	0	0	0
VT(0.001)DRS(0.001)HY(0.016)S(0.983)PL			VT(-31.81)DR	0	0	0
VT(0.996)ILWMGGS(0.003)		VTILWM(47.5	VT(24.72)ILW	0	0	0
VT(0.996)ILWMGGS(0.002)		VTILWM(42.3	VT(27.11)ILW	0	0	0
VT(0.999)ILWMGGS(0.001)		VTILWM(42.0	VT(32.61)ILW	0	0	0
VT(0.999)KSSSSK			VT(37.92)KS(-	0	0	0
VTRS(0.001)T(0.001)S(0.00		VTRSTSENIIK	VT(-38.2)RS(-	0	0	0
VT(0.007)S(0.018)KPT(0.035)LELLS(0.946)			VT(-22.82)S(-	0	0	0
				0	0	0
VVDT(0.012)I	VVDTLYQ(61.76)KAK		VVDT(-19.29)	0	1	0
WEEPFY(0.002)GGS(0.885)S(0.114)PAK			WEEPFY(-27.	0	0	0
WEEPFY(0.001)GGS(0.472)S(0.528)PAK			WEEPFY(-28.	0	0	0

Y(1)FIES(1)PH	YFIESPHPEVLQ(45.08)K		Y(45.08)FIES(	0	1	0
YKVPQLEIVPNS(0.166)AEER		YKVPQLEIVPN	Y(-53.17)KVP(	0	0	0
YKVPQLEIVPNS(0.211)AEER		YKVPQLEIVPN	Y(-51.88)KVP(	0	0	0
Y(1)LAVGLLDATVK			Y(60.29)LAVG	0	0	0
				0	0	0
Y(1)LNQWLHI	YLN(-30.03)Q(-7.5)WLHN(7		Y(56.92)LNQ	0	1	0
Y(0.999)LT(0.001)VLLS(0.5)LKT(0.5)K			Y(27.41)LT(-2	0	0	0
Y(1)MKLTQEI	YMKLTQ(70.94)EILQ(70.94)		Y(40.77)MKL	0	2	0
Y(0.32)NLKT(	YN(57.05)LKTPEAP		Y(-3.27)NLKT(	0	1	0
YQGQQNDYIL	YQ(0)GQ(0)Q(0)N(0)DYILISL		Y(-62.08)QGC	0	1	0
Y(0.999)RLLS(	YRLLSAN(53.38)RAAAVQ(5		Y(32.42)RLLS(	0	2	0
YRQAKMRHI	YRQ(47.73)A	YRQAKM(-46.	Y(-34.93)RQA	0	1	0

Oxidation (M	Phospho (STY	Missed cleava	Proteins	Leading Prote	Leading Razo	Gene Names
0	2	0	M9NG39;P41	M9NG39	M9NG39	Pep
0	2	0	M9NG39;P41	M9NG39	M9NG39	Pep
0	1	0	M9NG39;P41	M9NG39	M9NG39	Pep
0	1	0	M9NG39;P41	M9NG39	M9NG39	Pep
0	1	1	M9NG39;P41	M9NG39	M9NG39	Pep
0	1	1	M9NG39;P41	M9NG39	M9NG39	Pep
0	2	1	M9NG39;P41	M9NG39	M9NG39	Pep
0	2	1	M9NG39;P41	M9NG39	M9NG39	Pep
1	1	0	A0APA5;Q8M	A0APA5	A0APA5	CG3509;BigH
0	1	0	Q9VK33-2	Q9VK33-2	Q9VK33-2	Sfmbt
1	1	1	A0A0B4KHE9	A0A0B4KHE9	A0A0B4KHE9	Rpn2
0	1	0	E2QD63;Q86	E2QD63	E2QD63	HIP-R;HIP
0	1	0	E2QD63;Q86	E2QD63	E2QD63	HIP-R;HIP
0	3	2	A0A0B4LFB8;	A0A0B4LFB8	A0A0B4LFB8	Opa1;opa1-li
1	2	0	Q4V3Q5;Q8M	Q4V3Q5	Q4V3Q5	Obp22a CG3
1	2	0	Q4V3Q5;Q8M	Q4V3Q5	Q4V3Q5	Obp22a
0	1	1	Q8T9C5;Q9I7	Q8T9C5	Q8T9C5	MRP CG6214
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	M9PB68;Q9V	M9PB68	M9PB68	poe
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	2	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	2	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	1	A0A0B4LGC0	A0A0B4LGC0	A0A0B4LGC0	TppII
0	1	1	A0A0B4LGC0	A0A0B4LGC0	A0A0B4LGC0	TppII
0	1	1	A0A0B4LGC0	A0A0B4LGC0	A0A0B4LGC0	TppII
0	1	1	A0A0B4LGC0	A0A0B4LGC0	A0A0B4LGC0	TppII

0	1	1	A0A0B4LGC0	A0A0B4LGC0	A0A0B4LGC0	TppII
1	1	0	A4V201;E1JI1	A4V201	A4V201	Taf4
0	1	0		REV__Q8I725	REV__Q8I725	
0	1	0		REV__Q8I725	REV__Q8I725	
0	1	0		REV__Q8I725	REV__Q8I725	
0	1	0	Q9VTY6	Q9VTY6	Q9VTY6	vih
0	1	0	Q8T3J9	Q8T3J9	Q8T3J9	
0	1	0	Q8T3J9	Q8T3J9	Q8T3J9	
0	3	1	Q8I0A1	Q8I0A1	Q8I0A1	SNF4Agamma
0	3	1	Q8I0A1	Q8I0A1	Q8I0A1	SNF4Agamma
0	3	1	Q8I0A1	Q8I0A1	Q8I0A1	SNF4Agamma
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	2	0	Q8IH82	Q8IH82	Q8IH82	grsm
0	2	2	A4V449;Q6N	A4V449	A4V449	ND75
0	1	1	F3YDM3;Q6A	F3YDM3	F3YDM3	CG32068-RB;
0	1	1	F3YDM3;Q6A	F3YDM3	F3YDM3	CG32068-RB;
0	1	0	Q9V5R2;A1Z	Q9V5R2	Q9V5R2	Pex6
0	1	0	Q9V5R2;A1Z	Q9V5R2	Q9V5R2	Pex6
1	1	0	M9PBZ3;M9	M9PBZ3	M9PBZ3	spen
0	1	1	Q9VBX4	Q9VBX4	Q9VBX4	CG31510-RA
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp

0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	Q86BM5;Q9V	Q86BM5;Q9V	Q86BM5	Akap200
0	1	0	Q9VAN0	Q9VAN0	Q9VAN0	CG11899
0	1	0	Q9VAN0	Q9VAN0	Q9VAN0	CG11899
2	1	0	D7FAM9;D7F	D7FAM9	D7FAM9	gr97a;Gr97a-
1	1	1	P28668;H8F4	P28668	P28668	Aats-glupro;A
1	1	1	P28668;H8F4	P28668	P28668	Aats-glupro;A
1	1	1	P28668;H8F4	P28668	P28668	Aats-glupro;A
1	1	2	Q7KTG2	Q7KTG2	Q7KTG2	Apoltp
0	2	2	A0A0C4DHG	A0A0C4DHG	A0A0C4DHG	Gel
0	1	0	Q8SYN6;Q9V	Q8SYN6	Q8SYN6	CG8209
0	1	0	Q9VNH5	Q9VNH5	Q9VNH5	
0	1	0	Q9VNH5	Q9VNH5	Q9VNH5	
0	1	0	Q9VNH5	Q9VNH5	Q9VNH5	
0	1	1	Q9VP27;M9P	Q9VP27	Q9VP27	Glg1
0	2	2	O61380;A8D	O61380	O61380	eIF4G
0	1	1	Q9VHR8-2;Q	Q9VHR8-2	Q9VHR8-2	DppIII;CG561
0	2	0	M9NGE4;M9	M9NGE4	M9NGE4	mud
0	1	1	Q8T410;Q0K	Q8T410	Q8T410	Cnx99A;Cnx1
0	1	1	Q9V9Z1	Q9V9Z1	Q9V9Z1	mRpL32
0	1	0	Q9XZ34;Q4V	Q9XZ34	Q9XZ34	Rif1;CG30085
0	2	1	P91875	P91875	P91875	Rpl1
0	1	1	Q0PQ31;Q0P	Q0PQ31	Q0PQ31	Klp61F
0	1	1	M9PBL3;P02	M9PBL3	M9PBL3	Hsp83
1	1	0	Q9VUB8	Q9VUB8	Q9VUB8	endos
1	1	0	Q9VUB8	Q9VUB8	Q9VUB8	endos
1	1	0	Q9VUB8	Q9VUB8	Q9VUB8	endos
1	1	1	Q8IA36;Q9W	Q8IA36	Q8IA36	mRpS29
0	2	1	Q6V6U1;Q6V	Q6V6U1	Q6V6U1	nec
0	2	1	Q9U6X3;Q9V	Q9U6X3	Q9U6X3	MTA1-like
0	1	1	Q9VRQ4	Q9VRQ4	Q9VRQ4	
0	1	1	Q9VRQ4	Q9VRQ4	Q9VRQ4	
0	1	1	Q9VRQ4	Q9VRQ4	Q9VRQ4	
1	1	1	Q9VSM8;Q95	Q9VSM8	Q9VSM8	GAPsec
1	1	2	Q9VH81	Q9VH81	Q9VH81	PpD3
1	1	0	Q0E9E2;Q86	Q0E9E2;Q7K	Q7KN97	BcDNA:GH06
0	1	0	B4F4Z1;Q9W	B4F4Z1	B4F4Z1	CG12681
0	1	0	B4F4Z1;Q9W	B4F4Z1	B4F4Z1	CG12681
0	1	0	C0MJ66;P235	C0MJ66	C0MJ66	CG5363;cdc2

0	1	0	CON__P0076	CON__P0076	CON__P00761	
0	1	0	CON__P0076	CON__P0076	CON__P00761	
1	2	1	Q9VVI1	Q9VVI1	Q9VVI1	
1	1	1		REV__Q95S3	REV__Q95S34	
1	1	1		REV__Q95S3	REV__Q95S34	
1	1	1		REV__Q95S3	REV__Q95S34	
1	1	1		REV__Q95S3	REV__Q95S34	
1	1	1		REV__Q95S3	REV__Q95S34	
0	2	0		REV__Q9VPU	REV__Q9VPU	CG13950
0	2	0		REV__Q9VPU	REV__Q9VPU	CG13950
1	1	1	Q961E0;Q5BI	Q961E0	Q961E0	Cul4
1	1	1	M9PBI9;M9P	M9PBI9	M9PBI9	sls
1	1	1	M9PBI9;M9P	M9PBI9	M9PBI9	sls
0	1	1	M9PBI9;M9P	M9PBI9	M9PBI9	sls
0	3	0	P35875;P358	P35875	P35875	Parp
1	2	2	A8JV07;B4F5	A8JV07	A8JV07	CG9915;CG9
1	1	1	Q867Z4-3	Q867Z4-3	Q867Z4-3	lola
0	1	2	A0A0B4LFD2;	A0A0B4LFD2	A0A0B4LFD2	Hsc70-5
1	1	1	B7FNN6;P05	B7FNN6	B7FNN6	RpLP2-RB;Rp
1	1	1	B7FNN6;P05	B7FNN6	B7FNN6	RpLP2-RB;Rp
1	1	1	B7FNN6;P05	B7FNN6	B7FNN6	RpLP2-RB;Rp
0	1	1	M9NG39;P41	M9NG39	M9NG39	Pep
0	1	2	P05205	P05205	P05205	Su(var)205
0	1	2	P05205	P05205	P05205	Su(var)205
0	1	2	P05205	P05205	P05205	Su(var)205
0	1	2	P05205	P05205	P05205	Su(var)205
0	1	2	CON__P0266	CON__P0266	CON__P02666	
0	1	2	CON__P0266	CON__P0266	CON__P02666	
1	2	2	M9PBK5;P08	M9PBK5	M9PBK5	RpLP1
1	2	2	M9PBK5;P08	M9PBK5	M9PBK5	RpLP1
1	2	2	M9PBK5;P08	M9PBK5	M9PBK5	RpLP1
1	1	2	M9PBK5;P08	M9PBK5	M9PBK5	RpLP1
0	1	2	Q9VCC0	Q9VCC0	Q9VCC0	CHORD
0	1	1	M9PE74;Q9	M9PE74	M9PE74	nocte
0	1	1	Q7PLP4;A8Y5	Q7PLP4	Q7PLP4	CG41099;CG1
0	1	1	Q9VTI8	Q9VTI8	Q9VTI8	chrb
0	2	2	Q9VFR0	Q9VFR0	Q9VFR0	CG9286
0	1	2	Q6IHK8	Q6IHK8	Q6IHK8	HDC02276
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223

0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	1	Q9VCC0	Q9VCC0	Q9VCC0	CHORD
0	1	1		REV__D4G7E	REV__D4G7E0	
0	2	2	Q9VAA9	Q9VAA9	Q9VAA9	
0	2	1	Q9W1H4	Q9W1H4	Q9W1H4	DNA-ligI
0	1	1	X2JF19;Q9NB	X2JF19	X2JF19	hiw
0	1	1	Q8IR12;Q9VX	Q8IR12	Q8IR12	Cap;Cap-RA
1	2	1	Q9VZ30	Q9VZ30	Q9VZ30	
0	1	1	Q9Y162	Q9Y162	Q9Y162	Vps4
0	2	0	A8DYI1;Q7K5	A8DYI1	A8DYI1	CG5544
0	1	1	Q9VIF0	Q9VIF0	Q9VIF0	CG9246
0	1	0	Q9NH11;Q9V	Q9NH11	Q9NH11	RecQ4
0	2	2	T2FFB7;Q9VL	T2FFB7	T2FFB7	Aats-ala-RB;A
0	2	1	Q95RH7;F0JA	Q95RH7	Q95RH7	Rab35
0	1	0	Q7KUA4;Q7K	Q7KUA4	Q7KUA4	Uba2
1	1	0	Q9V4M2	Q9V4M2	Q9V4M2	wech
1	1	0	Q9V4M2	Q9V4M2	Q9V4M2	wech
1	1	0	Q9GP67;Q7K	Q9GP67	Q9GP67	Ret
1	1	0	D5AEK6;Q95	D5AEK6	D5AEK6	CG9795-RA
1	1	0	D5AEK6;Q95	D5AEK6	D5AEK6	CG9795-RA
1	1	0	Q6IKG0	Q6IKG0	Q6IKG0	
2	1	1		REV__Q8IN0	REV__Q8IN09	
1	2	0	Q9VWH1	Q9VWH1	Q9VWH1	
1	1	0	H1UUN5;Q9V	H1UUN5	H1UUN5	CG14043-RA;
1	1	0	H1UUN5;Q9V	H1UUN5	H1UUN5	CG14043-RA;
1	1	0	Q9VR91	Q9VR91	Q9VR91	HERC2
1	1	0	Q9VIH1;Q8SX	Q9VIH1	Q9VIH1	RPA2;CG9273
1	1	1	Q6IIC4	Q6IIC4	Q6IIC4	HDC19000
1	1	1	Q6IIC4	Q6IIC4	Q6IIC4	HDC19000
1	1	1	Q6IIC4	Q6IIC4	Q6IIC4	HDC19000
1	1	1	Q6IIC4	Q6IIC4	Q6IIC4	HDC19000
1	1	1	A0A0B4LEV8;	A0A0B4LEV8	A0A0B4LEV8	coil
0	1	1	Q8IGR0;P153	Q8IGR0	Q8IGR0	aru;RpS27A;
0	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
0	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
0	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
0	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
1	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
1	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
1	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
1	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB

1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	0	Q6IJT9	Q6IJT9	Q6IJT9	HDC14233
1	1	1	T2GFF4	T2GFF4	T2GFF4	
2	1	0	Q9W1X7	Q9W1X7	Q9W1X7	MED23
0	1	0	Q7KSW3	Q7KSW3	Q7KSW3	
0	2	0	Q9V3W0	Q9V3W0	Q9V3W0	UK114
1	1	1	CON__P2093	CON__P2093	CON__P20930	
1	1	0	Q9XZL7;A0A0	Q9XZL7	Q9XZL7	tacc;tacc-RA
1	1	0	Q9VA95	Q9VA95	Q9VA95	Bet5
1	1	0	B7YZZ9;P278	B7YZZ9	B7YZZ9	Rrp1
1	1	0	B7YZZ9;P278	B7YZZ9	B7YZZ9	Rrp1
1	1	0	B7YZZ9;P278	B7YZZ9	B7YZZ9	Rrp1
0	1	1	Q8IHE7;C9QF	Q8IHE7	Q8IHE7	CG6664
0	1	1	Q8IHE7;C9QF	Q8IHE7	Q8IHE7	CG6664
0	1	1	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	1	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	1	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	1	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	1	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	2	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	2	Q9VYV4	Q9VYV4	Q9VYV4	Amun
1	1	0	Q9VGZ3;Q9N	Q9VGZ3;Q9V	Q9VGZ3	Irp-1B;Irp-1A
0	1	2	E1NZC8;H8F4	E1NZC8	E1NZC8	MED1-RA;ME
1	1	2	Q7KKI0;A1Z8	Q7KKI0	Q7KKI0	Cct5;Cct5-RB
0	1	2	Q9VIE7;Q8W	Q9VIE7	Q9VIE7	bur
1	2	1		REV__A0A0B	REV__A0A0B4KEZ8	
0	1	2	Q967T2	Q967T2	Q967T2	pol
0	1	0	Q8INI3;Q86M	Q8INI3	Q8INI3	CG31347-RA;
0	1	0	Q8INI3;Q86M	Q8INI3	Q8INI3	CG31347-RA;
0	1	2	Q8IRG6;Q8IR	Q8IRG6	Q8IRG6	dre4
0	1	2	Q8IRG6;Q8IR	Q8IRG6	Q8IRG6	dre4
0	1	2	Q8IRG6;Q8IR	Q8IRG6	Q8IRG6	dre4
0	1	0	Q4V3L7;Q4V	Q4V3L7	Q4V3L7	BcDNA:GH10
0	1	0	E2QCZ8;Q0KI	E2QCZ8	E2QCZ8	CG43427
0	1	0	E2QCZ8;Q0KI	E2QCZ8	E2QCZ8	CG43427
2	1	0	Q7KNF3;Q8I	Q7KNF3	Q7KNF3	Trap1
0	2	0	E2QCZ8;Q0KI	E2QCZ8	E2QCZ8	CG43427
0	2	0	E2QCZ8;Q0KI	E2QCZ8	E2QCZ8	CG43427
0	1	1	A0A0B4LFL3;	A0A0B4LFL3	A0A0B4LFL3	Ef1beta
1	1	0	Q9VIV2;B1NL	Q9VIV2	Q9VIV2	swm

1	1	0	Q9VIV2;B1NL	Q9VIV2	Q9VIV2	swm
0	1	0	Q9VIV2;B1NL	Q9VIV2	Q9VIV2	swm
0	1	0	Q6IGL3	Q6IGL3	Q6IGL3	HDC05999
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A4UZZ4;Q9X	A4UZZ4	A4UZZ4	GlyP
0	1	0	A4UZZ4;Q9X	A4UZZ4	A4UZZ4	GlyP
0	1	1	A4UZZ4;Q9X	A4UZZ4	A4UZZ4	GlyP
0	1	1	A4UZZ4;Q9X	A4UZZ4	A4UZZ4	GlyP
0	1	0	Q9VY84	Q9VY84	Q9VY84	
0	1	1	A0ZWT4;A0Z	A0ZWT4	A0ZWT4	TepII;Tep2
1	1	1	M9PBI9;M9P	M9PBI9	M9PBI9	sls
0	1	0	A0A0B4JD95;	A0A0B4JD95	A0A0B4JD95	zip
0	1	0	A0A0B4JD95;	A0A0B4JD95	A0A0B4JD95	zip
0	1	1	Q1RKX3;A0A	Q1RKX3	Q1RKX3	
1	1	0	Q9VV82;Q8S	Q9VV82	Q9VV82	CG18861;CG
0	1	0	Q95RK9;Q6A	Q95RK9	Q95RK9	Cap-G
0	1	0	Q95RK9;Q6A	Q95RK9	Q95RK9	Cap-G
0	1	0	Q95RK9;Q6A	Q95RK9	Q95RK9	Cap-G
0	1	0	Q9VQ76;M9	Q9VQ76	Q9VQ76	tho2
1	1	0	C0PUW8;Q9	C0PUW8	C0PUW8	CG3305-RA;L
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1

0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	Q8MYL1	Q8MYL1	Q8MYL1	Fancd2
0	1	0	Q8MYL1	Q8MYL1	Q8MYL1	Fancd2
0	1	0	Q8MYL1	Q8MYL1	Q8MYL1	Fancd2
0	1	0	Q8MYL1	Q8MYL1	Q8MYL1	Fancd2
0	1	0	Q8MYL1	Q8MYL1	Q8MYL1	Fancd2
1	1	0	C9QPJ3;Q9V	C9QPJ3	C9QPJ3	pps-RA;pps
0	1	0		REV__Q961M	REV__Q961M1	
0	1	0		REV__Q961M	REV__Q961M1	
0	1	0	Q9VV74	Q9VV74	Q9VV74	Smn
0	1	0	Q9VV74	Q9VV74	Q9VV74	Smn
0	1	0	Q9VV74	Q9VV74	Q9VV74	Smn
0	1	1	Q9VZW4;A8V	Q9VZW4	Q9VZW4	CG32487
0	1	1	Q9VZW4;A8V	Q9VZW4	Q9VZW4	CG32487
0	1	1	Q9VZW4;A8V	Q9VZW4	Q9VZW4	CG32487
0	2	0	A0A0B4KFB8;	A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
0	2	0	A0A0B4KFB8;	A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
0	2	0	A0A0B4KFB8;	A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
0	1	1	Q7KK51;Q9W	Q7KK51	Q7KK51	BcDNA.GH04
0	1	0	M9PCD7;M9	M9PCD7	M9PCD7	
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
1	1	0	Q8MNR4	Q8MNR4	Q8MNR4	gag-pol
0	1	0	O02195	O02195	O02195	Trip1
0	1	0	O02195	O02195	O02195	Trip1
0	1	1	Q86BM5;Q9V	Q86BM5;Q9V	Q86BM5	Akap200
0	1	1	Q86BM5;Q9V	Q86BM5;Q9V	Q86BM5	Akap200
0	1	1	Q86BM5;Q9V	Q86BM5;Q9V	Q86BM5	Akap200
0	1	1	Q86BM5;Q9V	Q86BM5;Q9V	Q86BM5	Akap200
0	1	1	Q86BM5;Q9V	Q86BM5;Q9V	Q86BM5	Akap200
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223

0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
1	1	0	B9ER03	B9ER03	B9ER03	CG10597-RB
0	1	0	Q4AB54;P022	Q4AB54	Q4AB54	His1:CG3386
0	1	0	Q4AB54;P022	Q4AB54	Q4AB54	His1:CG3386
0	1	0	Q4AB54;P022	Q4AB54	Q4AB54	His1:CG3386
0	4	0	Q9VNH5	Q9VNH5	Q9VNH5	
0	1	0	Q95RN0-2	Q95RN0-2	Q95RN0-2	CG10038
0	1	0	Q9VZS3	Q9VZS3	Q9VZS3	CG17737
0	1	0	Q9VZS3	Q9VZS3	Q9VZS3	CG17737
0	1	0	Q8INM3;Q8I	Q8INM3	Q8INM3	sle
0	1	0	Q8INM3;Q8I	Q8INM3	Q8INM3	sle
1	2	1	A0A0H4Y1G5	A0A0H4Y1G5	A0A0H4Y1G5	hyd
2	2	1	A0A0H4Y1G5	A0A0H4Y1G5	A0A0H4Y1G5	hyd
2	2	1	A0A0H4Y1G5	A0A0H4Y1G5	A0A0H4Y1G5	hyd
0	2	2	Q9VPR5;Q4V	Q9VPR5	Q9VPR5	CG2807
1	1	0	Q9W5W8	Q9W5W8	Q9W5W8	
0	1	0	Q9W401	Q9W401	Q9W401	kdn
0	1	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	1	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	1	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	1	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc

0	1	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	2	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	2	0	M9PDK5;Q9	M9PDK5	M9PDK5	VhaSFD
0	1	2	Q4V3Z6	Q4V3Z6	Q4V3Z6	
0	2	0	A0A0C5K8A0	A0A0C5K8A0	A0A0C5K8A0	lds
0	2	1	M9NDM4;Q9	M9NDM4	M9NDM4	wds
0	1	0	Q86BJ3-3	Q86BJ3-3	Q86BJ3-3	
0	1	0	P81900;A8DY	P81900	P81900	Pka-R2
0	1	0	Q9V6U8	Q9V6U8	Q9V6U8	Uba3
0	1	0	Q9V6U8	Q9V6U8	Q9V6U8	Uba3
0	1	0	Q9V6U8	Q9V6U8	Q9V6U8	Uba3
0	1	0	Q9V6U8	Q9V6U8	Q9V6U8	Uba3
0	2	2	Q9VBX4	Q9VBX4	Q9VBX4	CG31510-RA
0	1	2	C7LAH9;C9Q	C7LAH9	C7LAH9	Moe;Moe-RA
0	2	2	Q967T2	Q967T2	Q967T2	pol
0	1	0	A1Z968;Q5KT	A1Z968	A1Z968	NAT1
0	3	0	Q9VKW5	Q9VKW5	Q9VKW5	
0	1	0	Q29QZ8	Q29QZ8	Q29QZ8	
1	1	0	Q9VIS5	Q9VIS5	Q9VIS5	
0	2	2	A8E774;P250	A8E774	A8E774	Cyp1;CG9916
0	1	2	Q9W335	Q9W335	Q9W335	l(1)G0320
0	1	2	Q9W335	Q9W335	Q9W335	l(1)G0320
0	2	1	A1A6R3;Q9V	A1A6R3	A1A6R3	
0	1	1	Q9VWF8	Q9VWF8	Q9VWF8	
0	1	0	C0MJE4;Q24	C0MJE4	C0MJE4	CG4236;Caf1
0	1	0	C0MJE4;Q24	C0MJE4	C0MJE4	CG4236;Caf1
0	1	0	C0MJE4;Q24	C0MJE4	C0MJE4	CG4236;Caf1
0	1	0	P20240	P20240	P20240	Ote
0	1	0	P20240	P20240	P20240	Ote
0	1	0	P20240	P20240	P20240	Ote
0	1	1	A0A0B4K7G4	A0A0B4K7G4	A0A0B4K7G4	mod
0	1	0	Q9VL18	Q9VL18	Q9VL18	eEF1delta
0	1	0	Q9VL18	Q9VL18	Q9VL18	eEF1delta
1	1	1	Q95SA9	Q95SA9	Q95SA9	spoon
1	1	1	Q95SA9	Q95SA9	Q95SA9	spoon
1	1	1	Q95SA9	Q95SA9	Q95SA9	spoon
0	1	1	Q9W384;Q9	Q9W384	Q9W384	dalao
1	1	1	X2JIN0;M9M	X2JIN0	X2JIN0	
0	2	2	Q24574-2;Q2	Q24574-2	Q24574-2	Ubp64E
0	2	2	Q24574-2;Q2	Q24574-2	Q24574-2	Ubp64E
0	1	1	A0A0B4K7Z5;	A0A0B4K7Z5	A0A0B4K7Z5	Rpn6
0	1	0	M9PFS8;Q9V	M9PFS8	M9PFS8	CG9705
0	1	0	M9PFS8;Q9V	M9PFS8	M9PFS8	CG9705

0	2	0	B7Z0G1;Q02	B7Z0G1	B7Z0G1	hay
1	1	1	CON__P0266	CON__P0266	CON__P02662	
1	1	1	CON__P0266	CON__P0266	CON__P02662	
0	1	0	Q9VE98	Q9VE98	Q9VE98	
0	1	0	Q9VE98	Q9VE98	Q9VE98	
0	1	0	Q9VIS5	Q9VIS5	Q9VIS5	
0	2	1	Q9V3U0	Q9V3U0	Q9V3U0	CG4500
0	1	1	E1JI68	E1JI68	E1JI68	
0	1	1	Q9VRV7	Q9VRV7	Q9VRV7	CG13298
0	1	0	Q8MSA2;Q8	Q8MSA2	Q8MSA2	CG14730
0	1	0	Q9VPW4	Q9VPW4	Q9VPW4	mtRNApol
1	1	1	A1ZBT6;Q96	A1ZBT6	A1ZBT6	

Protein Nam	Type	Labeling Stat	Raw file	Fraction	Experiment	MS/MS m/z
Zinc finger pr	MULTI-MSMS		PT5722-2	2	B1	761.34
Zinc finger pr	ISO-MSMS	0	PT5722-32	32	B3	761.67
Zinc finger pr	ISO-MSMS	0	PT5722-2	2	B1	735.02
Zinc finger pr	ISO-MSMS	0	PT5722-32	32	B3	734.69
Zinc finger pr	ISO-MSMS	0	PT5722-2	2	B1	777.72
Zinc finger pr	ISO-MSMS	0	PT5722-7	7	B1 SCX	777.38
Zinc finger pr	ISO-MSMS	0	PT5722-2	2	B1	804.37
Zinc finger pr	ISO-MSMS	0	PT5722-32	32	B3	804.38
1	MULTI-MSMS		PT5722-58	58	H/H TIO2	767.35
Polycomb pr	ISO-MSMS	1	PT5722-40	40	B3 SCX	913.44
26S proteaso	ISO-MSMS	0	PT5722-51	51	H/H SCX	631.25
Hsc70-intera	MULTI-MSMS		PT5722-23	23	B2 SCX	516.59
Hsc70-intera	MULTI-MSMS		PT5722-23	23	B2 SCX	774.39
e-RA	ISO-MSMS	0	PT5722-7	7	B1 SCX	757.02
Odorant bind	MSMS	1	PT5722-3	3	B1	753.86
	MSMS	1	PT5722-19	19	B2	753.85
Multidrug-re	MSMS	1	PT5722-48	48	H/H	489.94
Phosphogluc	MULTI-MSMS		PT5722-7	7	B1 SCX	782.38
Phosphogluc	MULTI-MSMS		PT5722-8	8	B1 SCX	782.38
Phosphogluc	MULTI-MSMS		PT5722-23	23	B2 SCX	782.05
Phosphogluc	ISO-MSMS	0	PT5722-33	33	B3	782.38
Phosphogluc	MULTI-MSMS		PT5722-38	38	B3 SCX	782.38
Phosphogluc	MULTI-MSMS		PT5722-38	38	B3 SCX	1173.07
Phosphogluc	ISO-MSMS	0	PT5722-51	51	H/H SCX	782.05
Phosphogluc	MULTI-MSMS		PT5722-53	53	H/H SCX	782.05
Phosphogluc	MULTI-MATCH		PT5722-6	6	B1 SCX	
Phosphogluc	MULTI-MATCH		PT5722-21	21	B2 SCX	
Phosphogluc	MULTI-MATCH		PT5722-22	22	B2 SCX	
Phosphogluc	ISO-MSMS	0	PT5722-38	38	B3 SCX	782.71
Protein purit	MSMS	1	PT5722-32	32	B3	687.36
Glycogen [sta	MULTI-MSMS		PT5722-2	2	B1	1106.52
Glycogen [sta	MULTI-MSMS		PT5722-7	7	B1 SCX	1106.02
Glycogen [sta	ISO-MSMS	0	PT5722-37	37	B3 SCX	1106.03
Glycogen [sta	MULTI-MSMS		PT5722-47	47	H/H	1106.52
Glycogen [sta	MULTI-MSMS		PT5722-57	57	H/H TIO2	1106.52
Glycogen [sta	MULTI-MATCH		PT5722-56	56	H/H TIO2	
Glycogen [sta	MULTI-MSMS		PT5722-57	57	H/H TIO2	1146.5
Glycogen [sta	MULTI-MSMS		PT5722-57	57	H/H TIO2	764.67
Tripeptidyl-p	ISO-MSMS	0	PT5722-6	6	B1 SCX	943.2
Tripeptidyl-p	ISO-MSMS	0	PT5722-7	7	B1 SCX	943.2
Tripeptidyl-p	ISO-MSMS	0	PT5722-21	21	B2 SCX	943.2
Tripeptidyl-p	ISO-MSMS	0	PT5722-37	37	B3 SCX	943.2

Tripeptidyl-pe	MULTI-MSMS		PT5722-51	51	H/H SCX	942.95
Transcription	MULTI-MSMS		PT5722-1	1	B1	812.4
	MULTI-MSMS		PT5722-3	3	B1	954.97
	MULTI-SECPEP		PT5722-3	3	B1	954.97
	MULTI-MATCH		PT5722-2	2	B1	
Ubiquitin-con	MULTI-MSMS		PT5722-20	20	B2	862.37
	MSMS	1	PT5722-19	19	B2	547.28
	MSMS	1	PT5722-20	20	B2	547.28
a	MSMS	1	PT5722-6	6	B1 SCX	956.93
a	MSMS	1	PT5722-6	6	B1 SCX	956.93
a	MSMS	1	PT5722-7	7	B1 SCX	956.93
Eukaryotic tra	MULTI-MSMS		PT5722-2	2	B1	841.84
Eukaryotic tra	MULTI-MSMS		PT5722-6	6	B1 SCX	841.34
Eukaryotic tra	MULTI-MSMS		PT5722-7	7	B1 SCX	841.34
Eukaryotic tra	MULTI-MSMS		PT5722-11	11	B1 TIO2	841.34
Eukaryotic tra	ISO-MSMS	0	PT5722-22	22	B2 SCX	841.34
Eukaryotic tra	ISO-MSMS	0	PT5722-27	27	B2 TIO2	841.34
Eukaryotic tra	MULTI-MSMS		PT5722-36	36	B3 SCX	841.33
Eukaryotic tra	MULTI-MSMS		PT5722-37	37	B3 SCX	841.34
Eukaryotic tra	MULTI-MSMS		PT5722-41	41	B3 TIO2	841.34
Eukaryotic tra	MULTI-MSMS		PT5722-51	51	H/H SCX	841.34
Eukaryotic tra	MULTI-MSMS		PT5722-52	52	H/H SCX	841.83
Eukaryotic tra	MULTI-MATCH		PT5722-42	42	B3 TIO2	
Cofilin/actin-	MULTI-MSMS		PT5722-5	5	B1	622.77
Cofilin/actin-	MULTI-MSMS		PT5722-15	15	B1 TIO2	622.77
Cofilin/actin-	MULTI-MSMS		PT5722-16	16	B2	626.77
Cofilin/actin-	MULTI-MSMS		PT5722-20	20	B2	622.77
Cofilin/actin-	MULTI-MSMS		PT5722-30	30	B2 TIO2	622.77
Cofilin/actin-	MULTI-MSMS		PT5722-32	32	B3	626.77
Cofilin/actin-	MULTI-MSMS		PT5722-34	34	B3	622.76
Cofilin/actin-	MULTI-MSMS		PT5722-49	49	H/H	622.77
Cofilin/actin-	MULTI-MSMS		PT5722-50	50	H/H	626.77
Cofilin/actin-	MULTI-MSMS		PT5722-60	60	H/H TIO2	622.76
Cofilin/actin-	MULTI-MATCH		PT5722-33	33	B3	
	MSMS	1	PT5722-48	48	H/H	729.36
NADH-ubiqui	ISO-MSMS	1	PT5722-7	7	B1 SCX	817.71
1,2-dihydroxy	MULTI-MSMS		PT5722-51	51	H/H SCX	659.82
1,2-dihydroxy	MULTI-MATCH		PT5722-52	52	H/H SCX	
	MULTI-MSMS		PT5722-8	8	B1 SCX	619.25
	MULTI-MSMS		PT5722-23	23	B2 SCX	619.25
Protein split e	MSMS	0	PT5722-18	18	B2	671.34
	ISO-MSMS	1	PT5722-24	24	B2 SCX	774.37
FACT comple	ISO-MSMS	0	PT5722-6	6	B1 SCX	822.02

FACT comple:	MULTI-MSMS		PT5722-7	7	B1 SCX	822.02
FACT comple:	MULTI-MSMS		PT5722-22	22	B2 SCX	821.69
FACT comple:	MULTI-MSMS		PT5722-36	36	B3 SCX	822.02
FACT comple:	MULTI-MSMS		PT5722-51	51	H/H SCX	822.02
FACT comple:	MULTI-MSMS		PT5722-52	52	H/H SCX	822.02
Akap200	ISO-MSMS	0	PT5722-32	32	B3	905.41
Probable pho	MULTI-MSMS		PT5722-7	7	B1 SCX	388.19
Probable pho	MULTI-SECPEP		PT5722-37	37	B3 SCX	388.46
Putative gust	MULTI-MSMS		PT5722-8	8	B1 SCX	926.9
Bifunctional g	ISO-MSMS	0	PT5722-21	21	B2 SCX	909.75
Bifunctional g	ISO-MSMS	0	PT5722-37	37	B3 SCX	909.75
Bifunctional g	MULTI-MSMS		PT5722-51	51	H/H SCX	909.75
	ISO-MSMS	0	PT5722-32	32	B3	741.37
Gelsolin	ISO-MSMS	1	PT5722-18	18	B2	684.32
	MULTI-MSMS		PT5722-58	58	H/H TIO2	788.38
	ISO-MSMS	0	PT5722-23	23	B2 SCX	1052.44
	ISO-MSMS	0	PT5722-38	38	B3 SCX	1052.78
	ISO-MSMS	0	PT5722-53	53	H/H SCX	1052.78
	MSMS	0	PT5722-48	48	H/H	901.94
	ISO-MSMS	0	PT5722-5	5	B1	812.36
Dipeptidyl pe	MULTI-MSMS		PT5722-22	22	B2 SCX	542.93
	MSMS	0	PT5722-28	28	B2 TIO2	697.72
4D	ISO-MSMS	0	PT5722-22	22	B2 SCX	612.8
39S ribosoma	MULTI-MSMS		PT5722-34	34	B3	786.04
	ISO-MSMS	1	PT5722-4	4	B1	791.04
DNA-directed	MSMS	1	PT5722-39	39	B3 SCX	847.09
	ISO-MSMS	1	PT5722-40	40	B3 SCX	919.1
Heat shock pı	MULTI-MSMS		PT5722-17	17	B2	730.78
	ISO-MSMS	1	PT5722-10	10	B1 SCX	707.27
	MULTI-MSMS		PT5722-40	40	B3 SCX	707.27
	MULTI-MSMS		PT5722-55	55	H/H SCX	702.76
	MSMS	0	PT5722-1	1	B1	948.6
	MSMS	0	PT5722-49	49	H/H	500.9
	MSMS	0	PT5722-39	39	B3 SCX	841.88
	ISO-MSMS	0	PT5722-18	18	B2	642.3
	MULTI-MSMS		PT5722-48	48	H/H	642.3
	MULTI-MSMS		PT5722-58	58	H/H TIO2	642.31
	MULTI-MSMS		PT5722-36	36	B3 SCX	693.37
	MSMS	1	PT5722-48	48	H/H	906.45
Pyruvate carb	MULTI-SECPEP		PT5722-37	37	B3 SCX	620.84
	ISO-MSMS	0	PT5722-36	36	B3 SCX	821.74
	MULTI-MSMS		PT5722-37	37	B3 SCX	821.74
Cyclin-depen	MULTI-MSMS		PT5722-34	34	B3	633.29

	MULTI-MSMS		PT5722-3	3	B1	792.38
	MULTI-MSMS		PT5722-18	18	B2	789.36
	MSMS	0	PT5722-22	22	B2 SCX	1287.06
	MULTI-SECPEP		PT5722-3	3	B1	913.45
	MULTI-MSMS		PT5722-39	39	B3 SCX	908.94
	MULTI-MATCH		PT5722-2	2	B1	
	MULTI-MATCH		PT5722-38	38	B3 SCX	
	MULTI-MATCH		PT5722-40	40	B3 SCX	
	MULTI-MSMS		PT5722-10	10	B1 SCX	837.71
	MULTI-SECPEP		PT5722-10	10	B1 SCX	837.71
	ISO-MSMS	1	PT5722-7	7	B1 SCX	924.41
Titin	ISO-MSMS	0	PT5722-33	33	B3	864.91
Titin	ISO-MSMS	0	PT5722-38	38	B3 SCX	864.91
Titin	MSMS	0	PT5722-37	37	B3 SCX	856.91
Poly [ADP-rib	MULTI-SECPEP		PT5722-48	48	H/H	713.99
915-RB	ISO-MSMS	0	PT5722-5	5	B1	911.95
Longitudinals	ISO-MSMS	0	PT5722-10	10	B1 SCX	721.68
Heat shock 7(	MSMS	0	PT5722-32	32	B3	496.93
60S acidic rib	MULTI-MSMS		PT5722-25	25	B2 SCX	1037.38
60S acidic rib	ISO-MSMS	0	PT5722-45	45	B3 TIO2	1037.38
60S acidic rib	MULTI-MSMS		PT5722-55	55	H/H SCX	1037.38
Zinc finger pr	MSMS	1	PT5722-8	8	B1 SCX	491.23
Heterochrom	ISO-MSMS	0	PT5722-9	9	B1 SCX	727.32
Heterochrom	MULTI-MSMS		PT5722-39	39	B3 SCX	969.42
Heterochrom	MULTI-MSMS		PT5722-39	39	B3 SCX	727.32
Heterochrom	ISO-MSMS	0	PT5722-54	54	H/H SCX	727.32
	ISO-MSMS	0	PT5722-10	10	B1 SCX	854.39
	ISO-MSMS	0	PT5722-39	39	B3 SCX	854.39
60S acidic rib	MSMS	0	PT5722-6	6	B1 SCX	1184.42
60S acidic rib	MSMS	0	PT5722-36	36	B3 SCX	789.95
60S acidic rib	MSMS	0	PT5722-40	40	B3 SCX	789.95
60S acidic rib	MULTI-MSMS		PT5722-55	55	H/H SCX	763.63
Cysteine and	MULTI-MSMS		PT5722-38	38	B3 SCX	732.32
	MULTI-MSMS		PT5722-37	37	B3 SCX	728.65
.7419	ISO-MSMS	1	PT5722-23	23	B2 SCX	671.36
Protein chary	MULTI-MSMS		PT5722-23	23	B2 SCX	847.4
Protein BCCIF	ISO-MSMS	0	PT5722-22	22	B2 SCX	915.96
	ISO-MSMS	0	PT5722-39	39	B3 SCX	714.86
Protein NASP	ISO-MSMS	0	PT5722-7	7	B1 SCX	632.94
Protein NASP	MULTI-MSMS		PT5722-18	18	B2	632.61
Protein NASP	MULTI-MSMS		PT5722-32	32	B3	632.61
Protein NASP	ISO-MSMS	0	PT5722-36	36	B3 SCX	632.94
Protein NASP	ISO-MSMS	0	PT5722-38	38	B3 SCX	632.61

Protein NASP	MULTI-MSMS		PT5722-52	52	H/H SCX	632.61
Cysteine and	MULTI-MSMS		PT5722-23	23	B2 SCX	1033.93
	MULTI-MSMS		PT5722-32	32	B3	758.05
	ISO-MSMS	0	PT5722-55	55	H/H SCX	765.87
DNA ligase 1	ISO-MSMS	1	PT5722-27	27	B2 TIO2	790.89
E3 ubiquitin-p	MSMS	0	PT5722-54	54	H/H SCX	586.95
	MULTI-MSMS		PT5722-33	33	B3	739.02
	ISO-MSMS	1	PT5722-34	34	B3	968.12
	MULTI-MSMS		PT5722-38	38	B3 SCX	777.4
	MULTI-SECPEP		PT5722-48	48	H/H	905.45
Nucleolar cor	ISO-MSMS	0	PT5722-37	37	B3 SCX	1108.79
	ISO-MSMS	0	PT5722-35	35	B3	758.35
Alanine--tRN/	MSMS	1	PT5722-3	3	B1	990.81
	MSMS	0	PT5722-18	18	B2	690.97
	ISO-MSMS	0	PT5722-32	32	B3	468.23
Protein wech	ISO-MSMS	0	PT5722-8	8	B1 SCX	991.94
Protein wech	ISO-MSMS	0	PT5722-51	51	H/H SCX	991.94
	MSMS	0	PT5722-38	38	B3 SCX	764.41
	MULTI-MSMS		PT5722-38	38	B3 SCX	567.61
	ISO-MSMS	0	PT5722-38	38	B3 SCX	850.9
	MULTI-MSMS		PT5722-40	40	B3 SCX	835.39
	ISO-MSMS	1	PT5722-34	34	B3	913.48
	MULTI-MSMS		PT5722-10	10	B1 SCX	745.02
Protein KBP h	MULTI-MSMS		PT5722-36	36	B3 SCX	859.41
Protein KBP h	MULTI-MATCH		PT5722-37	37	B3 SCX	
Probable E3 u	MULTI-MSMS		PT5722-33	33	B3	760.74
	MULTI-MSMS		PT5722-34	34	B3	837.68
	ISO-MSMS	1	PT5722-23	23	B2 SCX	818.4
	ISO-MSMS	1	PT5722-24	24	B2 SCX	818.4
	ISO-MSMS	1	PT5722-38	38	B3 SCX	817.9
	ISO-MSMS	1	PT5722-49	49	H/H	817.9
	MULTI-MSMS		PT5722-33	33	B3	632.61
Ubiquitin-40S	MSMS	0	PT5722-16	16	B2	694.8
	MULTI-MSMS		PT5722-10	10	B1 SCX	909.43
	MULTI-MSMS		PT5722-24	24	B2 SCX	609.63
	MULTI-MATCH		PT5722-23	23	B2 SCX	
	MULTI-MATCH		PT5722-25	25	B2 SCX	
	MULTI-MSMS		PT5722-23	23	B2 SCX	597.63
	MULTI-MSMS		PT5722-24	24	B2 SCX	896.44
	MULTI-MATCH		PT5722-23	23	B2 SCX	
	MULTI-MATCH		PT5722-25	25	B2 SCX	
sobremesa	ISO-MSMS	1	PT5722-8	8	B1 SCX	911.43
sobremesa	ISO-MSMS	1	PT5722-9	9	B1 SCX	911.43

sobremesa	ISO-MSMS	1	PT5722-10	10	B1 SCX	911.44
sobremesa	ISO-MSMS	1	PT5722-26	26	B2 TIO2	911.43
sobremesa	ISO-MSMS	1	PT5722-38	38	B3 SCX	911.43
sobremesa	ISO-MSMS	1	PT5722-40	40	B3 SCX	911.44
	ISO-MSMS	0	PT5722-49	49	H/H	793.86
	ISO-MSMS	0	PT5722-35	35	B3	801.37
Mediator of	ISO-MSMS	0	PT5722-53	53	H/H SCX	824.38
	ISO-MSMS	0	PT5722-52	52	H/H SCX	905.45
	MULTI-SECPEP		PT5722-10	10	B1 SCX	497.28
	ISO-MSMS	1	PT5722-38	38	B3 SCX	830.09
	ISO-MSMS	0	PT5722-41	41	B3 TIO2	930.46
	MULTI-SECPEP		PT5722-10	10	B1 SCX	750.85
Recombinati	ISO-MSMS	0	PT5722-12	12	B1 TIO2	914.74
Recombinati	ISO-MSMS	0	PT5722-32	32	B3	914.41
Recombinati	MULTI-MSMS		PT5722-57	57	H/H TIO2	914.74
	ISO-MSMS	1	PT5722-10	10	B1 SCX	635.32
	ISO-MSMS	1	PT5722-55	55	H/H SCX	634.82
	MULTI-MSMS		PT5722-2	2	B1	555.27
	MULTI-MSMS		PT5722-22	22	B2 SCX	832.41
	MULTI-MSMS		PT5722-36	36	B3 SCX	555.27
	MULTI-MSMS		PT5722-37	37	B3 SCX	832.4
	MULTI-MATCH		PT5722-36	36	B3 SCX	
	MULTI-MSMS		PT5722-2	2	B1	597.97
	MULTI-MSMS		PT5722-7	7	B1 SCX	597.97
	MULTI-MSMS		PT5722-52	52	H/H SCX	694.33
Mediator of	MSMS	0	PT5722-3	3	B1	719.36
	ISO-MSMS	0	PT5722-3	3	B1	766.07
	MSMS	0	PT5722-38	38	B3 SCX	883.43
	ISO-MSMS	1	PT5722-4	4	B1	799.37
	ISO-MSMS	1	PT5722-3	3	B1	799.4
CG31347	MULTI-MSMS		PT5722-33	33	B3	482.89
CG31347	MULTI-MATCH		PT5722-34	34	B3	
FACT comple	MULTI-MSMS		PT5722-21	21	B2 SCX	754.67
FACT comple	MULTI-MSMS		PT5722-22	22	B2 SCX	754.33
FACT comple	MULTI-MSMS		PT5722-36	36	B3 SCX	754.33
614;BcDNA.G	ISO-MSMS	-1	PT5722-35	35	B3	563.71
smallish, sma	MULTI-MSMS		PT5722-24	24	B2 SCX	558.59
smallish, sma	ISO-MSMS	0	PT5722-39	39	B3 SCX	558.58
	MULTI-MSMS		PT5722-39	39	B3 SCX	936.46
smallish, sma	MULTI-SECPEP		PT5722-16	16	B2	958.48
smallish, sma	MULTI-SECPEP		PT5722-33	33	B3	958.48
Probable elo	ISO-MSMS	0	PT5722-24	24	B2 SCX	926.15
	MULTI-MSMS		PT5722-20	20	B2	615.25

	MULTI-MSMS		PT5722-40	40	B3 SCX	615.25
	MULTI-MSMS		PT5722-50	50	H/H	602.75
	MULTI-SECPEP		PT5722-50	50	H/H	425.52
	ISO-MSMS	0	PT5722-6	6	B1 SCX	678.86
	ISO-MSMS	0	PT5722-7	7	B1 SCX	678.86
	ISO-MSMS	0	PT5722-8	8	B1 SCX	678.86
	ISO-MSMS	0	PT5722-19	19	B2	678.86
	ISO-MSMS	0	PT5722-20	20	B2	678.86
	ISO-MSMS	0	PT5722-21	21	B2 SCX	678.86
	ISO-MSMS	0	PT5722-22	22	B2 SCX	678.86
	ISO-MSMS	0	PT5722-24	24	B2 SCX	678.86
	ISO-MSMS	0	PT5722-31	31	B3	678.86
	ISO-MSMS	0	PT5722-32	32	B3	678.86
	ISO-MSMS	0	PT5722-36	36	B3 SCX	678.86
	ISO-MSMS	0	PT5722-37	37	B3 SCX	678.86
	ISO-MSMS	0	PT5722-39	39	B3 SCX	678.86
	ISO-MSMS	0	PT5722-46	46	H/H	678.86
	ISO-MSMS	0	PT5722-47	47	H/H	678.86
	ISO-MSMS	0	PT5722-50	50	H/H	678.86
	ISO-MSMS	0	PT5722-51	51	H/H SCX	678.86
	ISO-MSMS	0	PT5722-54	54	H/H SCX	678.86
Phosphorylas	ISO-MSMS	0	PT5722-36	36	B3 SCX	931.47
Phosphorylas	MULTI-MSMS		PT5722-37	37	B3 SCX	931.98
Phosphorylas	MULTI-MSMS		PT5722-37	37	B3 SCX	664.02
Phosphorylas	MULTI-MATCH		PT5722-36	36	B3 SCX	
	MULTI-MSMS		PT5722-25	25	B2 SCX	589.8
	MSMS	0	PT5722-38	38	B3 SCX	707.81
Titin	MSMS	1	PT5722-8	8	B1 SCX	806.39
Myosin heavy	ISO-MSMS	0	PT5722-10	10	B1 SCX	613.29
Myosin heavy	ISO-MSMS	0	PT5722-55	55	H/H SCX	613.29
	ISO-MSMS	0	PT5722-4	4	B1	689.38
2164-RA	ISO-MSMS	1	PT5722-25	25	B2 SCX	613.28
	ISO-MSMS	0	PT5722-37	37	B3 SCX	814.89
	ISO-MSMS	0	PT5722-50	50	H/H	814.89
	ISO-MSMS	0	PT5722-51	51	H/H SCX	814.89
	MULTI-SECPEP		PT5722-19	19	B2	908.98
amp1	MULTI-MSMS		PT5722-35	35	B3	620.77
Vitellogenin-	ISO-MSMS	0	PT5722-8	8	B1 SCX	717.63
Vitellogenin-	ISO-MSMS	0	PT5722-18	18	B2	717.3
Vitellogenin-	MULTI-MSMS		PT5722-33	33	B3	717.63
Vitellogenin-	MULTI-MSMS		PT5722-38	38	B3 SCX	717.63
Vitellogenin-	ISO-MSMS	0	PT5722-40	40	B3 SCX	717.63
Vitellogenin-	MULTI-MSMS		PT5722-48	48	H/H	720.63

Vitellogenin-	MULTI-MSMS		PT5722-53	53	H/H SCX	717.29	
Vitellogenin-	ISO-MSMS	0	PT5722-55	55	H/H SCX	717.63	
	MULTI-MSMS		PT5722-4	4	B1	990.98	
	MULTI-MSMS		PT5722-18	18	B2	990.98	
	MULTI-MSMS		PT5722-23	23	B2 SCX	990.98	
	MULTI-MATCH		PT5722-24	24	B2 SCX		
	MULTI-MATCH		PT5722-25	25	B2 SCX		
	MULTI-MSMS		PT5722-33	33	B3	887.1	
	MULTI-MSMS		PT5722-55	55	H/H SCX	715.84	
	MULTI-MATCH		PT5722-54	54	H/H SCX		
Survival mot	ISO-MSMS	0	PT5722-24	24	B2 SCX	1072.48	
Survival mot	ISO-MSMS	0	PT5722-39	39	B3 SCX	1072.47	
Survival mot	ISO-MSMS	0	PT5722-40	40	B3 SCX	1072.47	
	ISO-MSMS	0	PT5722-2	2	B1	753.05	
	ISO-MSMS	0	PT5722-22	22	B2 SCX	752.72	
	ISO-MSMS	0	PT5722-36	36	B3 SCX	753.05	
1367-RA	MULTI-MSMS		PT5722-23	23	B2 SCX	670.97	
1367-RA	MULTI-MATCH		PT5722-21	21	B2 SCX		
1367-RA	MULTI-MATCH		PT5722-22	22	B2 SCX		
637;BcDNA:G	MSMS	0	PT5722-24	24	B2 SCX	469.58	
	MSMS	0	PT5722-49	49	H/H	629.31	
Protein NASP	ISO-MSMS	0	PT5722-3	3	B1	727.67	
Protein NASP	MULTI-MSMS		PT5722-7	7	B1 SCX	546.01	
Protein NASP	MULTI-MSMS		PT5722-18	18	B2	727.68	
Protein NASP	ISO-MSMS	0	PT5722-18	18	B2	545.76	
Protein NASP	ISO-MSMS	0	PT5722-23	23	B2 SCX	546.01	
Protein NASP	ISO-MSMS	0	PT5722-32	32	B3	545.76	
Protein NASP	MULTI-MSMS		PT5722-36	36	B3 SCX	728.01	
Protein NASP	ISO-MSMS	0	PT5722-36	36	B3 SCX	546.01	
Protein NASP	ISO-MSMS	0	PT5722-37	37	B3 SCX	727.68	
	ISO-MSMS	0	PT5722-35	35	B3	953.43	
Eukaryotic tr	MULTI-MSMS		PT5722-36	36	B3 SCX	1016.01	
Eukaryotic tr	MULTI-MATCH		PT5722-37	37	B3 SCX		
Akap200	ISO-MSMS	0	PT5722-9	9	B1 SCX		738
Akap200	MULTI-MSMS		PT5722-37	37	B3 SCX	737.66	
Akap200	MULTI-MSMS		PT5722-39	39	B3 SCX	737.67	
Akap200	ISO-MSMS	0	PT5722-47	47	H/H	737.66	
Akap200	MULTI-MSMS		PT5722-54	54	H/H SCX	743.68	
Protein NASP	MULTI-MSMS		PT5722-3	3	B1	1029.47	
Protein NASP	MULTI-MSMS		PT5722-12	12	B1 TIO2	1028.97	
Protein NASP	MULTI-MSMS		PT5722-13	13	B1 TIO2	1028.97	
Protein NASP	MULTI-MSMS		PT5722-14	14	B1 TIO2	1028.97	
Protein NASP	MULTI-MSMS		PT5722-18	18	B2	1029.47	

Protein NASP	ISO-MSMS	0	PT5722-23	23	B2 SCX	1028.97
Protein NASP	MULTI-MSMS		PT5722-27	27	B2 TIO2	1028.97
Protein NASP	MULTI-MSMS		PT5722-28	28	B2 TIO2	1028.97
Protein NASP	MULTI-MSMS		PT5722-29	29	B2 TIO2	1028.97
Protein NASP	MULTI-MSMS		PT5722-32	32	B3	1029.47
Protein NASP	ISO-MSMS	0	PT5722-32	32	B3	686.65
Protein NASP	MULTI-MSMS		PT5722-33	33	B3	1028.97
Protein NASP	MULTI-MSMS		PT5722-33	33	B3	686.32
Protein NASP	ISO-MSMS	0	PT5722-38	38	B3 SCX	1028.98
Protein NASP	MULTI-MSMS		PT5722-42	42	B3 TIO2	1033.48
Protein NASP	MULTI-MSMS		PT5722-42	42	B3 TIO2	686.65
Protein NASP	MULTI-MSMS		PT5722-43	43	B3 TIO2	1029.47
Protein NASP	MULTI-MSMS		PT5722-44	44	B3 TIO2	1028.96
Protein NASP	ISO-MSMS	0	PT5722-44	44	B3 TIO2	686.65
Protein NASP	ISO-MSMS	0	PT5722-45	45	B3 TIO2	1028.98
Protein NASP	MULTI-MSMS		PT5722-47	47	H/H	1029.47
Protein NASP	MULTI-MSMS		PT5722-48	48	H/H	1028.96
Protein NASP	MULTI-MSMS		PT5722-52	52	H/H SCX	1028.96
Protein NASP	MULTI-MSMS		PT5722-57	57	H/H TIO2	1029.47
Protein NASP	MULTI-MSMS		PT5722-58	58	H/H TIO2	1028.97
Protein NASP	MSMS	0	PT5722-58	58	H/H TIO2	686.32
Protein NASP	MULTI-MSMS		PT5722-59	59	H/H TIO2	1028.97
Protein NASP	MULTI-MATCH		PT5722-2	2	B1	
	MULTI-MSMS		PT5722-4	4	B1	671.68
Histone H1	ISO-MSMS	0	PT5722-4	4	B1	693.66
Histone H1	ISO-MSMS	0	PT5722-19	19	B2	1039.49
Histone H1	MULTI-MSMS		PT5722-49	49	H/H	693.33
	MSMS	1	PT5722-23	23	B2 SCX	732.71
UPF0528 prot	ISO-MSMS	0	PT5722-14	14	B1 TIO2	700.65
Protein transl	MULTI-MSMS		PT5722-40	40	B3 SCX	963.46
Protein transl	ISO-MSMS	0	PT5722-45	45	B3 TIO2	963.47
Protein slend	MULTI-MSMS		PT5722-57	57	H/H TIO2	845.37
Protein slend	MULTI-MATCH		PT5722-58	58	H/H TIO2	
E3 ubiquitin-p	MULTI-MSMS		PT5722-19	19	B2	785.71
E3 ubiquitin-p	MULTI-MSMS		PT5722-24	24	B2 SCX	791.04
E3 ubiquitin-p	MULTI-MATCH		PT5722-25	25	B2 SCX	
	ISO-MSMS	0	PT5722-12	12	B1 TIO2	844.38
	MSMS	1	PT5722-33	33	B3	655.32
Probable citra	MULTI-SECPEP		PT5722-23	23	B2 SCX	608.32
tacc	ISO-MSMS	0	PT5722-7	7	B1 SCX	826.91
	MULTI-MSMS		PT5722-41	41	B3 TIO2	826.91
	ISO-MSMS	0	PT5722-51	51	H/H SCX	826.9
	MULTI-MSMS		PT5722-54	54	H/H SCX	826.9

	MULTI-MSMS		PT5722-57	57	H/H TIO2	826.4
	MULTI-MSMS		PT5722-57	57	H/H TIO2	866.39
V-type proto	MSMS	1	PT5722-31	31	B3	895.9
	MSMS	1	PT5722-38	38	B3 SCX	679.38
Transcription	MSMS	0	PT5722-56	56	H/H TIO2	755.73
Protein will d	MSMS	0	PT5722-49	49	H/H	749.34
	ISO-MSMS	1	PT5722-4	4	B1	982.46
cAMP-depen	MULTI-MSMS		PT5722-58	58	H/H TIO2	876.03
Nedd8-activa	MULTI-MSMS		PT5722-11	11	B1 TIO2	799.9
Nedd8-activa	MULTI-MSMS		PT5722-28	28	B2 TIO2	799.9
Nedd8-activa	MULTI-MSMS		PT5722-57	57	H/H TIO2	799.9
Nedd8-activa	MULTI-MSMS		PT5722-58	58	H/H TIO2	799.9
	ISO-MSMS	0	PT5722-38	38	B3 SCX	988.49
Moesin/ezrin	ISO-MSMS	0	PT5722-18	18	B2	410.24
	MSMS	0	PT5722-34	34	B3	696.01
	MULTI-MSMS		PT5722-2	2	B1	861.78
	MULTI-MSMS		PT5722-55	55	H/H SCX	1073.18
	ISO-MSMS	0	PT5722-2	2	B1	717.84
	MULTI-SECPEP		PT5722-22	22	B2 SCX	926.46
Peptidyl-prol	ISO-MSMS	1	PT5722-39	39	B3 SCX	747.37
	MULTI-MSMS		PT5722-19	19	B2	440.23
	MULTI-MSMS		PT5722-34	34	B3	440.56
	ISO-MSMS	1	PT5722-39	39	B3 SCX	988.48
	MULTI-MSMS		PT5722-22	22	B2 SCX	651.83
Probable hist	ISO-MSMS	0	PT5722-3	3	B1	1008.44
Probable hist	MULTI-MSMS		PT5722-38	38	B3 SCX	1008.44
Probable hist	MULTI-MSMS		PT5722-53	53	H/H SCX	1008.77
Otefin	ISO-MSMS	0	PT5722-3	3	B1	954.95
Otefin	ISO-MSMS	0	PT5722-33	33	B3	954.96
Otefin	ISO-MSMS	0	PT5722-38	38	B3 SCX	954.96
DNA-binding	ISO-MSMS	0	PT5722-32	32	B3	588.95
Probable elo	MULTI-MSMS		PT5722-24	24	B2 SCX	628.31
Probable elo	MULTI-MSMS		PT5722-54	54	H/H SCX	627.97
	MULTI-MSMS		PT5722-4	4	B1	672.02
	MULTI-MSMS		PT5722-18	18	B2	672.02
	MULTI-MSMS		PT5722-32	32	B3	671.69
Bap111 Brah	ISO-MSMS	0	PT5722-34	34	B3	903.72
	MULTI-MSMS		PT5722-54	54	H/H SCX	622.65
Ubiquitin car	MULTI-MSMS		PT5722-37	37	B3 SCX	766.07
Ubiquitin car	MULTI-MATCH		PT5722-36	36	B3 SCX	
26S proteaso	MSMS	0	PT5722-48	48	H/H	623.31
Cold shock d	MULTI-MSMS		PT5722-40	40	B3 SCX	767.82
Cold shock d	MULTI-MSMS		PT5722-55	55	H/H SCX	772.32

DNA excision	MULTI-MSMS		PT5722-39	39	B3 SCX	874.37
	ISO-MSMS	0	PT5722-23	23	B2 SCX	641.82
	ISO-MSMS	0	PT5722-48	48	H/H	642.07
	MULTI-MSMS		PT5722-37	37	B3 SCX	671.85
	MULTI-MATCH		PT5722-36	36	B3 SCX	
	MSMS	0	PT5722-20	20	B2	705.34
Long-chain-fa	ISO-MSMS	0	PT5722-54	54	H/H SCX	720.38
	ISO-MSMS	0	PT5722-33	33	B3	738.86
Splicing facto	ISO-MSMS	0	PT5722-52	52	H/H SCX	557.25
	MULTI-MSMS		PT5722-22	22	B2 SCX	710.36
DNA-directed	MULTI-MSMS		PT5722-39	39	B3 SCX	821.92
	ISO-MSMS	1	PT5722-39	39	B3 SCX	918.1

Charge	m/z	Mass	Resolution	Uncalibrated	Uncalibrated	Mass Error [p
3	761341567	228100287	48700.75	-0.6341	-0.00048276	-0.040968
3	761341567	228100287	NaN	NaN	NaN	0.14489
3	734686124	220103654	NaN	NaN	NaN	0.91062
3	734686124	220103654	NaN	NaN	NaN	0.23012
3	777384445	23291315	NaN	NaN	NaN	0.8582
3	777384445	23291315	NaN	NaN	NaN	0.78236
3	804039888	240909784	NaN	NaN	NaN	0.47731
3	804039888	240909784	NaN	NaN	NaN	0.28295
3	767354045	229904031	48876.38	0	0	-10011
2	908936794	181585904	NaN	NaN	NaN	13756
2	631254526	12604945	NaN	NaN	NaN	-0.29455
3	516592108	154675449	56958.66	0.15225	0.78649	-0.58953
2	774384523	154675449	48267.14	-0.51862	-0.00040161	-0.68776
3	757022497	226804566	NaN	NaN	NaN	-0.17349
2	749842461	149767037	NaN	NaN	NaN	NaN
2	749842461	149767037	NaN	NaN	NaN	NaN
3	484593449	145075852	NaN	NaN	NaN	NaN
3	782049285	234312603	49084.29	-0.31035	-0.00024271	-0.22733
3	782049285	234312603	47136.54	-0.6614	-0.00051725	-0.84304
3	782049285	234312603	48041.27	-0.65958	-0.00051582	-0.34588
3	782049285	234312603	NaN	NaN	NaN	0.32247
3	782049285	234312603	47180.82	-0.58054	-0.00045401	-0.46054
2	117257029	234312603	38721.94	-0.93501	-0.0010964	-0.19664
3	782049285	234312603	NaN	NaN	NaN	-0.60707
3	782049285	234312603	47256.8	-0.42933	-0.00033576	-0.70423
3	782049285	234312603	47104.99	-0.85091	-0.00066545	-0.34612
3	782049285	234312603	46783.95	-0.96112	-0.00075164	-0.95532
3	782049285	234312603	47026.67	-0.66347	-0.00051887	-0.428
3	78237729	234411004	NaN	NaN	NaN	0.13328
2	683360517	136470648	NaN	NaN	NaN	NaN
2	110601649	221001843	40031.52	-0.93809	-0.0010375	0.17847
2	110601649	221001843	39980.95	-0.7294	-0.00080672	0.064339
2	110601649	221001843	NaN	NaN	NaN	0.45069
2	110601649	221001843	40122.95	-0.48689	-0.00053851	0.11751
2	110601649	221001843	39421.7	-0.60565	-0.00066986	0.046545
2	110601649	221001843	39367.34	0	0	-0.48324
2	114599966	228998476	40352.94	-0.60563	-0.00069406	0.03998
3	764335531	228998476	48247.85	-0.60554	-0.00046284	-0.14232
4	942699453	376676871	NaN	NaN	NaN	0.7398
4	942699453	376676871	NaN	NaN	NaN	0.44133
4	942699453	376676871	NaN	NaN	NaN	0.57015
4	942699453	376676871	NaN	NaN	NaN	0.62828

4	942699453	376676871	43554.6	-0.24396	-0.00022998	-11793
3	812069803	243318758	47351.67	-0.33769	-0.00027423	0.75759
2	954971699	190792885	42136.86	0.16333	0.00015598	-12736
2	954971699	190792885	42136.86	0.16333	0.00015598	-12736
2	954971699	190792885	43141.78	-0.34128	-0.00032592	-0.27091
2	862367787	172272102	45493.23	-15807	-0.0013632	-0.2871
2	543273182	108453181	NaN	NaN	NaN	NaN
2	543273182	108453181	NaN	NaN	NaN	NaN
2	948917758	189582096	NaN	NaN	NaN	NaN
2	948917758	189582096	NaN	NaN	NaN	NaN
2	948917758	189582096	NaN	NaN	NaN	NaN
2	84133509	168065563	45027.15	-0.89245	-0.00075085	0.41865
2	84133509	168065563	44767.33	-0.58062	-0.0004885	-0.38377
2	84133509	168065563	44982.43	-0.63029	-0.00053029	0.24525
2	84133509	168065563	45711.25	0	0	-11744
2	84133509	168065563	NaN	NaN	NaN	0.69875
2	84133509	168065563	NaN	NaN	NaN	-0.11447
2	84133509	168065563	43560.81	-0.47621	-0.00040065	-0.33956
2	84133509	168065563	45250.93	-0.87036	-0.00073227	-0.046635
2	84133509	168065563	45688.7	-0.94427	-0.00079445	-0.28334
2	84133509	168065563	46313.07	-0.57953	-0.00048758	-0.35958
2	84133509	168065563	45818.69	-0.70187	-0.0005905	-0.055655
2	84133509	168065563	46058.67	-0.88319	-0.00074306	0.088149
2	622765061	124351557	49666.66	-11675	-0.00072709	0.72062
2	622765061	124351557	53750.39	0	0	-0.36105
2	622765061	124351557	53765.87	-0.68807	-0.00042851	-0.096821
2	622765061	124351557	49223.58	-0.70701	-0.0004403	0.21521
2	622765061	124351557	53622.12	0	0	-0.33432
2	622765061	124351557	52022.43	-0.23251	-0.0001448	-0.28415
2	622765061	124351557	53283.96	-0.8521	-0.00053066	-0.026131
2	622765061	124351557	54265.55	-0.51174	-0.0003187	0.47838
2	622765061	124351557	49801.67	-0.35894	-0.00022353	0.1143
2	622765061	124351557	53179.15	-0.50061	-0.00031176	0.29178
2	622765061	124351557	54084.26	-0.31982	-0.00019917	-0.43446
3	72669461	2177062	NaN	NaN	NaN	NaN
3	812032628	243307605	NaN	NaN	NaN	-11897
2	651301613	130058867	48959.03	-0.26603	-0.00017327	11725
2	651301613	130058867	50046.32	-0.73326	-0.00047757	14704
2	619254852	123649515	53106.32	-0.21324	-0.00013205	13032
2	619254852	123649515	51842.47	-0.24336	-0.0001507	15959
2	671344678	13406748	NaN	NaN	NaN	NaN
3	768697134	230306957	NaN	NaN	NaN	10683
3	821683108	246202749	NaN	NaN	NaN	0.72795

3	821683108	246202749	46390.55	-0.52842	-0.00043419	0.18359
3	821683108	246202749	46712.96	-0.49176	-0.00040407	-0.048026
3	821683108	246202749	46631.54	-0.5666	-0.00046556	0.12942
3	821683108	246202749	46837.07	-0.46708	-0.00038379	-0.087081
3	821683108	246202749	46733.58	-0.54819	-0.00045044	-0.36846
2	905411329	180880811	NaN	NaN	NaN	0.84056
4	385940632	153973342	66420.11	0.018018	0.069539	-13849
4	385940632	153973342	66350.92	-0.27129	-0.0001047	-13766
2	926902094	185178963	44362.79	-0.85174	-0.00078948	-23454
3	9094124	272521537	NaN	NaN	NaN	0.53441
3	9094124	272521537	NaN	NaN	NaN	0.7078
3	9094124	272521537	44209.95	-0.57909	-0.00052663	0.11881
3	74103403	222008026	NaN	NaN	NaN	-0.96098
3	676307141	202589959	NaN	NaN	NaN	13318
3	788043977	23611101	47177.56	0	0	-0.95449
3	105211134	315331218	NaN	NaN	NaN	0.088838
3	105211134	315331218	NaN	NaN	NaN	-0.079777
3	105211134	315331218	NaN	NaN	NaN	0.38664
2	901935928	18018573	NaN	NaN	NaN	NaN
2	811864979	16217154	NaN	NaN	NaN	-17282
3	542593843	16247597	56848.63	-0.085335	-0.46302	16839
2	697759845	139350514	NaN	NaN	NaN	NaN
2	612797218	122357988	NaN	NaN	NaN	0.87587
3	785378079	235311241	47347.99	-0.69284	-0.00054414	-18986
3	788036934	236108897	NaN	NaN	NaN	0.63878
2	839405956	167679736	NaN	NaN	NaN	NaN
3	913090604	273624998	NaN	NaN	NaN	13904
2	730277241	145853993	49649.55	0.0087363	0.063799	-0.4595
2	702762518	140351048	NaN	NaN	NaN	-14181
2	702762518	140351048	49509.86	-0.77163	-0.00054227	-0.70452
2	702762518	140351048	50982.97	-0.46099	-0.00032397	0.016504
2	948935405	189585626	NaN	NaN	NaN	NaN
3	500897748	149967141	NaN	NaN	NaN	NaN
2	84188116	168174777	NaN	NaN	NaN	NaN
2	64230521	128259587	NaN	NaN	NaN	0.85034
2	64230521	128259587	51321.98	-0.39844	-0.00025592	-0.30627
2	64230521	128259587	52150.46	0	0	-0.43276
2	692867121	138371969	50168.29	-0.27966	-0.00019377	-0.18817
2	894436096	178685764	NaN	NaN	NaN	NaN
2	620306364	123859818	49206.27	-0.79259	-0.00049165	-0.50163
3	821402721	246118633	NaN	NaN	NaN	0.32563
3	821402721	246118633	46888.1	-0.66651	-0.00054747	-0.93131
2	633294311	126457407	51009.8	-0.71716	-0.00045417	0.79737

3	789043031	236410726	47036.24	-0.52761	-0.00041631	-0.89262
3	789043031	236410726	46820.52	-0.33946	-0.00026785	-1513
2	128704259	257207063	NaN	NaN	NaN	NaN
2	908943753	181587295	43925.27	-0.15097	-0.00013722	-14113
2	908943753	181587295	43245.38	-0.87631	-0.00079652	0.13465
2	908943753	181587295	44846.23	-0.85025	-0.00077283	-0.24021
2	908943753	181587295	43456.12	-0.87947	-0.00079939	-0.30722
2	908943753	181587295	44681.04	-15423	-0.0014018	0.61805
3	83770283	251008666	44966.19	-0.54529	-0.00045679	13236
3	83770283	251008666	44966.19	-0.54529	-0.00045679	13236
2	915894989	182977542	NaN	NaN	NaN	18622
2	864915527	17278165	NaN	NaN	NaN	0.92292
2	864915527	17278165	NaN	NaN	NaN	0.22132
2	85691807	171182159	NaN	NaN	NaN	NaN
3	714652181	214093471	49880.31	-11474	-0.00082	-16852
2	911952217	182188988	NaN	NaN	NaN	-16267
3	721690041	216204829	NaN	NaN	NaN	11152
3	496928497	148776366	NaN	NaN	NaN	NaN
2	103737957	207274458	41426.96	-0.80348	-0.00083351	-0.3003
2	103737957	207274458	NaN	NaN	NaN	0.01813
2	103737957	207274458	41640.52	-0.73718	-0.00076473	-0.066447
2	483220615	964426677	NaN	NaN	NaN	NaN
4	727068215	290424375	NaN	NaN	NaN	10117
3	969088528	290424375	42884.98	-11746	-0.0011383	-0.24134
4	727068215	290424375	49911.34	-0.99858	-0.00072604	-0.1016
4	727068215	290424375	NaN	NaN	NaN	0.51106
3	8540532	255913777	NaN	NaN	NaN	0.60084
3	8540532	255913777	NaN	NaN	NaN	0.29601
2	118441603	23668175	NaN	NaN	NaN	NaN
3	789946443	23668175	NaN	NaN	NaN	NaN
3	789946443	23668175	NaN	NaN	NaN	NaN
3	763290999	228685117	47898.98	-0.71276	-0.00054404	-0.16419
3	732319107	219393549	49921.53	-0.59548	-0.00043608	0.32665
3	728314467	218192157	51794.11	-10257	-0.00074707	0.90945
2	66333925	132466395	NaN	NaN	NaN	15429
2	846904963	169179537	43777	-0.61085	-0.00051733	12207
2	914957825	18279011	NaN	NaN	NaN	-10979
2	71385613	142569771	NaN	NaN	NaN	10855
3	632607934	189480197	NaN	NaN	NaN	10578
3	632607934	189480197	52561.09	-0.94823	-0.00059985	-0.19406
3	632607934	189480197	54769.45	-0.55402	-0.00035048	0.0018982
3	632607934	189480197	NaN	NaN	NaN	0.58237
3	632607934	189480197	NaN	NaN	NaN	0.64711

3	632607934	189480197	52791.61	-0.51669	-0.00032686	-0.51163
2	103392754	206584053	40415.86	-0.79586	-0.00082286	0.25047
3	757710721	227011033	47473.69	-0.41805	-0.00031676	0.90588
2	76537244	152873033	NaN	NaN	NaN	-17092
2	782872804	156373105	NaN	NaN	NaN	-0.173
3	586953594	175783895	NaN	NaN	NaN	NaN
3	733013906	219601989	48116.09	-0.36865	-0.00027023	0.19886
3	962450349	288432922	NaN	NaN	NaN	0.46048
3	777065113	232817351	47861.34	-0.74969	-0.00058255	-20764
2	901931716	180184888	47012.53	-0.15586	-0.00014058	15503
3	110845052	332232973	NaN	NaN	NaN	0.45608
2	758352554	151469056	NaN	NaN	NaN	-0.029571
3	982795507	294536469	NaN	NaN	NaN	NaN
3	690976337	206990718	NaN	NaN	NaN	NaN
2	468233525	934452498	NaN	NaN	NaN	0.41775
2	991439898	198086524	NaN	NaN	NaN	0.23051
2	991439898	198086524	NaN	NaN	NaN	0.56887
3	764403789	229018954	NaN	NaN	NaN	NaN
3	567603685	169978922	56402.93	-0.56275	-0.00031942	0.77722
2	850901889	169978922	NaN	NaN	NaN	12041
2	830881291	165974803	44962.62	-0.60138	-0.00049967	-0.045227
2	904967374	18079202	NaN	NaN	NaN	12742
3	741017596	222003096	47644.57	-11412	-0.00084565	0.4771
2	859406284	171679801	45496.41	-0.79204	-0.00068069	17602
2	859406284	171679801	46122.58	-0.6682	-0.00057426	22269
3	760406638	227819809	45270.59	-0.7434	-0.00056529	0.6408
3	837675847	251000571	46192.75	0.27528	0.0002306	-10232
2	809886573	161775859	NaN	NaN	NaN	-13628
2	809886573	161775859	NaN	NaN	NaN	-0.79476
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3	6326071	189479947	55347.39	-0.66669	-0.00042175	10897
2	694848396	138768224	NaN	NaN	NaN	NaN
2	909435761	181685697	43696.7	-18642	-0.0016954	0.0030465
3	606626266	181685697	52622.78	-0.53676	-0.00032561	-11913
3	606626266	181685697	53944.11	-0.10199	-0.61868	-12749
3	606626266	181685697	53182.92	-0.37484	-0.00022739	-10728
3	597626378	17898573	52584.19	-0.2817	-0.00016835	-0.85859
2	895935928	17898573	42945.04	-0.27722	-0.00024837	-17824
2	895935928	17898573	43884.54	-11219	-0.0010051	-0.50313
3	597626378	17898573	51025.32	-0.64456	-0.00038521	-0.27575
2	903419923	180482529	NaN	NaN	NaN	0.48176
2	903419923	180482529	NaN	NaN	NaN	12271

2	903419923	180482529	NaN	NaN	NaN	17114
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2	903419923	180482529	NaN	NaN	NaN	13955
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2	793855273	158569599	NaN	NaN	NaN	-40766
2	801371287	160072802	NaN	NaN	NaN	-0.58927
2	824379735	164674492	NaN	NaN	NaN	14386
2	904952444	180789034	NaN	NaN	NaN	-15692
2	497713261	993411969	63181.4	-0.47068	-0.00023426	0.38491
3	824410832	247021067	NaN	NaN	NaN	-1.47
3	930129053	278736533	NaN	NaN	NaN	0.60166
2	750845854	149967715	47822.81	-10651	-0.00079971	12842
3	914401501	274018267	NaN	NaN	NaN	-0.36446
3	914401501	274018267	NaN	NaN	NaN	0.40981
3	914401501	274018267	43868.11	-0.60547	-0.00055364	-0.39734
2	626806	125159745	NaN	NaN	NaN	-13851
2	626806	125159745	NaN	NaN	NaN	-17886
3	555273215	166279782	57588.13	-0.64389	-0.00035753	-0.39201
2	832406184	166279782	45805.02	-0.90136	-0.0007503	-0.30556
3	555273215	166279782	57856	-0.18944	-0.00010519	-0.24905
2	832406184	166279782	45675.85	-0.69867	-0.00058158	0.5334
2	832406184	166279782	47421.39	-0.78716	-0.00065524	-0.099439
3	597971536	179089278	53542.4	-0.51142	-0.00030581	-11847
3	597971536	179089278	52488.26	-0.45983	-0.00027496	-13331
2	68832562	137463669	49598.84	-0.7459	-0.00051342	-14928
2	719360517	143670648	NaN	NaN	NaN	NaN
3	765739171	229419569	NaN	NaN	NaN	0.65819
3	883435756	264728544	NaN	NaN	NaN	NaN
2	790848806	157968306	NaN	NaN	NaN	-0.89867
3	791391554	237115283	NaN	NaN	NaN	-12631
3	482892334	144565517	60270.27	-0.078487	-0.37901	0.29151
3	482892334	144565517	56998.14	-0.33879	-0.0001636	10269
3	754333416	225997842	48501.36	-12935	-0.00097576	0.59531
3	754333416	225997842	48648.12	-0.68361	-0.00051567	0.44713
3	754333416	225997842	47620.15	-0.6986	-0.00052698	0.019261
2	563212456	112441036	NaN	NaN	NaN	13213
3	558251534	167173277	52879.02	-0.43009	-0.0002401	0.60775
3	558579539	167271679	NaN	NaN	NaN	10397
2	935956338	186989812	42893.06	-0.22415	-0.0002098	0.46973
2	958475759	191493696	42446.84	-10427	-0.00099945	14035
2	958475759	191493696	42782.33	-0.13625	-0.0001306	10331
4	925648089	369856325	NaN	NaN	NaN	0.99947
2	610743263	121947197	52952.65	-0.76413	-0.00046669	-12932

2	610743263	121947197	52520.14	-0.41241	-0.00025187	-14579
2	602745805	120347706	53745.4	-0.83504	-0.00050332	-11888
3	425186859	127253875	64696.68	0.35045	0.00014901	19649
2	678862361	135571017	NaN	NaN	NaN	-0.15588
2	678862361	135571017	NaN	NaN	NaN	-0.50484
2	678862361	135571017	NaN	NaN	NaN	-0.68469
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2	678862361	135571017	NaN	NaN	NaN	-0.2432
2	678862361	135571017	NaN	NaN	NaN	-10303
2	678862361	135571017	NaN	NaN	NaN	-0.52289
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2	678862361	135571017	NaN	NaN	NaN	-0.80944
2	678862361	135571017	NaN	NaN	NaN	-0.39322
2	931474598	186093464	NaN	NaN	NaN	11623
2	931474598	186093464	45039.56	-0.80878	-0.00075335	0.064491
3	664017145	198902961	52663.82	-0.50236	-0.00033357	0.087416
3	664017145	198902961	52017.14	-0.36311	-0.00024111	0.31241
2	585296323	116857809	54610.31	-0.32262	-0.00018883	-11838
2	707816139	141361773	NaN	NaN	NaN	NaN
3	80104169	240010324	NaN	NaN	NaN	NaN
3	612950689	183583024	NaN	NaN	NaN	17737
3	612950689	183583024	NaN	NaN	NaN	16463
2	68937871	137674287	NaN	NaN	NaN	-0.18966
3	610281047	182782131	NaN	NaN	NaN	-0.9206
2	814893244	162777193	NaN	NaN	NaN	-20437
2	814893244	162777193	NaN	NaN	NaN	-11287
2	814893244	162777193	NaN	NaN	NaN	-1196
2	909436338	181685812	43061.84	-13698	-0.0012458	-11923
2	620769615	123952468	54836.2	0.78559	0.00048767	-0.43215
3	71729563	214886506	NaN	NaN	NaN	10651
3	71729563	214886506	NaN	NaN	NaN	0.96299
3	71729563	214886506	50576.19	-0.81753	-0.00058641	-0.5649
3	71729563	214886506	48931.68	-11873	-0.00085165	-0.36907
3	71729563	214886506	NaN	NaN	NaN	0.82332
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3	71729563	214886506	48589.26	-0.93498	-0.00067066	-0.48078
3	71729563	214886506	NaN	NaN	NaN	0.61346
2	990473732	197893291	41371.02	-0.13943	-0.0001381	1129
2	990473732	197893291	41700.63	-0.8848	-0.00087637	17107
2	990473732	197893291	41721.6	-0.71732	-0.00071049	15135
2	990473732	197893291	41596.73	-0.78942	-0.0007819	10194
2	990473732	197893291	41791.86	-0.78107	-0.00077363	1597
3	883441965	264730407	43202.57	-0.69887	-0.00061741	-12377
2	711337239	142065992	46830.41	-0.42617	-0.00030315	-15062
2	711337239	142065992	48552.99	-0.28408	-0.00020208	-2123
3	107214017	321339869	NaN	NaN	NaN	10075
3	107214017	321339869	NaN	NaN	NaN	11244
3	107214017	321339869	NaN	NaN	NaN	0.064241
3	752716813	225512861	NaN	NaN	NaN	0.39857
3	752716813	225512861	NaN	NaN	NaN	0.6837
3	752716813	225512861	NaN	NaN	NaN	0.95028
3	670304899	200789287	50782.59	-12919	-0.00086598	-14228
3	670304899	200789287	50413.44	-0.92069	-0.00061714	-23988
3	670304899	200789287	49867.72	-0.80455	-0.00053929	-22151
3	46957791	14057119	NaN	NaN	NaN	NaN
2	629315578	12566166	NaN	NaN	NaN	NaN
3	727339959	217899805	NaN	NaN	NaN	0.67973
4	545756788	217899805	55200.6	-0.47673	-0.00026018	-11118
3	727339959	217899805	47298.66	-1453	-0.0010568	-0.28561
4	545756788	217899805	NaN	NaN	NaN	10085
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4	545756788	217899805	NaN	NaN	NaN	0.43893
3	727339959	217899805	49461.57	-0.8152	-0.00059293	-0.26477
4	545756788	217899805	NaN	NaN	NaN	0.29208
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2	953429864	190484518	NaN	NaN	NaN	16975
2	101600828	203000201	42507.05	-0.96301	-0.00097843	-13997
2	101600828	203000201	41054.1	-0.99274	-0.0010086	-20601
3	737665277	2209974	NaN	NaN	NaN	0.7087
3	737665277	2209974	48021.57	-0.81164	-0.00059872	-1022
3	737665277	2209974	49666.97	-0.73257	-0.00054039	-0.59356
3	737665277	2209974	NaN	NaN	NaN	0.063042
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2	102896974	205592493	40445.55	-0.72577	-0.0007468	-0.46537
2	102896974	205592493	40108.64	0	0	-17689
2	102896974	205592493	40719.98	0	0	-16878
2	102896974	205592493	42294.86	0	0	-15537
2	102896974	205592493	40144.92	-0.4439	-0.00045676	-10553

2	102896974	205592493	NaN	NaN	NaN	0.40686
2	102896974	205592493	40656.43	0	0	-17644
2	102896974	205592493	40637.25	0	0	-16164
2	102896974	205592493	41381.46	0	0	-11285
2	102896974	205592493	40644.64	-0.15679	-0.00016133	-12504
3	686315585	205592493	NaN	NaN	NaN	0.93733
2	102896974	205592493	41106.15	-0.72335	-0.0007443	-0.40616
3	686315585	205592493	50304.32	-0.18577	-0.0001275	-0.72788
2	102896974	205592493	NaN	NaN	NaN	0.12316
2	102896974	205592493	40951.85	-0.88397	-0.00090958	-0.59491
3	686315585	205592493	50827.29	-0.88301	-0.00060602	0.062175
2	102896974	205592493	40977.51	0	0	-14647
2	102896974	205592493	41019.25	0	0	-13648
3	686315585	205592493	NaN	NaN	NaN	0.036765
2	102896974	205592493	NaN	NaN	NaN	-0.070952
2	102896974	205592493	41467.31	-0.1204	-0.00012389	-0.57332
2	102896974	205592493	41073.05	-0.52115	-0.00053625	0.11019
2	102896974	205592493	42349.81	-0.25346	-0.0002608	-0.58571
2	102896974	205592493	41294.95	-0.6056	-0.00062315	-0.12905
2	102896974	205592493	41438.02	0	0	-0.67687
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2	102896974	205592493	41382.49	0	0	-0.21612
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3	671690264	201204896	51096.34	-0.04967	-0.33363	-18587
3	693327825	207696165	NaN	NaN	NaN	0.95663
2	10394881	207696165	NaN	NaN	NaN	0.78001
3	693327825	207696165	51124.58	-0.24826	-0.00017213	-0.90324
2	728702169	145538978	NaN	NaN	NaN	NaN
3	700653767	209893947	NaN	NaN	NaN	-0.27695
2	962961855	192390916	42497.58	-1186	-0.0011421	-0.19763
2	962961855	192390916	NaN	NaN	NaN	-0.18423
2	84536639	168871823	46651.53	-0.60604	-0.00051233	0.0019643
2	84536639	168871823	46361.82	0	0	-0.24501
3	785376455	235310754	47188.41	-0.56286	-0.00044205	-0.18373
3	790708094	236910245	46846.98	-0.63925	-0.00050546	-13783
3	790708094	236910245	46786.05	-0.61018	-0.00048247	-0.9336
2	844389487	168676442	NaN	NaN	NaN	-11825
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2	608315912	121461727	53822.03	-0.50827	-0.00030919	-15834
2	826402579	16507906	NaN	NaN	NaN	19666
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2	826402579	16507906	NaN	NaN	NaN	20438
2	826402579	16507906	44639.39	-0.90043	-0.00074412	0.59597

2	826402579	16507906	45362.56	-0.6055	-0.00050038	0.23264
2	866385744	173075693	46475.25	-0.60516	-0.0005243	0.48461
2	891894799	178177504	NaN	NaN	NaN	NaN
2	667353026	13326915	NaN	NaN	NaN	NaN
2	755736567	150945858	NaN	NaN	NaN	NaN
2	749335523	149665649	NaN	NaN	NaN	NaN
2	978457133	195489971	NaN	NaN	NaN	-0.84486
3	875689928	262404795	46945.66	0	0	-0.25452
2	799900538	159778652	45334.03	0	0	-14209
2	799900538	159778652	49691.38	0	0	-0.59866
2	799900538	159778652	47238.11	-0.60566	-0.00048447	0.065684
2	799900538	159778652	46978.66	0	0	-0.66459
3	988155981	296144611	NaN	NaN	NaN	-0.4279
3	410244091	122771044	NaN	NaN	NaN	-11645
3	696003393	208498835	NaN	NaN	NaN	NaN
3	86144196	258130405	45295.8	-0.52496	-0.00045222	0.18813
3	106950427	320549098	40548.52	-0.22543	-0.0002411	-0.015594
2	717842491	143367043	NaN	NaN	NaN	-12811
2	926900409	185178626	42856.25	-10051	-0.00093167	-0.69765
2	739356789	147669903	NaN	NaN	NaN	0.43958
3	440230399	131766937	62752.88	-0.20477	-0.90147	-0.60419
3	440230399	131766937	62672.29	-0.27832	-0.00012253	0.42741
3	982802767	294538647	NaN	NaN	NaN	14222
2	65182631	130163807	53177.34	-0.078739	-0.51324	13658
3	100810317	302128768	NaN	NaN	NaN	0.81854
3	100810317	302128768	41498.1	-0.1923	-0.00019385	-0.69867
3	100810317	302128768	41709.66	-0.69225	-0.00069786	-0.24163
4	954455923	381379459	NaN	NaN	NaN	-0.43112
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4	954455923	381379459	NaN	NaN	NaN	0.73047
3	58895203	176383426	NaN	NaN	NaN	0.42039
3	627975057	188090334	52572.27	-0.7764	-0.00048756	0.44512
3	627975057	188090334	53267.84	-0.11549	-0.72523	-0.59607
3	67168786	201204175	51096.34	-0.04967	-0.33363	17197
3	67168786	201204175	50391.08	0.0094576	0.063526	19131
3	67168786	201204175	47925.68	0.24981	0.0001678	13833
1	903418304	902411027	NaN	NaN	NaN	32655
3	616635936	184688598	53442.93	-0.70568	-0.00043514	-0.78204
3	765738599	229419397	47979.82	-0.85582	-0.00065534	0.29911
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2	623309961	124460537	NaN	NaN	NaN	NaN
2	767816139	153361773	47355.37	-0.91422	-0.00070196	0.32816
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2	874372637	174673072	45399.33	-0.94238	-0.00082399	0.8373
4	64181992	256325057	NaN	NaN	NaN	0.80509
4	64181992	256325057	NaN	NaN	NaN	0.58357
2	671854536	134169452	51400.14	-0.34084	-0.00022899	-0.88366
2	671854536	134169452	51149.23	-0.83208	-0.00055903	-0.96309
2	705334302	140865405	NaN	NaN	NaN	NaN
2	719871544	143772854	NaN	NaN	NaN	0.67791
2	738856418	147569828	NaN	NaN	NaN	-17285
2	55724683	111247911	NaN	NaN	NaN	-0.94221
3	707352305	211903509	50088.56	-0.81337	-0.00057534	0.54251
2	821919262	164182397	46434.6	-0.73217	-0.00060178	-11055
3	912426655	273425814	NaN	NaN	NaN	14577

Mass Error [D	Uncalibrated	Uncalibrated	Max intensity	Max intensity	Retention tim	Retention len
-0.03119	-0.67506	-0.00051395	7.6168E+14	7.6468E+14	73595	0.60837
0.00011031	NaN	NaN	NaN	NaN	78863	0.81698
0.00066902	NaN	NaN	NaN	NaN	67212	0.58141
0.00016907	NaN	NaN	NaN	NaN	71066	10799
0.00066715	NaN	NaN	NaN	NaN	58525	0.57363
0.0006082	NaN	NaN	NaN	NaN	63039	0.88077
0.00038378	NaN	NaN	NaN	NaN	63152	0.58234
0.0002275	NaN	NaN	NaN	NaN	67438	0.67523
-0.00076819	-10011	-0.00076819	7.6769E+14	7.7036E+14	70.19	0.49585
0.0012503	NaN	NaN	NaN	NaN	93.17	11154
-0.00018593	NaN	NaN	NaN	NaN	78.78	0.98734
-0.00030454	-0.43728	-0.0002259	5.1659E+14	5.196E+14	88265	0.5152
-0.00053259	-12064	-0.0009342	7.7438E+14	7.7889E+14	88249	13346
-0.00013134	NaN	NaN	NaN	NaN	75278	0.52748
NaN	NaN	NaN	NaN	NaN	73177	1
NaN	NaN	NaN	NaN	NaN	73417	1
NaN	NaN	NaN	NaN	NaN	89034	1
-0.00017778	-0.53768	-0.00042049	7.8238E+14	7.8506E+14	103.41	0.57672
-0.0006593	-15044	-0.0011765	7.8238E+14	7.8539E+13	100.42	0.85462
-0.0002705	-10055	-0.00078632	7.8205E+14	7.8539E+14	97275	10631
0.00025218	NaN	NaN	NaN	NaN	102.37	19762
-0.00036016	-10411	-0.00081417	7.8238E+13	7.8539E+14	97438	0.64938
-0.00023058	-11317	-0.0013269	1.1731E+14	1.1781E+14	97415	0.58425
-0.00047476	NaN	NaN	NaN	NaN	102.5	13302
-0.00055074	-11336	-0.0008865	7.8238E+14	7.8505E+14	97.99	10517
-0.00027068	-1197	-0.00093614	7.8238E+14	7.8539E+14	105.34	0.73146
-0.00074711	-19164	-0.0014987	7.8238E+14	7.8572E+13	100.21	0.42425
-0.00033472	-10915	-0.00085358	7.8238E+14	7.8539E+14	98.64	0.56222
0.00010427	NaN	NaN	NaN	NaN	98032	0.47295
NaN	NaN	NaN	NaN	NaN	83069	1
0.00019739	-0.75963	-0.00084016	1.1065E+14	1.1115E+14	116.29	0.62392
0.07116	-0.66506	-0.00073556	1.1065E+14	1.111E+14	119.5	0.31782
0.00049847	NaN	NaN	NaN	NaN	126.64	0.47802
0.00012997	-0.36938	-0.00040854	1.1065E+14	1.111E+14	136.54	0.56355
0.51479	-0.55911	-0.00061838	1.1065E+14	1.111E+14	116.89	0.64877
-0.00053448	-0.48324	-0.00053448	1.1065E+14	1.111E+14	117.13	0.53051
0.45817	-0.56565	-0.00064824	1.1465E+14	1.151E+14	126.86	0.8235
-0.00010878	-0.74786	-0.00057162	7.6467E+14	7.6767E+14	126.92	0.62176
0.00069741	NaN	NaN	NaN	NaN	79829	0.67028
0.00041604	NaN	NaN	NaN	NaN	78767	0.8231
0.00053748	NaN	NaN	NaN	NaN	77134	0.60345
0.00059228	NaN	NaN	NaN	NaN	81341	14287

-0.0011118	-14233	-0.0013418	9.4295E+13	9.4746E+14	78.16	10275
0.00061522	0.4199	0.00034099	8.1241E+14	8.1541E+14	127.2	15163
-0.0012163	-11103	-0.0010603	9.5547E+14	9.5998E+14	97553	13201
-0.0012163	-11103	-0.0010603	9.5547E+14	9.5998E+14	97553	13201
-0.00025871	-0.61219	-0.00058463	9.5497E+14	9.5948E+14	97.7	0.46027
-0.00024759	-18678	-0.0016107	8.6237E+14	8.6738E+14	53491	0.71414
NaN	NaN	NaN	NaN	NaN	68544	1
NaN	NaN	NaN	NaN	NaN	118.05	1
NaN	NaN	NaN	NaN	NaN	149.53	1
NaN	NaN	NaN	NaN	NaN	151.95	1
NaN	NaN	NaN	NaN	NaN	145.85	1
0.00035223	-0.47379	-0.00039862	8.4134E+14	8.4584E+14	81717	0.60141
-0.00032288	-0.9644	-0.00081138	8.4184E+14	8.4584E+14	85461	0.54626
0.00020634	-0.38504	-0.00032395	8.4134E+14	8.4584E+14	84705	0.659
-0.00098804	-11744	-0.00098804	8.4133E+14	8.4634E+14	81916	0.5723
0.00058788	NaN	NaN	NaN	NaN	83036	0.60281
-0.96311	NaN	NaN	NaN	NaN	81405	0.53769
-0.00028568	-0.81577	-0.00068633	8.4134E+14	8.4634E+14	95193	0.4995
-0.39236	-0.917	-0.0007715	8.4134E+14	8.4584E+14	94723	0.63361
-0.00023838	-12276	-0.0010328	8.4134E+14	8.4634E+14	82131	0.55059
-0.00030253	-0.93911	-0.00079011	8.4134E+14	8.4584E+14	84447	0.58243
-0.46825	-0.75752	-0.00063733	8.4134E+14	8.4634E+14	83209	0.60301
0.74163	-0.79504	-0.00066889	8.4184E+14	8.4684E+14	81927	0.48901
0.00044878	-0.44689	-0.00027831	6.2277E+14	6.2677E+14	76755	15688
-0.00022485	-0.36105	-0.00022485	6.2277E+14	6.2677E+14	76205	0.73231
-0.60297	-0.78489	-0.0004888	6.2277E+13	6.2677E+14	76587	0.50031
0.00013403	-0.4918	-0.00030627	6.2277E+14	6.2727E+14	77517	13885
-0.00020821	-0.33432	-0.00020821	6.2277E+14	6.2677E+11	77719	0.58629
-0.00017696	-0.51667	-0.00032176	6.2277E+14	6.2677E+14	87667	0.53617
-0.16273	-0.87823	-0.00054693	6.2277E+11	6.2677E+14	87765	0.65209
0.00029792	-0.033363	-0.20777	6.2277E+14	6.2677E+14	78112	0.86717
0.71185	-0.24463	-0.00015235	6.2277E+14	6.2677E+14	76455	16749
0.00018171	-0.20884	-0.00013006	6.2277E+14	6.2677E+14	78722	0.7103
-0.00027057	-0.75428	-0.00046974	6.2277E+14	6.2727E+14	87866	0.6384
NaN	NaN	NaN	NaN	NaN	122.52	1
-0.0009661	NaN	NaN	NaN	NaN	68.89	0.65425
0.00076365	0.90647	0.00059039	6.513E+14	6.5982E+14	51208	0.58456
0.00095766	0.73712	0.00048009	6.513E+13	6.5932E+14	48669	0.51516
0.000807	10899	0.00067495	6.1926E+14	6.2376E+14	94877	0.67711
0.00098824	13525	0.00083754	6.1926E+14	6.2376E+14	94214	0.52608
NaN	NaN	NaN	NaN	NaN	103.34	1
0.00082118	NaN	NaN	NaN	NaN	105.6	0.71088
0.00059814	NaN	NaN	NaN	NaN	103.01	0.75828

0.00015085	-0.34483	-0.00028334	8.2202E+14	8.2502E+14	101.81	0.72246
-0.39462	-0.53978	-0.00044353	8.2202E+14	8.2502E+14	100.02	0.75243
0.00010634	-0.43717	-0.00035922	8.2202E+13	8.2502E+14	110.97	10815
-0.71553	-0.55416	-0.00045534	8.2202E+14	8.2502E+13	102.64	0.68706
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89428	88928	89928	16251			
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104.8	104.24	105.3	75276			
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     68308 68.1            68534      16277
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     91648     91276     92046    -10707 -0.045914 -0.00071351 NaN
91.68          91441        92    -10484 -0.014114 0.0004307   NaN
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     96274     96034     96698     62184
     95981     95678     96715     53899 -0.14693  -0.00043725 NaN
     95931     95438     96824     14647
     95986     95643     97325     14609
     96007 95.73               96587     14849
131.04    130.73    131.67         19095
130.72    130.46    131.1          16528
130.23    129.91    130.5          68524
     77736     77388 78.11         14652
     78233 78.05               78437     11564 0.30605   -0.00075337 NaN
     77812     77542     78103     13018 -0.11486  -0.00038386 NaN
     56246     55746     56746     15247
107.58    107.08    108.08        -19476
     58848     58649     59224     16752
     57547 57.25               57904     75053
59.31          58947 59.67         16975
     59312     58829 59.76         16975
     58862     58414     59503     15253
     58767     58553     58876     83342
        59     58688     59348     15351
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     58935     58636     59263     34263
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     95918     95427     96133     28266 0.14866   -0.00067247 NaN
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     67702     67352     68128     28262
     68789     68474     69156     15308
     99005     98655     99685    -78752
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134.91    134.46    135.69         14748
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134.77    134.35    135.43         14277
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133.04	132.66	133.48	11854			
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129.9	129.62	130.4	-15667			
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62021	61684	62699	15153			
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89438	89273	89673	-11459			
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106.38     105.88     106.88         -19476
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     93802 93.59           94061       6398
     93687      93465      94031      77113
     90358      90157      90618      45403
     92529      92252      92877      69571
127.53     127.33     127.84          17564
     74955      74646      75252      16357
103.49     102.99     103.99           2122
145.78     145.57     146.04          14285
103.41     103.03     103.8           89251
     66494      66244 66.83           15086
105.73     105.28     106.03           6304
140.4      140.21     140.56          12213
     35537 35.11      35.89           17251
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137.31     136.42     137.73          70318
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     93295      92861      93581     -61941
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PEP	MS/MS Coun	MS/MS Scan	Score	Delta score	Combinatoric	Ratio H/L
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0.00066166	2	9811	63937	45532	10	0.39827
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0.015999	1	8380	54047	32371	5	0.27281
0.013065	1	5937	41615	26992	5	0.25025
0.0012876	1	6660	53625	31949	5	0.14797
0.00037934	1	6747	55302	26579	10	0.2281
0.0045661	1	7721	42209	20086	10	0.37424
0.014163	1	4648	48579	48579	5	0.31534
0.012897	1	13576	48467	20106	3	65582
0.01963	1	9065	80688	35.32	1	NaN
0.0063079	1	13327	73.36	51447	1	0.3703
0.033103	1	13329	80596	56065	1	0.58594
0.0053695	1	9268	50827	18461	1	NaN
0.02807	1	10887	45433	82528	1	
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0.0043557	2	8539	50226	29.26	7	0.35126
0.00029721	2	8791	85177	60509	7	0.18401
4.6423E-06	9	9905	115.56	89013	7	0.50312
0.94809	1	21020	94632	76316	7	0.49387
0.00046045	1	16782	85087	70065	7	0.39694
0.00011178	5	8495	111.3	72495	7	0.50955
0.00020613	4	8376	91926	74207	7	0.50597
0.0076101	1	8395	58864	30698	7	
0.22873	1	8671	97271	82391	7	0.35501
NaN	0		NaN	NaN	0	0.69868
0.0099691	1	13639	47016	64696	8	0.5026
0.020133	1	5593	41257	18627	6	0.25871
0.016457	1	8863	43091	25076	6	NaN
0.0021378	1	5542	50358	21809	6	0.46976
0.024512	1	23661	47187	14.62	1	
0.00060368	1	6010	71685	39494	3	0.39278
0.0045191	2	15975	68676	44269	2	0.63431
0.0027084	2	7149	66041	33.95	2	0.37721
0.024744	1	7074	86179	86179	2	0.7238
NaN	0		NaN	NaN	0	0.53294
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0.026924	1	10724	45357	12927	3	NaN
0.016234	1	12035	52579	65772	3	
0.029975	1	4702	65465	14213	3	0.18581
0.030294	1	15787	88283	41486	3	0.17475
0.021733	2	7087	90385	63123	3	0.27006
0.035888	1	14615	87676	60413	3	0.24707
0.0061697	1	13851	100.77	84926	3	0.8397

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0.0022498             1        6811 104.88          89939            3 0.30248
0.0065927             1        8043       69581     69581            3 0.27591
0.031                 1       11864       52008     67278           18
0.018399              1       19406       58592     17598            1
0.030004              1       11763       45653     22293           15
0.030708              1        9603 46.89           75515           10
   0.005004           1       13742       95429     50989           80 NaN
0.0097054             2        7441       51104     31948            3 0.33058
    0.86601           1        5983 106.31          85721            3 0.96199
    0.18711           1        5785 113.86          97118            3 0.26731
0.0017519             1        5830       89913     69677            3 0.38826
0.0023236             2        5682       85046     67418            3 0.50712
0.0045983             1       18690 47.05           21126           45 NaN
0.038563              1        7996       41427     17195            2 0.20728
0.011363              1       15517       59884     33112            3
0.011712              1       18688       51469     32533            7 0.51866
0.0043264             1       12296       40986     12895           35 0.35024
0.032187              1        4718       45115     14257            3 NaN
0.0060348             1       15472       63181     13847            2      13046
0.039321              1       24020       58172     87241            6 NaN
0.011627              1        1240       42629     30571            4 0.58787
0.0021129             2        1671       58274     47348            4 0.48042
0.0020297             1       18544       49497     75857           30      39007
0.003254              1       10400       61161     85827            2 0.60011
0.00011073            1       17054       63925     39718            3 0.47343
 0.00041089           2       16830       82942     82942            3 NaN
0.0030549             1       15804 47.05           27121            3 0.61585
 1.0221E-08           2       18995       75416     53565            2 0.1746
 1.2654E-08           1       22592       73603 49.58                2 0.30054
   0.040158           2       18880       57629     41819            2 0.2115
0.03597               1        4781       48907     25916            3 0.29631
0.0090881             1        7651       65887     46124            5 0.2541
0.013697              1        6573       62002     48379            5 0.44899
0.0025483             1       13644       47548 16.41                4 0.5026
0.0068367             1       20960       42314     13982            4 0.32278
0.0070169             1       20592       42095     26493            4 0.57424
0.03068               1       22205       40103     12983            5 NaN
0.0033688             1        5888       52966     67171            6 0.4069
0.00066613            1       14867       53551     37967           15 0.24014
NaN                   0             NaN         NaN                  0 0.34407
0.024356              1       10768       61765     20656            2
0.028584              1       11840       86803     67506            3 0.4286
0.024336              1       10297 89.44           42378            3 0.3455
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0.0025547	1	10770	54103	27742	3	0.73698
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0.025826	1	10358	56916	14705	3	
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0.004607	1	10195	70942	7761	2	NaN
0.034442	1	8310	57047	21603	2	0.044587
0.0095447	1	13692	62077	26979	16	29426
0.0075079	1	13370	53377	86432	2	0.19195
0.010466	1	14965	47726	61113	8	NaN

Ratio H/L nor	Ratio H/L shif	Intensity	Intensity L	Intensity H	Reverse	Potential con
0.57984	0	119240	84688	34548		
0.73098	0	88880	65772	23108		
0.35155	0	247460	209250	38214		
0.53892	0	229620	176360	53258		
0.51506	0	164080	137950	26132		
0.28614	0	192690	172720	19962		
0.44277	0	84864	78384	6480.6		
0.25798	0	90922	75426	15496		
0.38091	0	67903	46479	21424		
12628	0	173700	12556	161150		
NaN	0	142390	141990	407.64		
0.94138	0	313510	204840	108670		
14614	0	218980	132170	86805		
NaN	0	105780	98411	7367.4		
10247	0	313690	179890	133790		
0.86522	0	578820	331790	247040		
12257	0	756200	447440	308760		
0.65471	0	401910	277420	124490		
0.90773	0	4876900	2849900	2027100		
21426	0	813590	481360	332230		
0.45693	0	129650	112250	17405		
0.97177	0	707250	476140	231110		
0.90304	0	339740	185380	154350		
1655	0	114740	45031	69710		
13952	0	156460	80831	75629		
10078	0	359240	234560	124680		
11573	0	242390	145890	96503		
0.93693	0	80759	49713	31047		
0.87588	0	137250	112380	24868		
13616	0	599260	339050	260210		
13431	0	273570	164130	109440		
0.49196	0	90726	55894	34831		
11528	0	132120	81066	51050		
10819	0	65880	44312	21569		
0.21051	0	289450	271610	17837		
0.15605	0	231540	220620	10918		
0.18851	0	101150	97603	3548.5		
0.38686	0	439390	388300	51092		

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      10214 0   7382900   3846400   3536400 +
      12928 0     63270     43570     19700 +
0.69503     0     91083     60678     30406





0.50367     0    255820    208970     46851
0.68522     0    120480     85761     34715
0.36672     0    195370    160860     34513
0.57834     0    215610    156630     58975
0.29314     0    165720    146660     19056
0.11562     0     61337     54770 6566.9
0.78028     0    309790    261000     48791
0.67052     0    567380    403460    163920
       1057 0    122240     78061     44174
0.76923     0    259970    200520     59452
      10578 0    255800    185350     70457
0.37952     0     90624     68113     22511
0.68932     0   1099700    782150    317510
0.32049     0    288330    210060     78265
0.85198     0     92724     53318     39407
0.47149     0   1000500    723220    277270
0.38078     0    175680    126400     49279
      12283 0    226430    135120     91304
0.92394     0    245390    165200     80189
0.56326     0     91162     73823     17339
0.67576     0   1507900   1142600    365350
0.67518     0    313510    226040     87470
0.9039      0    216730    144730     72005

NaN         0    175250 2451.8       172800
0.70272     0    141990     90082     51908
0.42025     0     65000     39535     25465
       1205 0    249100    134730    114360
0.71817     0    101870     78338     23527

NaN         0     49661         0     49661
0.29435     0    222970    194040     28930
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0.99748	0	348080	237670	110410
10496	0	233940	157990	75949
0.71628	0	290030	203570	86459
0.96139	0	334750	215590	119160
0.94173	0	155670	108410	47258
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21855	0	129210	66144	63070
0.43474	0	781810	449920	331890
69727	0	673200	126020	547180
43778	0	405010	21418	383590
0.31421	0	51616	38672	12944
56773	0	61882	10820	51062
23934	0	141910	51627	90278
0.72155	0	59383	43312	16070
0.44605	0	52323	47569	4753.8
10384	0	63053	37972	25081
0.41515	0	48416	32483	15933
13198	0	257740	168290	89450
10617	0	82681	54727	27953
0.80221	0	267730	199900	67833
11831	0	235780	146960	88819
0.62867	0	192830	140670	52161

0.872	0	1201900	614420	587520		+
11019	0	382440	233280	149170		+
12567	0	4788200	2287400	2500800	+	
0.60287	0	5225400	3739200	1486200	+	
0.73885	0	40278	24927	15351	+	
0.95139	0	17833000	10411000	7421600	+	
0.47429	0	269230	216790	52439	+	
20359	0	1336400	547220	789140	+	
20359	0	1336400	547220	789140	+	
NaN	0	75545	3620.3	71925		
NaN	0	118170	113950	4228.6		
0.47712	0	704450	583790	120660		
19572	0	80164	43221	36943		
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NaN	0	118510	117450	1068.2		
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0.43446	0	113860	98979	14883		+
NaN	0	224060	210040	14027		+
0.8344	0	107580	74859	32725		
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0.83063	0	70607	51988	18619		
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0.37879	0	1415900	1036800	379070	+
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     41549          0    259330 8189.1          251140
     66059          0    458870      19718      439150
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     10192          0     79361      56407       22954
0.73437             0    148100      96002       52094
0.77457             0    121610      85316       36293
0.74515             0     86893      58523       28370
0.7399              0    145970      95549       50423
0.57051             0    169540     106950       62587
     13895          0   3667900    2133300     1534600

NaN                 0    313750     311870 1886.5

NaN                 0     48021          0       48021 +
     32448          0    117830 5923.9          111900
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0.4312              0    397460     267310      130150

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0.81982	0	406320	289960	116360	+
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0.57906	0	158280	103420	54860
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11579	0	453040	255010	198030
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0.29377	0	99281	75588	23692
12254	0	774480	428530	345950
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64681	16	7867	9030	105618	105618
64682	16	7867	9030	105619;1056	105620
64683	16	7867	9030	105621	105621
64684	16	7867	9030	105622	105622

64685	16	7867	9030	105623	105623
64686	16	7867	9031	105624	105624
65072	765	7923	9091	106283	106283
65090	1089	7929	9097	106297	106297
65206	185	7954	9125	106442	106442
65363	700	7977	9150	106669	106669
65727	1274	8036	9215	107257	107257
66336	1008	8094	9282	108310;1083	108311
66407	1567	8101	9290	108420	108420
66408	1567	8101	9290	108421	108421
66409	1567	8101	9290	108422	108422
66410	1567	8101	9290	108423;1084	108423
67995	1621	8249	9454	111166	111166
69221	480	8379	9598	113381	113381
69542	1481	8405	9630	114045	114045
70014	241	8457	9686	115037	115037
70212	1797	8469	9700	115290	115290
70611	1073	8523	9763	116065	116065
71295	1756	8615	9866	117351	117351
71481	317	8639	9894	117739	117739
71538	2101	8646	9902	117814	117814
71539	2101	8646	9902	117815;1178	117816
71634	208	8660	9917	117948	117948
72615	1988	8751	10018	119612	119612
74264	434	8922	10209	122344	122344
74265	434	8922	10209	122345;1223	122346
74266	434	8922	10209	122347	122347
77619	925	9284	10621	127839;1278	127839
77620	925	9284	10621	127841	127841
77621	925	9284	10621	127842;1278	127843
78230	38	9354	10698	128761	128761
79136	1801	9454	10810	130187	130187
79137	1801	9454	10810	130188	130188
79325	1455	9468	10826	130479	130479
79326	1455	9468	10826	130480	130480
79327	1455	9468	10826	130481	130481
79339	1483	9471	10829	130496	130496
79529	331	9487	10848	130771	130771
79541	1066	9490	10851	130784	130784
79542	1066	9490	10851		
79957	51	9524	10888	131513	131513
80825	788	9608	10982	132956	132956
80826	788	9608	10982	132957	132957

81631	415	9725	11109	134163	134163
82115	496	9792	11181	134919	134919
82116	496	9792	11181	134920	134920
82130	1665	9796	11185	134947	134947
82131	1665	9796	11185		
82248	1756	9817	11207	135143	135143
82327	1540	9830	11220	135244	135244
82455	566	9846	11238	135431	135431
82568	1908	9861	11255	135596	135596
82981	1252	9898	11300	136397	136397
83162	1869	9914	11318	136763	136763
83216	269	9920	11324	136833	136833

Deamidation	Oxidation (M	Phospho (STY) site IDs
		13;14
		13;14
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	204	
	1115	
	1115	
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172;173				
172;173				
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		1122		
709;710		727		33
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709;710				33
		343		
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776		
516		
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225		44
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471;472;473			22
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546			
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567	1712		
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617			
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	342		
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Sequence	Length	K Count	Modifications	Modified sequence	Deamidation (NQ) Probabilities	Oxidation (M) Probabilities
AAAPAAVASP	25	1	2 Phospho (S	_AAAPAAVAS(ph)PAAAATSADASPS(ph)PA		
AAAPAAVASP	25	1	2 Phospho (S	_AAAPAAVAS(ph)PAAAATSADASPS(ph)PA		
AAAPAAVASP	25	1	Phospho (STY	_AAAPAAVASPAAAATSADASPS(ph)PAK_		
AAAPAAVASP	25	1	Phospho (STY	_AAAPAAVASPAAAATSADASPS(ph)PAK_		
AAAPAAVASP	26	2	Phospho (STY	_AAAPAAVASPAAAATS(ph)ADASPSPAKK_		
AAAPAAVASP	26	2	Phospho (STY	_AAAPAAVASPAAAATSADASPS(ph)PAKK_		
AAAPAAVASP	26	2	2 Phospho (S	_AAAPAAVAS(ph)PAAAATSADASPS(ph)PA		
AAAPAAVASP	26	2	2 Phospho (S	_AAAPAAVAS(ph)PAAAATSADAS(ph)PSPA		
ALDLLMSYRL	11	1	Oxidation (M	_ALDLLM(ox)S(ph)Y(ph)RLK		ALDLLM(1)SY
ALDLLMSYRL	11	1	Oxidation (M	_ALDLLM(ox)S(ph)Y(ph)RLK		ALDLLM(1)SY
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLTAS(ph)HNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLTAS(ph)HNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLTAS(ph)HNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLTAS(ph)HNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLT(ph)ASHNPGGPENDFGIK_		
ALGGIVLTASH	23	1	Phospho (STY	_ALGGIVLT(p	ALGGIVLTASHN(0.529)PGG	
ALQAVYPDYV	19	1	Phospho (STY	_ALQAVYPDYVDELSLYGS(ph)K_		
ALQAVYPDYV	19	1	Phospho (STY	_ALQAVYPDYVDELSLYGS(ph)K_		
ALQAVYPDYV	19	1	Phospho (STY	_ALQAVYPDYVDELSLYGS(ph)K_		
ALQAVYPDYV	19	1	Phospho (STY	_ALQAVYPDYVDELSLYGS(ph)K_		
ALQAVYPDYV	19	1	Phospho (STY	_ALQAVYPDYVDELSLYGS(ph)K_		
ALQAVYPDYV	19	1	Phospho (STY	_ALQAVYPDYVDELSLYGS(ph)K_		
ALQAVYPDYV	19	1	2 Phospho (S	_ALQAVYPDYVDELS(ph)LYGS(ph)K_		
ALQAVYPDYV	19	1	2 Phospho (S	_ALQAVYPDYVDELS(ph)LYGS(ph)K_		
APATPQAATS	39	2	Phospho (STY	_APATPQAATSVTNPAAGDGISVQNDPPVD		
APATPQAATS	39	2	Phospho (STY	_APATPQAATSVTNPAAGDGISVQNDPPVD		
APATPQAATS	39	2	Phospho (STY	_APATPQAATSVTNPAAGDGISVQNDPPVD		
APATPQAATS	39	2	Phospho (STY	_APATPQAATSVTNPAAGDGISVQNDPPVD		

APATPQAATS	39	2	Phospho (STY	_APATPQAATSVTNPAAGDGISVQNDPPVD	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASAFQFSDDE	14	1	Phospho (STY	_ASAFQFS(ph)DDEEEVK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)AS(ph)GVTVSDVCK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)AS(ph)GVTVSDVCK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)AS(ph)GVTVSDVCK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)AS(ph)GVTVSDVCK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)AS(ph)GVTVSDVCK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)AS(ph)GVTVSDVCK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)ASGVT(ph)VSDVCK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)AS(ph)GVTVSDVCK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)AS(ph)GVTVSDVCK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)AS(ph)GVTVSDVCK_	
ASGVTVSDVC	11	1	Acetyl (Protei	_(ac)ASGVT(ph)VSDVCK_	
DLEYFNNLK	9	1	Phospho (STY	_DLEY(ph)FN	DLEYFN(1)N(1)LK
DLEYFNNLK	9	1	Phospho (STY	_DLEY(ph)FN	DLEYFN(1)N(1)LK
DVDFGDSDNI	21	1	Phospho (STY	_DVDFGDS(ph)DNENEPDAYLARLK_	
DVDFGDSDNI	21	1	Phospho (STY	_DVDFGDS(ph)DNENEPDAYLARLK_	
DVDFGDSDNI	21	1	Phospho (STY	_DVDFGDS(ph)DNENEPDAYLARLK_	
DVDFGDSDNI	21	1	Phospho (STY	_DVDFGDS(ph)DNENEPDAYLARLK_	
DVDFGDSDNI	21	1	Phospho (STY	_DVDFGDS(ph)DNENEPDAYLARLK_	
DVDFGDSDNI	21	1	Phospho (STY	_DVDFGDS(ph)DNENEPDAYLARLK_	
EAAQYGTVN	14	1	Phospho (STY	_EAAQY(ph)GTVNAVLPK_	
EAAQYGTVN	14	1	Phospho (STY	_EAAQY(ph)GTVNAVLPK_	
EASPVSMASP	25	2	Oxidation (M	_EASPVSM(ox)AS(ph)PAKD	EASPVSM(1)A

EASPVSMASP	25	2	Oxidation (M	_EASPVSM(ox)AS(ph)PAKD	EASPVSM(1)
EASPVSMASP	25	2	Oxidation (M	_EASPVS(ph)M(ox)ASPAKD	EASPVSM(1)
ELPDSDSLNV	27	1	Phospho (ST	_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_	
ELPDSDSLNV	27	1	Phospho (ST	_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_	
ELPDSDSLNV	27	1	Phospho (ST	_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_	
FFDSGDYQM	11	1	Oxidation (M	_FFDS(ph)GDYQM(ox)AK_	FFDSGDYQM
FFDSGDYQM	11	1	Oxidation (M	_FFDS(ph)GDYQM(ox)AK_	FFDSGDYQM
FFDSGDYQM	11	1	Oxidation (M	_FFDS(ph)GDYQM(ox)AK_	FFDSGDYQM
KEESESEDDD	17	1	Oxidation (M	_KEESES(ph)EDDDM(ox)GF	KEESESEDDD
KEESESEDDD	17	1	Oxidation (M	_KEESES(ph)EDDDM(ox)GF	KEESESEDDD
KEESESEDDD	17	1	Oxidation (M	_KEESES(ph)EDDDM(ox)GF	KEESESEDDD
KIDNPESSAK	25	3	Phospho (ST	_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_	
KIDNPESSAK	25	3	Phospho (ST	_KIDNPESSAKVS(ph)DAEEEEEEYAVEK_	
KIDNPESSAK	25	3	Phospho (ST	_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_	
KIDNPESSAK	25	3	Phospho (ST	_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_	
KKEEESDQSD	19	2	Oxidation (M	_KKEEES(ph)DQS(ph)DDD	KKEEESDQSD
KKEEESDQSD	19	2	Oxidation (M	_KKEEES(ph)DQS(ph)DDD	KKEEESDQSD
KKEEESDQSD	19	2	Oxidation (M	_KKEEES(ph)DQS(ph)DDD	KKEEESDQSD
KKEEESDQSD	19	2	Oxidation (M	_KKEEESDQS(ph)DDDM(ox	KKEEESDQSD
KPEDPSSEAE	17	2	Phospho (ST	_KPEDPSSEAEALCS(ph)PAK_	
KPEDPSSEAE	17	2	Phospho (ST	_KPEDPSSEAEALCS(ph)PAK_	
KPEDPSSEAE	17	2	Phospho (ST	_KPEDPSSEAEALCS(ph)PAK_	
KPEDPSSEAE	17	2	Phospho (ST	_KPEDPSSEAEALCS(ph)PAK_	
KPEDPSSEAE	17	2	Phospho (ST	_KPEDPSSEAEALCS(ph)PAK_	
KPEDPSSEAE	17	2	Phospho (ST	_KPEDPSSEAEALCS(ph)PAK_	
MPNLQSSIPH	13	2	Acetyl (Prote	_(ac)M(ox)PNLQS(ph)SIPHT	M(1)PNLQSSI
MPNLQSSIPH	13	2	Acetyl (Prote	_(ac)M(ox)PNLQS(ph)SIPHT	M(1)PNLQSSI
MPNLQSSIPH	13	2	Acetyl (Prote	_(ac)M(ox)PNLQS(ph)SIPHT	M(1)PNLQSSI
MPNLQSSIPH	13	2	Acetyl (Prote	_(ac)M(ox)PNLQS(ph)SIPHT	M(1)PNLQSSI
MQLILSYLQS	14	1	Acetyl (Prote	_(ac)MQLILS	MQ(0.212)LILSYLQ(0.848)S
MQLILSYLQS	14	1	Acetyl (Prote	_(ac)MQLILS	MQ(0.007)LILSYLQ(0.996)S
MQLILSYLQS	14	1	Acetyl (Prote	_(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_	
MQLILSYLQS	14	1	Acetyl (Prote	_(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_	
MQLILSYLQS	14	1	Oxidation (M	_M(ox)Q(de)	MQ(0.844)LIL	M(1)QLILSYL

MQLILSYLQS	14	1	Oxidation (M	_M(ox)QLILSY	MQ(0.066)LIL	M(1)QLILSYL
MQLILSYLQS	14	1	Oxidation (M	_M(ox)QLILSYLQ(de)S(ph)Q(de)QIK_		
MQLILSYLQS	14	1	Oxidation (M	_M(ox)Q(de)LILS(ph)YLQSQQ(de)IK_		
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)RD	MRDKISQ(0.0	M(1)RDKISQL
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)RD	MRDKISQ(0.0	M(1)RDKISQL
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)RD	MRDKISQ(0.0	M(1)RDKISQL
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)RD	MRDKISQ(0.0	M(1)RDKISQL
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)RD	MRDKISQ(0.0	M(1)RDKISQL
MRDKISQLFC	13	2	Acetyl (Protei	_(ac)M(ox)RD	MRDKISQ(0.2	M(1)RDKISQL
MVEPSPETVG	24	1	Oxidation (M	_M(ox)VEPSPETVGDFQSVQ	M(1)VEPSPET	
MVEPSPETVG	24	1	Oxidation (M	_M(ox)VEPSPETVGDFQSVQ	M(1)VEPSPET	
MVEPSPETVG	24	1	Oxidation (M	_M(ox)VEPSPETVGDFQSVQ	M(1)VEPSPET	
NAGGVGVGV	17	2	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLK_		
NAGGVGVGV	17	2	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLK_		
NAGGVGVGV	17	2	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLK_		
NAGGVGVGV	17	2	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLK_		
NAGGVGVGV	17	2	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLK_		
NAGGVGVGV	18	3	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLKK_		
NAGGVGVGV	18	3	Phospho (STY	_NAGGVGVGVGEKS(ph)PDLKK_		
NVGIFIKDDS	19	3	Phospho (STY	_NVGIFIKDDS(ph)DEEDVDDKK_		
NVGIFIKDDS	19	3	Phospho (STY	_NVGIFIKDDS(ph)DEEDVDDKK_		
NVGIFIKDDS	19	3	Phospho (STY	_NVGIFIKDDS(ph)DEEDVDDKK_		
PCNLYQTAQE	13	1	Phospho (STY	_PCNLY(ph)QTAQEQLK_		
PCNLYQTAQE	13	1	Phospho (STY	_PCN(de)LY(p	PCN(0.992)LYQ(0.004)TAQ(	
PLPSGRIPQIT	17	1	2 Phospho (S	_PLPS(ph)GRIPQIT(ph)PPASPK_		
PLPSGRIPQIT	17	1	2 Phospho (S	_PLPS(ph)GRIPQIT(ph)PPASPK_		
QELLQSYMK	9	1	Oxidation (M	_(gl)Q(de)ELL	Q(1)ELLQ(1)S	QELLQSYM(1)
QELLQSYMK	9	1	Oxidation (M	_(gl)Q(de)ELL	Q(1)ELLQ(1)S	QELLQSYM(1)
QELLQSYMK	9	1	Phospho (STY	_(gl)Q(de)ELL	Q(1)ELLQ(1)SYMK	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_		

QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	
QISIGIYELLK	11	1	Phospho (STY	_QISIGIY(ph)ELLK_	

QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_	
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_	
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_	
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_	
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_	
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_	
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_	
QSSYHGVHQ	18	1	Phospho (STY	_(gl)QSSYHGVHQAWNTNQDS(ph)K_	

QSVPQLANLT	16	1	Phospho (STY	_Q(de)SVPQ(	Q(0.987)SVPQ(0.987)LAN(0
QSVPQLANLT	16	1	Phospho (STY	_Q(de)SVPQ(	Q(0.962)SVPQ(0.972)LAN(0
QSVPQLANLT	16	1	Phospho (STY	_Q(de)SVPQ(	Q(0.942)SVPQ(0.985)LAN(0
QSVPQLANLT	16	1	Phospho (STY	_Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_	
QSVPQLANLT	16	1	Phospho (STY	_Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_	

REEENAAAAE	31	1	Phospho (STY	_REEENAAAAEEEAGEISATGGATS(ph)PEP	
REEENAAAAE	31	1	Phospho (STY	_REEENAAAAEEEAGEISATGGAT(ph)SPEP	
REEENAAAAE	31	1	Phospho (STY	_REEENAAAAEEEAGEISATGGAT(ph)SPEP	

RGCQILGLNK	18	2	Phospho (STY	_RGCQ(de)IL	RGCQ(0.965)ILGLN(0.024)K
RGCQILGLNK	18	2	Phospho (STY	_RGCQ(de)IL	RGCQ(0.838)ILGLN(0.155)K
RGCQILGLNK	18	2	Phospho (STY	_RGCQ(de)IL	RGCQ(0.999)ILGLNKYGIQQ

RGPPPPPTAS	17	1	2 Phospho (S	_RGPPPPPTA	RGPPPPPTASESTRRN(1)K
RGPPPPPTAS	17	1	2 Phospho (S	_RGPPPPPTASES(ph)T(ph)RRN(de)K_	
RGPPPPPTAS	17	1	2 Phospho (S	_RGPPPPPTASES(ph)T(ph)RRN(de)K_	

RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_	
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_	
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_	

RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_
RKKPEDPSSE	19	3	Phospho (STY	_RKKPEDPSSEAEALCS(ph)PAK_

SAAVAEGGD	23	2	Phospho (STY	_SAAVAEGGDAVAET(ph)AKGEEGSPK_
SAAVAEGGD	23	2	Phospho (STY	_SAAVAEGGDAVAET(ph)AKGEEGSPK_
SAAVAEGGD	23	2	Phospho (STY	_SAAVAEGGDAVAET(ph)AKGEEGSPK_
SAAVAEGGD	23	2	Phospho (STY	_SAAVAEGGDAVAET(ph)AKGEEGSPK_
SAAVAEGGD	23	2	Phospho (STY	_SAAVAEGGDAVAETAKGEEGS(ph)PK_

SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVS(ph)SPSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSSPS(ph)K_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSSPS(ph)K_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVS(ph)SPSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSSPS(ph)K_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSSPS(ph)K_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_
SAEAEAIVTTA	20	1	Acetyl (Protei	_(ac)SAEAEAIVTTATADVSS(ph)PSK_

SDSAVATSAS	21	1	Acetyl (Protei	_(ac)SDSAVAT(ph)SASPVAAPPATVEK_

SDSAVATSAS	21	1	Acetyl (Protei	_(ac)SDSAVATS(ph)ASPVAAPPATVEK_	
SDSAVATSAS	21	1	Acetyl (Protei	_(ac)SDSAVAT(ph)SASPVAAPPATVEK_	
SPIVFELTQPS	14	1	Phospho (STY	_SPIVFELTQPS(ph)PEK_	
SPIVFELTQPS	14	1	Phospho (STY	_SPIVFELTQPS(ph)PEK_	
SPIVFELTQPS	14	1	Phospho (STY	_SPIVFELTQPS(ph)PEK_	
SPIVFELTQPS	14	1	Phospho (STY	_SPIVFELTQPS(ph)PEK_	
SPIVFELTQPS	14	1	Phospho (STY	_SPIVFELTQPS(ph)PEK_	
SPIVFELTQPS	14	1	2 Phospho (S	_S(ph)PIVFELTQPS(ph)PEK_	
SVHSPNPGLIL	14	1	Acetyl (Protei	_(ac)SVHS(ph)PNPGLILQSK_	
SVHSPNPGLIL	14	1	Acetyl (Protei	_(ac)SVHS(ph)PNPGLILQSK_	
SVHSPNPGLIL	14	1	Acetyl (Protei	_(ac)SVHS(ph)PNPGLILQSK_	
SVHSPNPGLIL	14	1	Acetyl (Protei	_(ac)SVHS(ph)PNPGLILQSK_	
TSPKPTKPAS	12	3	Phospho (STY	_TSPKPTKPAS(ph)PK_	
TSPKPTKPAS	12	3	Phospho (STY	_TSPKPTKPAS(ph)PK_	
VDRSDNAAES	25	1	Acetyl (Protei	_(ac)VDRSDNAAES(ph)FDDAVEERVINEEY	
VDRSDNAAES	25	1	Acetyl (Protei	_(ac)VDRSDNAAES(ph)FDDAVEERVINEEY	
VDRSDNAAES	25	1	Acetyl (Protei	_(ac)VDRSDNAAES(ph)FDDAVEERVINEEY	
VNSLIVLESDE	33	1	Phospho (STY	_VNSLIVLES(ph)DEEEDEQLVQAADLVEQE	
VNSLIVLESDE	33	1	Phospho (STY	_VNSLIVLES(ph)DEEEDEQLVQAADLVEQE	
VNSLIVLESDE	33	1	Phospho (STY	_VNSLIVLES(ph)DEEEDEQLVQAADLVEQE	
VTILWMGGS	19	1	Oxidation (M	_VT(ph)ILWM(ox)GGSGSIV	VTILWM(1)G
VTILWMGGS	19	1	Oxidation (M	_VT(ph)ILWM(ox)GGSGSIV	VTILWM(1)G
VTILWMGGS	19	1	Oxidation (M	_VT(ph)ILWM(ox)GGSGSIV	VTILWM(1)G

Phospho (STY) Probabilities	Deamidation (NQ) Score Diffs	Oxidation (M) Score Diffs	Phospho (STY) Score Diffs	Acetyl (Protein N-term)	Deamidation (NQ)	Gln->pyro-Glu
AAAPAAVAS(0.997)PAAAAT(0.005)S(0.00			AAAPAAVAS(	0	0	0
AAAPAAVAS(0.995)PAAAAT(0.003)S(0.00			AAAPAAVAS(	0	0	0
AAAPAAVASPAAAAT(0.005)S(0.034)ADAS			AAAPAAVAS(	0	0	0
AAAPAAVASPAAAAT(0.006)S(0.042)ADAS			AAAPAAVAS(	0	0	0
AAAPAAVAS(0.078)PAAAAT(0.34)S(0.427			AAAPAAVAS(	0	0	0
AAAPAAVAS(0.004)PAAAAT(0.062)S(0.28			AAAPAAVAS(	0	0	0
AAAPAAVAS(0.993)PAAAAT(0.03)S(0.03)			AAAPAAVAS(	0	0	0
AAAPAAVAS(0.985)PAAAAT(0.077)S(0.08			AAAPAAVAS(	0	0	0
ALDLLMS(1)Y(1)RLK		ALDLLM(45.4	ALDLLMS(45.	0	0	0
ALDLLMS(1)Y(1)RLK		ALDLLM(57.1	ALDLLMS(57.	0	0	0
ALGGIVLT(0.066)AS(0.934)HNPGGPENDF			ALGGIVLT(-11	0	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK			ALGGIVLT(0)	0	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK			ALGGIVLT(0)	0	0	0
ALGGIVLT(0.784)AS(0.216)HNPGGPENDF			ALGGIVLT(5.6	0	0	0
ALGGIVLT(0.121)AS(0.879)HNPGGPENDF			ALGGIVLT(-8.	0	0	0
ALGGIVLT(0.098)AS(0.902)HNPGGPENDF			ALGGIVLT(-9.	0	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK			ALGGIVLT(0)	0	0	0
ALGGIVLT(0.204)AS(0.796)HNPGGPENDF			ALGGIVLT(-5.	0	0	0
				0	0	0
				0	0	0
				0	0	0
ALGGIVLT(0.5	ALGGIVLTASHN(-0.65)PGG		ALGGIVLT(0.6	0	1	0
ALQAVYPDYVDELS(0.161)LY(0.135)GS(0.7			ALQAVY(-67.3	0	0	0
ALQAVYPDYVDELS(0.021)LY(0.015)GS(0.9			ALQAVY(-63.3	0	0	0
ALQAVYPDYVDELS(0.001)LY(0.057)GS(0.9			ALQAVY(-81.2	0	0	0
ALQAVYPDYVDELS(0.001)LY(0.016)GS(0.9			ALQAVY(-70.6	0	0	0
ALQAVYPDY(0.002)VDELS(0.04)LY(0.004)			ALQAVY(-51.2	0	0	0
				0	0	0
ALQAVYPDYVDELS(0.996)LY(0.009)GS(0.9			ALQAVY(-75.9	0	0	0
ALQAVY(0.084)PDY(0.078)VDELS(0.605)L			ALQAVY(-10.4	0	0	0
APATPQAATSVTNPAAGDGIS(0.001)VQND			APAT(-56.02)	0	0	0
APATPQAATSVTNPAAGDGIS(0.001)VQND			APAT(-50.33)	0	0	0
APATPQAATSVTNPAAGDGIS(0.002)VQND			APAT(-39.76)	0	0	0
APATPQAATSVTNPAAGDGIS(0.004)VQND			APAT(-40.05)	0	0	0

APATPQAATSVTNPAAGDGIS(0.004)VQN		APAT(-44.28)	0	0	0
ASAFQFS(1)DDEEEVK		AS(-64.04)AF	0	0	0
ASAFQFS(1)DDEEEVK		AS(-48.64)AF	0	0	0
ASAFQFS(1)DDEEEVK		AS(-75.24)AF	0	0	0
ASAFQFS(1)DDEEEVK		AS(-54.82)AF	0	0	0
ASAFQFS(1)DDEEEVK		AS(-61.47)AF	0	0	0
ASAFQFS(1)DDEEEVK		AS(-59.12)AF	0	0	0
ASAFQFS(1)DDEEEVK		AS(-56.8)AFQ	0	0	0
ASAFQFS(1)DDEEEVK		AS(-42.65)AF	0	0	0
ASAFQFS(1)DDEEEVK		AS(-66.2)AFQ	0	0	0
ASAFQFS(1)DDEEEVK		AS(-67.24)AF	0	0	0
ASAFQFS(1)DDEEEVK		AS(-96.36)AF	0	0	0
			0	0	0
AS(1)GVTVSDVCK		AS(39.82)GVT	1	0	0
AS(1)GVTVSDVCK		AS(38.57)GVT	1	0	0
AS(1)GVTVSDVCK		AS(40.23)GVT	1	0	0
AS(1)GVTVSDVCK		AS(38.02)GVT	1	0	0
AS(0.977)GVT(0.022)VSDVCK		AS(16.42)GVT	1	0	0
AS(0.997)GVT(0.003)VSDVCK		AS(25.59)GVT	1	0	0
AS(0.42)GVT(0.568)VS(0.012)DVCK		AS(-1.31)GVT	1	0	0
AS(0.998)GVT(0.002)VSDVCK		AS(26.02)GVT	1	0	0
AS(1)GVTVSDVCK		AS(35.02)GVT	1	0	0
AS(0.976)GVT(0.023)VS(0.001)DVCK		AS(16.37)GVT	1	0	0
			1	0	0
DLEY(1)FNNL	DLEYFN(65.22)N(65.22)LK	DLEY(65.22)F	0	2	0
DLEY(1)FNNL	DLEYFN(54.07)N(54.07)LK	DLEY(54.07)F	0	2	0
DVDFGDS(1)DNENEPDAYLARLK		DVDFGDS(53.	0	0	0
DVDFGDS(1)DNENEPDAYLARLK		DVDFGDS(67.	0	0	0
DVDFGDS(1)DNENEPDAYLARLK		DVDFGDS(43.	0	0	0
DVDFGDS(1)DNENEPDAYLARLK		DVDFGDS(56.	0	0	0
DVDFGDS(0.994)DNENEPDAY(0.006)LARL		DVDFGDS(22.	0	0	0
DVDFGDS(0.999)DNENEPDAY(0.001)LARL		DVDFGDS(31.	0	0	0
EAAQY(0.933)GT(0.067)VNAVLPK		EAAQY(11.44	0	0	0
EAAQY(0.799)GT(0.201)VNAVLPK		EAAQY(6)GT(	0	0	0
EAS(0.012)PVS(0.157)MAS(	EASPVSM(53.	EAS(-18.36)P	0	0	0

EAS(0.014)PVS(0.221)MAS(	EASPVSM(53.	EAS(-17.37)PV	0	0	0
EAS(0.127)PVS(0.465)MAS(	EASPVSM(40.	EAS(-5.65)PVS	0	0	0
ELPDSDSLNVAPPEGFS(1)DEEPEERQCK		ELPDS(-46.35	0	0	0
ELPDSDSLNVAPPEGFS(1)DEEPEERQCK		ELPDS(-49.23	0	0	0
ELPDSDS(0.001)LNVAPPEGFS(0.999)DEEP		ELPDS(-38.75	0	0	0
FFDS(1)GDYQMAK	FFDSGDYQM(	FFDS(40.97)G	0	0	0
FFDS(0.994)GDY(0.006)QM	FFDSGDYQM(	FFDS(22.15)G	0	0	0
FFDS(1)GDYQMAK	FFDSGDYQM(	FFDS(36.09)G	0	0	0
KEES(0.181)ES(0.819)EDDD	KEESESEDDD	KEES(-6.55)ES	0	0	0
KEES(0.209)ES(0.791)EDDD	KEESESEDDD	KEES(-5.78)ES	0	0	0
KEES(0.074)ES(0.926)EDDD	KEESESEDDD	KEES(-10.98)E	0	0	0
KIDNPES(0.333)S(0.333)AKVS(0.333)DAE		KIDNPES(0)S(	0	0	0
KIDNPES(0.012)S(0.022)AKVS(0.966)DAE		KIDNPES(-19.	0	0	0
KIDNPES(0.489)S(0.489)AKVS(0.022)DAE		KIDNPES(0)S(	0	0	0
KIDNPES(0.567)S(0.41)AKVS(0.023)DAEE		KIDNPES(1.41	0	0	0
KKEEES(1)DQS(1)DDDMGF	KKEEESDQSD	KKEEES(46.14	0	0	0
KKEEES(1)DQS(1)DDDMGF	KKEEESDQSD	KKEEES(46.7)	0	0	0
KKEEES(1)DQS(1)DDDMGF	KKEEESDQSD	KKEEES(42.09	0	0	0
KKEEES(0.035)DQS(0.965)D	KKEEESDQSD	KKEEES(-14.3	0	0	0
KPEDPSSEAEALCS(1)PAK		KPEDPS(-47.0	0	0	0
KPEDPSSEAEALCS(1)PAK		KPEDPS(-37.5	0	0	0
KPEDPSSEAEALCS(1)PAK		KPEDPS(-41.9	0	0	0
KPEDPSSEAEALCS(1)PAK		KPEDPS(-51.7	0	0	0
KPEDPSSEAEALCS(1)PAK		KPEDPS(-69.7	0	0	0
KPEDPSSEAEALCS(1)PAK		KPEDPS(-49.5	0	0	0
MPNLQS(0.857)S(0.121)IPH	M(56.2)PNLQ	MPNLQS(8.49	1	0	0
MPNLQS(0.492)S(0.492)IPH	M(40.24)PNL	MPNLQS(0)S(	1	0	0
MPNLQS(0.778)S(0.175)IPH	M(47.71)PNL	MPNLQS(6.47	1	0	0
MPNLQS(0.497)S(0.497)IPH	M(58.89)PNL	MPNLQS(0)S(	1	0	0
MQLILS(0.695	MQ(-7.66)LILSYLQ(7.66)SQ(		MQLILS(7.66)	1	3	0
MQLILS(0.245	MQ(-25.8)LILSYLQ(25.8)SQ(		MQLILS(-4.01	1	3	0
			1	3	0
			1	3	0
MQLILS(0.974	MQ(7.74)LILS	M(44.25)QLIL	MQLILS(19.37	0	2	0

MQLILS(0.20	MQ(-13.61)LI	M(43.69)QLIL	MQLILS(-5.35	0	2	0
				0	2	0
				0	2	0
MRDKIS(1)QL	MRDKISQ(-15	M(62.09)RDK	MRDKIS(62.0	1	1	0
MRDKIS(1)QL	MRDKISQ(-15	M(54.34)RDK	MRDKIS(54.3	1	1	0
MRDKIS(1)QL	MRDKISQ(-10	M(56.2)RDKI	MRDKIS(56.2	1	1	0
MRDKIS(1)QL	MRDKISQ(-17	M(51.13)RDK	MRDKIS(51.1	1	1	0
MRDKIS(1)QL	MRDKISQ(-12	M(51.46)RDK	MRDKIS(51.4	1	1	0
MRDKIS(1)QL	MRDKISQ(-4.	M(43.8)RDKI	MRDKIS(43.8	1	1	0
MVEPSPETVGDFQSVQEEVE		M(86.56)VEP	MVEPS(-69.6	0	0	0
MVEPSPETVGDFQS(0.245)		M(50.26)VEP	MVEPS(-41.7	0	0	0
MVEPSPETVGDFQS(0.001)		M(50.32)VEP	MVEPS(-37.1	0	0	0
NAGGVGVGVGEKS(1)PDLK			NAGGVGVGV	0	0	0
NAGGVGVGVGEKS(1)PDLK			NAGGVGVGV	0	0	0
NAGGVGVGVGEKS(1)PDLK			NAGGVGVGV	0	0	0
NAGGVGVGVGEKS(1)PDLK			NAGGVGVGV	0	0	0
				0	0	0
NAGGVGVGVGEKS(1)PDLKK			NAGGVGVGV	0	0	0
NAGGVGVGVGEKS(1)PDLKK			NAGGVGVGV	0	0	0
NVGIFIKDDS(1)DEEDVDDKK			NVGIFIKDDS(	0	0	0
NVGIFIKDDS(1)DEEDVDDKK			NVGIFIKDDS(	0	0	0
NVGIFIKDDS(1)DEEDVDDKK			NVGIFIKDDS(	0	0	0
PCNLY(0.854)QT(0.146)AQEQLK			PCNLY(7.67)	0	0	0
PCNLY(0.962)	PCN(24.93)LYQ(-24.93)TAQ		PCNLY(14.07)	0	1	0
PLPS(1)GRIPQIT(0.999)PPAS(0.001)PK			PLPS(41.55)G	0	0	0
PLPS(1)GRIPQIT(0.997)PPAS(0.004)PK			PLPS(33.2)GR	0	0	0
QELLQS(0.87	Q(51.95)ELL	QELLQSYM(5	QELLQS(8.31)	0	2	1
QELLQS(0.84	Q(41.43)ELL	QELLQSYM(4	QELLQS(7.5)Y	0	2	1
QELLQS(0.24	Q(45.02)ELLQ(45.02)SYMK		QELLQS(-4.96	0	2	1
QISIGIY(1)ELLK			QIS(-47.73)IG	0	0	0
QISIGIY(1)ELLK			QIS(-48.31)IG	0	0	0
QISIGIY(1)ELLK			QIS(-46.94)IG	0	0	0
QIS(0.001)IGIY(0.999)ELLK			QIS(-32.34)IG	0	0	0
QISIGIY(1)ELLK			QIS(-55.01)IG	0	0	0
QISIGIY(1)ELLK			QIS(-38.47)IG	0	0	0

QISIGIY(1)ELLK		QIS(-43.94)IG	0	0	0
QISIGIY(1)ELLK		QIS(-39.86)IG	0	0	0
QISIGIY(1)ELLK		QIS(-57.55)IG	0	0	0
QISIGIY(1)ELLK		QIS(-35.76)IG	0	0	0
QISIGIY(1)ELLK		QIS(-50.69)IG	0	0	0
QISIGIY(1)ELLK		QIS(-47.93)IG	0	0	0
QISIGIY(1)ELLK		QIS(-49.83)IG	0	0	0
QISIGIY(1)ELLK		QIS(-53)IGIY(	0	0	0
QISIGIY(1)ELLK		QIS(-39.44)IG	0	0	0
QISIGIY(1)ELLK		QIS(-55.72)IG	0	0	0
QISIGIY(1)ELLK		QIS(-52.88)IG	0	0	0
QISIGIY(1)ELLK		QIS(-36.23)IG	0	0	0
QSSYHGVHQAWNT(0.042)NQDS(0.957)K		QS(-41.5)S(-4	0	0	1
QSSYHGVHQAWNT(0.028)NQDS(0.972)K		QS(-47.65)S(-	0	0	1
QSSYHGVHQAWNT(0.042)NQDS(0.958)K		QS(-80.23)S(-	0	0	1
QSSYHGVHQAWNT(0.001)NQDS(0.999)K		QS(-87.48)S(-	0	0	1
QSSYHGVHQAWNT(0.01)NQDS(0.99)K		QS(-52.27)S(-	0	0	1
QSSYHGVHQAWNT(0.025)NQDS(0.975)K		QS(-60.4)S(-6	0	0	1
QSSYHGVHQAWNT(0.005)NQDS(0.995)K		QS(-73.94)S(-	0	0	1
QSSYHGVHQAWNT(0.128)NQDS(0.872)K		QS(-48.42)S(-	0	0	1
QS(0.014)VP	Q(21.8)SVPQ(21.8)LAN(20.	QS(-21.8)VPC	0	3	0
QS(0.005)VP	Q(13.41)SVPQ(14.75)LAN(5	QS(-25.08)VP	0	3	0
QS(0.006)VP	Q(11.59)SVPQ(18.04)LAN(6	QS(-24.64)VP	0	3	0
			0	3	0
			0	3	0
REEENAAAAEEEAGEISAT(0.01)GGAT(0.21		REEENAAAAE	0	0	0
REEENAAAAEEEAGEISAT(0.001)GGAT(0.4		REEENAAAAE	0	0	0
REEENAAAAEEEAGEIS(0.005)AT(0.02)GG		REEENAAAAE	0	0	0
RGCQILGLNK	RGCQ(16.13)ILGLN(-16.13)	RGCQILGLNK	0	1	0
RGCQILGLNK	RGCQ(7.33)ILGLN(-7.33)KY	RGCQILGLNK	0	1	0
RGCQILGLNK	RGCQ(33.24)ILGLN(-33.24)	RGCQILGLNK	0	1	0
RGPPPPPT(0.	RGPPPPPTASESTRRN(43.11	RGPPPPPT(-2	0	1	0
			0	1	0
			0	1	0
RKKPEDPSSEAEALCS(1)PAK		RKKPEDPS(-5	0	0	0
RKKPEDPSSEAEALCS(1)PAK		RKKPEDPS(-4	0	0	0
RKKPEDPSSEAEALCS(1)PAK		RKKPEDPS(-4	0	0	0

RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-3	0	0	0
RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-4	0	0	0
RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-3	0	0	0
RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-4	0	0	0
RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-4	0	0	0
RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-5	0	0	0

SAAVAEGGDAVAET(0.733)AKGEEGS(0.26	S(-42.23)AAV	0	0	0
SAAVAEGGDAVAET(0.901)AKGEEGS(0.09	S(-58.47)AAV	0	0	0
SAAVAEGGDAVAET(0.614)AKGEEGS(0.38	S(-39.38)AAV	0	0	0
S(0.001)AAVAEGGDAVAET(0.702)AKGEE	S(-28.94)AAV	0	0	0
SAAVAEGGDAVAET(0.209)AKGEEGS(0.79	S(-48.44)AAV	0	0	0

SAEAEAIVTTATADVS(0.307)S(0.514)PS(0.	S(-107.65)AE	1	0	0
SAEAEAIVTTATADVS(0.034)S(0.483)PS(0.	S(-78.78)AEA	1	0	0
SAEAEAIVTTATADVS(0.051)S(0.77)PS(0.1	S(-102.74)AE	1	0	0
SAEAEAIVTTATADVS(0.007)S(0.496)PS(0.	S(-76.49)AEA	1	0	0
SAEAEAIVT(0.022)T(0.02)AT(0.067)ADVS(	S(-61.37)AEA	1	0	0
SAEAEAIVTTATADVS(0.01)S(0.495)PS(0.4	S(-54.67)AEA	1	0	0
SAEAEAIVTT(0.001)AT(0.004)ADVS(0.046	S(-61.79)AEA	1	0	0
SAEAEAIVTTATADVS(0.019)S(0.957)PS(0.	S(-108.85)AE	1	0	0
SAEAEAIVTTATADVS(0.041)S(0.479)PS(0.	S(-81.76)AEA	1	0	0
SAEAEAIVTTATADVS(0.047)S(0.743)PS(0.	S(-102.8)AEA	1	0	0
SAEAEAIVTTATADVS(0.48)S(0.329)PS(0.1	S(-50.28)AEA	1	0	0
SAEAEAIVTTATADVS(0.045)S(0.421)PS(0.	S(-119.63)AE	1	0	0
SAEAEAIVTTAT(0.001)ADVS(0.035)S(0.37	S(-66.49)AEA	1	0	0
SAEAEAIVTTATADVS(0.007)S(0.783)PS(0.	S(-112.12)AE	1	0	0
SAEAEAIVTTATADVS(0.052)S(0.762)PS(0.	S(-82.71)AEA	1	0	0
SAEAEAIVT(0.01)T(0.012)AT(0.04)ADVS(0	S(-39.1)AEAE	1	0	0
SAEAEAIVTTATADVS(0.067)S(0.467)PS(0.	S(-77.93)AEA	1	0	0
SAEAEAIVTTATADVS(0.021)S(0.489)PS(0.	S(-77.91)AEA	1	0	0
SAEAEAIVTT(0.002)AT(0.006)ADVS(0.174	S(-40.69)AEA	1	0	0
SAEAEAIVTTATADVS(0.035)S(0.71)PS(0.2	S(-81.87)AEA	1	0	0
SAEAEAIVTTATADVS(0.175)S(0.771)PS(0.	S(-108.29)AE	1	0	0
SAEAEAIVTTATADVS(0.035)S(0.813)PS(0.	S(-91.77)AEA	1	0	0
SAEAEAIVTTATADVS(0.008)S(0.158)PS(0.	S(-76.74)AEA	1	0	0
SAEAEAIVTTATADVS(0.066)S(0.717)PS(0.	S(-108.3)AEA	1	0	0
SAEAEAIVTTATADVS(0.185)S(0.408)PS(0.	S(-80.53)AEA	1	0	0
SAEAEAIVTTATADVS(0.018)S(0.396)PS(0.	S(-55.82)AEA	1	0	0
SAEAEAIVTTATADVS(0.068)S(0.878)PS(0.	S(-89.55)AEA	1	0	0
		1	0	0

S(0.015)DS(0.015)AVAT(0.71)S(0.194)AS(	S(-16.63)DS(-	1	0	0

S(0.01)DS(0.01)AVAT(0.112)S(0.693)AS(0	S(-18.26)DS(-	1	0	0
SDSAVAT(0.333)S(0.333)AS(0.333)PVAAP	S(-34.71)DS(-	1	0	0
SPIVFELT(0.001)QPS(0.999)PEK	S(-54.97)PIVF	0	0	0
SPIVFELT(0.001)QPS(0.999)PEK	S(-67.16)PIVF	0	0	0
SPIVFELT(0.001)QPS(0.999)PEK	S(-63.62)PIVF	0	0	0
SPIVFELTQPS(1)PEK	S(-86.11)PIVF	0	0	0
SPIVFELTQPS(1)PEK	S(-70.03)PIVF	0	0	0
S(1)PIVFELT(0.009)QPS(0.991)PEK	S(40.41)PIVFE	0	0	0
S(0.06)VHS(0.94)PNPGLILQSK	S(-11.98)VHS	1	0	0
S(0.003)VHS(0.997)PNPGLILQSK	S(-25.47)VHS	1	0	0
S(0.002)VHS(0.998)PNPGLILQSK	S(-27.48)VHS	1	0	0
S(0.008)VHS(0.992)PNPGLILQSK	S(-21.15)VHS	1	0	0
TSPKPT(0.028)KPAS(0.972)PK	T(-33.19)S(-3	0	0	0
TSPKPT(0.079)KPAS(0.921)PK	T(-51.25)S(-4	0	0	0
VDRS(0.006)DNAAES(0.994)FDDAVEERVI	VDRS(-22.51)	1	0	0
VDRS(0.003)DNAAES(0.997)FDDAVEERVI	VDRS(-24.86)	1	0	0
VDRS(0.007)DNAAES(0.993)FDDAVEERVI	VDRS(-21.63)	1	0	0
VNS(0.002)LIVLES(0.998)DEEEDEQLVQAA	VNS(-28.14)LI	0	0	0
VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA	VNS(-29.34)LI	0	0	0
VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA	VNS(-31.63)LI	0	0	0
VT(0.996)ILWMGGS(0.003) VTILWM(47.5	VT(24.72)ILW	0	0	0
VT(0.996)ILWMGGS(0.002) VTILWM(42.3	VT(27.11)ILW	0	0	0
VT(0.999)ILWMGGS(0.001) VTILWM(42.0	VT(32.61)ILW	0	0	0

Oxidation (M)	Phospho (STY)	Missed cleavages	Proteins	Leading Proteins	Leading Razor Protein	Gene Names
0	2	0	M9NG39;P41	M9NG39	M9NG39	Pep
0	2	0	M9NG39;P41	M9NG39	M9NG39	Pep
0	1	0	M9NG39;P41	M9NG39	M9NG39	Pep
0	1	0	M9NG39;P41	M9NG39	M9NG39	Pep
0	1	1	M9NG39;P41	M9NG39	M9NG39	Pep
0	1	1	M9NG39;P41	M9NG39	M9NG39	Pep
0	2	1	M9NG39;P41	M9NG39	M9NG39	Pep
0	2	1	M9NG39;P41	M9NG39	M9NG39	Pep
1	2	0	Q4V3Q5;Q8M	Q4V3Q5	Q4V3Q5	Obp22a CG31941
1	2	0	Q4V3Q5;Q8M	Q4V3Q5	Q4V3Q5	Obp22a
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	2	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	2	0	A0A0B4KHJ5;	A0A0B4KHJ5	A0A0B4KHJ5	CG6904-RA;G
0	1	1	A0A0B4LGC0	A0A0B4LGC0	A0A0B4LGC0	TppII
0	1	1	A0A0B4LGC0	A0A0B4LGC0	A0A0B4LGC0	TppII
0	1	1	A0A0B4LGC0	A0A0B4LGC0	A0A0B4LGC0	TppII
0	1	1	A0A0B4LGC0	A0A0B4LGC0	A0A0B4LGC0	TppII

0	1	1	A0A0B4LGC0;	A0A0B4LGC0	A0A0B4LGC0	TppII
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	A0A0B4LFL2;	A0A0B4LFL2	A0A0B4LFL2	eIF3-S8
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	P45594	P45594	P45594	tsr
0	1	0	Q9V5R2;A1Z	Q9V5R2	Q9V5R2	Pex6
0	1	0	Q9V5R2;A1Z	Q9V5R2	Q9V5R2	Pex6
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	B5RJ65;Q053	B5RJ65	B5RJ65	Ssrp-RA;Ssrp
0	1	0	Q9VAN0	Q9VAN0	Q9VAN0	CG11899
0	1	0	Q9VAN0	Q9VAN0	Q9VAN0	CG11899
1	1	1	P28668;H8F4	P28668	P28668	Aats-glupro;Aats-glupro-RB

1	1	1	P28668;H8F4	P28668	P28668	Aats-glupro;A
1	1	1	P28668;H8F4	P28668	P28668	Aats-glupro;A
0	1	0	Q9VNH5	Q9VNH5	Q9VNH5	
0	1	0	Q9VNH5	Q9VNH5	Q9VNH5	
0	1	0	Q9VNH5	Q9VNH5	Q9VNH5	
1	1	0	Q9VUB8	Q9VUB8	Q9VUB8	endos
1	1	0	Q9VUB8	Q9VUB8	Q9VUB8	endos
1	1	0	Q9VUB8	Q9VUB8	Q9VUB8	endos
1	1	1	B7FNN6;P053	B7FNN6	B7FNN6	RpLP2-RB;Rpl
1	1	1	B7FNN6;P053	B7FNN6	B7FNN6	RpLP2-RB;Rpl
1	1	1	B7FNN6;P053	B7FNN6	B7FNN6	RpLP2-RB;Rpl
0	1	2	P05205	P05205	P05205	Su(var)205
0	1	2	P05205	P05205	P05205	Su(var)205
0	1	2	P05205	P05205	P05205	Su(var)205
0	1	2	P05205	P05205	P05205	Su(var)205
1	2	2	M9PBK5;P085	M9PBK5	M9PBK5	RpLP1
1	2	2	M9PBK5;P085	M9PBK5	M9PBK5	RpLP1
1	2	2	M9PBK5;P085	M9PBK5	M9PBK5	RpLP1
1	1	2	M9PBK5;P085	M9PBK5	M9PBK5	RpLP1
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	1	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
1	1	1	Q6IIC4	Q6IIC4	Q6IIC4	HDC19000
1	1	1	Q6IIC4	Q6IIC4	Q6IIC4	HDC19000
1	1	1	Q6IIC4	Q6IIC4	Q6IIC4	HDC19000
1	1	1	Q6IIC4	Q6IIC4	Q6IIC4	HDC19000
0	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
0	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
0	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
0	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
1	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3

1	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
1	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
1	1	0	B7Z0H3	B7Z0H3	B7Z0H3	RhoGEF3
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	1	X2JDR1;Q8IR	X2JDR1	X2JDR1	CG9413-RB
1	1	0	B7YZZ9;P278	B7YZZ9	B7YZZ9	Rrp1
1	1	0	B7YZZ9;P278	B7YZZ9	B7YZZ9	Rrp1
1	1	0	B7YZZ9;P278	B7YZZ9	B7YZZ9	Rrp1
0	1	1	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	1	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	1	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	1	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	1	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	2	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	2	Q9VYV4	Q9VYV4	Q9VYV4	Amun
0	1	2	Q8IRG6;Q8IR	Q8IRG6	Q8IRG6	dre4
0	1	2	Q8IRG6;Q8IR	Q8IRG6	Q8IRG6	dre4
0	1	2	Q8IRG6;Q8IR	Q8IRG6	Q8IRG6	dre4
0	1	0	E2QCZ8;Q0KI	E2QCZ8	E2QCZ8	CG43427
0	1	0	E2QCZ8;Q0KI	E2QCZ8	E2QCZ8	CG43427
0	2	0	E2QCZ8;Q0KI	E2QCZ8	E2QCZ8	CG43427
0	2	0	E2QCZ8;Q0KI	E2QCZ8	E2QCZ8	CG43427
1	1	0	Q9VIV2;B1NL	Q9VIV2	Q9VIV2	swm
1	1	0	Q9VIV2;B1NL	Q9VIV2	Q9VIV2	swm
0	1	0	Q9VIV2;B1NL	Q9VIV2	Q9VIV2	swm
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz

0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	A1Z8W9;A0A	A1Z8W9	A1Z8W9	garz
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	X2JD55;Q29C	X2JD55	X2JD55	Yp1
0	1	0	Q8MYL1	Q8MYL1	Q8MYL1	Fancd2
0	1	0	Q8MYL1	Q8MYL1	Q8MYL1	Fancd2
0	1	0	Q8MYL1	Q8MYL1	Q8MYL1	Fancd2
0	1	0	Q8MYL1	Q8MYL1	Q8MYL1	Fancd2
0	1	0	Q8MYL1	Q8MYL1	Q8MYL1	Fancd2
0	1	0	Q9VV74	Q9VV74	Q9VV74	Smn
0	1	0	Q9VV74	Q9VV74	Q9VV74	Smn
0	1	0	Q9VV74	Q9VV74	Q9VV74	Smn
0	1	1	Q9VZW4;A8V	Q9VZW4	Q9VZW4	CG32487
0	1	1	Q9VZW4;A8V	Q9VZW4	Q9VZW4	CG32487
0	1	1	Q9VZW4;A8V	Q9VZW4	Q9VZW4	CG32487
0	2	0	A0A0B4KFB8;	A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
0	2	0	A0A0B4KFB8;	A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
0	2	0	A0A0B4KFB8;	A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223

0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	2	Q9I7K6	Q9I7K6	Q9I7K6	CG8223

0	1	1	Q86BM5;Q9	Q86BM5;Q9	Q86BM5	Akap200
0	1	1	Q86BM5;Q9	Q86BM5;Q9	Q86BM5	Akap200
0	1	1	Q86BM5;Q9	Q86BM5;Q9	Q86BM5	Akap200
0	1	1	Q86BM5;Q9	Q86BM5;Q9	Q86BM5	Akap200
0	1	1	Q86BM5;Q9	Q86BM5;Q9	Q86BM5	Akap200

0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223
0	1	0	Q9I7K6	Q9I7K6	Q9I7K6	CG8223

0	1	0	Q4AB54;P022	Q4AB54	Q4AB54	His1:CG3386

0	1	0	Q4AB54;P02	Q4AB54	Q4AB54	His1:CG3386
0	1	0	Q4AB54;P02	Q4AB54	Q4AB54	His1:CG3386
0	1	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	1	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	1	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	1	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	1	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	2	0	Q9XZL7;A0A	Q9XZL7	Q9XZL7	tacc
0	1	0	Q9V6U8	Q9V6U8	Q9V6U8	Uba3
0	1	0	Q9V6U8	Q9V6U8	Q9V6U8	Uba3
0	1	0	Q9V6U8	Q9V6U8	Q9V6U8	Uba3
0	1	0	Q9V6U8	Q9V6U8	Q9V6U8	Uba3
0	1	2	Q9W335	Q9W335	Q9W335	l(1)G0320
0	1	2	Q9W335	Q9W335	Q9W335	l(1)G0320
0	1	0	C0MJE4;Q24	C0MJE4	C0MJE4	CG4236;Caf1
0	1	0	C0MJE4;Q24	C0MJE4	C0MJE4	CG4236;Caf1
0	1	0	C0MJE4;Q24	C0MJE4	C0MJE4	CG4236;Caf1
0	1	0	P20240	P20240	P20240	Ote
0	1	0	P20240	P20240	P20240	Ote
0	1	0	P20240	P20240	P20240	Ote
1	1	1	Q95SA9	Q95SA9	Q95SA9	spoon
1	1	1	Q95SA9	Q95SA9	Q95SA9	spoon
1	1	1	Q95SA9	Q95SA9	Q95SA9	spoon

Protein Names	Type	Labeling State	Raw file	Fraction	Experiment	MS/MS m/z
Zinc finger pr	MULTI-MSMS		PT5722-2	2	B1	761.34
Zinc finger pr	ISO-MSMS	0	PT5722-32	32	B3	761.67
Zinc finger pr	ISO-MSMS	0	PT5722-2	2	B1	735.02
Zinc finger pr	ISO-MSMS	0	PT5722-32	32	B3	734.69
Zinc finger pr	ISO-MSMS	0	PT5722-2	2	B1	777.72
Zinc finger pr	ISO-MSMS	0	PT5722-7	7	B1 SCX	777.38
Zinc finger pr	ISO-MSMS	0	PT5722-2	2	B1	804.37
Zinc finger pr	ISO-MSMS	0	PT5722-32	32	B3	804.38
Odorant bind	MSMS	1	PT5722-3	3	B1	753.86
	MSMS	1	PT5722-19	19	B2	753.85
Phosphogluc	MULTI-MSMS		PT5722-7	7	B1 SCX	782.38
Phosphogluc	MULTI-MSMS		PT5722-8	8	B1 SCX	782.38
Phosphogluc	MULTI-MSMS		PT5722-23	23	B2 SCX	782.05
Phosphogluc	ISO-MSMS	0	PT5722-33	33	B3	782.38
Phosphogluc	MULTI-MSMS		PT5722-38	38	B3 SCX	782.38
Phosphogluc	MULTI-MSMS		PT5722-38	38	B3 SCX	1173.07
Phosphogluc	ISO-MSMS	0	PT5722-51	51	H/H SCX	782.05
Phosphogluc	MULTI-MSMS		PT5722-53	53	H/H SCX	782.05
Phosphogluc	MULTI-MATCH		PT5722-6	6	B1 SCX	
Phosphogluc	MULTI-MATCH		PT5722-21	21	B2 SCX	
Phosphogluc	MULTI-MATCH		PT5722-22	22	B2 SCX	
Phosphogluc	ISO-MSMS	0	PT5722-38	38	B3 SCX	782.71
Glycogen [sta	MULTI-MSMS		PT5722-2	2	B1	1106.52
Glycogen [sta	MULTI-MSMS		PT5722-7	7	B1 SCX	1106.02
Glycogen [sta	ISO-MSMS	0	PT5722-37	37	B3 SCX	1106.03
Glycogen [sta	MULTI-MSMS		PT5722-47	47	H/H	1106.52
Glycogen [sta	MULTI-MSMS		PT5722-57	57	H/H TIO2	1106.52
Glycogen [sta	MULTI-MATCH		PT5722-56	56	H/H TIO2	
Glycogen [sta	MULTI-MSMS		PT5722-57	57	H/H TIO2	1146.5
Glycogen [sta	MULTI-MSMS		PT5722-57	57	H/H TIO2	764.67
Tripeptidyl-p	ISO-MSMS	0	PT5722-6	6	B1 SCX	943.2
Tripeptidyl-p	ISO-MSMS	0	PT5722-7	7	B1 SCX	943.2
Tripeptidyl-p	ISO-MSMS	0	PT5722-21	21	B2 SCX	943.2
Tripeptidyl-p	ISO-MSMS	0	PT5722-37	37	B3 SCX	943.2

Tripeptidyl-p	MULTI-MSMS		PT5722-51	51	H/H SCX	942.95

Eukaryotic tr	MULTI-MSMS		PT5722-2	2	B1	841.84
Eukaryotic tr	MULTI-MSMS		PT5722-6	6	B1 SCX	841.34
Eukaryotic tr	MULTI-MSMS		PT5722-7	7	B1 SCX	841.34
Eukaryotic tr	MULTI-MSMS		PT5722-11	11	B1 TIO2	841.34
Eukaryotic tr	ISO-MSMS	0	PT5722-22	22	B2 SCX	841.34
Eukaryotic tr	ISO-MSMS	0	PT5722-27	27	B2 TIO2	841.34
Eukaryotic tr	MULTI-MSMS		PT5722-36	36	B3 SCX	841.33
Eukaryotic tr	MULTI-MSMS		PT5722-37	37	B3 SCX	841.34
Eukaryotic tr	MULTI-MSMS		PT5722-41	41	B3 TIO2	841.34
Eukaryotic tr	MULTI-MSMS		PT5722-51	51	H/H SCX	841.34
Eukaryotic tr	MULTI-MSMS		PT5722-52	52	H/H SCX	841.83
Eukaryotic tr	MULTI-MATCH		PT5722-42	42	B3 TIO2	

Cofilin/actin-	MULTI-MSMS		PT5722-5	5	B1	622.77
Cofilin/actin-	MULTI-MSMS		PT5722-15	15	B1 TIO2	622.77
Cofilin/actin-	MULTI-MSMS		PT5722-16	16	B2	626.77
Cofilin/actin-	MULTI-MSMS		PT5722-20	20	B2	622.77
Cofilin/actin-	MULTI-MSMS		PT5722-30	30	B2 TIO2	622.77
Cofilin/actin-	MULTI-MSMS		PT5722-32	32	B3	626.77
Cofilin/actin-	MULTI-MSMS		PT5722-34	34	B3	622.76
Cofilin/actin-	MULTI-MSMS		PT5722-49	49	H/H	622.77
Cofilin/actin-	MULTI-MSMS		PT5722-50	50	H/H	626.77
Cofilin/actin-	MULTI-MSMS		PT5722-60	60	H/H TIO2	622.76
Cofilin/actin-	MULTI-MATCH		PT5722-33	33	B3	

	MULTI-MSMS		PT5722-8	8	B1 SCX	619.25
	MULTI-MSMS		PT5722-23	23	B2 SCX	619.25

FACT comple	ISO-MSMS	0	PT5722-6	6	B1 SCX	822.02
FACT comple	MULTI-MSMS		PT5722-7	7	B1 SCX	822.02
FACT comple	MULTI-MSMS		PT5722-22	22	B2 SCX	821.69
FACT comple	MULTI-MSMS		PT5722-36	36	B3 SCX	822.02
FACT comple	MULTI-MSMS		PT5722-51	51	H/H SCX	822.02
FACT comple	MULTI-MSMS		PT5722-52	52	H/H SCX	822.02

Probable pho	MULTI-MSMS		PT5722-7	7	B1 SCX	388.19
Probable pho	MULTI-SECPEP		PT5722-37	37	B3 SCX	388.46

Bifunctional	ISO-MSMS	0	PT5722-21	21	B2 SCX	909.75

Bifunctional	ISO-MSMS	0	PT5722-37	37	B3 SCX	909.75
Bifunctional	MULTI-MSMS		PT5722-51	51	H/H SCX	909.75

	ISO-MSMS	0	PT5722-23	23	B2 SCX	1052.44
	ISO-MSMS	0	PT5722-38	38	B3 SCX	1052.78
	ISO-MSMS	0	PT5722-53	53	H/H SCX	1052.78

	ISO-MSMS	1	PT5722-10	10	B1 SCX	707.27
	MULTI-MSMS		PT5722-40	40	B3 SCX	707.27
	MULTI-MSMS		PT5722-55	55	H/H SCX	702.76

60S acidic rib	MULTI-MSMS		PT5722-25	25	B2 SCX	1037.38
60S acidic rib	ISO-MSMS	0	PT5722-45	45	B3 TIO2	1037.38
60S acidic rib	MULTI-MSMS		PT5722-55	55	H/H SCX	1037.38

Heterochrom	ISO-MSMS	0	PT5722-9	9	B1 SCX	727.32
Heterochrom	MULTI-MSMS		PT5722-39	39	B3 SCX	969.42
Heterochrom	MULTI-MSMS		PT5722-39	39	B3 SCX	727.32
Heterochrom	ISO-MSMS	0	PT5722-54	54	H/H SCX	727.32

60S acidic rib	MSMS	0	PT5722-6	6	B1 SCX	1184.42
60S acidic rib	MSMS	0	PT5722-36	36	B3 SCX	789.95
60S acidic rib	MSMS	0	PT5722-40	40	B3 SCX	789.95
60S acidic rib	MULTI-MSMS		PT5722-55	55	H/H SCX	763.63

Protein NASP	ISO-MSMS	0	PT5722-7	7	B1 SCX	632.94
Protein NASP	MULTI-MSMS		PT5722-18	18	B2	632.61
Protein NASP	MULTI-MSMS		PT5722-32	32	B3	632.61
Protein NASP	ISO-MSMS	0	PT5722-36	36	B3 SCX	632.94
Protein NASP	ISO-MSMS	0	PT5722-38	38	B3 SCX	632.61
Protein NASP	MULTI-MSMS		PT5722-52	52	H/H SCX	632.61

	ISO-MSMS	1	PT5722-23	23	B2 SCX	818.4
	ISO-MSMS	1	PT5722-24	24	B2 SCX	818.4
	ISO-MSMS	1	PT5722-38	38	B3 SCX	817.9
	ISO-MSMS	1	PT5722-49	49	H/H	817.9

	MULTI-MSMS		PT5722-10	10	B1 SCX	909.43
	MULTI-MSMS		PT5722-24	24	B2 SCX	609.63
	MULTI-MATCH		PT5722-23	23	B2 SCX	
	MULTI-MATCH		PT5722-25	25	B2 SCX	
	MULTI-MSMS		PT5722-23	23	B2 SCX	597.63

	MULTI-MSMS		PT5722-24	24	B2 SCX	896.44
	MULTI-MATCH		PT5722-23	23	B2 SCX	
	MULTI-MATCH		PT5722-25	25	B2 SCX	
sobremesa	ISO-MSMS	1	PT5722-8	8	B1 SCX	911.43
sobremesa	ISO-MSMS	1	PT5722-9	9	B1 SCX	911.43
sobremesa	ISO-MSMS	1	PT5722-10	10	B1 SCX	911.44
sobremesa	ISO-MSMS	1	PT5722-26	26	B2 TIO2	911.43
sobremesa	ISO-MSMS	1	PT5722-38	38	B3 SCX	911.43
sobremesa	ISO-MSMS	1	PT5722-40	40	B3 SCX	911.44
Recombinatic	ISO-MSMS	0	PT5722-12	12	B1 TIO2	914.74
Recombinatic	ISO-MSMS	0	PT5722-32	32	B3	914.41
Recombinatic	MULTI-MSMS		PT5722-57	57	H/H TIO2	914.74
Amun	MULTI-MSMS		PT5722-2	2	B1	555.27
	MULTI-MSMS		PT5722-22	22	B2 SCX	832.41
	MULTI-MSMS		PT5722-36	36	B3 SCX	555.27
	MULTI-MSMS		PT5722-37	37	B3 SCX	832.4
	MULTI-MATCH		PT5722-36	36	B3 SCX	
	MULTI-MSMS		PT5722-2	2	B1	597.97
	MULTI-MSMS		PT5722-7	7	B1 SCX	597.97
FACT comple:	MULTI-MSMS		PT5722-21	21	B2 SCX	754.67
FACT comple:	MULTI-MSMS		PT5722-22	22	B2 SCX	754.33
FACT comple:	MULTI-MSMS		PT5722-36	36	B3 SCX	754.33
smallish, sma	MULTI-MSMS		PT5722-24	24	B2 SCX	558.59
smallish, sma	ISO-MSMS	0	PT5722-39	39	B3 SCX	558.58
smallish, sma	MULTI-SECPEP		PT5722-16	16	B2	958.48
smallish, sma	MULTI-SECPEP		PT5722-33	33	B3	958.48
swm	MULTI-MSMS		PT5722-20	20	B2	615.25
	MULTI-MSMS		PT5722-40	40	B3 SCX	615.25
	MULTI-MSMS		PT5722-50	50	H/H	602.75
garz	ISO-MSMS	0	PT5722-6	6	B1 SCX	678.86
	ISO-MSMS	0	PT5722-7	7	B1 SCX	678.86
	ISO-MSMS	0	PT5722-8	8	B1 SCX	678.86
	ISO-MSMS	0	PT5722-19	19	B2	678.86
	ISO-MSMS	0	PT5722-20	20	B2	678.86
	ISO-MSMS	0	PT5722-21	21	B2 SCX	678.86

	ISO-MSMS	0	PT5722-22	22	B2 SCX	678.86
	ISO-MSMS	0	PT5722-24	24	B2 SCX	678.86
	ISO-MSMS	0	PT5722-31	31	B3	678.86
	ISO-MSMS	0	PT5722-32	32	B3	678.86
	ISO-MSMS	0	PT5722-36	36	B3 SCX	678.86
	ISO-MSMS	0	PT5722-37	37	B3 SCX	678.86
	ISO-MSMS	0	PT5722-39	39	B3 SCX	678.86
	ISO-MSMS	0	PT5722-46	46	H/H	678.86
	ISO-MSMS	0	PT5722-47	47	H/H	678.86
	ISO-MSMS	0	PT5722-50	50	H/H	678.86
	ISO-MSMS	0	PT5722-51	51	H/H SCX	678.86
	ISO-MSMS	0	PT5722-54	54	H/H SCX	678.86

Vitellogenin-	ISO-MSMS	0	PT5722-8	8	B1 SCX	717.63
Vitellogenin-	ISO-MSMS	0	PT5722-18	18	B2	717.3
Vitellogenin-	MULTI-MSMS		PT5722-33	33	B3	717.63
Vitellogenin-	MULTI-MSMS		PT5722-38	38	B3 SCX	717.63
Vitellogenin-	ISO-MSMS	0	PT5722-40	40	B3 SCX	717.63
Vitellogenin-	MULTI-MSMS		PT5722-48	48	H/H	720.63
Vitellogenin-	MULTI-MSMS		PT5722-53	53	H/H SCX	717.29
Vitellogenin-	ISO-MSMS	0	PT5722-55	55	H/H SCX	717.63

Fancd2	MULTI-MSMS		PT5722-4	4	B1	990.98
	MULTI-MSMS		PT5722-18	18	B2	990.98
	MULTI-MSMS		PT5722-23	23	B2 SCX	990.98
	MULTI-MATCH		PT5722-24	24	B2 SCX	
	MULTI-MATCH		PT5722-25	25	B2 SCX	

Survival mot	ISO-MSMS	0	PT5722-24	24	B2 SCX	1072.48
Survival mot	ISO-MSMS	0	PT5722-39	39	B3 SCX	1072.47
Survival mot	ISO-MSMS	0	PT5722-40	40	B3 SCX	1072.47

CG32487	ISO-MSMS	0	PT5722-2	2	B1	753.05
	ISO-MSMS	0	PT5722-22	22	B2 SCX	752.72
	ISO-MSMS	0	PT5722-36	36	B3 SCX	753.05

1367-RA	MULTI-MSMS		PT5722-23	23	B2 SCX	670.97
1367-RA	MULTI-MATCH		PT5722-21	21	B2 SCX	
1367-RA	MULTI-MATCH		PT5722-22	22	B2 SCX	

Protein NASP	ISO-MSMS	0	PT5722-3	3	B1	727.67
Protein NASP	MULTI-MSMS		PT5722-7	7	B1 SCX	546.01
Protein NASP	MULTI-MSMS		PT5722-18	18	B2	727.68

Protein NASP	ISO-MSMS	0	PT5722-18	18	B2	545.76
Protein NASP	ISO-MSMS	0	PT5722-23	23	B2 SCX	546.01
Protein NASP	ISO-MSMS	0	PT5722-32	32	B3	545.76
Protein NASP	MULTI-MSMS		PT5722-36	36	B3 SCX	728.01
Protein NASP	ISO-MSMS	0	PT5722-36	36	B3 SCX	546.01
Protein NASP	ISO-MSMS	0	PT5722-37	37	B3 SCX	727.68

Akap200	ISO-MSMS	0	PT5722-9	9	B1 SCX	738
Akap200	MULTI-MSMS		PT5722-37	37	B3 SCX	737.66
Akap200	MULTI-MSMS		PT5722-39	39	B3 SCX	737.67
Akap200	ISO-MSMS	0	PT5722-47	47	H/H	737.66
Akap200	MULTI-MSMS		PT5722-54	54	H/H SCX	743.68

Protein NASP	MULTI-MSMS		PT5722-3	3	B1	1029.47
Protein NASP	MULTI-MSMS		PT5722-12	12	B1 TIO2	1028.97
Protein NASP	MULTI-MSMS		PT5722-13	13	B1 TIO2	1028.97
Protein NASP	MULTI-MSMS		PT5722-14	14	B1 TIO2	1028.97
Protein NASP	MULTI-MSMS		PT5722-18	18	B2	1029.47
Protein NASP	ISO-MSMS	0	PT5722-23	23	B2 SCX	1028.97
Protein NASP	MULTI-MSMS		PT5722-27	27	B2 TIO2	1028.97
Protein NASP	MULTI-MSMS		PT5722-28	28	B2 TIO2	1028.97
Protein NASP	MULTI-MSMS		PT5722-29	29	B2 TIO2	1028.97
Protein NASP	MULTI-MSMS		PT5722-32	32	B3	1029.47
Protein NASP	ISO-MSMS	0	PT5722-32	32	B3	686.65
Protein NASP	MULTI-MSMS		PT5722-33	33	B3	1028.97
Protein NASP	MULTI-MSMS		PT5722-33	33	B3	686.32
Protein NASP	ISO-MSMS	0	PT5722-38	38	B3 SCX	1028.98
Protein NASP	MULTI-MSMS		PT5722-42	42	B3 TIO2	1033.48
Protein NASP	MULTI-MSMS		PT5722-42	42	B3 TIO2	686.65
Protein NASP	MULTI-MSMS		PT5722-43	43	B3 TIO2	1029.47
Protein NASP	MULTI-MSMS		PT5722-44	44	B3 TIO2	1028.96
Protein NASP	ISO-MSMS	0	PT5722-44	44	B3 TIO2	686.65
Protein NASP	ISO-MSMS	0	PT5722-45	45	B3 TIO2	1028.98
Protein NASP	MULTI-MSMS		PT5722-47	47	H/H	1029.47
Protein NASP	MULTI-MSMS		PT5722-48	48	H/H	1028.96
Protein NASP	MULTI-MSMS		PT5722-52	52	H/H SCX	1028.96
Protein NASP	MULTI-MSMS		PT5722-57	57	H/H TIO2	1029.47
Protein NASP	MULTI-MSMS		PT5722-58	58	H/H TIO2	1028.97
Protein NASP	MSMS	0	PT5722-58	58	H/H TIO2	686.32
Protein NASP	MULTI-MSMS		PT5722-59	59	H/H TIO2	1028.97
Protein NASP	MULTI-MATCH		PT5722-2	2	B1	

Histone H1	ISO-MSMS	0	PT5722-4	4	B1	693.66

Histone H1	ISO-MSMS	0	PT5722-19	19	B2	1039.49
Histone H1	MULTI-MSMS		PT5722-49	49	H/H	693.33

tacc	ISO-MSMS	0	PT5722-7	7	B1 SCX	826.91
	MULTI-MSMS		PT5722-41	41	B3 TIO2	826.91
	ISO-MSMS	0	PT5722-51	51	H/H SCX	826.9
	MULTI-MSMS		PT5722-54	54	H/H SCX	826.9
	MULTI-MSMS		PT5722-57	57	H/H TIO2	826.4
	MULTI-MSMS		PT5722-57	57	H/H TIO2	866.39

Nedd8-activa	MULTI-MSMS		PT5722-11	11	B1 TIO2	799.9
Nedd8-activa	MULTI-MSMS		PT5722-28	28	B2 TIO2	799.9
Nedd8-activa	MULTI-MSMS		PT5722-57	57	H/H TIO2	799.9
Nedd8-activa	MULTI-MSMS		PT5722-58	58	H/H TIO2	799.9

	MULTI-MSMS		PT5722-19	19	B2	440.23
	MULTI-MSMS		PT5722-34	34	B3	440.56

Probable hist	ISO-MSMS	0	PT5722-3	3	B1	1008.44
Probable hist	MULTI-MSMS		PT5722-38	38	B3 SCX	1008.44
Probable hist	MULTI-MSMS		PT5722-53	53	H/H SCX	1008.77

Otefin	ISO-MSMS	0	PT5722-3	3	B1	954.95
Otefin	ISO-MSMS	0	PT5722-33	33	B3	954.96
Otefin	ISO-MSMS	0	PT5722-38	38	B3 SCX	954.96

spoon	MULTI-MSMS		PT5722-4	4	B1	672.02
	MULTI-MSMS		PT5722-18	18	B2	672.02
	MULTI-MSMS		PT5722-32	32	B3	671.69

Charge	m/z	Mass	Resolution	Uncalibrated - Calibrated m/z [ppm]	Uncalibrated - Calibrated m/z [Da]	Mass Error [ppm]
3	761,341,567	228,100,287	48700.75	-0.6341	-0.00048276	-0.040968
3	761,341,567	228,100,287	NaN	NaN	NaN	0.14489
3	734,686,124	220,103,654	NaN	NaN	NaN	0.91062
3	734,686,124	220,103,654	NaN	NaN	NaN	0.23012
3	777,384,445	23,291,315	NaN	NaN	NaN	0.8582
3	777,384,445	23,291,315	NaN	NaN	NaN	0.78236
3	804,039,888	240,909,784	NaN	NaN	NaN	0.47731
3	804,039,888	240,909,784	NaN	NaN	NaN	0.28295
2	749,842,461	149,767,037	NaN	NaN	NaN	NaN
2	749,842,461	149,767,037	NaN	NaN	NaN	NaN
3	782,049,285	234,312,603	49084.29	-0.31035	-0.00024271	-0.22733
3	782,049,285	234,312,603	47136.54	-0.6614	-0.00051725	-0.84304
3	782,049,285	234,312,603	48041.27	-0.65958	-0.00051582	-0.34588
3	782,049,285	234,312,603	NaN	NaN	NaN	0.32247
3	782,049,285	234,312,603	47180.82	-0.58054	-0.00045401	-0.46054
2	117,257,029	234,312,603	38721.94	-0.93501	-0.0010964	-0.19664
3	782,049,285	234,312,603	NaN	NaN	NaN	-0.60707
3	782,049,285	234,312,603	47256.8	-0.42933	-0.00033576	-0.70423
3	782,049,285	234,312,603	47104.99	-0.85091	-0.00066545	-0.34612
3	782,049,285	234,312,603	46783.95	-0.96112	-0.00075164	-0.95532
3	782,049,285	234,312,603	47026.67	-0.66347	-0.00051887	-0.428
3	78,237,729	234,411,004	NaN	NaN	NaN	0.13328
2	110,601,649	221,001,843	40031.52	-0.93809	-0.0010375	0.17847
2	110,601,649	221,001,843	39980.95	-0.7294	-0.00080672	0.064339
2	110,601,649	221,001,843	NaN	NaN	NaN	0.45069
2	110,601,649	221,001,843	40122.95	-0.48689	-0.00053851	0.11751
2	110,601,649	221,001,843	39421.7	-0.60565	-0.00066986	0.046545
2	110,601,649	221,001,843	39367.34	0	0	-0.48324
2	114,599,966	228,998,476	40352.94	-0.60563	-0.00069406	0.03998
3	764,335,531	228,998,476	48247.85	-0.60554	-0.00046284	-0.14232
4	942,699,453	376,676,871	NaN	NaN	NaN	0.7398
4	942,699,453	376,676,871	NaN	NaN	NaN	0.44133
4	942,699,453	376,676,871	NaN	NaN	NaN	0.57015
4	942,699,453	376,676,871	NaN	NaN	NaN	0.62828

4	942,699,453	376,676,871	43554.6	-0.24396	-0.00022998	-11,793

2	84,133,509	168,065,563	45027.15	-0.89245	-0.00075085	0.41865
2	84,133,509	168,065,563	44767.33	-0.58062	-0.0004885	-0.38377
2	84,133,509	168,065,563	44982.43	-0.63029	-0.00053029	0.24525
2	84,133,509	168,065,563	45711.25	0	0	-11,744
2	84,133,509	168,065,563	NaN	NaN	NaN	0.69875
2	84,133,509	168,065,563	NaN	NaN	NaN	-0.11447
2	84,133,509	168,065,563	43560.81	-0.47621	-0.00040065	-0.33956
2	84,133,509	168,065,563	45250.93	-0.87036	-0.00073227	-0.046635
2	84,133,509	168,065,563	45688.7	-0.94427	-0.00079445	-0.28334
2	84,133,509	168,065,563	46313.07	-0.57953	-0.00048758	-0.35958
2	84,133,509	168,065,563	45818.69	-0.70187	-0.0005905	-0.055655
2	84,133,509	168,065,563	46058.67	-0.88319	-0.00074306	0.088149

2	622,765,061	124,351,557	49666.66	-11,675	-0.00072709	0.72062
2	622,765,061	124,351,557	53750.39	0	0	-0.36105
2	622,765,061	124,351,557	53765.87	-0.68807	-0.00042851	-0.096821
2	622,765,061	124,351,557	49223.58	-0.70701	-0.0004403	0.21521
2	622,765,061	124,351,557	53622.12	0	0	-0.33432
2	622,765,061	124,351,557	52022.43	-0.23251	-0.0001448	-0.28415
2	622,765,061	124,351,557	53283.96	-0.8521	-0.00053066	-0.026131
2	622,765,061	124,351,557	54265.55	-0.51174	-0.0003187	0.47838
2	622,765,061	124,351,557	49801.67	-0.35894	-0.00022353	0.1143
2	622,765,061	124,351,557	53179.15	-0.50061	-0.00031176	0.29178
2	622,765,061	124,351,557	54084.26	-0.31982	-0.00019917	-0.43446

2	619,254,852	123,649,515	53106.32	-0.21324	-0.00013205	13,032
2	619,254,852	123,649,515	51842.47	-0.24336	-0.0001507	15,959

3	821,683,108	246,202,749	NaN	NaN	NaN	0.72795
3	821,683,108	246,202,749	46390.55	-0.52842	-0.00043419	0.18359
3	821,683,108	246,202,749	46712.96	-0.49176	-0.00040407	-0.048026
3	821,683,108	246,202,749	46631.54	-0.5666	-0.00046556	0.12942
3	821,683,108	246,202,749	46837.07	-0.46708	-0.00038379	-0.087081
3	821,683,108	246,202,749	46733.58	-0.54819	-0.00045044	-0.36846

4	385,940,632	153,973,342	66420.11	0.018018	6.95E-02	-13,849
4	385,940,632	153,973,342	66350.92	-0.27129	-0.0001047	-13,766

3	9,094,124	272,521,537	NaN	NaN	NaN	0.53441

3	9,094,124	272,521,537	NaN	NaN	NaN	0.7078
3	9,094,124	272,521,537	44209.95	-0.57909	-0.00052663	0.11881

3	105,211,134	315,331,218	NaN	NaN	NaN	0.088838
3	105,211,134	315,331,218	NaN	NaN	NaN	-0.079777
3	105,211,134	315,331,218	NaN	NaN	NaN	0.38664

2	702,762,518	140,351,048	NaN	NaN	NaN	-14,181
2	702,762,518	140,351,048	49509.86	-0.77163	-0.00054227	-0.70452
2	702,762,518	140,351,048	50982.97	-0.46099	-0.00032397	0.016504

2	103,737,957	207,274,458	41426.96	-0.80348	-0.00083351	-0.3003
2	103,737,957	207,274,458	NaN	NaN	NaN	0.01813
2	103,737,957	207,274,458	41640.52	-0.73718	-0.00076473	-0.066447

4	727,068,215	290,424,375	NaN	NaN	NaN	10,117
3	969,088,528	290,424,375	42884.98	-11,746	-0.0011383	-0.24134
4	727,068,215	290,424,375	49911.34	-0.99858	-0.00072604	-0.1016
4	727,068,215	290,424,375	NaN	NaN	NaN	0.51106

2	118,441,603	23,668,175	NaN	NaN	NaN	NaN
3	789,946,443	23,668,175	NaN	NaN	NaN	NaN
3	789,946,443	23,668,175	NaN	NaN	NaN	NaN
3	763,290,999	228,685,117	47898.98	-0.71276	-0.00054404	-0.16419

3	632,607,934	189,480,197	NaN	NaN	NaN	10,578
3	632,607,934	189,480,197	52561.09	-0.94823	-0.00059985	-0.19406
3	632,607,934	189,480,197	54769.45	-0.55402	-0.00035048	0.0018982
3	632,607,934	189,480,197	NaN	NaN	NaN	0.58237
3	632,607,934	189,480,197	NaN	NaN	NaN	0.64711
3	632,607,934	189,480,197	52791.61	-0.51669	-0.00032686	-0.51163

2	809,886,573	161,775,859	NaN	NaN	NaN	-13,628
2	809,886,573	161,775,859	NaN	NaN	NaN	-0.79476
2	809,886,573	161,775,859	NaN	NaN	NaN	-11,434
2	809,886,573	161,775,859	NaN	NaN	NaN	-15,373

2	909,435,761	181,685,697	43696.7	-18,642	-0.0016954	0.0030465
3	606,626,266	181,685,697	52622.78	-0.53676	-0.00032561	-11,913
3	606,626,266	181,685,697	53944.11	-0.10199	-6.19E-01	-12,749
3	606,626,266	181,685,697	53182.92	-0.37484	-0.00022739	-10,728
3	597,626,378	17,898,573	52584.19	-0.2817	-0.00016835	-0.85859

2	895,935,928	17,898,573	42945.04	-0.27722	-0.00024837	-17,824
2	895,935,928	17,898,573	43884.54	-11,219	-0.0010051	-0.50313
3	597,626,378	17,898,573	51025.32	-0.64456	-0.00038521	-0.27575

2	903,419,923	180,482,529	NaN	NaN	NaN	0.48176
2	903,419,923	180,482,529	NaN	NaN	NaN	12,271
2	903,419,923	180,482,529	NaN	NaN	NaN	17,114
2	903,419,923	180,482,529	NaN	NaN	NaN	0.061222
2	903,419,923	180,482,529	NaN	NaN	NaN	13,955
2	903,419,923	180,482,529	NaN	NaN	NaN	14,456

3	914,401,501	274,018,267	NaN	NaN	NaN	-0.36446
3	914,401,501	274,018,267	NaN	NaN	NaN	0.40981
3	914,401,501	274,018,267	43868.11	-0.60547	-0.00055364	-0.39734

3	555,273,215	166,279,782	57588.13	-0.64389	-0.00035753	-0.39201
2	832,406,184	166,279,782	45805.02	-0.90136	-0.0007503	-0.30556
3	555,273,215	166,279,782	57856	-0.18944	-0.00010519	-0.24905
2	832,406,184	166,279,782	45675.85	-0.69867	-0.00058158	0.5334
2	832,406,184	166,279,782	47421.39	-0.78716	-0.00065524	-0.099439
3	597,971,536	179,089,278	53542.4	-0.51142	-0.00030581	-11,847
3	597,971,536	179,089,278	52488.26	-0.45983	-0.00027496	-13,331

3	754,333,416	225,997,842	48501.36	-12,935	-0.00097576	0.59531
3	754,333,416	225,997,842	48648.12	-0.68361	-0.00051567	0.44713
3	754,333,416	225,997,842	47620.15	-0.6986	-0.00052698	0.019261

3	558,251,534	167,173,277	52879.02	-0.43009	-0.0002401	0.60775
3	558,579,539	167,271,679	NaN	NaN	NaN	10,397

2	958,475,759	191,493,696	42446.84	-10,427	-0.00099945	14,035
2	958,475,759	191,493,696	42782.33	-0.13625	-0.0001306	10,331

2	610,743,263	121,947,197	52952.65	-0.76413	-0.00046669	-12,932
2	610,743,263	121,947,197	52520.14	-0.41241	-0.00025187	-14,579
2	602,745,805	120,347,706	53745.4	-0.83504	-0.00050332	-11,888

2	678,862,361	135,571,017	NaN	NaN	NaN	-0.15588
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.50484
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.68469
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.20306
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.24851
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.2432

2	678,862,361	135,571,017	NaN	NaN	NaN	-10,303
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.52289
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.85876
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.46929
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.22617
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.41926
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.37923
2	678,862,361	135,571,017	NaN	NaN	NaN	-10,336
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.5864
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.89777
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.80944
2	678,862,361	135,571,017	NaN	NaN	NaN	-0.39322

3	71,729,563	214,886,506	NaN	NaN	NaN	10,651
3	71,729,563	214,886,506	NaN	NaN	NaN	0.96299
3	71,729,563	214,886,506	50576.19	-0.81753	-0.00058641	-0.5649
3	71,729,563	214,886,506	48931.68	-11,873	-0.00085165	-0.36907
3	71,729,563	214,886,506	NaN	NaN	NaN	0.82332
3	71,729,563	214,886,506	48935.83	-0.89124	-0.00063928	-0.42935
3	71,729,563	214,886,506	48589.26	-0.93498	-0.00067066	-0.48078
3	71,729,563	214,886,506	NaN	NaN	NaN	0.61346

2	990,473,732	197,893,291	41371.02	-0.13943	-0.0001381	1,129
2	990,473,732	197,893,291	41700.63	-0.8848	-0.00087637	17,107
2	990,473,732	197,893,291	41721.6	-0.71732	-0.00071049	15,135
2	990,473,732	197,893,291	41596.73	-0.78942	-0.0007819	10,194
2	990,473,732	197,893,291	41791.86	-0.78107	-0.00077363	1,597

3	107,214,017	321,339,869	NaN	NaN	NaN	10,075
3	107,214,017	321,339,869	NaN	NaN	NaN	11,244
3	107,214,017	321,339,869	NaN	NaN	NaN	0.064241

3	752,716,813	225,512,861	NaN	NaN	NaN	0.39857
3	752,716,813	225,512,861	NaN	NaN	NaN	0.6837
3	752,716,813	225,512,861	NaN	NaN	NaN	0.95028

3	670,304,899	200,789,287	50782.59	-12,919	-0.00086598	-14,228
3	670,304,899	200,789,287	50413.44	-0.92069	-0.00061714	-23,988
3	670,304,899	200,789,287	49867.72	-0.80455	-0.00053929	-22,151

3	727,339,959	217,899,805	NaN	NaN	NaN	0.67973
4	545,756,788	217,899,805	55200.6	-0.47673	-0.00026018	-11,118
3	727,339,959	217,899,805	47298.66	-1,453	-0.0010568	-0.28561

4	545,756,788	217,899,805	NaN	NaN	NaN	10,085
4	545,756,788	217,899,805	NaN	NaN	NaN	0.51477
4	545,756,788	217,899,805	NaN	NaN	NaN	0.43893
3	727,339,959	217,899,805	49461.57	-0.8152	-0.00059293	-0.26477
4	545,756,788	217,899,805	NaN	NaN	NaN	0.29208
3	727,339,959	217,899,805	NaN	NaN	NaN	0.67912

3	737,665,277	2,209,974	NaN	NaN	NaN	0.7087
3	737,665,277	2,209,974	48021.57	-0.81164	-0.00059872	-1,022
3	737,665,277	2,209,974	49666.97	-0.73257	-0.00054039	-0.59356
3	737,665,277	2,209,974	NaN	NaN	NaN	0.063042
3	737,665,277	2,209,974	48325.57	-0.67641	-0.00049896	-0.688

2	102,896,974	205,592,493	40445.55	-0.72577	-0.0007468	-0.46537
2	102,896,974	205,592,493	40108.64	0	0	-17,689
2	102,896,974	205,592,493	40719.98	0	0	-16,878
2	102,896,974	205,592,493	42294.86	0	0	-15,537
2	102,896,974	205,592,493	40144.92	-0.4439	-0.00045676	-10,553
2	102,896,974	205,592,493	NaN	NaN	NaN	0.40686
2	102,896,974	205,592,493	40656.43	0	0	-17,644
2	102,896,974	205,592,493	40637.25	0	0	-16,164
2	102,896,974	205,592,493	41381.46	0	0	-11,285
2	102,896,974	205,592,493	40644.64	-0.15679	-0.00016133	-12,504
3	686,315,585	205,592,493	NaN	NaN	NaN	0.93733
2	102,896,974	205,592,493	41106.15	-0.72335	-0.0007443	-0.40616
3	686,315,585	205,592,493	50304.32	-0.18577	-0.0001275	-0.72788
2	102,896,974	205,592,493	NaN	NaN	NaN	0.12316
2	102,896,974	205,592,493	40951.85	-0.88397	-0.00090958	-0.59491
3	686,315,585	205,592,493	50827.29	-0.88301	-0.00060602	0.062175
2	102,896,974	205,592,493	40977.51	0	0	-14,647
2	102,896,974	205,592,493	41019.25	0	0	-13,648
3	686,315,585	205,592,493	NaN	NaN	NaN	0.036765
2	102,896,974	205,592,493	NaN	NaN	NaN	-0.070952
2	102,896,974	205,592,493	41467.31	-0.1204	-0.00012389	-0.57332
2	102,896,974	205,592,493	41073.05	-0.52115	-0.00053625	0.11019
2	102,896,974	205,592,493	42349.81	-0.25346	-0.0002608	-0.58571
2	102,896,974	205,592,493	41294.95	-0.6056	-0.00062315	-0.12905
2	102,896,974	205,592,493	41438.02	0	0	-0.67687
3	686,315,585	205,592,493	NaN	NaN	NaN	NaN
2	102,896,974	205,592,493	41382.49	0	0	-0.21612
2	102,896,974	205,592,493	40875.37	-0.67242	-0.0006919	-0.46279

3	693,327,825	207,696,165	NaN	NaN	NaN	0.95663

2	10,394,881	207,696,165	NaN	NaN	NaN	0.78001
3	693,327,825	207,696,165	51124.58	-0.24826	-0.00017213	-0.90324

2	826,402,579	16,507,906	NaN	NaN	NaN	19,666
2	826,402,579	16,507,906	44413.07	-0.71751	-0.00059296	-0.17386
2	826,402,579	16,507,906	NaN	NaN	NaN	20,438
2	826,402,579	16,507,906	44639.39	-0.90043	-0.00074412	0.59597
2	826,402,579	16,507,906	45362.56	-0.6055	-0.00050038	0.23264
2	866,385,744	173,075,693	46475.25	-0.60516	-0.0005243	0.48461

2	799,900,538	159,778,652	45334.03	0	0	-14,209
2	799,900,538	159,778,652	49691.38	0	0	-0.59866
2	799,900,538	159,778,652	47238.11	-0.60566	-0.00048447	0.065684
2	799,900,538	159,778,652	46978.66	0	0	-0.66459

3	440,230,399	131,766,937	62752.88	-0.20477	-9.01E-01	-0.60419
3	440,230,399	131,766,937	62672.29	-0.27832	-0.00012253	0.42741

3	100,810,317	302,128,768	NaN	NaN	NaN	0.81854
3	100,810,317	302,128,768	41498.1	-0.1923	-0.00019385	-0.69867
3	100,810,317	302,128,768	41709.66	-0.69225	-0.00069786	-0.24163

4	954,455,923	381,379,459	NaN	NaN	NaN	-0.43112
4	954,455,923	381,379,459	NaN	NaN	NaN	0.51079
4	954,455,923	381,379,459	NaN	NaN	NaN	0.73047

3	67,168,786	201,204,175	51096.34	-0.04967	-3.34E-01	17,197
3	67,168,786	201,204,175	50391.08	0.0094576	6.35E-02	19,131
3	67,168,786	201,204,175	47925.68	0.24981	0.0001678	13,833

Mass Error [Da]	Uncalibrated Mass Error [ppm]	Uncalibrated Mass Error [Da]	Max intensity m/z 0	Max intensity m/z 1	Retention time	Retention length
-3.12E-02	-0.67506	-0.00051395	##########	##########	73,595	0.60837
0.00011031	NaN	NaN	NaN	NaN	78,863	0.81698
0.00066902	NaN	NaN	NaN	NaN	67,212	0.58141
0.00016907	NaN	NaN	NaN	NaN	71,066	10,799
0.00066715	NaN	NaN	NaN	NaN	58,525	0.57363
0.0006082	NaN	NaN	NaN	NaN	63,039	0.88077
0.00038378	NaN	NaN	NaN	NaN	63,152	0.58234
0.0002275	NaN	NaN	NaN	NaN	67,438	0.67523
NaN	NaN	NaN	NaN	NaN	73,177	1
NaN	NaN	NaN	NaN	NaN	73,417	1
-0.00017778	-0.53768	-0.00042049	##########	##########	103.41	0.57672
-0.0006593	-15,044	-0.0011765	##########	##########	100.42	0.85462
-0.0002705	-10,055	-0.00078632	##########	##########	97,275	10,631
0.00025218	NaN	NaN	NaN	NaN	102.37	19,762
-0.00036016	-10,411	-0.00081417	##########	##########	97,438	0.64938
-0.00023058	-11,317	-0.0013269	##########	##########	97,415	0.58425
-0.00047476	NaN	NaN	NaN	NaN	102.5	13,302
-0.00055074	-11,336	-0.0008865	##########	##########	97.99	10,517
-0.00027068	-1,197	-0.00093614	##########	##########	105.34	0.73146
-0.00074711	-19,164	-0.0014987	##########	##########	100.21	0.42425
-0.00033472	-10,915	-0.00085358	##########	##########	98.64	0.56222
0.00010427	NaN	NaN	NaN	NaN	98,032	0.47295
0.00019739	-0.75963	-0.00084016	##########	##########	116.29	0.62392
7.12E-02	-0.66506	-0.00073556	##########	##########	119.5	0.31782
0.00049847	NaN	NaN	NaN	NaN	126.64	0.47802
0.00012997	-0.36938	-0.00040854	##########	##########	136.54	0.56355
5.15E-01	-0.55911	-0.00061838	##########	##########	116.89	0.64877
-0.00053448	-0.48324	-0.00053448	##########	##########	117.13	0.53051
4.58E-01	-0.56565	-0.00064824	##########	##########	126.86	0.8235
-0.00010878	-0.74786	-0.00057162	##########	##########	126.92	0.62176
0.00069741	NaN	NaN	NaN	NaN	79,829	0.67028
0.00041604	NaN	NaN	NaN	NaN	78,767	0.8231
0.00053748	NaN	NaN	NaN	NaN	77,134	0.60345
0.00059228	NaN	NaN	NaN	NaN	81,341	14,287

-0.0011118	-14,233	-0.0013418	##########	##########	78.16	10,275

0.00035223	-0.47379	-0.00039862	##########	##########	81,717	0.60141
-0.00032288	-0.9644	-0.00081138	##########	##########	85,461	0.54626
0.00020634	-0.38504	-0.00032395	##########	##########	84,705	0.659
-0.00098804	-11,744	-0.00098804	##########	##########	81,916	0.5723
0.00058788	NaN	NaN	NaN	NaN	83,036	0.60281
-9.63E-01	NaN	NaN	NaN	NaN	81,405	0.53769
-0.00028568	-0.81577	-0.00068633	##########	##########	95,193	0.4995
-3.92E-01	-0.917	-0.0007715	##########	##########	94,723	0.63361
-0.00023838	-12,276	-0.0010328	##########	##########	82,131	0.55059
-0.00030253	-0.93911	-0.00079011	##########	##########	84,447	0.58243
-4.68E-01	-0.75752	-0.00063733	##########	##########	83,209	0.60301
7.42E-01	-0.79504	-0.00066889	##########	##########	81,927	0.48901

0.00044878	-0.44689	-0.00027831	##########	##########	76,755	15,688
-0.00022485	-0.36105	-0.00022485	##########	##########	76,205	0.73231
-6.03E-01	-0.78489	-0.0004888	##########	##########	76,587	0.50031
0.00013403	-0.4918	-0.00030627	##########	##########	77,517	13,885
-0.00020821	-0.33432	-0.00020821	##########	##########	77,719	0.58629
-0.00017696	-0.51667	-0.00032176	##########	##########	87,667	0.53617
-1.63E-01	-0.87823	-0.00054693	##########	##########	87,765	0.65209
0.00029792	-0.033363	-2.08E-01	##########	##########	78,112	0.86717
7.12E-01	-0.24463	-0.00015235	##########	##########	76,455	16,749
0.00018171	-0.20884	-0.00013006	##########	##########	78,722	0.7103
-0.00027057	-0.75428	-0.00046974	##########	##########	87,866	0.6384

0.000807	10,899	0.00067495	##########	##########	94,877	0.67711
0.00098824	13,525	0.00083754	##########	##########	94,214	0.52608

0.00059814	NaN	NaN	NaN	NaN	103.01	0.75828
0.00015085	-0.34483	-0.00028334	##########	##########	101.81	0.72246
-3.95E-01	-0.53978	-0.00044353	##########	##########	100.02	0.75243
0.00010634	-0.43717	-0.00035922	##########	##########	110.97	10,815
-7.16E-01	-0.55416	-0.00045534	##########	##########	102.64	0.68706
-0.00030275	-0.91665	-0.0007532	##########	##########	101.37	0.67909

-0.00053448	-13,669	-0.00052752	##########	##########	51,006	0.59747
-0.0005313	-16,479	-0.000636	##########	##########	57,204	0.60443

0.000486	NaN	NaN	NaN	NaN	78,509	0.36842

0.00064369	NaN	NaN	NaN	NaN	87,301	0.7648
0.00010804	-0.46028	-0.00041858	##########	##########	79,768	0.59363

9.35E-01	NaN	NaN	NaN	NaN	88,133	0.81361
-8.39E-01	NaN	NaN	NaN	NaN	88.65	0.6924
0.00040679	NaN	NaN	NaN	NaN	88.85	0.88759

-0.00099659	NaN	NaN	NaN	NaN	70,489	0.52867
-0.00049511	-14,762	-0.0010374	##########	##########	71,545	0.62837
1.16E-01	-0.44449	-0.00031237	##########	##########	70,618	0.64713

-0.00031152	-11,038	-0.001145	##########	##########	108.15	0.59637
1.88E-01	NaN	NaN	NaN	NaN	108.99	0.44384
-6.89E-01	-0.80363	-0.00083366	##########	##########	108.84	0.54576

			y			
0.00073559	NaN	NaN	NaN	NaN	66,421	0.63902
-0.00023388	-1,416	-0.0013722	##########	##########	64,623	0.91163
-7.39E-01	-11,002	-0.00079991	##########	##########	64,653	0.91163
0.00037158	NaN	NaN	NaN	NaN	64,588	0.61862

NaN	NaN	NaN	NaN	NaN	94,476	1
NaN	NaN	NaN	NaN	NaN	113.66	1
NaN	NaN	NaN	NaN	NaN	101.06	1
-0.00012533	-0.87695	-0.00066937	##########	##########	87,498	0.53297

0.00066917	NaN	NaN	NaN	NaN	57,495	0.41724
-0.00012276	-11,423	-0.00072262	##########	##########	53,759	0.55851
1.20E-02	-0.55212	-0.00034928	##########	##########	63,476	0.71551
0.00036841	NaN	NaN	NaN	NaN	66.49	0.72619
0.00040937	NaN	NaN	NaN	NaN	57,738	0.36544
-0.00032366	-10,283	-0.00065052	##########	##########	55,677	0.57108

-0.0011037	NaN	NaN	NaN	NaN	59,949	0.91953
-0.00064366	NaN	NaN	NaN	NaN	59,764	0.9465
-0.00092598	NaN	NaN	NaN	NaN	61,765	1,128
-0.0012451	NaN	NaN	NaN	NaN	123.93	0.76739

2.77E-02	-18,612	-0.0016926	##########	##########	88,764	0.6004
-0.00072269	-17,281	-0.0010483	##########	##########	89,718	14,088
-0.00077341	-13,769	-0.00083528	##########	##########	89.86	11,759
-0.0006508	-14,476	-0.00087818	##########	##########	89,509	0.76118
-0.00051312	-11,403	-0.00068147	##########	##########	68,206	19,744

-0.0015969	-20,596	-0.0018453	##########	##########	74,517	0.44894
-0.00045077	-1,625	-0.0014559	##########	##########	74,981	0.66922
-0.00016479	-0.92031	-0.00055	##########	##########	67,525	0.73146
0.00043523	NaN	NaN	NaN	NaN	86,999	0.7193
0.0011086	NaN	NaN	NaN	NaN	85,962	0.63573
0.0015461	NaN	NaN	NaN	NaN	84,968	0.63683
5.53E-02	NaN	NaN	NaN	NaN	82,974	0.69716
0.0012608	NaN	NaN	NaN	NaN	84,321	0.64992
0.001306	NaN	NaN	NaN	NaN	83.74	0.96486
-0.00033326	NaN	NaN	NaN	NaN	95,998	0.73493
0.00037473	NaN	NaN	NaN	NaN	105	0.64604
-0.00036333	-10,028	-0.00091697	##########	##########	95,819	0.87028
-0.00021767	-10,359	-0.00057521	##########	##########	55,913	0.41409
-0.00025435	-12,069	-0.0010046	##########	##########	57,181	0.44668
-0.00013829	-0.43849	-0.00024348	##########	##########	65,694	0.53619
0.000444	-0.16528	-0.00013758	##########	##########	64,475	0.49722
-8.28E-01	-0.8866	-0.00073801	##########	##########	65,717	0.48075
-0.0007084	-16,961	-0.0010142	##########	##########	46,122	0.3931
-0.00079715	-17,929	-0.0010721	##########	##########	52,587	0.64492
0.00044906	-0.69823	-0.00052669	##########	##########	71,015	0.46674
0.00033729	-0.23648	-0.00017839	##########	##########	69,722	0.74473
1.45E-01	-0.67934	-0.00051245	##########	##########	81,242	0.67423
0.00033928	0.17765	9.92E-01	##########	##########	46,373	13,627
0.00058073	NaN	NaN	NaN	NaN	48,931	0.67912
0.0013452	0.36076	0.00034578	##########	##########	130.53	1,487
0.00099024	0.89689	0.00085964	##########	##########	132	15,108
-0.00078979	-20,573	-0.0012565	##########	##########	116.71	0.92902
-0.00089042	-18,703	-0.0011423	##########	##########	46,818	0.65672
-0.00071657	-20,239	-0.0012199	##########	##########	126.59	17,975
-0.00010582	NaN	NaN	NaN	NaN	73,446	0.85529
-0.00034272	NaN	NaN	NaN	NaN	71,689	0.95847
-0.00046481	NaN	NaN	NaN	NaN	68,475	0.57893
-0.00013785	NaN	NaN	NaN	NaN	63,488	0.81966
-0.0001687	NaN	NaN	NaN	NaN	128.62	23,097
-0.0001651	NaN	NaN	NaN	NaN	68,041	0.80257

-0.00069943	NaN	NaN	NaN	NaN	66,515	11,619
-0.00035497	NaN	NaN	NaN	NaN	64,425	1,019
-0.00058298	NaN	NaN	NaN	NaN	121.77	39,073
-0.00031859	NaN	NaN	NaN	NaN	71,122	0.53815
-0.00015354	NaN	NaN	NaN	NaN	77,373	10,956
-0.00028462	NaN	NaN	NaN	NaN	75,968	12,429
-0.00025744	NaN	NaN	NaN	NaN	64,014	10,419
-0.00070165	NaN	NaN	NaN	NaN	118.8	25,957
-0.00039808	NaN	NaN	NaN	NaN	125.72	29,955
-0.00060946	NaN	NaN	NaN	NaN	129.27	2,961
-0.0005495	NaN	NaN	NaN	NaN	69.77	10,571
-0.00026694	NaN	NaN	NaN	NaN	63,333	0.77888

0.00076401	NaN	NaN	NaN	NaN	54,759	0.54944
0.00069075	NaN	NaN	NaN	NaN	52,031	0.43327
-0.0004052	-13,824	-0.00099161	##########	##########	62,327	11,715
-0.00026473	-15,564	-0.0011164	##########	##########	56,364	0.55442
0.00059057	NaN	NaN	NaN	NaN	52,195	0.50599
-0.00030797	-13,206	-0.00094725	##########	##########	51,827	0.88256
-0.00034486	-14,158	-0.0010155	##########	##########	52,567	0.85705
0.00044003	NaN	NaN	NaN	NaN	50.78	0.51909

0.0011183	0.98959	0.00098016	##########	##########	130.2	14,043
0.0016944	0.82589	0.00081803	##########	##########	101.65	2,687
0.0014991	0.79621	0.00078863	##########	##########	102.56	18,499
0.0010097	0.22998	0.00022779	##########	##########	102.36	0.76945
0.0015818	0.81593	0.00080816	##########	##########	102.16	0.55981

0.0010802	NaN	NaN	NaN	NaN	81,284	13,858
0.0012056	NaN	NaN	NaN	NaN	81,377	16,813
6.89E-01	NaN	NaN	NaN	NaN	81,158	0.85651

0.00030001	NaN	NaN	NaN	NaN	111.95	0.94267
0.00051464	NaN	NaN	NaN	NaN	114.19	0.63842
0.00071529	NaN	NaN	NaN	NaN	123.38	0.5867

-0.00095371	-27,147	-0.0018197	##########	##########	63,084	0.72208
-0.001608	-33,195	-0.0022251	##########	##########	66.67	0.38632
-0.0014848	-30,196	-0.0020241	##########	##########	64,794	0.56033

0.00049439	NaN	NaN	NaN	NaN	42,096	0.57529
-0.00060678	-15,885	-0.00086696	##########	##########	50,042	0.65393
-0.00020773	-17,386	-0.0012645	##########	##########	42,335	0.72315

0.00055042	NaN	NaN	NaN	NaN	42,336	0.93044
0.00028094	NaN	NaN	NaN	NaN	43,609	10,889
0.00023955	NaN	NaN	NaN	NaN	50,433	0.32283
-0.00019258	-1.08	-0.00078551	##########	##########	57,465	0.65966
0.00015941	NaN	NaN	NaN	NaN	57,517	0.85898
0.00049395	NaN	NaN	NaN	NaN	55,509	0.62685

0.00052278	NaN	NaN	NaN	NaN	54,745	0.51048
-0.00075392	-18,337	-0.0013526	##########	##########	64,875	0.77584
-0.00043785	-13,261	-0.00097824	##########	##########	53,482	0.68179
4.65E-01	NaN	NaN	NaN	NaN	106.88	10,294
-0.00050752	-13,644	-0.0010065	##########	##########	52.9	0.56873

-0.00047885	-11,911	-0.0012256	##########	##########	120.16	12,281
-0.0018201	-17,689	-0.0018201	##########	##########	119.81	11,799
-0.0017367	-16,878	-0.0017367	##########	##########	119.92	1,068
-0.0015987	-15,537	-0.0015987	##########	##########	119.98	0.58934
-0.0010859	-14,992	-0.0015427	##########	##########	120.5	10,766
0.00041865	NaN	NaN	NaN	NaN	120.4	0.50204
-0.0018155	-17,644	-0.0018155	##########	##########	120.97	0.6772
-0.0016632	-16,164	-0.0016632	##########	##########	121.12	13,278
-0.0011612	-11,285	-0.0011612	##########	##########	121.39	0.68147
-0.0012866	-14,072	-0.001448	##########	##########	133.17	0.95207
0.0006433	NaN	NaN	NaN	NaN	133.21	0.64886
-0.00041792	-11,295	-0.0011622	##########	##########	133.07	1,098
-0.00049955	-0.91365	-0.00062705	##########	##########	133.09	0.57579
0.00012673	NaN	NaN	NaN	NaN	121.19	0.82292
-0.00061214	-14,789	-0.0015217	##########	##########	121.83	0.82023
4.27E-01	-0.82083	-0.00056335	##########	##########	121.79	0.83508
-0.0015071	-14,647	-0.0015071	##########	##########	121.84	0.78532
-0.0014044	-13,648	-0.0014044	##########	##########	121.85	0.75122
2.52E-01	NaN	NaN	NaN	NaN	121.87	0.56217
-7.30E-01	NaN	NaN	NaN	NaN	122.13	0.63235
-0.00058993	-0.69372	-0.00071382	##########	##########	123.85	24,877
0.00011339	-0.41096	-0.00042286	##########	##########	121.54	0.76222
-0.00060268	-0.83917	-0.00086349	##########	##########	120.81	0.62215
-0.00013279	-0.73465	-0.00075593	##########	##########	121.92	18,693
-0.00069648	-0.67687	-0.00069648	##########	##########	122.16	0.78681
NaN	NaN	NaN	NaN	NaN	122.13	1
-0.00022238	-0.21612	-0.00022238	##########	##########	122.46	0.56194
-0.0004762	-11,352	-0.0011681	##########	##########	120.15	0.95764

0.00066326	NaN	NaN	NaN	NaN	82,514	0.82999

0.00081082	NaN	NaN	NaN	NaN	83,068	0.49942
-0.00062624	-11,515	-0.00079837	##########	##########	84,379	0.89329

0.0016252	NaN	NaN	NaN	NaN	105.61	0.69661
-0.00014368	-0.89137	-0.00073663	##########	##########	100.9	0.40081
0.001689	NaN	NaN	NaN	NaN	105.18	0.58349
0.00049251	-0.30446	-0.00025161	##########	##########	101.02	0.55649
0.00019225	-0.37286	-0.00030813	##########	##########	99,569	0.63045
0.00041986	-0.12055	-0.00010444	##########	##########	116.48	0.51491

-0.0011366	-14,209	-0.0011366	##########	##########	87,404	0.47132
-0.00047887	-0.59866	-0.00047887	##########	##########	85,976	0.56593
5.25E-01	-0.53997	-0.00043193	##########	##########	85,818	0.46095
-0.00053161	-0.66459	-0.00053161	##########	##########	85,572	0.62428

-0.00026598	-0.80896	-0.00035613	##########	##########	18,285	0.77988
0.00018816	0.14909	6.56E-01	##########	##########	23,095	0.53612

0.00082517	NaN	NaN	NaN	NaN	100.73	0.78802
-0.00070433	-0.89096	-0.00089818	##########	##########	101.71	0.80127
-0.00024359	-0.93389	-0.00094145	##########	##########	102.32	0.64181

-0.00041149	NaN	NaN	NaN	NaN	109.77	12,359
0.00048753	NaN	NaN	NaN	NaN	123.32	24,183
0.00069721	NaN	NaN	NaN	NaN	110.69	0.79527

0.0011551	Jan-67	0.0011217	##########	##########	136.58	0.83658
0.001285	19,226	0.0012914	##########	##########	123.02	49,787
0.00092914	16,331	0.0010969	##########	##########	130.28	13,125

Calibrated retention time	Calibrated retention time start	Calibrated retention time finish	Retention time calibration	Match time difference	Match m/z difference	Match q-value
88,682	88,396	89,005	15,086			
86,296	85.84	86,657	7,433			
82,298	82.03	82,611	15,086			
78,199	77,715	78,795	71,326			
73,611	73,316	73.89	15,086			
70,516	70,158	71,039	74,774			
78,238	78,026	78,608	15,086			
74.77	74,446	75,121	73,329			
89,428	88,928	89,928	16,251			
89.57	89.07	90.07	16,153			
104.38	104.12	104.7	0.96355			
104.58	104.14	104.99	4,162			
104.8	104.24	105.3	75,276			
103.74	103.3	105.28	13,625			
104.52	104.19	104.84	7,082			
104.53	104.22	104.81	71,179			
104.52	103.97	105.3	20,194			
104.5	104.11	105.16	65,146			
104.15	103.85	104.58	-11,905	-0.2187	0.00029497	NaN
104.86	104.64	105.06	46,491	-0.0084508	-0.00093103	NaN
104.94	104.7	105.26	6,304	0.074542	0.00030615	NaN
105.27	104.99	105.47	72,397			
135.39	135.12	135.75	19,095			
132.19	132.02	132.34	12,687			
134.08	133.79	134.27	74,366			
128.76	128.37	128.94	-7,775			
100.99	100.72	101.37	-15,894			
101.36	101.13	101.66	-15,771	0.183	-0.0006071	NaN
110.96	110.53	111.36	-15,894			
111.02	110.62	111.24	-15,894			
85,153	84,797	85,467	5,324			
86,045	85,642	86,465	72,776			
88,198	87,942	88,546	11,064			
84,867	84,016	85,445	35,258			

86,894	86,285	87,312	87,342			

100.91	100.66	101.26	19,196			
90,685	90,438	90,985	5,224			
91,882	91,522	92,181	71,776			
95,804	95,551	96,123	13,888			
95,855	95.55	96,152	12,818			
88,706	88,454	88,991	73,008			
100.46	100.21	100.71	52,721			
101.56	101.28	101.91	68,355			
97,518	97,303	97,853	15,387			
93,081	92.79	93,372	86,341			
95,115	94.78	95,383	11,906			
97,608	97,316	97,805	15,681	0.045101	0.00031363	NaN

83,294	82,811	84,379	65,389			
74,634	74,321	75,054	-15,717			
92,495	92,273	92,774	15,908			
81,551	81,135	82,523	40,333			
85,429	85,159	85,746	Jul-71			
94.9	94,616	95,153	72,329			
96,211	95,907	96,559	84,453			
88,911	88.57	89,437	10,799			
93.44	93,001	94,676	16,985			
104.69	104.38	105.09	25,969			
96,344	96,047	96,686	84,784	0.066776	-0.00027052	NaN

96,434	96,099	96,776	15,562			
101.75	101.4	101.93	75,363			

101.92	101.66	102.42	-10,905			
102.87	102.55	103.27	10,635			
106.32	105.95	106.71	63,039			
106.6	106.18	107.26	-43,689			
104.66	104.32	105.01	20,194			
106.06	105.76	106.44	46,915			

58,484	58,195	58,792	74,781			
60.63	60,381	60,985	34,263			

89,573	89,404	89,773	11,064			

90,527	90.11	90,874	32,259			
88,402	88,072	88,666	86,341			

93,264	92,876	93,689	51,308			
93,584	93,163	93,855	49,337			
93,358	92,951	93,838	45,084			

84.35	84,065	84,594	13,861			
86,597	86,306	86,935	15,052			
87,258	86,975	87,622	16.64			

127.03	126.78	127.37	18,882			
92,842	92,689	93,133	-16,152			
127.99	127.68	128.23	19,151			

78,645	78.34	78,979	12,223			
79,931	79,545	80,457	15,308			
79,961	79,545	80,457	15,308			
80,397	80,116	80,734	15,809			

104.01	103.51	104.51	95,334			
91,039	90,539	91,539	-22.62			
90,247	89,747	90,747	-10,808			
93,917	93,654	94,187	64,188			

64,873	64,649	65,066	73,776			
70,036	69.74	70,298	16,277			
71.41	70,984	71.7	79,337			
67,525	67.14	67,866	10,349			
70,505	70,325	70.69	12,767			
67,784	67,514	68,086	12,107			

74,601	74,277	75,196	14,652			
74.91	74,549	75,496	15,146			
74,532	74,252	75.38	12,766			
104.46	104.26	105.03	-19,476			

92,904	92,636	93,236	41,393			
94,746	94,091	95.5	50,272			
94,791	94,313	95,489	49,305	-0.041153	-0.00017331	NaN
94,959	94,602	95,363	54,503	0.12724	0.00019452	NaN
82,757	81,481	83,455	14,552			

89,364	89,119	89,568	14,847			
89,433	89,182	89,851	14,452	0.034115	0.00081033	NaN
82,596	82,258	82.99	15,072	-0.024422	0.00039573	NaN

101.78	101.32	102.04	14,786			
102.39	102.07	102.71	16,433			
102.64	102.25	102.89	17,669			
89,947	89,633	90.33	69,729			
102.68	102.23	102.88	18,364			
102.6	102.23	103.19	18,858			

89,819	89,454	90,189	-61,797			
106.31	106.07	106.72	1,319			
102.66	102.21	103.08	68,448			

70,999	70,781	71,195	15,086			
69,999	69.77	70,217	12,818			
66,729	66,453	66,989	10,349			
67,301	67,076	67,574	28,262			
66,751	66,453	66,934	10,349	-0.27472	-0.00060714	NaN
61,208	61,025	61,419	15,086			
60,065	59,868	60,513	74,781			

82,279	82,057	82,523	11,264			
82.54	82,217	82,961	12,818			
83,176	82,873	83,547	19,343			

61.82	61,491	62,854	15,446			
64,376	63,856	64,536	15,445			

132.31	131.6	133.09	17,792			
138.47	137.36	138.88	64,748			

125.7	125.43	126.36	89,881			
62,572	62,327	62,984	15,754			
110.3	109.5	111.29	-16,286			

79.07	78,797	79,652	5,624			
79,267	78,869	79,828	75,776			
79,353	79,035	79,614	10,877			
79,841	79,541	80,361	16,353			
137.41	136.35	138.66	Aug-79			
79,605	79,349	80,152	11,564			

79,533	79.2	80,362	13,018			
79,571	79,233	80,252	15,146			
117.36	115.3	119.21	-4.41			
78,254	78,052	78.59	71,326			
78,607	78,338	79,434	12,349			
78,795	78,468	79,711	28,264			
79,322	78,967	80,009	15,308			
117.33	115.93	118.52	-1,474			
117.94	116.54	119.54	-7,775			
112.99	111.61	114.57	-16,286			
78,905	78,599	79,657	91,348			
79,142	78,859	79,638	15,809			

65,937	65.78	66,329	11,178			
68,308	68.1	68,534	16,277			
70,805	70,492	71,663	84,783			
69,031	68,797	69,352	12,667			
67,748	67,541	68,047	15,553			
67,992	67,722	68,604	16,165			
67,095	66,778	67,635	14,528			
68,119	67,908	68,427	17,339			

127.38	126.72	128.13	-28,205			
91,871	91,424	94,111	-97,767			
91,754	91,367	93,217	-10,805			
91,648	91,276	92,046	-10,707	-0.045914	-0.00071351	NaN
91.68	91,441	92	-10,484	-0.014114	0.0004307	NaN

95,931	95,438	96,824	14,647			
95,986	95,643	97,325	14,609			
96,007	95.73	96,587	14,849			

131.04	130.73	131.67	19,095			
130.72	130.46	131.1	16,528			
130.23	129.91	130.5	68,524			

77,736	77,388	78.11	14,652			
78,233	78.05	78,437	11,564	0.30605	-0.00075337	NaN
77,812	77,542	78,103	13,018	-0.11486	-0.00038386	NaN

58,848	58,649	59,224	16,752			
57,547	57.25	57,904	75,053			
59.31	58,947	59.67	16,975			

59,312	58,829	59.76	16,975
58,862	58,414	59,503	15,253
58,767	58,553	58,876	83,342
59	58,688	59,348	15,351
59,052	58,547	59,406	15,351
58,935	58,636	59,263	34,263

66,968	66.75	67,261	12,223
67,702	67,352	68,128	28,262
68,789	68,474	69,156	15,308
99,005	98,655	99,685	-78,752
69,009	68,747	69,316	16,109

134.91	134.46	135.69	14,748			
95,223	94,798	95,978	-24,592			
95,257	94,854	95,922	-24,667			
96,836	96,597	97,186	-23,143			
134.77	134.35	135.43	14,277			
132.85	132.62	133.12	12,449			
101.21	100.93	101.61	-19,762			
101.57	101.1	102.43	-19,551			
101.9	101.6	102.28	-19.49			
140.2	139.77	140.72	70,318			
140.24	139.96	140.6	70,318			
139.44	139	140.1	63,746			
139.46	139.14	139.72	63,746			
133.04	132.66	133.48	11,854			
106.04	105.62	106.44	-15,786			
106.01	105.69	106.53	-15,786			
105.47	105.17	105.96	-16.37			
110.64	110.29	111.05	-11,217			
110.65	110.38	110.95	-11,217			
107.67	107.41	108.04	-14,454			
116.08	115.68	118.17	-7,775			
133.51	133.11	133.87	11,971			
131.31	131.05	131.67	10,506			
106.02	105.52	107.39	-15,894			
102.68	102.32	103.11	-19,482			
102.65	102.15	103.15	-19,482			
119.33	119.06	119.62	-31,306			
134.43	134.07	135.03	14,285	-0.2373	2.57E-02	NaN

74,493	74,168	74,998	-80,209

103.13	102.89	103.39	20,062
95,077	94,701	95,594	10,699

106.57	106.13	106.83	0.96355
89,438	89,273	89,673	-11,459
107.2	106.99	107.57	20,194
90,677	90,413	90,969	-10,344
106.41	106.01	106.64	68,448
100.59	100.37	100.88	-15,894

93,802	93.59	94,061	6,398
93,687	93,465	94,031	77,113
90,358	90,157	90,618	45,403
92,529	92,252	92,877	69,571

35,537	35.11	35.89	17,251
33,624	33,368	33,904	10,529

91.62	91,221	92,009	-91,056
90,709	90,255	91,056	-11
90,794	90,466	91,107	-11,525

129.53	129.05	130.29	19,759
134.2	132.87	135.29	10,886
128.26	127.84	128.64	17,564

133.66	133.44	134.27	-29,207
137.09	135.07	140.05	14,078
137.31	136.42	137.73	70,318

Match score	Number of data points	Number of scans	Number of isotopic peaks	PIF	Fraction of total spectrum	Base peak fraction
	51	13	7	0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
	54	7	12	0	0	0
	74	11	12	0	0	0
	79	13	13	0	0	0
				0	0	0
	89	9	14	0	0	0
	49	8	10	0	0	0
				0	0	0
	91	14	13	0	0	0
76,533	72	12	13	NaN	NaN	NaN
87,352	152	21	11	NaN	NaN	NaN
87,352	75	13	11	NaN	NaN	NaN
				0	0	0
	138	22	12	0	0	0
	96	21	6	0	0	0
				0	0	0
	42	7	10	0	0	0
	338	43	11	0	0	0
63,883	203	35	9	NaN	NaN	NaN
	337	55	9	0	0	0
	171	41	7	0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0

	102	14	16	0	0	0

	128	23	9	0	0	0
	40	7	9	0	0	0
	40	8	8	0	0	0
	248	38	9	0	0	0
				0	0	0
				0	0	0
	33	6	9	0	0	0
	49	8	10	0	0	0
	228	36	9	0	0	0
	44	7	9	0	0	0
	61	8	10	0	0	0
101.23	153	33	8	NaN	NaN	NaN

	633	102	9	0	0	0
	252	48	8	0	0	0
	135	33	6	0	0	0
	539	91	9	0	0	0
	167	39	6	0	0	0
	72	17	6	0	0	0
	61	16	7	0	0	0
	218	57	6	0	0	0
	594	111	9	0	0	0
	221	48	7	0	0	0
48,532	25	8	5	NaN	NaN	NaN

	36	8	6	0	0	0
	21	6	5	0	0	0

				0	0	0
	45	9	7	0	0	0
	240	32	12	0	0	0
	109	14	13	0	0	0
	76	11	11	0	0	0
	297	33	12	0	0	0

	158	32	7	0	0	0
	103	22	7	0	0	0

				0	0	0

				0	0	0
	45	7	9	0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
	74	16	7	0	0	0
	39	14	5	0	0	0
	149	34	8	0	0	0
				0	0	0
	190	32	10	0	0	0
				0	0	0
	124	13	15	0	0	0
	114	13	13	0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
	73	15	7	0	0	0
				0	0	0
	120	28	7	0	0	0
	88	33	6	0	0	0
				0	0	0
				0	0	0
	208	31	10	0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
	62	11	8	0	0	0
	170	23	11	0	0	0
41,621	115	15	10	NaN	NaN	NaN
41,621	127	25	9	NaN	NaN	NaN
	194	28	10	0	0	0

	38	7	7	0	0	0
43.69	49	8	10	NaN	NaN	NaN
44,246	164	38	7	NaN	NaN	NaN
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
	488	58	12	0	0	0
	138	25	8	0	0	0
	44	9	8	0	0	0
	42	12	6	0	0	0
	24	6	6	0	0	0
72,316	32	10	7	NaN	NaN	NaN
	163	24	9	0	0	0
	160	30	11	0	0	0
	104	21	9	0	0	0
	42	10	8	0	0	0
	50	8	10	0	0	0
	497	80	15	0	0	0
				0	0	0
	701	98	10	0	0	0
	157	20	9	0	0	0
	58	14	8	0	0	0
	179	40	6	0	0	0
	173	77	4	0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0

				0	0	0
				0	0	0
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				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0
				0	0	0

				0	0	0
				0	0	0
	67	16	11	0	0	0
	56	7	12	0	0	0
				0	0	0
	239	30	12	0	0	0
	346	40	12	0	0	0
				0	0	0

	136	20	10	0	0	0
	301	34	14	0	0	0
	196	26	16	0	0	0
47,622	217	25	13	NaN	NaN	NaN
47,622	219	30	12	NaN	NaN	NaN

				0	0	0
				0	0	0
				0	0	0

				0	0	0
				0	0	0
				0	0	0

	66	11	10	0	0	0
43,115	123	24	8	NaN	NaN	NaN
43,115	45	8	9	NaN	NaN	NaN

				0	0	0
	287	34	12	0	0	0
	161	32	8	0	0	0

				0	0	0
				0	0	0
				0	0	0
	79	25	5	0	0	0
				0	0	0
				0	0	0

				0	0	0
	86	10	13	0	0	0
	61	10	9	0	0	0
				0	0	0
	235	30	12	0	0	0

	130	15	14	0	0	0
	752	79	15	0	0	0
	709	71	15	0	0	0
	190	39	8	0	0	0
	130	13	14	0	0	0
				0	0	0
	282	45	10	0	0	0
	865	89	14	0	0	0
	211	45	7	0	0	0
	135	15	13	0	0	0
				0	0	0
	109	15	13	0	0	0
	41	7	9	0	0	0
				0	0	0
	442	54	12	0	0	0
	170	55	6	0	0	0
	421	52	11	0	0	0
	428	50	11	0	0	0
				0	0	0
				0	0	0
	834	147	10	0	0	0
	48	9	8	0	0	0
	214	42	8	0	0	0
	1043	126	15	0	0	0
	391	55	10	0	0	0
				0	0	0
	194	38	8	0	0	0
128.33	556	63	12	NaN	NaN	NaN

				0	0	0

			0	0	0
342	59	9	0	0	0
			0	0	0
88	27	5	0	0	0
			0	0	0
81	21	7	0	0	0
154	42	7	0	0	0
132	34	5	0	0	0
172	31	9	0	0	0
147	37	7	0	0	0
152	30	7	0	0	0
255	41	9	0	0	0
258	50	7	0	0	0
112	37	6	0	0	0
			0	0	0
92	10	13	0	0	0
76	10	11	0	0	0
			0	0	0
			0	0	0
			0	0	0
93	12	15	0	0	0
510	76	10	0	0	0
72	17	7	0	0	0

PEP	MS/MS Count	MS/MS Scan Number	Score	Delta score	Combinatorics	Ratio H/L
0.0024998	1	8758	50,873	36,926	10	0.32364
0.00066166	2	9811	63,937	45,532	10	0.39827
0.011114	1	7485	56.48	27,381	5	0.189
0.015999	1	8380	54,047	32,371	5	0.27281
0.013065	1	5937	41,615	26,992	5	0.25025
0.0012876	1	6660	53,625	31,949	5	0.14797
0.00037934	1	6747	55,302	26,579	10	0.2281
0.0045661	1	7721	42,209	20,086	10	0.37424
0.02807	1	10887	45,433	82,528	1	
0.014498	1	7441	57,149	22.38	1	
0.0025375	3	15318	67,396	61,087	2	0.54438
0.0010496	2	15421	76,533	55,254	2	0.49769
9.88E-01	1	15234	87,352	62,871	2	0.49671
0.0093801	1	17999	56.48	28,389	2	0.34323
0.0030875	1	15853	58,796	39,861	2	0.49439
2.20E-11	1	15878	118.67	103.82	2	11,087
0.011985	1	14078	54.15	28,274	2	0.16628
1.39E-03	1	14879	99,409	80,404	2	0.46245
NaN	0		NaN	NaN	0	0.55402
NaN	0		NaN	NaN	0	12,755
NaN	0		NaN	NaN	0	0.57747
0.022911	1	16018	47,603	15.25	4	0.51852
0.0096279	1	16802	83.31	83.31	5	0.62157
0.038931	1	18314	65,207	45,627	5	0.53203
0.02059	1	20557	96,391	63,022	5	0.43102
0.001369	1	12202	95,444	95,444	5	0.63294
0.044014	1	8067	63,883	44,861	5	0.59556
NaN	0		NaN	NaN	0	0.43797
0.0004661	2	8847	90.78	72.2	10	0.51119
0.019791	1	8859	43,794	43,794	10	0.47973
2.37E-03	1	9284	56,099	33,977	9	0.1246
5.44E-03	1	10051	51,264	31,511	9	0.081331
0.00031051	1	7891	42,301	20,735	9	0.12181
0.00078287	1	10748	40,129	24,923	9	0.18889

0.013428	1	8952	45,842	29,153	9	NaN

0.00011047	1	10305	114.99	71,032	2	0.27122
0.021028	1	10475	90,755	46,157	2	0.41465
2.74E-02	1	11305	128.79	86,731	2	0.19931
0.0087381	1	5589	98,077	44,682	2	0.42649
0.00059842	1	12030	103.99	70,796	2	0.12084
0.0099793	1	5466	94,973	53,491	2	0.12082
1.62E-01	1	13652	131.54	84,649	2	0.38566
4.09E-01	1	13835	125.51	65,422	2	0.35571
0.005735	1	5602	101.23	78	2	0.62417
7.66E-09	1	10295	154.48	111.1	2	0.27884
6.83E-03	2	10693	139.74	84,787	2	0.47856
NaN	0		NaN	NaN	0	0.21525

0.0027448	3	5000	113.69	81,986	3	0.34725
0.0027173	1	5304	99,991	75,481	3	0.34253
0.022825	1	5646	64,313	50,913	3	0.74067
0.0024174	2	5047	112.42	75,976	3	0.31066
0.013363	1	5352	69,314	42,956	3	0.29144
0.012442	1	11571	70,438	43,549	3	0.62239
0.017913	1	12775	48,532	19,229	3	0.48128
0.0060641	1	5110	79,886	54,922	3	0.259
0.0034134	3	5036	91,307	61,303	3	0.29809
0.0036161	2	5500	86,803	58,598	3	0.2857
NaN	0		NaN	NaN	0	0.46249

0.0057169	1	14238	65,224	65,947	1	0.70699
0.013013	1	14612	54,066	15,763	1	0.3297

0.026132	1	14173	64,346	42,864	2	0.17971
0.00017333	1	14967	91,414	66,183	2	0.24866
0.0012865	1	15524	72,793	53.63	2	0.11958
0.0024762	1	17094	66,777	66,777	2	0.19281
0.0046037	1	14113	60,938	60,938	2	0.39613
0.016277	1	14290	50,722	31,033	2	0.4492

0.0066911	1	4389	47,039	15,317	2	0.37845
0.023679	1	5542	40,767	24,827	2	0.47176

0.0036427	1	8183	53,603	35,982	4	NaN

0.0037112	1	12115	53,444	27,084	4	0.20669
0.0087212	1	9313	40,086	22,324	4	0.32137
0.0053796	1	13274	55,588	34,365	3	0.20466
0.005144	1	13684	55,846	32.21	3	0.28266
0.0092671	1	12933	51,323	30,538	3	0.41583
0.033384	1	7994	72,321	24,037	2	31,103
0.018663	1	8978	62,166	15.76	2	12,633
0.0037806	1	7516	80,632	50.02	2	0.33563
0.01242	1	14018	46,099	26-May	2	0.43173
0.025403	1	7613	44,045	15,496	2	NaN
0.0075169	1	14614	49,326	27,441	2	0.4862
0.0062369	1	7138	42,863	25,104	4	0.2213
1.63E-04	1	10094	80,664	58.9	4	NaN
3.58E-04	1	10118	76,807	57,114	4	0.26256
9.41E-01	1	6563	66,845	42.34	4	0.2477
0.039708	1	12403	46,145	20,121	1	
0.03181	1	17663	46,701	20,706	1	
0.03593	1	15186	42,095	26,854	1	
0.005205	1	10972	42,059	31,197	2	0.37748
0.023872	1	5568	50,831	30,601	3	0.41778
0.018293	1	6974	40,602	27,181	3	0.5327
0.0056349	2	6932	48,711	27,745	3	0.2539
0.018465	1	7406	54,004	34,831	3	0.3153
0.0010818	1	6609	76,586	54,589	3	0.3185
0.0024738	3	5136	56,121	36,823	3	0.39543
0.0055099	1	7239	56,205	11,358	3	NaN
0.020928	1	6553	40,242	88,942	3	NaN
0.011604	1	7470	47,712	97,173	3	NaN
0.0041436	1	9143	58,885	23,208	3	10,111
0.014343	1	11748	44,252	11,745	12	0.74268
0.0099871	1	12753	41,621	41,621	12	0.64113
NaN	0		NaN	NaN	0	0.29793
NaN	0		NaN	NaN	0	0.83982
0.0093154	1	9040	44,246	15,175	18	0.26957

0.035826	1	9568	43.69	19,606	18	0.60977
NaN	0		NaN	NaN	0	0.26093
NaN	0		NaN	NaN	0	10,618

0.0055019	1	12566	62,088	Dec-79	2	60,165
0.011075	1	11100	54,343	26,289	2	NaN
0.0094476	1	10950	56,205	22.94	2	14,999
0.013879	1	5804	51,135	13,958	2	11,805
0.013592	1	12656	51,463	18,198	2	7,004
0.028261	1	11531	43,798	68,534	2	NaN

0.00034151	1	6543	86,557	67,693	4	0.14147
0.004696	1	15133	50,255	26,363	4	NaN
0.0096204	1	6510	50,323	22,645	4	0.35956

0.011481	1	5455	44,468	27,256	1	0.42219
0.011523	1	6599	64,749	50,445	1	0.449
0.0026626	1	7257	55,575	38.65	1	0.36541
0.0058585	1	7079	72,316	72,316	1	0.39553
NaN	0		NaN	NaN	0	0.44217
0.004046	1	3914	43.05	33.25	1	0.54788
0.0036301	1	4652	43,861	35,553	1	0.41072

0.0040337	1	6817	41,446	19,745	1	0.22528
0.0010549	1	9182	50,178	14,686	1	0.093787
0.0023183	1	10573	45,363	26,499	1	0.34137

0.0070692	1	4275	64,224	81,371	2	0.21532
0.0026817	1	6598	75,416	25,933	8	0.35198

0.032575	1	14601	47,537	20,404	3	0.40559
0.040478	1	24658	43,861	43,861	3	0.41982

0.010757	2	8200	51,949	37.48	2	0.84105
0.022437	1	4435	41,427	18,865	2	0.75432
0.041501	1	9477	45,022	20,768	2	0.34812

0.0182	1	7944	61,815	21-Mar	2	NaN
0.011692	1	8473	67,214	18,266	2	NaN
0.011692	1	8462	67,214	11,235	2	0.086717
0.041234	1	6118	51,998	16,961	2	NaN
0.0052422	1	10100	76,927	32,734	2	0.096784
0.0059889	1	6288	75,416	26,118	2	0.01201

0.0081995	1	8492	70,942	25,289	2	0.013381
0.024685	1	7463	58,274	24,187	2	0.018572
0.0017384	1	11862	90,827	56,827	2	0.21213
0.038559	1	8382	53,013	68,068	2	0.044513
0.018769	1	9720	61,344	10,335	2	NaN
0.011692	1	9542	67,214	24,897	2	0.018412
0.0059149	1	9958	75,566	35,693	2	NaN
0.016684	1	9018	63,073	29,024	2	0.0723
0.011855	2	10057	67.08	39,166	2	0.11481
0.0076293	1	10005	72,096	31.62	2	0.047213
0.0068534	1	7195	73,666	32,283	2	0.0062677
0.031417	1	6332	55,721	20,953	2	0.024096

0.024113	1	5678	41,703	21,943	5	NaN
0.0081741	1	6673	50,891	21,615	5	NaN
0.00022932	2	9121	80,314	49,982	5	0.43213
0.00015138	1	6309	89,043	56.69	5	0.68121
0.0052321	1	5346	55,844	30,942	5	0.24467
0.0011627	3	6431	60,761	37,535	5	0.61086
0.00029277	2	5360	75,703	50,748	5	0.59265
0.010752	1	4126	48,961	25,563	5	0.1266

0.0044681	1	12023	49,066	20-Sep	12	0.69795
0.010474	1	16835	43,042	13,943	12	0.42738
0.0050612	1	16316	47,622	13,729	12	0.4548
NaN	0		NaN	NaN	0	0.96313
NaN	0		NaN	NaN	0	0.65978

6.44E-02	1	11010	63,316	38,686	5	0.29767
3.57E-04	2	13917	76,109	52,094	5	0.18027
0.00044264	1	11006	49,912	30,606	5	0.27171

0.027894	1	16020	40,187	12,661	4	0.083061
0.023762	1	17589	42,257	17,835	4	NaN
0.0047553	1	19634	56,872	35,513	4	0.052186

0.014065	1	7899	43,115	65,234	6	0.5391
NaN	0		NaN	NaN	0	29,714
NaN	0		NaN	NaN	0	12,702

0.0090328	1	4505	84,436	56,117	3	NaN
0.00050631	1	4212	54,004	54,004	3	0.66971
0.00014728	2	4879	70,316	41,689	3	0.60681

0.017538	1	4864	44,391	99,957	3	0.78079
0.0061945	1	4148	52,172	23,545	3	0.42382
0.020574	1	4797	42,708	20,468	3	0.49494
0.00013482	2	5616	71,376	52,796	3	0.84281
0.0070897	1	5597	50,376	31,796	3	0.45843
0.029933	1	5209	71,929	46,772	3	0.38952

0.026547	1	5129	44,029	24,268	3	0.15335
0.000655	1	7126	62,617	41,939	3	0.5177
0.016141	1	7635	42,639	22,609	3	0.35349
0.02124	1	7642	45,844	28,419	3	NaN
0.00062315	2	4701	56,748	39,862	3	0.63442

4.37E-16	3	21272	128.33	90,339	7	0.62808
0.00048003	1	8209	84,249	66,015	7	0.74161
2.01E-04	1	8303	107.75	90,506	7	0.63761
0.00048098	1	8283	84,208	84,208	7	0.58945
0.00045259	3	20748	85,423	46,147	7	0.55036
0.0034012	1	19553	56,719	35.15	7	NaN
0.0016868	2	8222	69,361	69,361	7	0.75594
6.03E-16	2	8373	125.73	108.49	7	0.56281
0.00039938	1	8323	87,228	65,659	7	0.50359
3.58E-03	3	21145	105.91	55,867	7	0.6626
0.0034179	1	21208	53,327	24.25	7	0.28191
9.33E-10	3	24871	122.6	93,847	7	0.66951
0.00050727	1	24926	69,612	46,275	7	0.80047
3.01E-07	2	21071	127.49	89,834	7	0.42587
0.00026142	3	9741	90,581	70,893	7	0.66297
0.0043172	1	9764	47,942	22,119	7	0.52528
0.00061323	4	8707	78,552	57,309	7	0.62127
0.00044057	5	8523	85,937	64,364	7	0.62092
0.0043557	2	8539	50,226	29.26	7	0.35126
0.00029721	2	8791	85,177	60,509	7	0.18401
4.64E-06	9	9905	115.56	89,013	7	0.50312
9.48E-01	1	21020	94,632	76,316	7	0.49387
0.00046045	1	16782	85,087	70,065	7	0.39694
1.12E-04	5	8495	111.3	72,495	7	0.50955
0.00020613	4	8376	91,926	74,207	7	0.50597
0.0076101	1	8395	58,864	30,698	7	
2.29E-01	1	8671	97,271	82,391	7	0.35501
NaN	0		NaN	NaN	0	0.69868

0.020133	1	5593	41,257	18,627	6	0.25871

0.016457	1	8863	43,091	25,076	6	NaN
0.0021378	1	5542	50,358	21,809	6	0.46976

0.030294	1	15787	88,283	41,486	3	0.17475
0.021733	2	7087	90,385	63,123	3	0.27006
0.035888	1	14615	87,676	60,413	3	0.24707
0.0061697	1	13851	100.77	84,926	3	0.8397
0.0022498	1	6811	104.88	89,939	3	0.30248
0.0065927	1	8043	69,581	69,581	3	0.27591

8.66E-01	1	5983	106.31	85,721	3	0.96199
1.87E-01	1	5785	113.86	97,118	3	0.26731
0.0017519	1	5830	89,913	69,677	3	0.38826
0.0023236	2	5682	85,046	67,418	3	0.50712

0.011627	1	1240	42,629	30,571	4	0.58787
0.0021129	2	1671	58,274	47,348	4	0.48042

0.00011073	1	17054	63,925	39,718	3	0.47343
4.11E-04	2	16830	82,942	82,942	3	NaN
0.0030549	1	15804	47.05	27,121	3	0.61585

1.02E-08	2	18995	75,416	53,565	2	0.1746
1.27E-08	1	22592	73,603	49.58	2	0.30054
4.02E-02	2	18880	57,629	41,819	2	0.2115

0.0025483	1	13644	47,548	16.41	4	0.5026
0.0068367	1	20960	42,314	13,982	4	0.32278
0.0070169	1	20592	42,095	26,493	4	0.57424

Ratio H/L normalized	Ratio H/L shift	Intensity	Intensity L	Intensity H	Reverse	Potential contaminant
0.57984	0	119240	84688	34548		
0.73098	0	88880	65772	23108		
0.35155	0	247460	209250	38214		
0.53892	0	229620	176360	53258		
0.51506	0	164080	137950	26132		
0.28614	0	192690	172720	19962		
0.44277	0	84864	78384	6480.6		
0.25798	0	90922	75426	15496		
10,247	0	313690	179890	133790		
0.86522	0	578820	331790	247040		
12,257	0	756200	447440	308760		
0.65471	0	401910	277420	124490		
0.90773	0	4876900	2849900	2027100		
21,426	0	813590	481360	332230		
0.45693	0	129650	112250	17405		
0.97177	0	707250	476140	231110		
0.90304	0	339740	185380	154350		
1,655	0	114740	45031	69710		
13,952	0	156460	80831	75629		
10,078	0	359240	234560	124680		
11,573	0	242390	145890	96503		
0.93693	0	80759	49713	31047		
0.87588	0	137250	112380	24868		
13,616	0	599260	339050	260210		
13,431	0	273570	164130	109440		
0.49196	0	90726	55894	34831		
11,528	0	132120	81066	51050		
10,819	0	65880	44312	21569		
0.21051	0	289450	271610	17837		
0.15605	0	231540	220620	10918		
0.18851	0	101150	97603	3548.5		
0.38686	0	439390	388300	51092		

NaN	0	948710	618890	329820

0.50367	0	255820	208970	46851
0.68522	0	120480	85761	34715
0.36672	0	195370	160860	34513
0.57834	0	215610	156630	58975
0.29314	0	165720	146660	19056
0.11562	0	61337	54770	6566.9
0.78028	0	309790	261000	48791
0.67052	0	567380	403460	163920
1,057	0	122240	78061	44174
0.76923	0	259970	200520	59452
10,578	0	255800	185350	70457
0.37952	0	90624	68113	22511

0.68932	0	1099700	782150	317510
0.32049	0	288330	210060	78265
0.85198	0	92724	53318	39407
0.47149	0	1000500	723220	277270
0.38078	0	175680	126400	49279
12,283	0	226430	135120	91304
0.92394	0	245390	165200	80189
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0.67518	0	313510	226040	87470
0.9039	0	216730	144730	72005

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0.71817	0	101870	78338	23527

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0.29647	0	412880	368280	44599
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12,681	0	157470	77181	80285
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0.4312	0	397460	267310	130150

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14,941	0	706560	347160	359400
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0.92615	0	102710	69948	32766
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0.9251	0	466950	286540	180400
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