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*Published in:*  
Fly

*DOI:*  
[10.1080/19336934.2019.1705118](https://doi.org/10.1080/19336934.2019.1705118)

*Publication date:*  
2019

*Document Version*  
Peer reviewed version

[Link to publication in Discovery Research Portal](#)

#### *Citation for published version (APA):*

Beati, H., Langlands, A., ten Have, S., & Müller, H. -A. J. (2019). SILAC-based quantitative proteomic analysis of *Drosophila* gastrula stage embryos mutant for fibroblast growth factor signalling. *Fly*.  
<https://doi.org/10.1080/19336934.2019.1705118>

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

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**keywords:** *Drosophila*, SILAC, Fibroblast Growth Factor, cell signaling, proteomics

## **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<sup>1</sup>. 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 <sup>2</sup>. SILAC labeling has also proven successful for global quantitative proteomic comparisons of entire organisms including mammalian model systems<sup>3</sup>. Since then various multicellular model organisms were successfully labeled with stable, non-radioactive isotopes (SILAC or <sup>15</sup>N labeling) including the plant *Arabidopsis thaliana*, the nematode *Caenorhabditis elegans*, the insect *Drosophila melanogaster* and the mammal *Mus musculus*<sup>4-13</sup>.

*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 <sup>15</sup>N labeling of *Drosophila* are based on feeding flies with yeast that has been labeled with stable isotopes<sup>4, 9, 11</sup>. Stable isotope labeling in flies has been used to determine sex-specific differences in the proteome of somatic cells<sup>9</sup>, differences in the proteome during ageing<sup>14</sup>, and differences in proteomes between adults, larvae and pupae<sup>15, 16</sup>. Recently, a quantitative proteomic study investigated the developmental profile of the *Drosophila*

proteome throughout the life cycle using label-free approaches<sup>15</sup>. 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)<sup>8, 17, 18</sup>. 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<sup>19</sup>. 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<sup>20-26</sup>. 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<sup>27</sup>. 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<sup>27, 28</sup>.

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 detected 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<sup>29</sup>. 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<sup>29, 30</sup>. 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<sup>AJ</sup>* allele and a stock harboring a transgene with the *halo* genomic locus (*p[halo<sup>+</sup>]*) were gifts of M.A. Welte (Univ. of Rochester, U.S.A.)<sup>31, 32</sup>. We used a chromosome harboring transposase  $\Delta$ 2,3 under the control of a *hsp70* promoter to mobilize the *p[halo<sup>+</sup>]* transposon insertion in the genome and isolated insertions on the autosomal balancer chromosomes TM3, TM6 and CyO. The loss-of-function *htf<sup>AB42</sup>* allele was maintained over a TM6B, *Hu*, *Tb*, *e*, *p[halo<sup>+</sup>]* balancer chromosome and crossed into a homozygous *halo<sup>AJ</sup>* 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  $\mu$ l of heavy lysine (Lys-8; stock: 30 mg/ml) (L-lysine: 2HCl, U-<sup>13</sup>C<sub>6</sub>, 99%; U-<sup>15</sup>N<sub>2</sub>, 99%, Cambridge Isotope Laboratories, Inc.). The culture was incubated at 30°C for 24 hours. 5  $\mu$ l 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<sub>2</sub>O 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*<sup>9</sup>. 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<sup>33</sup>. The labeling efficiency 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<sub>2</sub>O 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 % trichloroacetic 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, cComplete™, 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<sub>4</sub>HCO<sub>3</sub> : 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<sub>4</sub>CO<sub>3</sub> 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<sub>4</sub>HCO<sub>3</sub> : 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<sub>2</sub>PO<sub>4</sub>, 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<sub>2</sub>PO<sub>4</sub>, 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<sub>2</sub> binding

The unbound fraction of the SCX chromatography was subjected to phosphopeptide enrichment using affinity binding to TiO<sub>2</sub> beads. The TiO<sub>2</sub> 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<sub>2</sub> 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<sub>2</sub> beads with 400 mM NH<sub>4</sub>OH, 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<sup>34</sup> version 1.5.2.8 and searched against the Uniprot *Drosophila* January 2016 database. The modifications used for L-lysine quantitations were: Lys-0: <sup>12</sup>C<sub>6</sub>, 99%; <sup>14</sup>N<sub>2</sub>, 99% (MW: 182.65); Lys-8: <sup>13</sup>C<sub>6</sub>, 99%; <sup>15</sup>N<sub>2</sub>, 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<sup>35</sup> and Microsoft Excel. Protein network analyses of down- and upregulated proteins were conducted with STRING version 10.5 (<https://string-db.org/>)<sup>36</sup>. 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<sup>9, 11</sup>. 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<sup>37, 38</sup>. 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<sup>20, 28</sup>. Embryos heterozygously mutant for *htl* are viable, but homozygous *htl* mutant embryos exhibit severe mesoderm spreading defects and die during late embryogenesis<sup>21-23</sup>. 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<sup>30,32</sup>. 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<sup>+</sup>]*<sup>31</sup>. We linked the *halo* rescue transgene *p[halo<sup>+</sup>]* 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<sup>+</sup>]* 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<sup>AJ</sup> ; htl<sup>AB42</sup>* / TM6 *p[halo<sup>+</sup>]* 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<sup>39</sup> (Fig. 2A',B'). We have chosen this developmental stage for the sampling, because we were interested to identify protein changes that are involved in Htl-dependent mesoderm spreading<sup>27</sup>. 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<sup>AJ</sup>* homozygous mutant embryos with Lys-8 as control sample for comparison with *halo<sup>AJ</sup> ; htl<sup>AB42</sup>* heterozygous embryos. Additionally, we compared Lys-8 labeled *halo<sup>AJ</sup>* embryos with Lys-0 unlabeled *halo<sup>AJ</sup>* 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<sup>AJ</sup>* 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<sup>AJ</sup>* 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<sup>AJ</sup>*

; *htl*<sup>+</sup> stock and Lys-0 labeled homozygous *halo*<sup>AJ</sup>; *htl*<sup>AB42</sup> 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*<sup>AJ</sup> 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*<sup>AB42</sup> 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<sup>35</sup>. 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<sup>AB42</sup>* 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<sup>36</sup>. 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<sup>AB42</sup>* mutant embryos (Table 1). To a smaller extent we detected downregulation of some metabolic and cytoskeletal components in *htl<sup>AB42</sup>* embryos. In contrast to the downregulated proteins, the largest network detected to be upregulated in *htl<sup>AB42</sup>* 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<sub>2</sub> 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<sub>2</sub> 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<sub>2</sub> enriched fractions (Table 4). Among the 12 phosphopeptides found in all three bioreplicates, 9 phosphopeptides exhibited log<sub>2</sub> 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<sup>40-42</sup>. One protein, ADF/cofilin encoded by the *twinstar (tsr)* gene, is a well characterized regulator of the actin cytoskeleton in cell migration<sup>43</sup>. 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<sup>9, 11, 12</sup>. 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<sup>44</sup>. 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<sup>16</sup>. 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 quantitation 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<sup>9, 11</sup>. 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<sup>29</sup>. 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<sup>32</sup>. The establishment of balancers containing the transgenic *p[halo<sup>+</sup>]* 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)*<sup>45</sup>. Msk was previously shown to function in RTK signaling, including EGF signaling and FGF signaling<sup>45</sup>, and found to mediate the nuclear transport of activated ERK in the EGF receptor pathway<sup>46</sup>. 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<sup>45, 47, 48</sup>.

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<sup>28</sup>. 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<sup>49</sup>. 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<sup>50</sup>. 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<sup>51, 52</sup>.

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)<sup>25, 48, 53</sup>. 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<sup>25, 48</sup>. We previously found that Pbl acts downstream of Htl, but the mechanism of this regulation by Htl is not understood<sup>25</sup>. 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<sub>2</sub> 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<sub>2</sub> or Ti-IMAC<sup>54, 55</sup>. Alternatively, large-scale quantification of phosphorylated peptides can be also combined by the spike-in SILAC method<sup>56, 57</sup>. 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<sup>58</sup>. 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<sup>59</sup>. 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<sup>60</sup>, expression of phosphosite mutant variants or tissue-specific protein knock-down<sup>61</sup>.

**Acknowledgements:** We thank Michael Welte (Univ. Rochester, U.S.A) for the gift of the *halo* fly stocks and insightful discussions. We thank Angus Lamond (University of Dundee, U.K.) and Matthias Trost (University of Newcastle, U.K.) for support and discussions throughout this study. We thank Ryan Webster (University of Dundee, U.K.) for expert technical assistance, Kelly Hodge for assistance with LC-MS/MS, Elham Gheisari for help with preparing figures and Katja Kapp for discussions and critical comments on the manuscript. We thank two anonymous reviewers for their excellent comments and suggestions that helped to improve the manuscript. Stocks obtained from the Bloomington Drosophila Stock Center (NIH P40OD018537) were used in this study. This study was funded by an MRC project grant (KO18531/1) to HAJM and the collaborative research centre PhosMOrg funded by the University of Kassel. HB obtained a University of Kassel stipend 'future programme leader award'.

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## **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<sub>2</sub> chromatography. The SCX fractions, TiO<sub>2</sub>-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<sup>AJ/-</sup>* / Lys-0 *halo<sup>AJ/-</sup>* comparison are shown after SDS-PAGE and Coomassie staining. Red lines indicate separation of the sample lines for further preparation. (D) Rearing *halo<sup>AJ</sup>* 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<sup>1118</sup> ; halo<sup>AJ/halo<sup>AJ</sup></sup>* ; *htl<sup>AB42</sup>,e/Tm6,e,Hu,Tb, p[halo<sup>+</sup>]*. 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<sup>AJ</sup>* develop an opaque ring in cellular blastoderm stages due to defect in clearing of lipid droplets. (**A**) The *halo<sup>AJ</sup>* mutant phenotype is fully rescued by the TM6 *p[halo<sup>+</sup>]* balancer chromosome. *htl<sup>AB42</sup>* embryos were therefore identified by the *halo<sup>AJ</sup>* 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<sup>AB42</sup>* 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 FALGQQGVGVILCIGETLEEK 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<sup>AJ</sup>* with Lys-0 unlabeled *halo<sup>AJ</sup>* 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<sup>AJ</sup>* 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<sup>AJ</sup>* 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 I(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<sup>AB42</sup>* 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<sup>AB42</sup>* 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**

<b>Downregulated proteins</b>	<b>T-Test Difference</b>
elf2B-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

<b>Upregulated proteins</b>	<b>T-Test Difference</b>
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
<sup>1</sup> QISIGIY*ELLK	- 5.13	1.40	Garz, CG8487	-3.50**	0.09
<sup>1</sup> APATP....PVDS*SGSPASPKK	- 2.90	0.45	TppII, CG3991	0.06	1.04
<sup>1</sup> DVDFGDS*DNENEPDAYLARLK	-2.55	0.45	Ssrp1, CG4817	- 1.25	0.27
<sup>1</sup> ASAFQFS*DDEEEVK	- 2.06	0.87	eIF3c, CG4954	- 0.71	0.61
<sup>2</sup> ASAFQFS*DDEEEVK	- 1.61	1.24	eIF3c, CG4954	- 0.71	0.61
<sup>3</sup> VT*ILWMGGSGSIVGKSVLL	- 1.14	0.14	Spoon, CG3249	- 0.16	0.89
<sup>3</sup> AS*GTVSDVCK	- 1.13	0.34	Tsr, CG4254	- 0.14	0.91
<sup>1</sup> NAGGVGVGVGEKS*PDLK	- 1.12	0.18	Amun, CG2446	- 0.28	0.82
<sup>1</sup> RKKPEDPSSEAEALCS*PAK	- 0.88	0.33	NASP, CG8223	0.12	1.09
<sup>2</sup> SAEAEAIVTTTADVSS*PSK	- 0.80	0.21	NASP, CG8223	0.12	1.09
<sup>3</sup> SAEAEAIVTTTADVSS*PSK	- 0.80	0.21	NASP, CG8223	0.12	1.09
<sup>1</sup> ALGGIVLTAS*HNPAGGPENDFGIK	1.10	1.75	Pgm1, CG5165	0.07	1.05

Phosphopeptides that were detected in all three SCX-enriched samples<sup>1</sup> or in all three TiO<sub>2</sub>-enriched samples<sup>2</sup> or detected in all three unenriched bioreplicates<sup>3</sup>. 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](http://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 APATPQAATSVTNPAAGDGISVQNDPPVDS\*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.

*halo*<sup>-/-</sup>; *htl*<sup>-/+</sup> TM6 p[*halo*+]

**A**

*halo*<sup>-/-</sup>; *htl*<sup>-/-</sup>

t = 0

**A'**

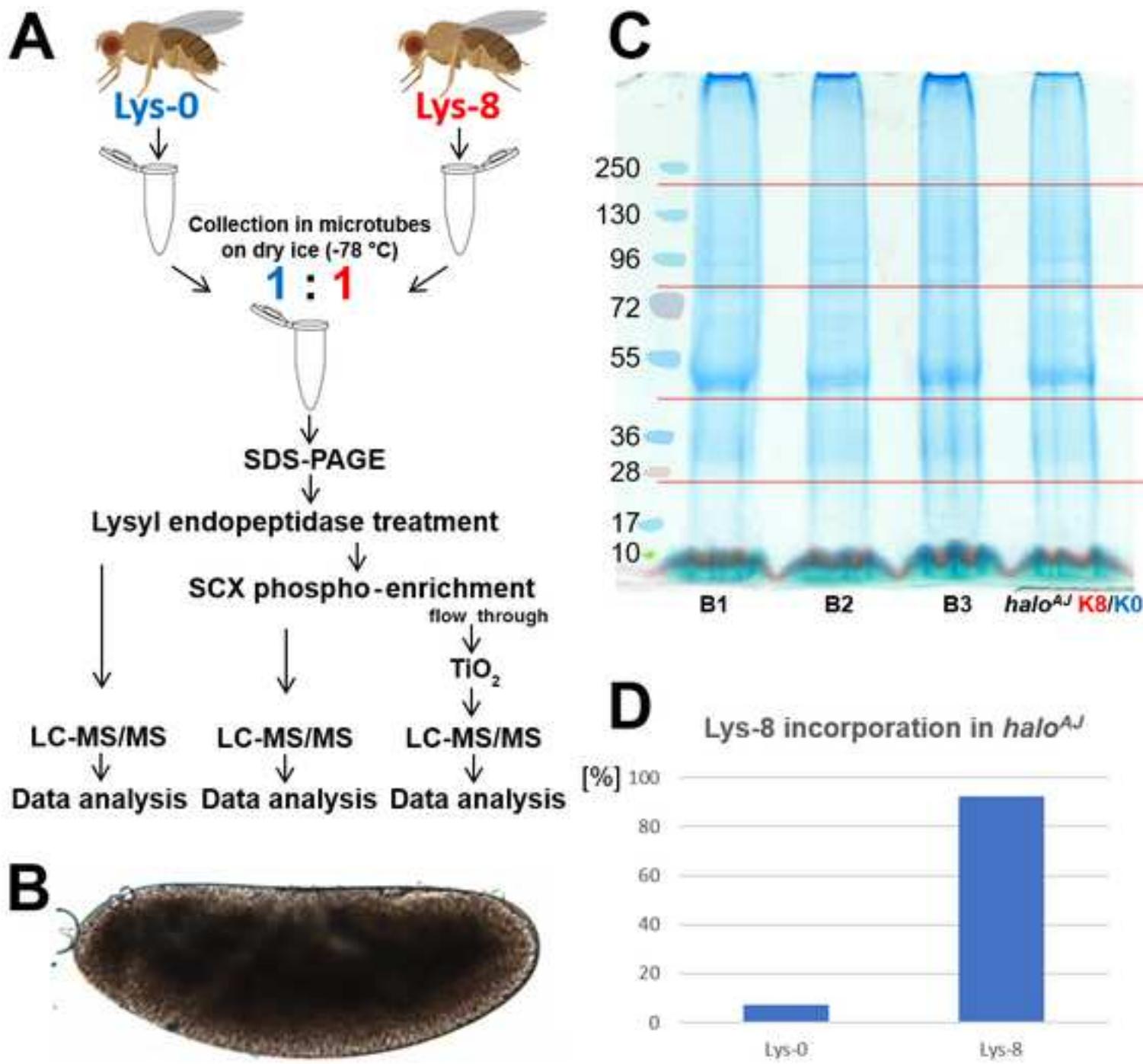
+45 minutes

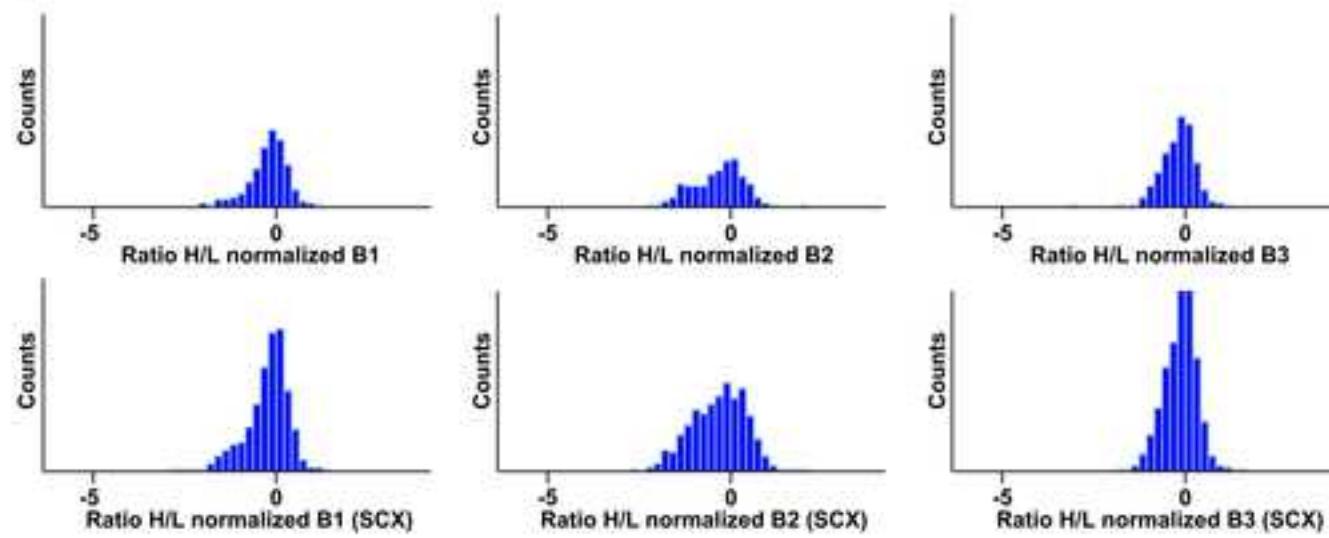
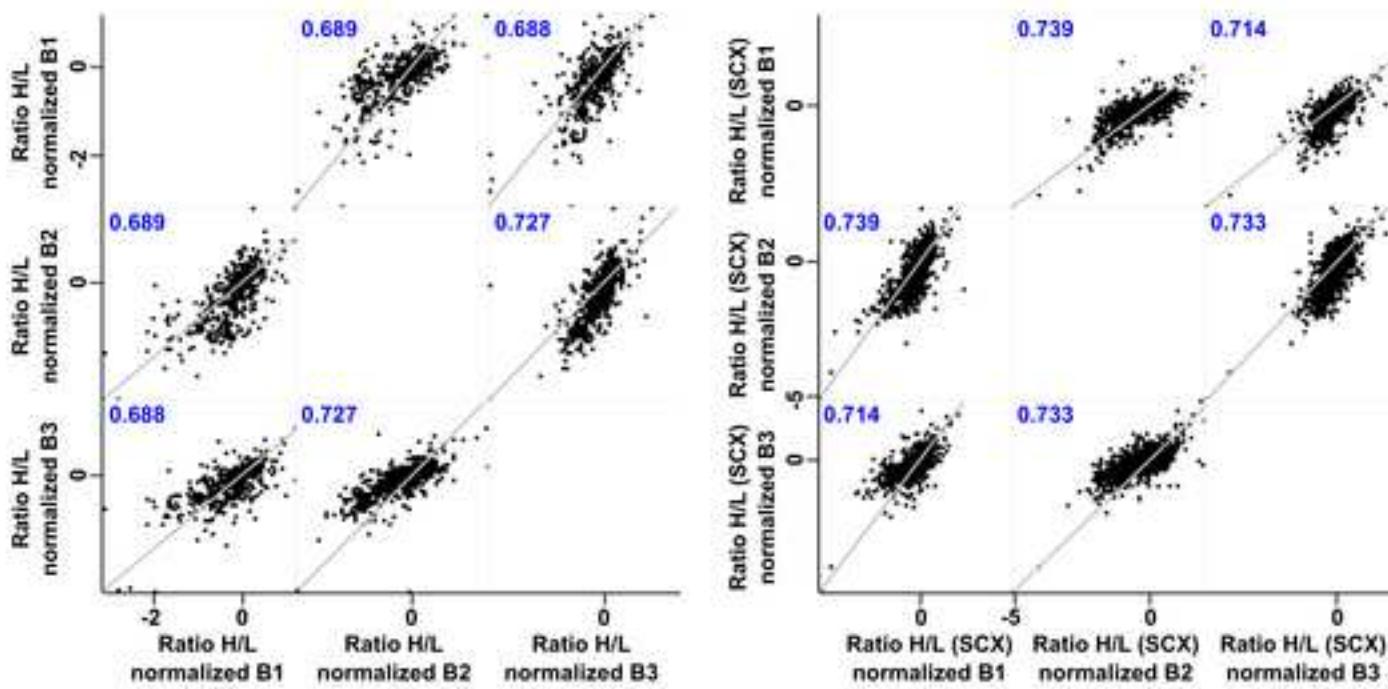
**B**

t = 0

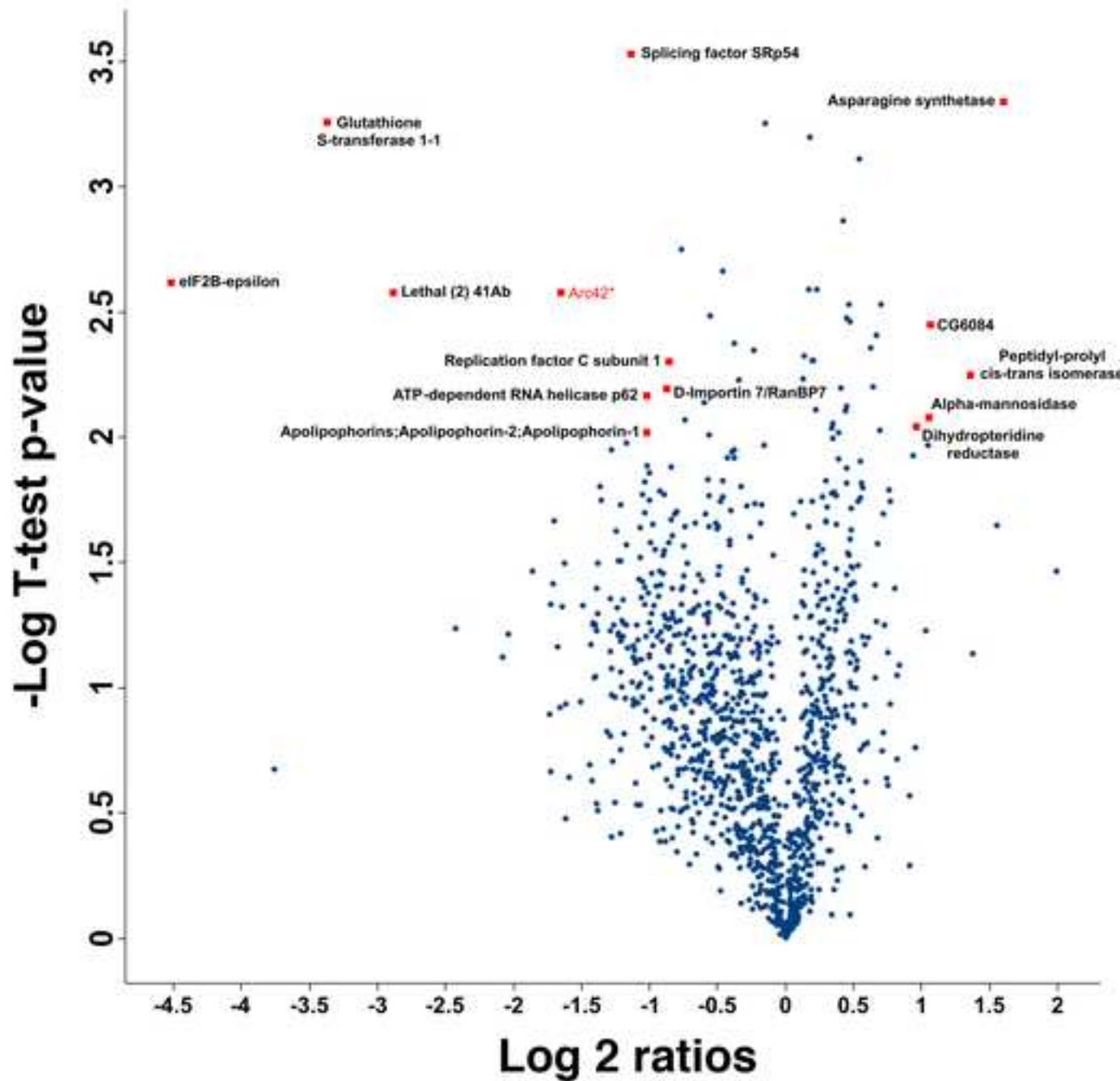
**B'**

+45 minutes

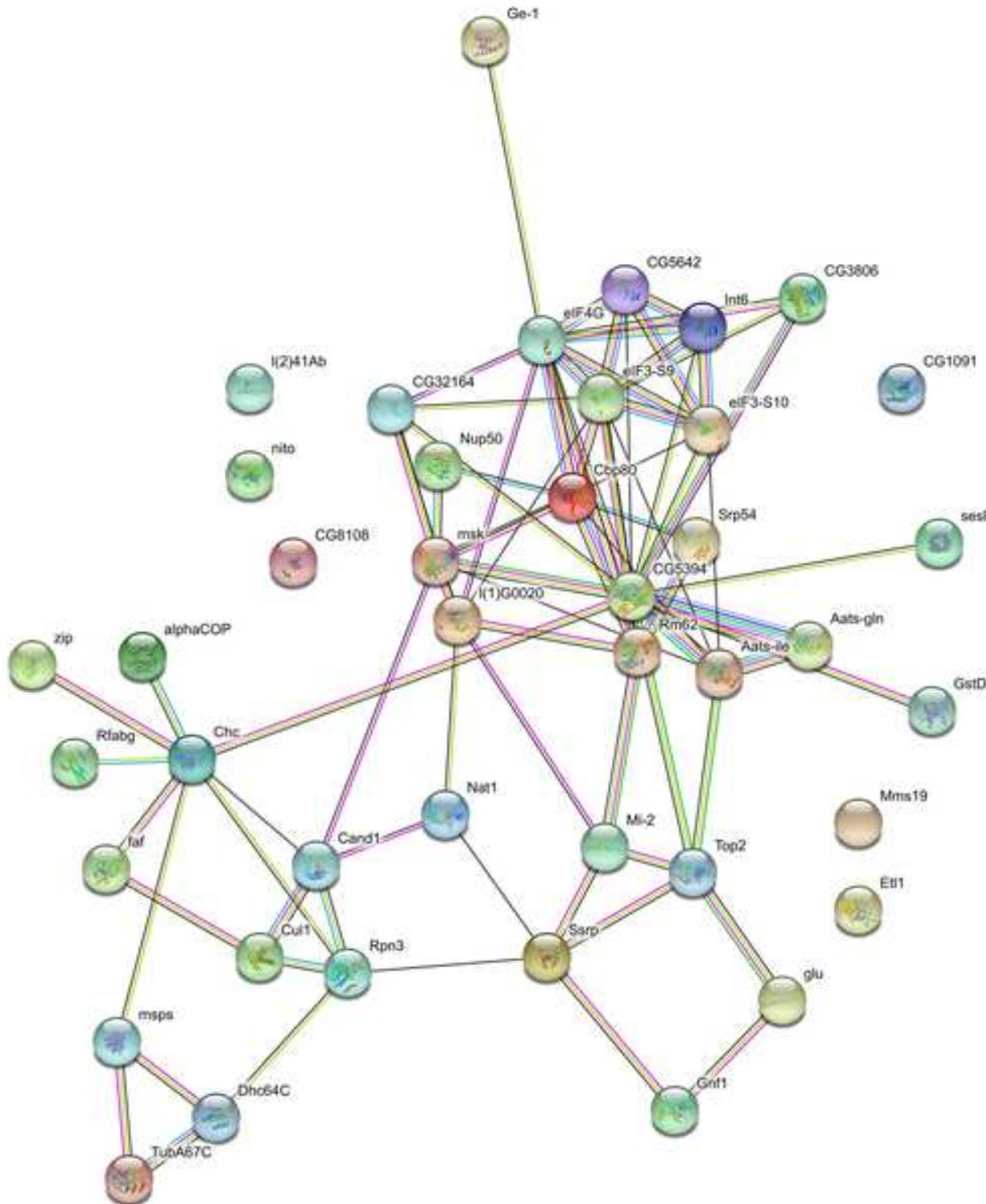


**A****B**

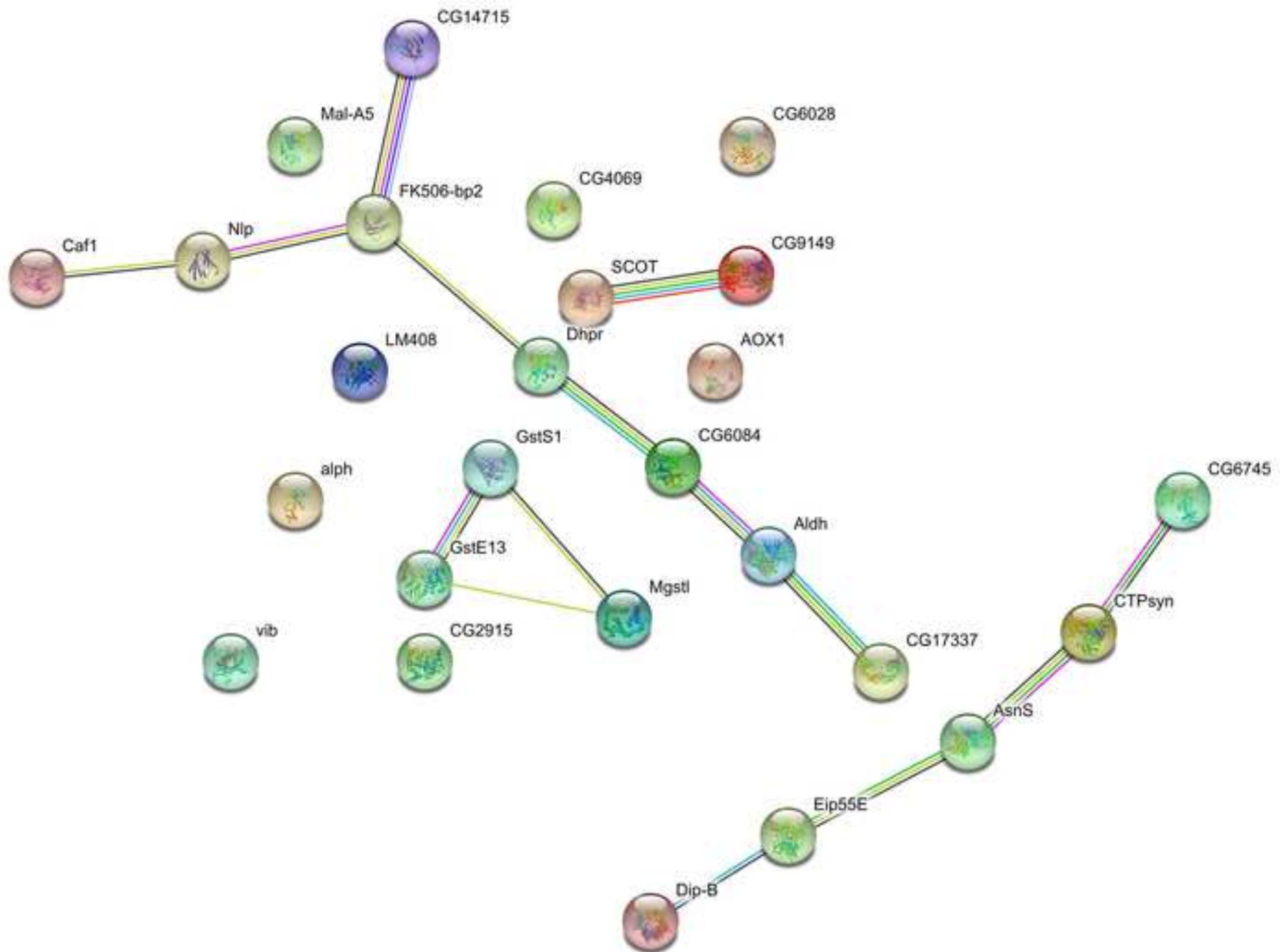
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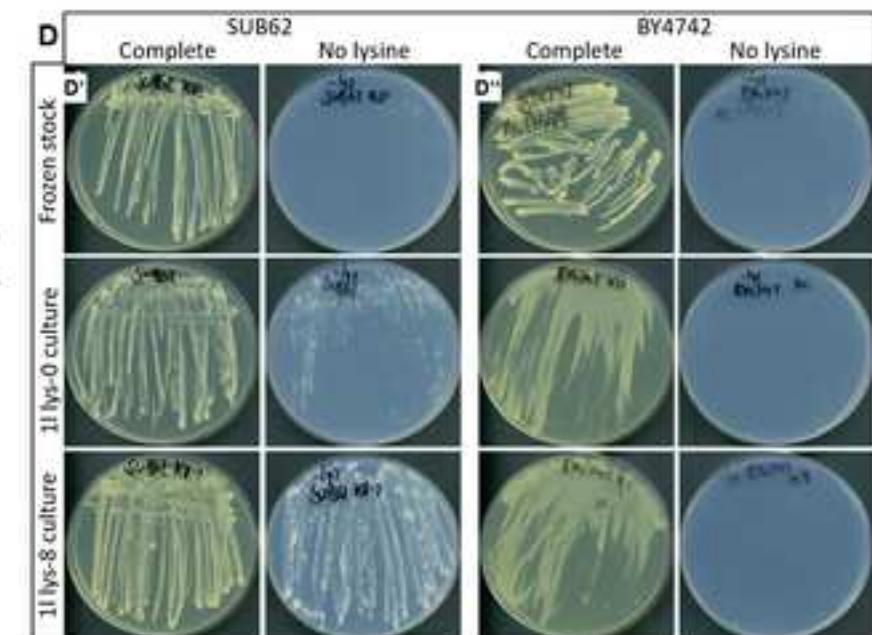
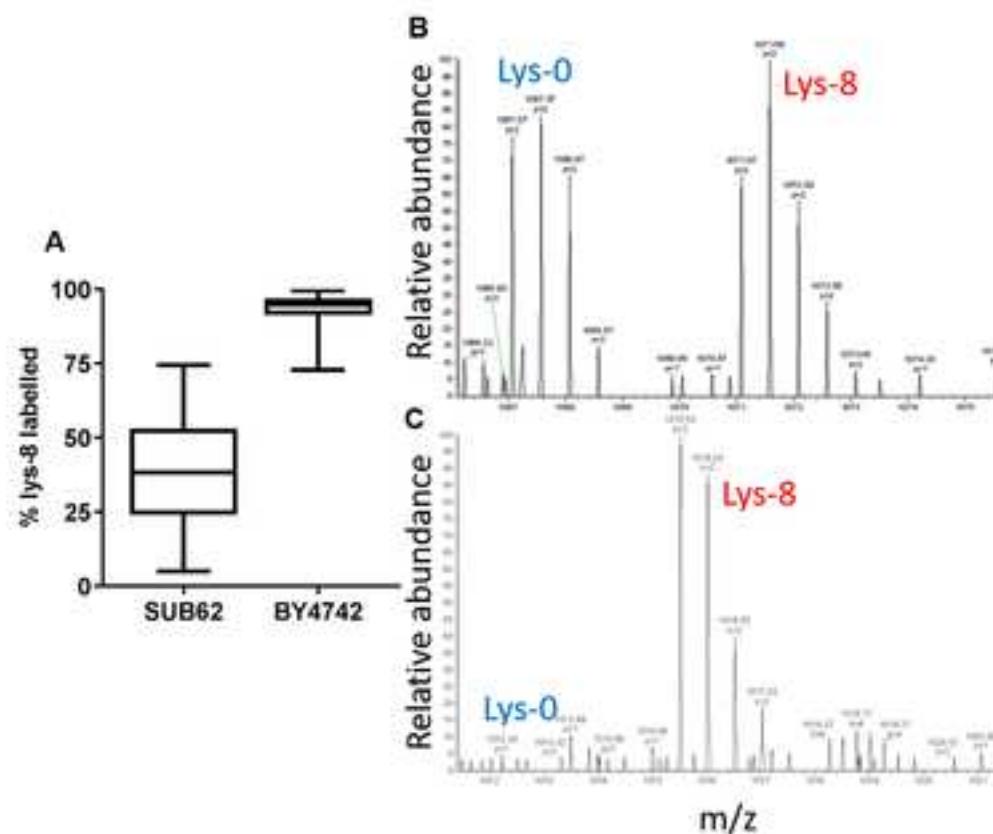
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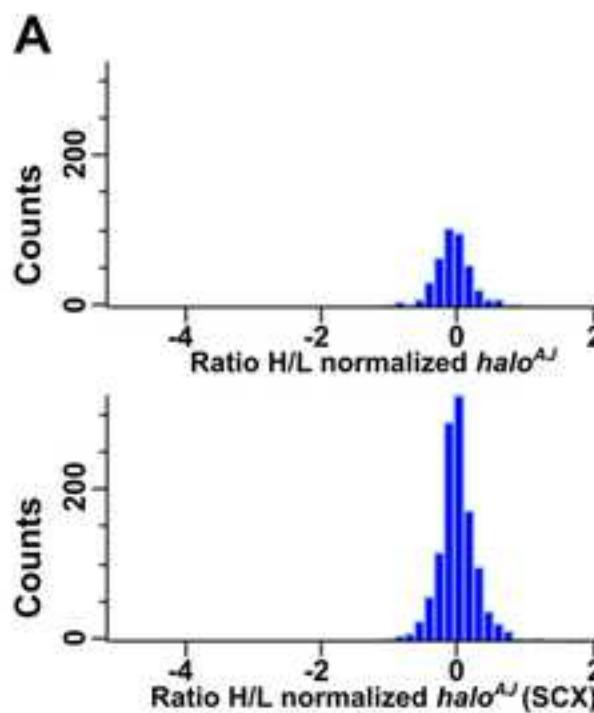
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**B**

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

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

	Sequence	Length	K Count	Modifications	Modified seq	Deamidation	Oxidation (M)
1	AAAPAAVASP	25		1 2 Phospho (S`_AAAPAAVAS(ph)PAAAATSADASPS(ph)PA			
2	AAAPAAVASP	25		1 2 Phospho (S`_AAAPAAVAS(ph)PAAAATSADASPS(ph)PA			
3	AAAPAAVASP	25		1 Phospho (STY_AAAPAAVASPAAAATSADASPS(ph)PAK_			
4	AAAPAAVASP	25		1 Phospho (STY_AAAPAAVASPAAAATSADASPS(ph)PAK_			
5	AAAPAAVASP	26		2 Phospho (STY_AAAPAAVASPAAAATS(ph)ADASPSPAKK_			
6	AAAPAAVASP	26		2 Phospho (STY_AAAPAAVASPAAAATS(ph)PAKK_			
7	AAAPAAVASP	26		2 2 Phospho (S`_AAAPAAVAS(ph)PAAAATSADASPS(ph)PA			
8	AAAPAAVASP	26		2 2 Phospho (S`_AAAPAAVAS(ph)PAAAATSADAS(ph)PSP			
9	AASSAAAQAM	23		1 Oxidation (M_AASSAAAQAM(ox)LETS(pI AASSAAAQAM			
10	ACARGELYSLV	15		1 Acetyl (Protei_(ac)ACARGELY(ph)SLVLNTK_			
11	ADEKMVTDEI	10		2 Oxidation (M_ADEKM(ox)VT(ph)DEK_ ADEKM(1)VTI			
12	AIELSPGNALF	14		1 Phospho (STY_AIELS(ph)PGNALFHAK_			
13	AIELSPGNALF	14		1 Phospho (STY_AIELS(ph)PGNALFHAK_			
14	AKGEILDEVV1	19		3 3 Phospho (S`_AKGEILDEVVT(ph)LS(ph)QIS(ph)AKK_			
15	ALDLLMSYRLI	11		1 Oxidation (M_ALDLLM(ox)S(ph)Y(ph)RLK ALDLLM(1)SY			
16	ALDLLMSYRLI	11		1 Oxidation (M_ALDLLM(ox)S(ph)Y(ph)RLK ALDLLM(1)SY			
17	ALELSHLKSFV	12		2 Phospho (STY_ALELSHLKS(ph)FVK_			
18	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLTAS(ph)HNPGGPENDFGIK_			
19	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
20	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
21	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
22	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
23	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
24	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
25	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
26	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
27	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
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41	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
42	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ASHNPGGPENDFGIK_			
43	ALGGIVLTASF	23		1 Phospho (STY_ALGGIVLT(ph)ALGGIVLTASHN(0.529)PGG			
44	ALILNRTGALN	12		1 Phospho (STY_ALILN(de)RT ALILN(1)RTGALN(1)K			
45	ALQAVYPDYV	19		1 Phospho (STY_ALQAVYPDYVDESLYGS(ph)K_			
46	ALQAVYPDYV	19		1 Phospho (STY_ALQAVYPDYVDESLYGS(ph)K_			
47	ALQAVYPDYV	19		1 Phospho (STY_ALQAVYPDYVDESLYGS(ph)K_			
48	ALQAVYPDYV	19		1 Phospho (STY_ALQAVYPDYVDESLYGS(ph)K_			
49	ALQAVYPDYV	19		1 Phospho (STY_ALQAVYPDYVDESLYGS(ph)K_			
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53	ALQAVYPDYV	19		1 Phospho (STY_ALQAVYPDYVDESLYGS(ph)K_			
54	ALQAVYPDYV	19		1 2 Phospho (S`_ALQAVYPDYVDELS(ph)LYGS(ph)K_			
55	ALQAVYPDYV	19		1 2 Phospho (S`_ALQAVYPDYVDELS(ph)LYGS(ph)K_			
56	APATPQAATS	39		2 Phospho (STY_APATPQAATSVTNPAAAGDGISVQNDPPVD			
57	APATPQAATS	39		2 Phospho (STY_APATPQAATSVTNPAAAGDGISVQNDPPVD			
58	APATPQAATS	39		2 Phospho (STY_APATPQAATSVTNPAAAGDGISVQNDPPVD			
59	APATPQAATS	39		2 Phospho (STY_APATPQAATSVTNPAAAGDGISVQNDPPVD			
60	APATPQAATS	39		2 Phospho (STY_APATPQAATSVTNPAAAGDGISVQNDPPVD			
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3	APATPQAATS	39	2 Phospho (STY_APATPQAATSVTNPAAGDGISVQNDPPVD
4	APSLHPPHME	22	1 Oxidation (M_AP5(ph)LHPIAPSLHPPHMEAPSLHPPHM(
5	AQDVVGRGA	17	1 Phospho (STY_AQDVVGRGAT(ph)NILICNK_
6	AQDVVGRGA	17	1 Phospho (STY_AQDVVGRGAT(ph)NILICNK_
7	AQDVVGRGA	17	1 Phospho (STY_AQDVVGRGAT(ph)NILICNK_
8	AQDVVGRGA	17	1 Acetyl (Protei_(ac)AQNIS(ph)PEQSGGAGGGGSK_
9	AQNISPEQSG	18	1 Acetyl (Protei_(ac)ARLVFT(ph)EK_
10	ARLVFTEK	8	1 Acetyl (Protei_(ac)ARLVFT(ph)EK_
11	ARLVFTEK	8	1 Acetyl (Protei_(ac)ARLVFT(ph)EK_
12	ARSLNSPLYF	14	2 3 Phospho (S'_ARS(ph)LS(ph)NS(ph)PLYHRKK_
13	ARSLNSPLYF	14	2 3 Phospho (S'_ARS(ph)LS(ph)NS(ph)PLYHRKK_
14	ARSLNSPLYF	14	2 3 Phospho (S'_ARS(ph)LS(ph)NS(ph)PLYHRKK_
15	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
16	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
17	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
18	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
19	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
20	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
21	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
22	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
23	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
24	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
25	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
26	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
27	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
28	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
29	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
30	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
31	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
32	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
33	ASAFQFSDDDE	14	1 Phospho (STY_ASAFQFS(ph)DDEEEVK_
34	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
35	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
36	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
37	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
38	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
39	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
40	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
41	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
42	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
43	ASGVTVDVC	11	1 Acetyl (Protei_(ac)ASGVT(ph)VSDVCK_
44	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
45	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
46	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
47	ASGVTVDVC	11	1 Acetyl (Protei_(ac)AS(ph)GVTVDVCK_
48	ASGVTVDVC	11	1 Acetyl (Protei_(ac)ASGVT(ph)VSDVCK_
49	ASRHTASRA	18	1 2 Phospho (S'_AS(ph)RHN(1)ASRHN(1)TASRAHVITRLVK
50	CISAVNKQQR	20	2 2 Phospho (S'_CIS(ph)AVN(CISAVNKQ(0.001)Q(0.007)F
51	CLPDYANKLK	10	2 Phospho (STY_CLPDY(ph)ANKLK_
52	CLPDYANKLK	10	2 Phospho (STY_CLPDY(ph)ANKLK_
53	DLEYFNNLK	9	1 Phospho (STY_DLEY(ph)FN(DLEYFN(1)N(1)LK
54	DLEYFNNLK	9	1 Phospho (STY_DLEY(ph)FN(DLEYFN(1)N(1)LK
55	DMRGTLRRK	10	1 Oxidation (M_DM(ox)RGT(ph)ILRRK_DM(1)RGTLR
56	DRQLFTQVY	18	2 Phospho (STY_DRQ(de)SLF DRQ(0.991)SLFTQ(0.004)VY
57	DVDFGDSNDI	21	1 Phospho (STY_DVDFGDS(ph)DNENEPDAYLARLK_

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63  
64  
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1 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_
   
 2 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_
   
 3 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_
   
 4 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_
   
 5 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_
   
 6 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_
   
 7 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_
   
 8 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_
   
 9 EAAAGEDITPI 17 1 Phospho (STY\_EAAAGEDITPLADES(ph)IK\_
   
 10 EAAQYGTVN/ 14 1 Phospho (STY\_EAAQY(ph)GTVNAVLPK\_
   
 11 EAAQYGTVN/ 14 1 Phospho (STY\_EAAQY(ph)GTVNAVLPK\_
   
 12 EANMLQSPV( 15 1 2 Oxidation (I\_EANM(ox)LC EAN(0.004)M EANM(1)LQSI
   
 13 EASPVSMASP 25 2 Oxidation (M\_EASPVSM(ox)AS(ph)PAKD| EASPVSM(1)A
   
 14 EASPVSMASP 25 2 Oxidation (M\_EASPVSM(ox)AS(ph)PAKD| EASPVSM(1)A
   
 15 EASPVSMASP 25 2 Oxidation (M\_EASPVSM(ox)AS(ph)PAKD| EASPVSM(1)A
   
 16 EFVFQLHGKM 18 3 Oxidation (M\_EFVFQLHGKM(ox)SNY(ph) EFVFQLHGKM
   
 17 EKTDAMAKA( 16 3 2 Phospho (S\_EKT(ph)DAMAKAQEFLRT(ph)K\_
   
 18 ELGNAEPAPS' 24 1 Phospho (STY\_ELGNAEPAPSVSSTTVSS(ph)PPAGVK\_
   
 19 ELPDSDSLNV/ 27 1 Phospho (STY\_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK\_
   
 20 ELPDSDSLNV/ 27 1 Phospho (STY\_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK\_
   
 21 ELPDSDSLNV/ 27 1 Phospho (STY\_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK\_
   
 22 EMIKILQEQAII 14 2 Phospho (STY\_EMIKILQ(de)EMIKILQ(0.503)EQ(0.503)A
   
 23 ENSPSNVAKK 13 3 2 Phospho (S\_ENS(ph)PS(p EN(0.039)SPSN(0.961)VAKK
   
 24 ENTKNLVTGE 14 2 Phospho (STY\_EN(de)TKN(c EN(1)TKN(1)LVTGEPIK
   
 25 ESAQQLEAQQT 11 1 2 Phospho (S\_ES(ph)AQ(d ES AQ(0.854)Q(0.147)LEAQ(
   
 26 ESTPLSASP KK 11 2 Phospho (STY\_ESTPLSAS(ph)PKK\_
   
 27 ETELMQSKIQ 20 2 Phospho (STY\_ETELMQSKIQET(ph)LGLDPVDK\_
   
 28 ETEQVAQPQF 20 1 Phospho (STY\_ETEQVAQPC ETEQ(0.085)VAQ(0.085)PQF
   
 29 ETIADIMRVK 13 2 2 Phospho (S\_ET(ph)IADIMRVKT(ph)IK\_
   
 30 EVCAQSLQDC 23 2 Phospho (STY\_EVCAQS(ph) EVCAQ(0.12)SLQ(0.116)DQ
   
 31 EVSDDEADDE 12 2 Phospho (STY\_EVS(ph)DDEADDEKK\_
   
 32 FFDSGDYQM/ 11 1 Oxidation (M\_FFDS(ph)GDYQM(ox)AK\_ FFDSGDYQM/
   
 33 FFDSGDYQM/ 11 1 Oxidation (M\_FFDS(ph)GDYQM(ox)AK\_ FFDSGDYQM/
   
 34 FFDSGDYQM/ 11 1 Oxidation (M\_FFDS(ph)GDYQM(ox)AK\_ FFDSGDYQM/
   
 35 FMSNKNPYS L 15 2 Oxidation (M\_FMSNKN(de FMSN(0.008)| FMSNKNPYS L
   
 36 FSSELFKEIIK 11 2 2 Phospho (S\_FS(ph)S(ph)ELFKEIIK\_
   
 37 GEALT SKQR Y 13 2 2 Phospho (S\_GEALT(ph)S| GEALT SKQ(0.991)RYQ(0.00
   
 38 GELQAGKSPF 11 2 Acetyl (Protei\_(ac)GELQAGKS(ph)PFK\_
   
 39 GELQAGKSPF 11 2 Acetyl (Protei\_(ac)GELQAGKS(ph)PFK\_
   
 40 GELQAGKSPF 11 2 Acetyl (Protei\_(ac)GELQAGKS(ph)PFK\_
   
 41 GLGMTKINLI 12 2 Oxidation (M\_GLGM(ox)T(ph)KINLITK\_ GLGM(1)TKIN
   
 42 GPQLEDGKV T 15 3 Oxidation (M\_GPQ(de)LED GPQ(1)LEDG| GPQLEDGKV T
   
 43 GQPLVVLSAM 11 1 Oxidation (M\_GQ(de)PLVV GQ(1)PLVVLS GQPLVVLSAM
   
 44 HNNSPNTNL/ 20 1 Phospho (STY\_HN(de)NSPN HN(0.468)N(0.468)SPN(0.0
   
 45 HNNSPNTNL/ 20 1 Phospho (STY\_HN(de)NSPN HN(0.371)N(0.371)SPN(0.1
   
 46 IGE GTYGVV YI 11 1 Phospho (STY\_IGEGTY(ph)GVVYK\_

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2			
3	IITHPNFNGN1	20	1 Phospho (STY_IITHPN(de)F IITHPN(0.59)FN(0.205)GN(C
4	IITHPNFNGN1	20	1 Phospho (STY_IITHPN(de)F IITHPN(0.65)FN(0.268)GN(C
5	IAEHEYRTSN	20	2 Oxidation (M_IAEHEYRTS IAEHEYRTSN IAEHEYRTSN
6	IKPILQATQTSD	15	1 Oxidation (M_IKPILQAT(ph)IKPILQ(0.026)IKPILQATQTSD
7	IKPILQATQTSD	15	1 Oxidation (M_IKPILQAT(ph)IKPILQ(0.005)IKPILQATQTSD
8	IKPILQATQTSD	15	1 Oxidation (M_IKPILQAT(ph)Q(de)TSQ(de)LFM(ox)_
9	IKPILQATQTSD	15	1 Oxidation (M_IKPILQAT(ph)Q(de)TSQ(de)LFM(ox)_
10	IKPILQATQTSD	15	1 Oxidation (M_IKPILQAT(ph)Q(de)TSQ(de)LFM(ox)_
11	IKPILQATQTSD	15	1 2 Phospho (S_ILFVTESEN(c ILFVTESEN(0.919)Q(0.08)AI
12	ILFVTESENQA	21	1 2 Phospho (S_ILFVTESEN(c ILFVTESEN(0.919)Q(0.08)AI
13	ILFVTESENQA	21	2 Oxidation (M_INQIQ(de)M IN(0.033)Q(0.INQIQM(1)KE
14	INQIQMKETN	14	2 Oxidation (M_IQVQTKQ(d IQ(0.001)VQ(IQVQTKQIAQ
15	IQVQTKQIAQ	14	2 Oxidation (M_IQVQTKQ(d IQ(0.011)VQ(IQVQTKQIAQ
16	IQVQTKQIAQ	14	2 Phospho (STY_IQ(de)VQTKIQ(0.502)VQ(0.502)TKQ(0.C
17	ISENTIAIISTEL	17	1 3 Phospho (S_IS(ph)ENT(ph)IAIIST(ph)ELEIQK_
18	ISMLKQVMSC	14	3 Oxidation (M_IS(ph)M(ox)LKQVMS(ph)Q ISM(0.818)LK
19	KDFLPLAFQM	19	2 Oxidation (M_KDFLPLAFQM(ox)QASTGIA KDFLPLAFQM
20	KDITNLSYKVVK	12	3 Phospho (STY_KDIT(ph)N(d KDITN(1)LSYKVVK
21	KEESESEDDDI	17	1 Oxidation (M_KEESES(ph)EDDDM(ox)GF.KEESESEDDDI
22	KEESESEDDDI	17	1 Oxidation (M_KEESES(ph)EDDDM(ox)GF.KEESESEDDDI
23	KEESESEDDDI	17	1 Oxidation (M_KEESES(ph)EDDDM(ox)GF.KEESESEDDDI
24	KEPTPGEK	8	2 Phospho (STY_KEPT(ph)PGEK_
25	KIDNPESAKV	25	3 Phospho (STY_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_
26	KIDNPESAKV	25	3 Phospho (STY_KIDNPESAKVS(ph)DAEEEEEEYAVEK_
27	KIDNPESAKV	25	3 Phospho (STY_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_
28	KIDNPESAKV	25	3 Phospho (STY_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_
29	KIEKFQSEEQC	20	3 Phospho (STY_KIEKFQS(ph)EEQQQTEDELQDK_
30	KIEKFQSEEQC	20	3 Phospho (STY_KIEKFQS(ph)EEQQQTEDELQDK_
31	KKEEESDQSD	19	2 Oxidation (M_KKEEES(ph)DQS(ph)DDDM KKEEESDQSD
32	KKEEESDQSD	19	2 Oxidation (M_KKEEES(ph)DQS(ph)DDDM KKEEESDQSD
33	KKEEESDQSD	19	2 Oxidation (M_KKEEES(ph)DQS(ph)DDDM KKEEESDQSD
34	KKEEESDQSD	19	2 Oxidation (M_KKEEESDQ(ph)DDDM(ox)KKEEESDQSD
35	KKQEESDEEF	17	3 Phospho (STY_KKQEES(ph)DEEFFDLDDIK_
36	KLAFSDESTF	19	2 Phospho (STY_KLAFFS(ph)DDESTPEEHQGQGK_
37	KLIVNGASSNI	12	2 Phospho (STY_KLIVN(de)G/KLIVN(1)GASSN(1)LK
38	KMEVLSVQNI	14	2 Phospho (STY_KMEVLS(ph)KMEVLSVQ(0.215)N(0.84)H
39	KMKYDFGTLL	14	3 2 Phospho (S_KMKY(ph)DFGT(ph)LLLLVK_
40	KNKTNRQLSS	11	3 Acetyl (Protei_(ac)KN(de)K KN(0.97)KTN(0.029)RQ(0.0
41	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
42	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
43	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
44	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
45	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
46	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
47	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
48	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
49	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
50	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
51	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
52	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
53	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
54	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
55	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
56	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
57	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
58	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
59	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
60	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
61	KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_

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2	KPEDPSSEAE\	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
3	KQEESDEEFFI	16	2 Phospho (STY_KQEES(ph)DEEFFDLDDIK_
4	KSAPQRQSC	18	2 Phospho (STY_KS(ph)APQ(\u03b1 KSAPQ(1)SRQ(1)SCFRSRPRL
5	KSPTAAVTPI	13	3 2 Phospho (S\u207b_KS(ph)KPT(p KSKPTAAVTPIQ(1)K
6	KVTTIGLNSTA	14	2 2 Phospho (S\u207b_KVT(ph)T(ph)IGLNSTAATK_
7	KVTWIGANGI	15	2 Phospho (STY_KVT(ph)WIG KVTWIGAN(0.771)GDQ(0.2.
8	LDLTIVDLNDE	19	2 Phospho (STY_LDLTIVDLND LDLTIVDLN(0.079)DEVQ(0.2
9	LENLAYEKSEC	24	2 Oxidation (M_LENLAYEKS(ph)EDLLT(ph)'LENLAYEKS
10	LFEPPVTMRD	19	2 Phospho (STY_LFEPPVTMRDMLKSLSRT(ph)K_
11	LGIDIGDRLQA	15	1 2 Phospho (S\u207b_LGIDIGDRLQAT(ph)S(ph)RK_
12	LLDFNLLDTD\	28	2 Phospho (STY_LLDFNLLDT(ph)DDDDDEEGDEEDKEDTVT
13	LNENFVTINIC	12	1 Phospho (STY_LN(de)EN(de)LN(0.913)EN(0.913)FVTIN(C
14	LRFDNFNSKAII	24	3 2 Phospho (S\u207b_LRFDNFNS(ph)LRFDNFN(0.002)SKAAMTIEQI
15	LRTSPNEQQK	16	2 2 Phospho (S\u207b_LRTS(ph)PN(LRTSPN(1)EQ(1)Q(1)KDTLHI
16	LSVQSPPK	8	1 Phospho (STY_LSVQS(ph)PPK_
17	LTNGQRQME	16	1 Oxidation (M_LT(ph)NGQR LTN(0.008)GC LTNGQRQM(:
18	LTNGQRQME	16	1 Oxidation (M_LT(ph)NGQR LTN(0.016)GC LTNGQRQM(:
19	MESTTIVFVTI	19	1 Oxidation (M_M(ox)ESTTIV MESTTIVFVTI M(1)ESTTIVF\
20	MFLTQQQQQL	13	1 Oxidation (M_M(ox)FLT(p\u03b1 MFLTQ(0.015 M(1)FLTQQQ
21	MFLTQQQQQL	13	1 Oxidation (M_M(ox)FLT(p\u03b1 MFLTQ(0.138 M(1)FLTQQQ
22	MGHLQLDFH:	13	1 Acetyl (Protei_(ac)M(ox)GHLQLDFHS(ph) M(1)GHLQLD
23	MHKLIMRSVI	14	2 2 Oxidation (I_M(ox)HKLIM(ox)RS(ph)VII M(1)HKLIM(1
24	MIRATSCALS\	18	1 Oxidation (M_M(ox)IRATSCALS(ph)TRPLI M(1)IRATSCA
25	MLNRCLELVT	13	1 Oxidation (M_M(ox)LN(de)MLN(1)RCLEL M(1)LNRCLEL
26	MLNRCLELVT	13	1 Oxidation (M_M(ox)LN(de)RCLELVT(ph)PFK_
27	MLVRRLLQEL	18	1 Oxidation (M_M(ox)LVRRRL MLVRRLLQ(1) M(1)LVRRLLQ
28	MNDSFGDFN	23	1 Acetyl (Protei_(ac)M(ox)NDS(ph)FGDFNA M(1)NDSFGD
29	MPNLQSSIPH	13	2 Acetyl (Protei_(ac)M(ox)PNLQSQ(ph)SIPHT M(1)PNLQSSI
30	MPNLQSSIPH	13	2 Acetyl (Protei_(ac)M(ox)PNLQSQ(ph)SIPHT M(1)PNLQSSI
31	MPNLQSSIPH	13	2 Acetyl (Protei_(ac)M(ox)PNLQSQ(ph)SIPHT M(1)PNLQSSI
32	MQHSSMKV\	15	2 Oxidation (M_M(ox)Q(de)\ MQ(1)HSSMK M(0.989)QHS
33	MQIFVKTLTG	11	2 Acetyl (Protei_(ac)MQ(de)\ MQ(1)IFVKTLTGK
34	MQLILSYLQSC	14	1 Acetyl (Protei_(ac)MQLILS( MQ(0.212)LILSYLQ(0.848)SI
35	MQLILSYLQSC	14	1 Acetyl (Protei_(ac)MQLILSY MQ(0.007)LILSYLQ(0.996)SI
36	MQLILSYLQSC	14	1 Acetyl (Protei_(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_
37	MQLILSYLQSC	14	1 Acetyl (Protei_(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_
38	MQLILSYLQSC	14	1 Oxidation (M_M(ox)Q(de)\ MQ(0.844)LIL M(1)QLILSYLC
39	MQLILSYLQSC	14	1 Oxidation (M_M(ox)QLILSY MQ(0.066)LIL M(1)QLILSYLC
40	MQLILSYLQSC	14	1 Oxidation (M_M(ox)QLILSYLQ(de)S(ph)Q(de)QIK_
41	MQLILSYLQSC	14	1 Oxidation (M_M(ox)Q(de)LILS(ph)YLQSQQ(de)IK_
42	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
43	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL

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3	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RC MRDKISQ(0.0 M(1)RDKISQL
4	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RC MRDKISQ(0.0 M(1)RDKISQL
5	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RC MRDKISQ(0.0 M(1)RDKISQL
6	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RC MRDKISQ(0.2 M(1)RDKISQL
7	MRFISQHNSS	12	1 Acetyl (Protei_(ac)M(ox)RF MRFISQ(0.53 M(1)RFISQHN
8	MSGALKSQQI	13	2 Acetyl (Protei_(ac)M(ox)SG MSGALKSQ(0 M(1)SGALKSC
9	MSLIHSFVTQI	13	1 2 Oxidation (I_M(ox)S(ph)L MSLIHSFVTQ(M(1)SLIHSFV
10	MSQGASEVPI	16	1 Acetyl (Protei_(ac)MSQGASEVPLS(ph)ALRLK_
11	MSTIVRK	7	1 2 Phospho (S_MS(ph)T(ph)IVRK_
12	MSTLLENIFAI	20	2 Oxidation (M_M(ox)S(ph)T MSTLLEN(0.9 M(1)STLLENIF
13	MTEIELPVESV	26	1 Oxidation (M_M(ox)TEIELPVESVPSASLS(I M(1)TEIELPV
14	MTIFNLYIFDK	11	1 Oxidation (M_M(ox)TIFNLY(ph)IFDK_ M(1)TIFNLYIF
15	MVEPSPETVC	24	1 Oxidation (M_M(ox)VEPSPETVGDFQSVQ M(1)VEPSPET
16	MVEPSPETVC	24	1 Oxidation (M_M(ox)VEPSPETVGDFQSVQ M(1)VEPSPET
17	MVEPSPETVC	24	1 Oxidation (M_M(ox)VEPSPETVGDFQSVQ M(1)VEPSPET
18	MYNIYVLKK	9	2 Phospho (STY_MYN(de)IY(f MYN(1)IYVLKK
19	MYNIYVLKK	9	2 Phospho (STY_MY(ph)N(de MYN(1)IYVLKK
20	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
21	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
22	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
23	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
24	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
25	NAGGVGVGV	18	3 Phospho (STY_NAGGVGVGVGEKS(ph)PDLKK_
26	NAGGVGVGV	18	3 Phospho (STY_NAGGVGVGVGEKS(ph)PDLKK_
27	NGGILNYMIR	11	1 Oxidation (M_N(de)GGILN N(0.96)GGILN NGGILNYM(1
28	NIWKDKTPNL	11	3 Phospho (STY_N(de)IWKDK N(0.999)IWKDKTPN(0.001)I
29	NKEPLIQIAM	20	3 Oxidation (M_N(de)KEPLIC N(0.823)KEPL NKEPLIQIAM(
30	NKLQKNHALII	23	3 Phospho (STY_N(de)KLQ(d N(0.999)KLQ(0.999)KN(0.99
31	NLKLMQMASTF	12	2 Oxidation (M_N(de)LKLQN N(0.938)LKLC NLKLM(1)A
32	NNIKLKCLIDT	20	3 Acetyl (Protei_(ac)NNIKLKCN(0.023)N(0.023)IKLKCLIDT
33	NSQYERESLLK	11	1 Phospho (STY_NSQY(ph)ERESLLK_
34	NSQYERESLLK	11	1 Phospho (STY_NSQY(ph)ERESLLK_
35	NVGIFIKDDSE	19	3 Phospho (STY_NVGIFIKDDS(ph)DEEDVDDKK_
36	NVGIFIKDDSE	19	3 Phospho (STY_NVGIFIKDDS(ph)DEEDVDDKK_
37	NVGIFIKDDSE	19	3 Phospho (STY_NVGIFIKDDS(ph)DEEDVDDKK_
38	NYPFNIEF	8	0 Phospho (STY_N(de)Y(ph)P N(1)YPFN(1)IEF
39	PCNLYQTAQE	13	1 Phospho (STY_PCNLY(ph)QTAQEQLK_
40	PCNLYQTAQE	13	1 Phospho (STY_PCN(de)LY(p PCN(0.992)LYQ(0.004)TAQ(
41	PLMQLIIQDT	16	1 2 Oxidation (I_PLM(ox)QLIIQDTGIGM(ox) PLM(1)QLIIQD
42	PLPSGRIPQITI	17	1 2 Phospho (S_PLPS(ph)GRIPQIT(ph)PPASPK_
43	PLPSGRIPQITI	17	1 2 Phospho (S_PLPS(ph)GRIPQIT(ph)PPASPK_
44	PTVAAAACKPA	34	2 Phospho (STY_PTVAAAACKPAADDVDLFGS(ph)DDEE
45	QELLQSYMK	9	1 Oxidation (M_(gl)Q(de)ELL Q(1)ELLQ(1)S QELLQSYM(1)

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3	QELLQSYM <b>K</b>	9	1 Oxidation (M_(gl)Q(de)ELL Q(1)ELLQ(1)S) QELLQSYM(1)
4	QELLQSYM <b>K</b>	9	1 Phospho (STY_(gl)Q(de)ELL Q(1)ELLQ(1)SYM <b>K</b> )
5	QHSFTSSSALK	11	1 Phospho (STY_Q(de)HSFTS! Q(1)HSFTSSSALK)
6	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
7	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
8	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
9	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
10	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
11	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
12	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
13	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
14	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
15	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
16	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
17	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
18	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
19	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
20	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
21	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
22	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
23	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
24	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
25	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
26	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
27	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
28	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
29	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
30	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_)
31	QISVRGIAEV <b>C</b>	17	1 Phospho (STY_(gl)QIS(ph)VRGIAEVGVNVTEVK_)
32	QISVRGIAEV <b>C</b>	17	1 Phospho (STY_(gl)QIS(ph)VRGIAEVGVNVTEVK_)
33	QISVRGIAEV <b>C</b>	18	2 Phospho (STY_(gl)QIS(ph)VRGIAEVGVNVTEVKK_)
34	QISVRGIAEV <b>C</b>	18	2 Phospho (STY_(gl)QIS(ph)VRGIAEVGVNVTEVKK_)
35	QIVPLLN <b>YK</b>	9	1 Phospho (STY_Q(de)IVPLLN Q(1)IVPLLN(1)YK)
36	QKESGEFPEV <b>I</b>	12	2 Phospho (STY_QKES(ph)GEFPEVGK_)
37	QKFITTEDVNI	19	2 Oxidation (M_Q(de)KFIT(p Q(0.941)KFIT QKFITTEDVNI)
38	QLRDLET <b>ELDE</b>	14	1 Phospho (STY_(gl)QLRDLET(ph)ELDEERK_)
39	QLRDLET <b>ELDE</b>	14	1 Phospho (STY_(gl)QLRDLET(ph)ELDEERK_)
40	QLSIIHQKSLK	11	2 Phospho (STY_(gl)Q(de)LSII Q(0.999)LSIIHQ(0.001)KSLK)
41	QMPDVET <b>TES</b>	16	1 Oxidation (M_Q(de)M(ox)I Q(1)MPDVET QM(1)PDVET)
42	QNDLIHDRSLI	13	1 Phospho (STY_(gl)QNDLIHDRS(ph)LINK_)
43	QNDLIHDRSLI	13	1 Phospho (STY_(gl)QNDLIHDRS(ph)LINK_)
44	QNDLIHDRSLI	13	1 Phospho (STY_(gl)QNDLIHDRS(ph)LINK_)
45	QRDLPAPRES	15	1 Phospho (STY_(gl)QRDLPAPRES(ph)QSRSK_)
46	QSLIMYFNK	9	1 Oxidation (M_Q(de)SLIM(c Q(0.998)SLIM QSLIM(1)YFN)
47	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
48	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
49	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
50	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
51	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
52	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
53	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
54	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
55	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
56	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
57	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
58	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
59	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
60	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)
61	QSSYHGVHQ/ <b>Y</b>	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_)

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3	QSSYHGVHQ/	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
4	QSSYHGVHQ/	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
5	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(IQ(0.987)SVPQ(0.987)LAN(0
6	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(IQ(0.962)SVPQ(0.972)LAN(0
7	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(IQ(0.942)SVPQ(0.985)LAN(0
8	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_
9	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_
10	QVEPRQLVRN	22	1 Oxidation (M_QVEPRQLVRQ(0.001)VEPF QVEPRQLVRN
11	QVRTNLQEIQ	11	1 Phospho (STY_(gl)Q(de)VRTQ(0.334)VRTN(0.334)LQ(0.:
12	QVRTNLQEIQ	11	1 Phospho (STY_(gl)Q(de)VRT(ph)NLQEIQ(de)K_
13	REEENAAAAAE	31	1 Phospho (STY_REEENAAAAEEEAGEISATGGATS(ph)PEP\
14	REEENAAAAAE	31	1 Phospho (STY_REEENAAAAEEEAGEISATGGAT(ph)SPEP\
15	REEENAAAAAE	31	1 Phospho (STY_REEENAAAAEEEAGEISATGGAT(ph)SPEP\
16	RGCQILGLNK'	18	2 Phospho (STY_RGCQ(de)IL(RGCQ(0.965)ILGLN(0.024)K
17	RGCQILGLNK'	18	2 Phospho (STY_RGCQ(de)IL(RGCQ(0.838)ILGLN(0.155)K
18	RGCQILGLNK'	18	2 Phospho (STY_RGCQ(de)IL(RGCQ(0.999)ILGLNKYGIQQ)
19	RGPPPPPPTASI	17	1 2 Phospho (S'_RGPPPPPPTA(RGPPPPPPTASESTRRN(1)K
20	RGPPPPPPTASI	17	1 2 Phospho (S'_RGPPPPPPTASES(ph)T(ph)RRN(de)K_
21	RGPPPPPPTASI	17	1 2 Phospho (S'_RGPPPPPPTASES(ph)T(ph)RRN(de)K_
22	RIASFKNYISK	11	2 Phospho (STY_RIASFKNY(ph)ISK_
23	RHQEVYLQK	9	1 Phospho (STY_RHQEVY(ph)RHQI(0.049)EVYLQ(0.951)K
24	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
25	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
26	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
27	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
28	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
29	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
30	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
31	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
32	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
33	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
34	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
35	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
36	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
37	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
38	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
39	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
40	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
41	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
42	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
43	RKKPEDPSSE/	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
44	RMASSEQPTF	17	1 Oxidation (M_RM(ox)ASSE RMASEQ(0.5 RM(1)ASSEQF
45	RPLMLQGHEF	16	1 Acetyl (Protei_(ac)RPLMLQ RPLMLQ(1)GHERSITQ(1)IK
46	RPLMLQGHEF	16	1 Acetyl (Protei_(ac)RPLMLQ(de)GHERS(ph)ITQ(de)IK_
47	SAAVAEGGD/	23	2 Phospho (STY_SAAVAEGGDAVAET(ph)AKGEEGSPK_
48	SAAVAEGGD/	23	2 Phospho (STY_SAAVAEGGDAVAET(ph)AKGEEGSPK_
49	SAAVAEGGD/	23	2 Phospho (STY_SAAVAEGGDAVAET(ph)AKGEEGSPK_
50	SAAVAEGGD/	23	2 Phospho (STY_SAAVAEGGDAVAET(ph)AKGEEGSPK_
51	SAAVAEGGD/	23	2 Phospho (STY_SAAVAEGGDAVAET(ph)AKGEEGSPK_
52	SAAVAEGGD/	23	2 Phospho (STY_SAAVAEGGDAVAET(ph)AKGEEGSPK_
53	SAAVAEGGD/	23	2 Phospho (STY_SAAVAEGGDAVAET(ph)AKGEEGSPK_
54	SAAVAEGGD/	23	2 Phospho (STY_SAAVAEGGDAVAETAKGEEGS(ph)PK_
55	SAEAEAIVTTA	20	1 Acetyl (Protei_(ac)SAEAEAIVTTATADVSS(ph)PSK_
56	SAEAEAIVTTA	20	1 Acetyl (Protei_(ac)SAEAEAIVTTATADVSS(ph)PSK_
57	SAEAEAIVTTA	20	1 Acetyl (Protei_(ac)SAEAEAIVTTATADVSS(ph)PSK_
58	SAEAEAIVTTA	20	1 Acetyl (Protei_(ac)SAEAEAIVTTATADVSS(ph)PSK_
59	SAEAEAIVTTA	20	1 Acetyl (Protei_(ac)SAEAEAIVTTATADVSS(ph)PSK_
60	SAEAEAIVTTA	20	1 Acetyl (Protei_(ac)SAEAEAIVTTATADVSS(ph)PSK_
61	SAEAEAIVTTA	20	1 Acetyl (Protei_(ac)SAEAEAIVTTATADVSS(ph)PSK_

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3	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
4	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
5	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
6	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
7	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
8	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
9	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
10	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVS(ph)SPSK_
11	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSSPS(ph)K_
12	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSSPS(ph)K_
13	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
14	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
15	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
16	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVS(ph)SPSK_
17	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
18	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
19	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
20	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
21	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
22	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
23	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
24	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
25	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
26	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSSPS(ph)K_
27	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
28	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
29	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
30	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSSPS(ph)K_
31	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
32	SAEAEAVTTA	20	1 Acetyl (Protei_(ac)SAEAEAVTTATADVSS(ph)PSK_
33	SASIRILNLINS	17	1 Oxidation (M_SASIRILNLIN SASIRILN(0.0:SASIRILNLINS
34	SDSAVATSASI	21	1 Acetyl (Protei_(ac)SDSAVAT(ph)SASPVAAPPATVEK_
35	SDSAVATSASI	21	1 Acetyl (Protei_(ac)SDSAVATS(ph)ASPVAAPPATVEK_
36	SDSAVATSASI	21	1 Acetyl (Protei_(ac)SDSAVAT(ph)SASPVAAPPATVEK_
37	SETVDSTEVK	10	1 Acetyl (Protei_(ac)S(ph)ET(ph)VDS(ph)T(ph)EVK_
38	SHSPPPASNCL	18	1 Acetyl (Protei_(ac)S(ph)HSPPPASNCEEALIQLK_
39	SIQNLNTRDPI	16	1 Acetyl (Protei_(ac)S(ph)IQNLNTRDPFADAIIK_
40	SIQNLNTRDPI	16	1 Acetyl (Protei_(ac)S(ph)IQNLNTRDPFADAIIK_
41	SISEFVDLEAEI	15	1 Phospho (STY_S(ph)ISETVDLEAEIAGK_
42	SISEFVDLEAEI	15	1 Phospho (STY_S(ph)ISETVDLEAEIAGK_
43	SITMSTISLPAI	21	2 Oxidation (M_SIT(ph)MS(ph)TISLPAM(ox)SITM(0.078)S
44	SITMSTISLPAI	21	2 2 Oxidation (I_SITM(ox)S(ph)T(ph)ISLPAM SITM(1)STISLI
45	SITMSTISLPAI	21	2 2 Oxidation (I_SITM(ox)S(ph)T(ph)ISLPAM(ox)LSGVNLK
46	SKKSWQARH <sup>-</sup>	13	3 2 Phospho (S_S(ph)KKSWC SKKSWQ(1)ARHTGIK
47	SLSRLNTLMK	10	1 Acetyl (Protei_(ac)S(ph)LSR SLSRLN(1)TLN SLSRLNTLM(1
48	SLYRISARK	9	1 Acetyl (Protei_(ac)S(ph)LYRISARK_
49	SPIVFELTQPSI	14	1 Phospho (STY_SPIVFELTQPS(ph)PEK_
50	SPIVFELTQPSI	14	1 Phospho (STY_SPIVFELTQPS(ph)PEK_
51	SPIVFELTQPSI	14	1 Phospho (STY_SPIVFELTQPS(ph)PEK_
52	SPIVFELTQPSI	14	1 Phospho (STY_SPIVFELTQPS(ph)PEK_

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2	SPIVFELTQPSI	14	1 Phospho (STY_SPIVFELTQPS(ph)PEK_
3	SPIVFELTQPSI	14	1 2 Phospho (S`_S(ph)PIVFELTQPS(ph)PEK_
4	SRASFLAQNSI	15	1 2 Phospho (S`_S(ph)RASFLA\$RASFLAQ(0.715)N(0.27)SS
5	SRKHKENLLK	10	3 Phospho (STY_S(ph)RKHKEI\$RKHEN(1)LLK
6	SSENSEYYSDK	11	1 Acetyl (Protei_(ac)S(ph)SENSEYY\$(ph)DK_
7	SSL SVKP NYTL	12	2 2 Phospho (S`_S(ph)SLS(ph)SSL SVKP N(1)YTLK
8	STGQLQQQLSA	17	1 Phospho (STY_STGQLQQQLS STGQ(0.007)LQ(0.107)Q(0.:
9	SVFAEAYDPE,	24	1 Phospho (STY_S(ph)VFAEAYDPEADDDDDGATAVFPK_
10	SVHSPNPGLIL	14	1 Acetyl (Protei_(ac)SVHS(ph)PNPGLILQSK_
11	SVHSPNPGLIL	14	1 Acetyl (Protei_(ac)SVHS(ph)PNPGLILQSK_
12	SVHSPNPGLIL	14	1 Acetyl (Protei_(ac)SVHS(ph)PNPGLILQSK_
13	SVHSPNPGLIL	14	1 Acetyl (Protei_(ac)SVHS(ph)PNPGLILQSK_
14	TELAAKLASSL	26	3 2 Phospho (S`_TELAAKLAS(TELAAKCLASSLVSQ(0.165)GK
15	TIKYLKRVK	9	3 Phospho (STY_TIKY(ph)LKRVK_
16	TKIKIHYIEMTI	16	3 2 Phospho (S`_T(ph)KIKIHYIEMT(ph)NVHAK_
17	TLLNTSPNLLP	23	1 Phospho (STY_TLLNTS(ph)PNLLPITTATDTFNNLK_
18	TLPRNYIHREL	26	1 3 Phospho (S`_TLPRNY(ph)IHRELPS(ph)NLT(ph)RAMPSI
19	TNISRLGNYFK	11	1 Acetyl (Protei_(ac)TNIS(ph)RLGNYFK_
20	TRRFDEVQMI	14	1 Oxidation (M_T(ph)RRFDE'TRRFDEVQ(1)TRRFDEVQM(
21	TSKKIIVANSG	13	2 2 Phospho (S`_T(ph)SKKIIIVANS(ph)GSL_
22	TSPKPTKPKASF	12	3 Phospho (STY_TSPKPTKPKAS(ph)PK_
23	TSPKPTKPKASF	12	3 Phospho (STY_TSPKPTKPKAS(ph)PK_
24	TSWIANPSAV	26	2 2 Phospho (S`_T(ph)SWIAN TSWIAN(0.999)PSAVDKLLTI
25	TVNRLSFEKK	10	2 Phospho (STY_T(ph)VN(de)TVN(1)RLSFEKK
26	VDRSDNAAES	25	1 Acetyl (Protei_(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI
27	VDRSDNAAES	25	1 Acetyl (Protei_(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI
28	VDRSDNAAES	25	1 Acetyl (Protei_(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI
29	VNSLIVLESDE	33	1 Phospho (STY_VNSLIVLES(ph)DEEEDEQLVQAADLVEQEFT
30	VNSLIVLESDE	33	1 Phospho (STY_VNSLIVLES(ph)DEEEDEQLVQAADLVEQEFT
31	VNSLIVLESDE	33	1 Phospho (STY_VNSLIVLES(ph)DEEEDEQLVQAADLVEQEFT
32	VQEEETVVPO	15	2 Phospho (STY_VQEEETVVPO(ph)PSKK_
33	VTDRSHYSPL	16	1 Phospho (STY_VTDRSHYS(ph)PLVSEIAK_
34	VTDRSHYSPL	16	1 Phospho (STY_VTDRSHYS(ph)PLVSEIAK_
35	VTILWMGGSC	19	1 Oxidation (M_VT(ph)ILWM(ox)GGSGSIV(VTILWM(1)G)
36	VTILWMGGSC	19	1 Oxidation (M_VT(ph)ILWM(ox)GGSGSIV(VTILWM(1)G)
37	VTILWMGGSC	19	1 Oxidation (M_VT(ph)ILWM(ox)GGSGSIV(VTILWM(1)G)
38	VTKSSSSK	8	2 Phospho (STY_VT(ph)KSSSSK_
39	VTRSTSENIKKI	16	2 Oxidation (M_VTRSTSENIKKM(ox)SGT(ph)VTRSTSENIKKI
40	VTSKPTLELLSI	20	3 2 Phospho (S`_VTSKPTLELLS(ph)PIKPSS(ph)PIK_
41	VTSKPTLELLSI	20	3 2 Phospho (S`_VTSKPTLELLS(ph)PIKPSS(ph)PIK_
42	VVDTLYQKAK	10	2 Phospho (STY_VVDTLY(ph)VVDTLYQ(1)KAK
43	WEEPFYGGSS	13	1 Phospho (STY_WEEPFYGGSS(ph)SPA K_
44	WEEPFYGGSS	13	1 Phospho (STY_WEEPFYGGSS(ph)PAK_

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3 YFIESPHPEVL<sup>1</sup> 13 1 2 Phospho (S<sup>-</sup>Y(ph)FIES(p<sup>+</sup>)YFIESPHPEVLQ(1)K  
4 YKVPQLEIVP<sup>1</sup> 21 2 Oxidation (M<sup>-</sup>YKVPQLEIVPNSAEERLHS(p YKVPQLEIVP<sup>1</sup>  
5 YKVPQLEIVP<sup>1</sup> 21 2 Oxidation (M<sup>-</sup>YKVPQLEIVPNSAEERLHS(p YKVPQLEIVP<sup>1</sup>  
6 YLAVGLLDAT<sup>1</sup> 12 1 Phospho (STY<sup>-</sup>Y(ph)LAVGLLDATVK\_  
7 YLAVGLLDAT<sup>1</sup> 12 1 Phospho (STY<sup>-</sup>Y(ph)LAVGLLDATVK\_  
8 YLNQWLHNLI 10 1 Phospho (STY<sup>-</sup>Y(ph)LNQWIYLN(0.001)Q(0.151)WLHN((  
9 YLTVLLSLTK 11 2 2 Phospho (S<sup>-</sup>Y(ph)LTVLLS(ph)LTK\_  
10 YMKLTCYMKLTQ(1)EILQ(1)K  
11 YNLKTPEAP 9 1 Phospho (STY<sup>-</sup>YN(de)LKT(p YN(1)LKTPEAP  
12 YQGQQNDYIL 17 1 Phospho (STY<sup>-</sup>YQ(de)GQQIYQ(0.25)GQ(0.25)Q(0.25)N|  
13 YRLLSANRAA 14 1 Phospho (STY<sup>-</sup>Y(ph)RLLSAMYRLLSAN(1)RAAAVQ(1)K  
14 YRQAKMRHIC 22 2 Oxidation (M<sup>-</sup>YRQ(de)AKN YRQ(1)AKMR|YRQAKMRHIC  
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	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
AAAPAAVAS(0.995)PAAAAT(0.003)S(0.00	AAAPAAVAS(:	0	0
AAAPAAVASPAAAAT(0.005)S(0.034)ADAS	AAAPAAVAS(:	0	0
AAAPAAVASPAAAAT(0.006)S(0.042)ADAS	AAAPAAVAS(:	0	0
AAAPAAVAS(0.078)PAAAAT(0.34)S(0.427	AAAPAAVAS(:	0	0
AAAPAAVAS(0.004)PAAAAT(0.062)S(0.28	AAAPAAVAS(:	0	0
AAAPAAVAS(0.993)PAAAAT(0.03)S(0.03)	/AAAPAAVAS(:	0	0
AAAPAAVAS(0.985)PAAAAT(0.077)S(0.08	AAAPAAVAS(:	0	0
AAS(0.001)S(0.001)AAAQAI AASSAAAQAM	AAS(-27.34)SI	0	0
ACARGELY(0.814)S(0.183)LVLNT(0.003)K	ACARGELY(6..	1	0
ADEKMVT(1)DEK	ADEKM(80.69ADEKMVT(80	0	0
AIELS(1)PGNALFHAK	AIELS(73.36)F	0	0
AIELS(1)PGNALFHAK	AIELS(80.6)PC	0	0
AKGEILDEVVT(1)LS(1)QIS(1)AKK	AKGEILDEVV	0	0
ALDLLMS(1)Y(1)RLK	ALDLLM(45.4 ALDLLMS(45..	0	0
ALDLLMS(1)Y(1)RLK	ALDLLM(57.1 ALDLLMS(57.	0	0
ALELS(0.008)HLKS(0.992)FVK	ALELS(-21.07)	0	0
ALGGIVLT(0.066)AS(0.934)HNPGGPENDF	ALGGIVLT(-11	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK	ALGGIVLT(0)A	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK	ALGGIVLT(0)A	0	0
ALGGIVLT(0.784)AS(0.216)HNPGGPENDF	ALGGIVLT(5.6	0	0
ALGGIVLT(0.121)AS(0.879)HNPGGPENDF	ALGGIVLT(-8.	0	0
ALGGIVLT(0.098)AS(0.902)HNPGGPENDF	ALGGIVLT(-9.	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK	ALGGIVLT(0)A	0	0
ALGGIVLT(0.204)AS(0.796)HNPGGPENDF	ALGGIVLT(-5.)	0	0
		0	0
		0	0
		0	0
ALGGIVLT(0.5 ALGGIVLTASHN(-0.65)PGGF	ALGGIVLT(0.6	0	1
ALILNRT(1)G/ ALILN(44.61)RTGALN(44.61	ALILNRT(44.6	0	2
ALQAVYPDYVDELS(0.161)LY(0.135)GS(0.7	ALQAVY(-67.3	0	0
ALQAVYPDYVDELS(0.021)LY(0.015)GS(0.9	ALQAVY(-63.3	0	0
ALQAVYPDYVDELS(0.001)LY(0.057)GS(0.9	ALQAVY(-81.2	0	0
ALQAVYPDYVDELS(0.001)LY(0.016)GS(0.9	ALQAVY(-70.6	0	0
ALQAVYPDY(0.002)VDELS(0.04)LY(0.004)I	ALQAVY(-51.2	0	0
		0	0
ALQAVYPDYVDELS(0.996)LY(0.009)GS(0.9	ALQAVY(-75.9	0	0
ALQAVY(0.084)PDY(0.078)VDELS(0.605)L	ALQAVY(-10.4	0	0
APATPQAATSVTNPAAGDGIS(0.001)VQNE APAT(-56.02)		0	0
APATPQAATSVTNPAAGDGIS(0.001)VQNE APAT(-50.33)		0	0
APATPQAATSVTNPAAGDGIS(0.002)VQNE APAT(-39.76)		0	0
APATPQAATSVTNPAAGDGIS(0.004)VQNE APAT(-40.05)		0	0

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2	APATPQAATSVTNPAAGDGIS(0.004)VQNC APAT(-44.28)	0	0	0
3	APS(0.997)LHAPSLHPPHMEAPSLHPPHM(APS(26.22)LH	0	1	0
4	AQDVVGRGAT(1)NILICNK	AQDVVGRGA	0	0
5	AQDVVGRGAT(1)NILICNK	AQDVVGRGA	0	0
6			0	0
7			0	0
8			0	0
9			0	0
10	AQNIS(0.997)PEQS(0.003)GGAGGGGSK	AQNIS(24.87)	1	0
11	ARLVFT(1)EK	ARLVFT(64.82)	1	0
12	ARLVFT(1)EK	ARLVFT(106.2)	1	0
13	ARS(0.999)LS(0.999)NS(0.964)PLY(0.038) ARS(32.82)LS	0	0	0
14	ARS(1)LS(0.989)NS(0.852)PLY(0.16)HRKK	ARS(33.29)LS	0	0
15	ARS(1)LS(1)NS(0.998)PLY(0.003)HRKK	ARS(46.06)LS	0	0
16	ASAFQFS(1)DDEEEVK	AS(-64.04)AFI	0	0
17	ASAFQFS(1)DDEEEVK	AS(-48.64)AFI	0	0
18	ASAFQFS(1)DDEEEVK	AS(-75.24)AFI	0	0
19	ASAFQFS(1)DDEEEVK	AS(-54.82)AFI	0	0
20	ASAFQFS(1)DDEEEVK	AS(-61.47)AFI	0	0
21	ASAFQFS(1)DDEEEVK	AS(-59.12)AFI	0	0
22	ASAFQFS(1)DDEEEVK	AS(-56.8)AFQ	0	0
23	ASAFQFS(1)DDEEEVK	AS(-42.65)AFI	0	0
24	ASAFQFS(1)DDEEEVK	AS(-66.2)AFQ	0	0
25	ASAFQFS(1)DDEEEVK	AS(-67.24)AFI	0	0
26	ASAFQFS(1)DDEEEVK	AS(-96.36)AFI	0	0
27			0	0
28			0	0
29			0	0
30			0	0
31			0	0
32			0	0
33			0	0
34	AS(1)GVTVSDVCK	AS(39.82)GV1	1	0
35	AS(1)GVTVSDVCK	AS(38.57)GV1	1	0
36	AS(1)GVTVSDVCK	AS(40.23)GV1	1	0
37	AS(1)GVTVSDVCK	AS(38.02)GV1	1	0
38	AS(0.977)GVT(0.022)VSDVCK	AS(16.42)GV1	1	0
39	AS(0.997)GVT(0.003)VSDVCK	AS(25.59)GV1	1	0
40	AS(0.42)GVT(0.568)VS(0.012)DVCK	AS(-1.31)GVT	1	0
41	AS(0.998)GVT(0.002)VSDVCK	AS(26.02)GV1	1	0
42	AS(1)GVTVSDVCK	AS(35.02)GV1	1	0
43	AS(0.976)GVT(0.023)VS(0.001)DVCK	AS(16.37)GV1	1	0
44			1	0
45			0	0
46			0	0
47			0	0
48			1	0
49	AS(0.748)RHM ASRHN(47.22)TASRAHVITRI AS(5.52)RHN	0	1	0
50	CIS(1)AVNKQ CISAVN(-36.09)KQ(-29.43)C CIS(58.63)AVI	0	1	0
51	CLPDY(1)ANKLK	CLPDY(43.63)	0	0
52			0	0
53			0	0
54	DLEY(1)FNNL DLEYFN(65.22)N(65.22)LK	DLEY(65.22)F	0	2
55	DLEY(1)FNNL DLEYFN(54.07)N(54.07)LK	DLEY(54.07)F	0	2
56	DMRGTR(1)ILRRK	DM(57.55)RG DMRGTR(57.5)	0	0
57	DRQLSLFT(0.0) DRQ(24.42)SLFTQ(-24.42)V DRQ(44.49)	0	1	0
58	DVDFGDS(1)DNENEPDAYLARLK	DVDFGDS(53.	0	0
59			0	0
60			0	0
61			0	0
62			0	0
63			0	0
64			0	0
65			0	0

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2	DVDFGDS(1)DNENEPDAYLARLK	DVDFGDS(67.	0	0	0
3	DVDFGDS(1)DNENEPDAYLARLK	DVDFGDS(43.	0	0	0
4	DVDFGDS(1)DNENEPDAYLARLK	DVDFGDS(56.	0	0	0
5	DVDFGDS(0.994)DNENEPDAY(0.006)LARI DVDFGDS(22.	0	0	0	
6	DVDFGDS(0.999)DNENEPDAY(0.001)LARI DVDFGDS(31.	0	0	0	
7	EAAAGEDIT(0.001)PLADES(0.999)IK	EAAAGEDIT(-	0	0	0
8	EAAQY(0.933)GT(0.067)VNAVLPK	EAAQY(11.44	0	0	0
9	EAAQY(0.799)GT(0.201)VNAVLPK	EAAQY(6)GT(	0	0	0
10	EANMLQS(1)I EAN(-24.31)N EANM(56.46) EANMLQS(56	0	1	0	
11	EAS(0.012)PVS(0.157)MAS( EASPVSM(53. EAS(-18.36)P\	0	0	0	
12	EAS(0.014)PVS(0.221)MAS( EASPVSM(53. EAS(-17.37)P\	0	0	0	
13	EAS(0.127)PVS(0.465)MAS( EASPVSM(40. EAS(-5.65)PV	0	0	0	
14	EFVFQLHGKMS(0.255)NY(0 EFVFQLHGKM EFVFQLHGKM	0	0	0	
15	EKT(1)DAMAKAQEFLRT(1)K	EKT(46.68)DA	0	0	0
16	ELGNAEPAPSVSSTTVS(0.286)S(0.713)PPA ELGNAEPAPS	0	0	0	
17	ELPDSDSLNVAPPEGFS(1)DEEPEERQCK	ELPDS(-46.35	0	0	0
18	ELPDSDSLNVAPPEGFS(1)DEEPEERQCK	ELPDS(-49.23	0	0	0
19	ELPDSDS(0.001)LNVAPPEGFS(0.999)DEEP ELPDS(-38.75	0	0	0	
20	EMIKILQEQA1 EMIKILQ(0)EQ(0)ALN(19.11 EMIKILQEQA1	0	2	0	
21	ENS(1)PS(1)N EN(-13.93)SPSN(13.93)VAK ENS(49.45)PS	0	1	0	
22	ENTKNLVT(0.1 EN(40.01)TKN(40.01)LVTGE ENT(-37.23)K	0	2	0	
23	ES(1)AQQLEA ESAQ(7.67)Q(-7.67)LEAQ(2! ES(40.73)AQ	0	2	0	
24	ESTPLS(0.351)AS(0.649)PKK	ES(-36.54)T(-	0	0	0
25	ETELMQS(0.001)KIQET(0.999)LGLDPVDK ET(-43.05)EL	0	0	0	
26	ETEQVAQPQF ETEQ(-11.49)VAQ(-11.49)P( ET(-42.33)EQ	0	2	0	
27	ET(1)IADIMRVKT(1)IK	ET(47.55)IADI	0	0	0
28	EVCAQS(0.88 EVCAQ(-12.82)SLQ(-12.82)I EVCAQS(12.8	0	2	0	
29	EVS(1)DDEADDEKK	EVS(51.07)DC	0	0	0
30	FFDS(1)GDYQMAK	FFDSGDYQM(FFDS(40.97)G	0	0	0
31	FFDS(0.994)GDY(0.006)QM FFDSDGYQM(FFDS(22.15)G	0	0	0	
32	FFDS(1)GDYQMAK	FFDSDGYQM(FFDS(36.09)G	0	0	0
33	FMSKNNPY(0 FMSN(-21.26 FM(-38.75)SN FMS(-39.87)N	0	1	0	
34	FS(1)S(1)ELFKEIIK	FS(42.43)S(42	0	0	0
35	GEALT(0.8)S(I GEALTSKQ(20.61)RYQ(-20.6 GEALT(5.85)S	0	1	0	
36	GELQAGKS(1)PFK	GELQAGKS(6:	1	0	0
37	GELQAGKS(1)PFK	GELQAGKS(6(	1	0	0
38	GELQAGKS(1)PFK	GELQAGKS(6(	1	0	0
39	GLGMT(0.906)KINLIT(0.094 GLGM(45.65) GLGMT(9.84)	0	0	0	
40	GPQLEDGKVT GPQ(67.17)LE GPQLEDGKVT GPQLEDGKVT	0	1	0	
41	GQPLVVLS(1) GQ(40.62)PLV GQPLVVLSAM GQPLVVLS(4C	0	1	0	
42	HNNSPNTNL/ HN(0)N(0)SPN(-9.76)TN(-15 HNNS(-46.33)	0	1	0	
43	HNNSPNTNL/ HN(0)N(0)SPN(-4.61)TN(-4. HNNS(-52.12)	0	1	0	
44	IGEGT(0.186)Y(0.809)GVVY(0.006)K	IGEGT(-6.39)\	0	0	0

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2	IIT(0.001)HPN IITHPN(4.6)FN(-4.6)GN(-4.6)IIT(-32.2)HPN	0	2	0
3	IITHPNFNGN1IITHPN(3.85)FN(-3.85)GN(-IIT(-38.2)HPN	0	2	0
4	IKAEHEYRTS((IKAEHEYRTSN IKAEHEYRTSN IKAEHEY(-42..	0	1	0
5	IKPILQAT(0.4!IKPILQ(-16.83IKPILQATQTSIKPILQAT(0)Q	0	2	0
6	IKPILQAT(0.3`IKPILQ(-23.57IKPILQATQTSIKPILQAT(0)Q	0	2	0
7		0	2	0
8		0	2	0
9		0	2	0
10		0	2	0
11		0	2	0
12		0	2	0
13		0	2	0
14	ILFVTESENQA ILFVTESEN(10.6)Q(-10.6)AN ILFVT(-51.46)	0	1	0
15	ILFVTESENQA ILFVTESEN(10.6)Q(-10.6)AN ILFVT(-51.46)	0	1	0
16	INQIQMKET(1IN(-12.2)Q(-1 INQIQM(54.2 INQIQMKET(5	0	2	0
17	IQVQTKQIAQ IQ(-30.74)VQ IQVQTKQIAQ IQVQT(-61.06	0	2	0
18	IQVQTKQIAQ IQ(-21.7)VQ(-IQVQTKQIAQ IQVQT(-54.25	0	2	0
19	IQVQTKQIAQ IQ(0)VQ(0)TKQ(-12.69)IAQ( IQVQT(-41.78	0	2	0
20	IS(1)ENT(0.999)IAIIS(0.061)T(0.94)ELEIQK IS(34.56)ENT(	0	0	0
21	IS(1)MLKQVMS(1)QLIKK ISM(6.54)LKQ IS(57.43)MLK	0	0	0
22	KDFLPLAFQM QAS(0.227)T(KDFLPLAFQM KDFLPLAFQM	0	0	0
23	KDIT(0.837)N KDITN(56.04)LSYKVVK KDIT(9.69)NL	0	1	0
24	KEES(0.181)ES(0.819)EDDD KEESESEDDDI KEES(-6.55)ES	0	0	0
25	KEES(0.209)ES(0.791)EDDD KEESESEDDDI KEES(-5.78)ES	0	0	0
26	KEES(0.074)ES(0.926)EDDD KEESESEDDDI KEES(-10.98)E	0	0	0
27	KEPT(1)PGEK KEPT(41.43)P	0	0	0
28	KIDNPES(0.333)S(0.333)AKVS(0.333)DAEIKIDNPES(0)S(	0	0	0
29	KIDNPES(0.012)S(0.022)AKVS(0.966)DAEIKIDNPES(-19.	0	0	0
30	KIDNPES(0.489)S(0.489)AKVS(0.022)DAEIKIDNPES(0)S(	0	0	0
31	KIDNPES(0.567)S(0.41)AKVS(0.023)DAEEIKIDNPES(1.41	0	0	0
32	KIEKFQS(1)EEQQQTEDELQDK KIEKFQS(34.8	0	0	0
33	KIEKFQS(1)EEQQQTEDELQDK KIEKFQS(54.1	0	0	0
34	KKEEES(1)DQS(1)DDDMGFC KKEEESDQSD  KKEEES(46.14	0	0	0
35	KKEEES(1)DQS(1)DDDMGFC KKEEESDQSD  KKEEES(46.7)	0	0	0
36	KKEEES(1)DQS(1)DDDMGFC KKEEESDQSD  KKEEES(42.09	0	0	0
37	KKEEES(0.035)DQS(0.965)D KKEEESDQSD  KKEEES(-14.3	0	0	0
38	KKQEES(1)DEEFFDLDDIK KKQEES(93.2)	0	0	0
39	KLAFS(0.939)DDES(0.054)T(0.007)PEEHQ  KLAFS(12.41)	0	0	0
40	KLIVNGAS(0.5 KLIVN(62.53)GASSN(62.53) KLIVNGAS(31	0	2	0
41	KMEVLS(1)VC KMEVLSVQ(-6.9)N(6.9)HIQ( KMEVLS(44.5	0	2	0
42	KMKY(1)DFGT(1)LLLLVK KMKY(58.46)I	0	0	0
43	KNKT(0.997)N KN(15.36)KTN(-15.36)RQ(-3 KNKT(30.06)N	1	1	0
44	KPEDPSSEAEALCS(1)PAK KPEDPS(-47.0	0	0	0
45	KPEDPSSEAEALCS(1)PAK KPEDPS(-37.5	0	0	0
46	KPEDPSSEAEALCS(1)PAK KPEDPS(-41.9	0	0	0
47	KPEDPSSEAEALCS(1)PAK KPEDPS(-51.7	0	0	0
48	KPEDPSSEAEALCS(1)PAK KPEDPS(-69.7	0	0	0

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2	KPEDPSSEAEALCS(1)PAK	KPEDPS(-49.5	0	0	0
3	KQEES(1)DEEFFDLDDIK	KQEES(130.5	0	0	0
4	KS(0.928)APC KSAPQ(47.92)SRQ(47.92)SC KS(13.71)APC	0	2	0	
5	KS(1)KPT(0.95) KSKPTAAVTPIQ(46.34)K	KS(43.28)KPT	0	1	0
6	KVT(1)T(0.997)IGLNS(0.003)TAATK	KVT(37.94)T(	0	0	0
7	KVT(1)WIGAN KVTWIGAN(5.27)GDQ(-5.27)KVT(40.09)W	0	1	0	
8	LDLT(0.002)I\ LDLTIVDLM(-9.21)DEVQ(-3.8)LDLT(-26.77)I	0	1	0	
9	LENLAY(0.472)EKS(0.53)EDI LENLAYEKSEL LENLAY(-0.55	0	0	0	
10	LFEPPVT(0.001)MRDMLKS(0.016)LS(0.20)LFEPPVT(-31.	0	0	0	
11	LGIDIGDRLQAT(1)S(1)RK	LGIDIGDRLQA	0	0	0
12	LLDFNLLDT(0.999)DDDDDEEGDEEDKEDT\ LLDFNLLDT(3	0	0	0	
13	LNENFVT(1)I\ LN(9)EN(9)FVTIN(-7.29)IQ(7 LNENFVT(41.	0	3	0	
14	LRFDNFNS(0.95 LRFDFN(-32.02)SKAAMTIEC LRFDNFNS(20.	0	1	0	
15	LRT(0.242)S(C LRTSPN(50.04)EQ(50.04)Q( LRT(-4.96)S(4	0	3	0	
16	LSVQS(1)PPK	LS(-82.61)VQ	0	0	0
17	LT(1)NGQRQI LTN(-22.9)GC LTNGQRQM(\ LT(53.12)NGC	0	2	0	
18	LT(0.999)NGC LTN(-20.27)G LTNGQRQM(\ LT(40.05)NGC	0	2	0	
19	MESTTIVFVTI MESTTIVFVTI M(54.95)EST\ MES(-53.59)T	0	1	0	
20	MFLT(1)QQQ MFLTQ(-17.6)M(49.63)FLTC MFLT(49.63)C	0	2	0	
21	MFLT(1)QQQ MFLTQ(-8.51)M(68.68)FLTC MFLT(68.68)C	0	2	0	
22	MGHLQLDFHS(1)IPK	M(44.69)GHL MGHLQLDFH	1	0	0
23	MHKLIMRS(1)VINNLK	M(59.98)HKLI MHKLIMRS(5	0	0	0
24	MIRAT(0.001)S(0.001)CALSM(42.82)IRAT MIRAT(-36.1)	0	0	0	
25	MLNRCLELVT MLN(55.75)R M(55.75)LNR MLNRCLELVT	0	1	0	
26			0	1	0
27	MLVRRLLQEL MLVRRLLQ(4:M(41.42)LVRI MLVRRLLQEL	0	2	0	
28	MNDS(0.993)FGDFNAT(0.0)M(76.82)NDS MNDS(22.16)	1	0	0	
29	MPNLQS(0.857)S(0.121)IP\ M(56.2)PNLQ MPNLQS(8.45	1	0	0	
30	MPNLQS(0.492)S(0.492)IP\ M(40.24)PNL\ MPNLQS(0)S(	1	0	0	
31	MPNLQS(0.778)S(0.175)IP\ M(47.71)PNL\ MPNLQS(6.47	1	0	0	
32	MPNLQS(0.497)S(0.497)IP\ M(58.89)PNL\ MPNLQS(0)S(	1	0	0	
33	MQHS(0.5)S(I MQ(38.01)HS M(19.78)QHS MQHS(0)S(0)I	0	1	0	
34	MQIFVKT(0.5 MQ(42.8)IFVKTLTGK	MQIFVKT(0)L	1	1	0
35	MQLILS(0.69)MQ(-7.66)LILSYLQ(7.66)SQ( MQLILS(7.66)	1	3	0	
36	MQLILS(0.24)MQ(-25.8)LILSYLQ(25.8)SQ( MQLILS(-4.01	1	3	0	
37			1	3	0
38			1	3	0
39	MQLILS(0.97)MQ(7.74)LILS M(44.25)QLIL MQLILS(19.37	0	2	0	
40	MQLILS(0.20)MQ(-13.61)LI M(43.69)QLIL MQLILS(-5.35	0	2	0	
41			0	2	0
42			0	2	0
43	MRDKIS(1)QL MRDKISQ(-15 M(62.09)RDK MRDKIS(62.0	1	1	0	
44	MRDKIS(1)QL MRDKISQ(-15 M(54.34)RDK MRDKIS(54.3	1	1	0	
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3	MRDKIS(1)QL MRDKISQ(-10 M(56.2)RDKIS MRDKIS(56.2)	1	1	0
4	MRDKIS(1)QL MRDKISQ(-17 M(51.13)RDK MRDKIS(51.1)	1	1	0
5	MRDKIS(1)QL MRDKISQ(-12 M(51.46)RDK MRDKIS(51.4)	1	1	0
6	MRDKIS(1)QL MRDKISQ(-4. M(43.8)RDKIS MRDKIS(43.8)	1	1	0
7	MRFIS(0.025) MRFISQ(0.64 M(45.21)RFIS MRFIS(-15.4)	1	1	0
8	MSGALKS(0.7 MSGALKSQ(-1 M(50.15)SGA MS(-33.15)GA	1	1	0
9	MS(0.417)LIH MSЛИHSFVTQ(M(54.77)SLIH MS(0)LIHS(0)	0	1	0
10	MS(0.002)QGAS(0.01)EVPLS(0.988)ALRLK MS(-26.68)QC	1	0	0
11	MS(1)T(1)IVRK	MS(44.98)T(4	0	0
12	MS(0.5)T(0.5)MSTLLEN(7.5 M(43.21)STLL MS(0)T(0)LLE	0	2	0
13	MTEIELPVESVPS(0.051)AS(( M(60.73)TEIE MT(-56.15)EII	0	0	0
14	MTIFNLY(1)IFDK	M(46.88)TIFN MT(-34.52)IFI	0	0
15	MVEPSPETVGDFQSVQEEVE M(86.56)VEP! MVEPS(-69.6	0	0	0
16	MVEPSPETVGDFQS(0.245)\ M(50.26)VEP! MVEPS(-41.7	0	0	0
17	MVEPSPETVGDFQS(0.001)\ M(50.32)VEP! MVEPS(-37.1	0	0	0
18	MY(0.401)NI\ MYN(63.42)IYVLKK	MY(-1.74)NIY	0	1
19	MY(0.636)NI\ MYN(53.77)IYVLKK	MY(2.43)NIY(	0	1
20	NAGGVGVGVGEKS(1)PDLK	NAGGVGVGV	0	0
21	NAGGVGVGVGEKS(1)PDLK	NAGGVGVGV	0	0
22	NAGGVGVGVGEKS(1)PDLK	NAGGVGVGV	0	0
23	NAGGVGVGVGEKS(1)PDLK	NAGGVGVGV	0	0
24			0	0
25			0	0
26			0	0
27			0	0
28			0	0
29			0	0
30			0	0
31			0	0
32			0	0
33	NAGGVGVGVGEKS(1)PDLKK	NAGGVGVGV	0	0
34	NAGGVGVGVGEKS(1)PDLKK	NAGGVGVGV	0	0
35	NGGILNY(1)\ N(13.8)GGILN NGGILNY(4 NGGILNY(49.	0	1	0
36	NIWKDKT(1)F N(31.96)IWKDKTPN(-31.96)NIWKDKT(52.	0	1	0
37	NKEPLIQIAM\ N(8)KEPLIQ(-\ NKEPLIQIAM( NKEPLIQIAM\	0	1	0
38	NKLQKNHALI\ N(32.5)KLQ(32.5)KN(32.5)H NKLQKNHALI\	0	4	0
39	NLKLMQMAS(1 N(12.81)LKLC NLKLQM(41.€ NLKLQMAS(4	0	1	0
40	NNIKLKCLIDT\ N(-18.42)N(-18.42)IKLKCLID NNIKLKCLIDT\	1	1	0
41	NS(0.002)QY(0.97)ERES(0.029)LLK	NS(-27.81)QY	0	0
42			0	0
43			0	0
44			0	0
45			0	0
46			0	0
47	NVGIFIKDDS(1)DEEDVDDKK	NVGIFIKDDS(	0	0
48	NVGIFIKDDS(1)DEEDVDDKK	NVGIFIKDDS(	0	0
49	NVGIFIKDDS(1)DEEDVDDKK	NVGIFIKDDS(	0	0
50	NY(1)PFNIEF N(41.43)YPFN(41.43)IEF	NY(41.43)PFN	0	2
51	PCNLY(0.854)QT(0.146)AQEQLK	PCNLY(7.67)C	0	0
52	PCNLY(0.962) PCN(24.93)LYQ(-24.93)TAQ PCNLY(14.07)	0	1	0
53	PLMQLIIQDTGIGMT(1)K	PLM(40.86)Q PLMQLIIQDT(	0	0
54	PLPS(1)GRIPQIT(0.999)PPAS(0.001)PK	PLPS(41.55)G	0	0
55	PLPS(1)GRIPQIT(0.997)PPAS(0.004)PK	PLPS(33.2)GR	0	0
56	PTVAAAACKPAADDDEDVDLFGS(1)DDEEDE PT(-35.3)VAA	0	0	0
57	QELLQS(0.87\ Q(51.95)ELLC QELLQS(5\ QELLQS(8.31)	0	2	1
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3	QELLQS(0.84)Q(41.43)ELLC QELLQSYM(4)QELLQS(7.5)Y	0	2	1
4	QELLQS(0.24)Q(45.02)ELLQ(45.02)SYMK QELLQS(-4.96	0	2	1
5	QHS(0.009)F1Q(50.79)HSFTSSSALK	QHS(-16.7)FT	0	1
6				0
7	QISIGIY(1)ELLK	QIS(-47.73)IG	0	0
8	QISIGIY(1)ELLK	QIS(-48.31)IG	0	0
9	QISIGIY(1)ELLK	QIS(-46.94)IG	0	0
10	QIS(0.001)IGIY(0.999)ELLK	QIS(-32.34)IG	0	0
11	QISIGIY(1)ELLK	QIS(-55.01)IG	0	0
12	QISIGIY(1)ELLK	QIS(-38.47)IG	0	0
13	QISIGIY(1)ELLK	QIS(-43.94)IG	0	0
14	QISIGIY(1)ELLK	QIS(-39.86)IG	0	0
15	QISIGIY(1)ELLK	QIS(-57.55)IG	0	0
16	QISIGIY(1)ELLK	QIS(-35.76)IG	0	0
17	QISIGIY(1)ELLK	QIS(-50.69)IG	0	0
18	QISIGIY(1)ELLK	QIS(-47.93)IG	0	0
19	QISIGIY(1)ELLK	QIS(-49.83)IG	0	0
20	QISIGIY(1)ELLK	QIS(-53)IGIY(1)	0	0
21	QISIGIY(1)ELLK	QIS(-39.44)IG	0	0
22	QISIGIY(1)ELLK	QIS(-55.72)IG	0	0
23	QISIGIY(1)ELLK	QIS(-52.88)IG	0	0
24	QISIGIY(1)ELLK	QIS(-36.23)IG	0	0
25	QIS(1)VRGIAEVGNVTEVK	QIS(75.86)VR	0	0
26	QIS(1)VRGIAEVGNVTEVK	QIS(45.62)VR	0	0
27	QIS(1)VRGIAEVGNVTEVKK	QIS(87.21)VR	0	0
28		0	0	1
29		0	0	1
30		0	0	1
31		0	0	1
32		0	0	1
33		0	0	1
34		0	0	1
35		0	0	1
36		0	0	1
37	QIVPLLNY(1)Q(75.74)IVPLLN(75.74)YK	QIVPLLNY(75.	0	2
38	QKES(1)GEFPEVGK	QKES(64.64)C	0	0
39	QKFIT(0.5)T(CQ(12.07)KFIT QKFITTEDVNI QKFIT(0)T(0)E	0	1	0
40	QLRDLET(1)ELDEERK	QLRDLET(50.9	0	0
41	QLRDLET(1)ELDEERK	QLRDLET(46.8	0	1
42	QLRDLET(1)ELDEERK	QLRDLET(46.8	0	1
43	QLSIIRQKS(1)Q(28.76)LSIIRQ(-28.76)KSLIQLS(-42.53)III	0	1	1
44	QMPDVETTEQ(47.51)MPDQM(47.51)PDQMPDVET(-3	0	1	0
45	QNDLIHDRS(1)LINK	QNDLIHDRS(E	0	0
46	QNDLIHDRS(1)LINK	QNDLIHDRS(E	0	1
47	QNDLIHDRS(1)LINK	QNDLIHDRS(E	0	1
48	QRDLPAAPRES(0.569)QS(0.42)RS(0.011)K	QRDLPAAPRES	0	0
49	QS(0.023)LIMQ(28.35)SLIMQSLIM(45.37)QS(-16.46)LIN	0	1	0
50	QSSYHGVHQAWNT(0.042)NQDS(0.957)K	QS(-41.5)S(-4	0	0
51	QSSYHGVHQAWNT(0.028)NQDS(0.972)K	QS(-47.65)S(-	0	1
52	QSSYHGVHQAWNT(0.042)NQDS(0.958)K	QS(-80.23)S(-	0	1
53	QSSYHGVHQAWNT(0.001)NQDS(0.999)K	QS(-87.48)S(-	0	1
54	QSSYHGVHQAWNT(0.01)NQDS(0.99)K	QS(-52.27)S(-	0	1
55	QSSYHGVHQAWNT(0.025)NQDS(0.975)K	QS(-60.4)S(-6	0	1

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3	QSSYHGVHQAWNT(0.005)NQDS(0.995)K QS(-73.94)S(-	0	0	1
4	QSSYHGVHQAWNT(0.128)NQDS(0.872)K QS(-48.42)S(-	0	0	1
5	QS(0.014)VPC Q(21.8)SVPQ(21.8)LAN(20.:QS(-21.8)VPC	0	3	0
6	QS(0.005)VPC Q(13.41)SVPQ(14.75)LAN(5 QS(-25.08)VP	0	3	0
7	QS(0.006)VPC Q(11.59)SVPQ(18.04)LAN(6 QS(-24.64)VP	0	3	0
8		0	3	0
9		0	3	0
10				
11				
12	QVEPRQLVRN Q(-32.88)VEP QVEPRQLVRN QVEPRQLVRN	0	1	0
13	QVRT(1)NLQE Q(0)VRTN(0)LQ(0)EIQ(30.0)QVRT(64.82)I	0	2	1
14		0	2	1
15				
16	REEENAAAAAEEEAGEISAT(0.01)GGAT(0.21 REEENAAAAAE	0	0	0
17	REEENAAAAAEEEAGEISAT(0.001)GGAT(0.4 REEENAAAAAE	0	0	0
18	REEENAAAAAEEEAGEIS(0.005)AT(0.02)GG/REEENAAAAAE	0	0	0
19	RGCQILGLNK' RGCQ(16.13)ILGLN(-16.13)I RGCQILGLNK'	0	1	0
20	RGCQILGLNK' RGCQ(7.33)ILGLN(-7.33)KY( RGCQILGLNK'	0	1	0
21	RGCQILGLNK' RGCQ(33.24)ILGLN(-33.24)I RGCQILGLNK'	0	1	0
22	RGPPPPPT(0.1 RGPPPPPTASESTRRN(43.11 RGPPPPPT(-2	0	1	0
23		0	1	0
24				
25		0	1	0
26				
27		0	1	0
28				
29	RIAS(0.064)FKNY(0.898)IS(0.037)K RIAS(-11.45)F	0	0	0
30	RIQEYV(1)LQI RIQ(-12.87)EVYLQ(12.87)K RIQEYV(55.06	0	1	0
31	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-5)	0	0	0
32	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-4)	0	0	0
33	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-4)	0	0	0
34	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-3)	0	0	0
35	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-4)	0	0	0
36	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-3)	0	0	0
37	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-4)	0	0	0
38	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-3)	0	0	0
39	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-4)	0	0	0
40	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-4)	0	0	0
41	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-4)	0	0	0
42	RKKPEDPSSEAEALCS(1)PAK RKKPEDPS(-5)	0	0	0
43	RMASSEQPT( RMASSEQ(0)FRM(67.65)AS:RMAS(-37.42	0	1	0
44	RPLMLQGHEF RPLMLQ(40.43)GHERSITQ( RPLMLQGHEF	1	2	0
45		1	2	0
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48	SAAVAEGGDAVAET(0.733)AKGEEGS(0.26 S(-42.23)AAV	0	0	0
49	SAAVAEGGDAVAET(0.901)AKGEEGS(0.09 S(-58.47)AAV	0	0	0
50	SAAVAEGGDAVAET(0.614)AKGEEGS(0.38 S(-39.38)AAV	0	0	0
51	S(0.001)AAVAEGGDAVAET(0.702)AKGEECS(-28.94)AAV	0	0	0
52	SAAVAEGGDAVAET(0.209)AKGEEGS(0.79 S(-48.44)AAV	0	0	0
53	SAEAEAIVTTATADVS(0.307)S(0.514)PS(0..S(-107.65)AE/	1	0	0
54	SAEAEAIVTTATADVS(0.034)S(0.483)PS(0..S(-78.78)AE/	1	0	0
55	SAEAEAIVTTATADVS(0.051)S(0.77)PS(0.1 S(-102.74)AE/	1	0	0
56	SAEAEAIVTTATADVS(0.007)S(0.496)PS(0..S(-76.49)AE/	1	0	0
57	SAEAEAIVT(0.022)T(0.02)AT(0.067)ADVS(S(-61.37)AEA/	1	0	0
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2	SAEAEAI <sup>T</sup> TATADVS(0.01)S(0.495)PS(0.4)S(-54.67)AEA	1	0	0
3	SAEAEAI <sup>T</sup> T(0.001)AT(0.004)ADVS(0.046 S(-61.79)AEA	1	0	0
4	SAEAEAI <sup>T</sup> TATADVS(0.019)S(0.957)PS(0.1)S(-108.85)AE	1	0	0
5	SAEAEAI <sup>T</sup> TATADVS(0.041)S(0.479)PS(0.)S(-81.76)AEA	1	0	0
6	SAEAEAI <sup>T</sup> TATADVS(0.047)S(0.743)PS(0.)S(-102.8)AEA	1	0	0
7	SAEAEAI <sup>T</sup> TATADVS(0.48)S(0.329)PS(0.1)S(-50.28)AEA	1	0	0
8	SAEAEAI <sup>T</sup> TATADVS(0.045)S(0.421)PS(0.)S(-119.63)AE	1	0	0
9	SAEAEAI <sup>T</sup> TAT(0.001)ADVS(0.035)S(0.37 S(-66.49)AEA	1	0	0
10	SAEAEAI <sup>T</sup> TATADVS(0.007)S(0.783)PS(0.)S(-112.12)AE	1	0	0
11	SAEAEAI <sup>T</sup> TATADVS(0.052)S(0.762)PS(0.)S(-82.71)AEA	1	0	0
12	SAEAEAI <sup>T</sup> (0.01)T(0.012)AT(0.04)ADVS(0 S(-39.1)AEAE	1	0	0
13	SAEAEAI <sup>T</sup> TATADVS(0.067)S(0.467)PS(0.)S(-77.93)AEA	1	0	0
14	SAEAEAI <sup>T</sup> TATADVS(0.021)S(0.489)PS(0.)S(-77.91)AEA	1	0	0
15	SAEAEAI <sup>T</sup> T(0.002)AT(0.006)ADVS(0.174 S(-40.69)AEA	1	0	0
16	SAEAEAI <sup>T</sup> TATADVS(0.035)S(0.71)PS(0.2)S(-81.87)AEA	1	0	0
17	SAEAEAI <sup>T</sup> TATADVS(0.175)S(0.771)PS(0.)S(-108.29)AE	1	0	0
18	SAEAEAI <sup>T</sup> TATADVS(0.035)S(0.813)PS(0.)S(-91.77)AEA	1	0	0
19	SAEAEAI <sup>T</sup> TATADVS(0.008)S(0.158)PS(0.)S(-76.74)AEA	1	0	0
20	SAEAEAI <sup>T</sup> TATADVS(0.066)S(0.717)PS(0.)S(-108.3)AEA	1	0	0
21	SAEAEAI <sup>T</sup> TATADVS(0.185)S(0.408)PS(0.)S(-80.53)AEA	1	0	0
22	SAEAEAI <sup>T</sup> TATADVS(0.018)S(0.396)PS(0.)S(-55.82)AEA	1	0	0
23	SAEAEAI <sup>T</sup> TATADVS(0.068)S(0.878)PS(0.)S(-89.55)AEA	1	0	0
24		1	0	0
25	SASIRILNLINS SASIRILN(-15. SASIRILNLINS S(-45.57)AS(-	0	1	0
26	S(0.015)DS(0.015)AVAT(0.71)S(0.194)AS( S(-16.63)DS(-	1	0	0
27	S(0.01)DS(0.01)AVAT(0.112)S(0.693)AS(0 S(-18.26)DS(-	1	0	0
28	SDSAVAT(0.333)S(0.333)AS(0.333)PVAAP S(-34.71)DS(-	1	0	0
29	S(1)ET(1)VDS(1)T(1)EVK S(47.19)ET(47	1	0	0
30	S(0.55)HS(0.449)PPPAS(0.001)NCEEALIQL S(0.88)HS(-0.	1	0	0
31	S(0.984)IQNLNT(0.016)RDPFADAIIK S(17.92)IQNL	1	0	0
32	S(0.955)IQNLNT(0.045)RDPFADAIIK S(13.27)IQNL	1	0	0
33	S(0.89)IS(0.11)EFVDLEAEDAGK S(9.1)IS(-9.1)I	0	0	0
34		0	0	0
35	S(0.193)IT(0.578)MS(0.578)SITM(-11.71)S(-6.05)IT(0)I	0	0	0
36	S(0.239)IT(0.275)MS(0.533)SITM(40.18)S S(-4.82)IT(-4.8	0	0	0
37	SK_	0	0	0
38	S(0.5)KKS(0.5 SKSWQ(45.36)ARHTGIK S(0)KKS(0)WC	0	1	0
39	S(0.5)LS(0.5)FSLSRLN(52.58 SLSRLNTLM(5 S(0)LS(0)RLN1	1	1	0
40	S(0.889)LY(0.111)RISARK S(9.03)LY(-9.0	1	0	0
41	SPIVFELT(0.001)QPS(0.999)PEK S(-54.97)PIVF	0	0	0
42	SPIVFELT(0.001)QPS(0.999)PEK S(-67.16)PIVF	0	0	0
43	SPIVFELT(0.001)QPS(0.999)PEK S(-63.62)PIVF	0	0	0
44	SPIVFELTQPS(1)PEK S(-86.11)PIVF	0	0	0

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2	SPIVFELTQPS(1)PEK	S(-70.03)PIVF	0	0	0
3	S(1)PIVFELT(0.009)QPS(0.991)PEK	S(40.41)PIVFE	0	0	0
4	S(0.773)RAS((S)RASFLAQ(4.71)N(-4.71)SS(S(6.47)RAS(-6	0	1	0	
5	S(1)RKHKENL SRKHKEN(58.59)LLK	S(58.59)RKHK	0	1	0
6	S(0.397)S(0.397)ENS(0.206)EY(0.038)Y(0. S(0)S(0)ENS(-	1	0	0	
7	S(0.51)S(0.51 SSLSVKPN(46.89)YTLK	S(0)S(0)LS(9.2	0	1	0
8	STGQLQQLS(( STGQ(-23.59)LQ(-11.38)Q(- S(-72.86)T(-7:	0	3	0	
9	S(0.997)VFAEAY(0.003)DPEADDDDGAT/S(24.92)VFAE	0	0	0	
10	S(0.06)VHS(0.94)PNPGLILQSK	S(-11.98)VHS	1	0	0
11	S(0.003)VHS(0.997)PNPGLILQSK	S(-25.47)VHS	1	0	0
12	S(0.002)VHS(0.998)PNPGLILQSK	S(-27.48)VHS	1	0	0
13	S(0.008)VHS(0.992)PNPGLILQSK	S(-21.15)VHS	1	0	0
14	T(0.001)ELAA TELAAKCLASSLVSQ(-4.24)GK' T(-28.81)ELA/	0	1	0	
15	T(0.016)IKY(0.984)LKRVK	T(-17.9)IKY(1	0	0	0
16	T(1)KIKIHYIEMT(1)NVHAK	T(39.99)KIKIH	0	0	0
17	T(0.232)LLNT(0.322)S(0.426)PNLLPIT(0.0:T(-2.64)LLNT(	0	0	0	
18	T(0.235)LPRNY(0.765)IHRELP(S(0.839)NLT T(-5.33)LPRN'	0	0	0	
19	T(0.032)NIS(0.963)RLGNY(0.005)FK	T(-14.81)NIS(	1	0	0
20	T(1)RRFDEVQ TRRFDEVQ(6:TRRFDEVQM(T(56.33)RRFD	0	2	0	
21	T(0.971)S(0.03)KKIVANS(0.992)GS(0.006 T(15.33)S(-15	0	0	0	
22	TSPKPT(0.028)KPAS(0.972)PK	T(-33.19)S(-3:	0	0	0
23	TSPKPT(0.079)KPAS(0.921)PK	T(-51.25)S(-4:	0	0	0
24	T(0.432)S(0.4 TSWIAN(33.19)PSAVDKLLTIT(0)S(0)WIAN	0	1	0	
25	T(0.98)VNRLS TVN(61.16)RLSFEKK	T(16.84)VNRL	0	1	0
26	VDRS(0.006)DNAAES(0.994)FDDAVEERVII VDRS(-22.51)	1	0	0	
27	VDRS(0.003)DNAAES(0.997)FDDAVEERVII VDRS(-24.86)	1	0	0	
28	VDRS(0.007)DNAAES(0.993)FDDAVEERVII VDRS(-21.63)	1	0	0	
29	VNS(0.002)LIVLES(0.998)DEEEDEQLVQAA VNS(-28.14)L	0	0	0	
30	VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA VNS(-29.34)L	0	0	0	
31	VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA VNS(-31.63)L	0	0	0	
32	VQEEET(0.008)VVPQS(0.566)PS(0.426)KK VQEEET(-18.4	0	0	0	
33	VTDRS(0.002)HY(0.002)S(0.996)PLVSEIAK VT(-36.61)DR	0	0	0	
34	VT(0.001)DRS(0.001)HY(0.016)S(0.983)PL VT(-31.81)DR	0	0	0	
35	VT(0.996)ILWMGG(S(0.003) VTILWM(47.5 VT(24.72)ILW	0	0	0	
36	VT(0.996)ILWMGG(S(0.002) VTILWM(42.3 VT(27.11)ILW	0	0	0	
37	VT(0.999)ILWMGG(S(0.001) VTILWM(42.0 VT(32.61)ILW	0	0	0	
38	VT(0.999)KSSSSK	VT(37.92)KS(-	0	0	0
39	VTRS(0.001)T(0.001)S(0.00:VTRSTSENIKVT(-38.2)RS(-	0	0	0	
40	VT(0.007)S(0.018)KPT(0.035)LELLS(0.946)VT(-22.82)S(-	0	0	0	
41	0	0	0	0	0
42	VVDT(0.012)VVDTLYQ(61.76)KAK	VVDT(-19.29)	0	1	0
43	WEEPFY(0.002)GGS(0.885)S(0.114)PAK	WEEPFY(-27.1	0	0	0
44	WEEPFY(0.001)GGS(0.472)S(0.528)PAK	WEEPFY(-28.4	0	0	0

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3 Y(1)FIES(1)PH YFIESPHPEVLQ(45.08)K Y(45.08)FIES(· 0 1 0  
4 YKVPQLEIVPNS(0.166)AEER YKVPQLEIVPN Y(-53.17)KVP( 0 0 0  
5 YKVPQLEIVPNS(0.211)AEER YKVPQLEIVPN Y(-51.88)KVP( 0 0 0  
6 Y(1)LAVGLLDATVK Y(60.29)LAVG 0 0 0  
7 0 0 0  
8 0 0 0  
9 Y(1)LNQWLHI YLN(-30.03)Q(-7.5)WLHN(7 Y(56.92)LNQ\ 0 1 0  
10 Y(0.999)LT(0.001)VLLS(0.5)LKT(0.5)K Y(27.41)LT(-2 0 0 0  
11 Y(1)MKLTQEII YMKLTO(70.94)EILQ(70.94) Y(40.77)MKL\ 0 2 0  
12 Y(0.32)NLKT(I YN(57.05)LKTPEAP Y(-3.27)NLKT( 0 1 0  
13 YQGQQNDYIL YQ(0)GQ(0)Q(0)N(0)DYILISLY(-62.08)QGC 0 1 0  
14 Y(0.999)RLLS(YRLLSAN(53.38)RAAAVQ(53 Y(32.42)RLLS( 0 2 0  
15 YRQAKMRHIC YRQ(47.73)A YRQAKM(-46. Y(-34.93)RQA 0 1 0  
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Oxidation (M)	Phospho (STY)	Missed cleavages	Proteins	Leading Protein	Ratio	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;Q86I E2QD63	E2QD63	HIP-R;HIP	
0	1	0	E2QD63;Q86I E2QD63	E2QD63	HIP-R;HIP	
0	3	2	A0A0B4LFB8; A0A0B4LFB8	A0A0B4LFB8	Opa1;opa1-lil	
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	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	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	

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3	0	1	1 AOA0B4LGC0;AOA0B4LGC0 AOA0B4LGC0 TppII		
4	1	1	0 A4V201;E1JI1A4V201 A4V201 Taf4		
5	0	1	0 REV__Q8I725 REV__Q8I725		
6	0	1	0 REV__Q8I725 REV__Q8I725		
7	0	1	0 REV__Q8I725 REV__Q8I725		
8	0	1	0 Q9VTY6 Q9VTY6 Q9VTY6 vih		
9	0	1	0 Q8T3J9 Q8T3J9 Q8T3J9		
10	0	1	0 Q8T3J9 Q8T3J9 Q8T3J9		
11	0	1	1 Q8I0A1 Q8I0A1 Q8I0A1 SNF4Agamma		
12	0	3	1 Q8I0A1 Q8I0A1 Q8I0A1 SNF4Agamma		
13	0	3	1 Q8I0A1 Q8I0A1 Q8I0A1 SNF4Agamma		
14	0	3	1 Q8I0A1 Q8I0A1 Q8I0A1 SNF4Agamma		
15	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
16	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
17	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
18	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
19	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
20	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
21	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
22	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
23	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
24	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
25	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
26	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
27	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
28	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
29	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
30	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
31	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
32	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
33	0	1	0 AOA0B4LFL2;AOA0B4LFL2 AOA0B4LFL2 eIF3-S8		
34	0	1	0 P45594 P45594 P45594 tsr		
35	0	1	0 P45594 P45594 P45594 tsr		
36	0	1	0 P45594 P45594 P45594 tsr		
37	0	1	0 P45594 P45594 P45594 tsr		
38	0	1	0 P45594 P45594 P45594 tsr		
39	0	1	0 P45594 P45594 P45594 tsr		
40	0	1	0 P45594 P45594 P45594 tsr		
41	0	1	0 P45594 P45594 P45594 tsr		
42	0	1	0 P45594 P45594 P45594 tsr		
43	0	1	0 P45594 P45594 P45594 tsr		
44	0	1	0 P45594 P45594 P45594 tsr		
45	0	1	0 P45594 P45594 P45594 tsr		
46	0	1	0 P45594 P45594 P45594 tsr		
47	0	1	0 P45594 P45594 P45594 tsr		
48	0	1	0 P45594 P45594 P45594 tsr		
49	0	2	0 Q8IH82 Q8IH82 Q8IH82 grsm		
50	0	2	2 A4V449;Q6N A4V449 A4V449 ND75		
51	0	1	1 F3YDM3;Q6A F3YDM3 F3YDM3 CG32068-RB;		
52	0	1	1 F3YDM3;Q6A F3YDM3 F3YDM3 CG32068-RB;		
53	0	1	0 Q9V5R2;A1Z Q9V5R2 Q9V5R2 Pex6		
54	0	1	0 Q9V5R2;A1Z Q9V5R2 Q9V5R2 Pex6		
55	0	1	0 M9PBZ3;M9F M9PBZ3 M9PBZ3 spen		
56	0	1	1 Q9VBX4 Q9VBX4 Q9VBX4 CG31510-RA		
57	0	1	0 B5RJ65;Q053 B5RJ65 B5RJ65 Ssrp-RA;Ssrp		
58	1				
59	0				
60	0				
61	0				

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3	0	1	0 B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
4	0	1	0 B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
5	0	1	0 B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
6	0	1	0 B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
7	0	1	0 B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
8	0	1	0 B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
9	0	1	0 Q86BM5;Q9\ Q86BM5;Q9\ Q86BM5	Akap200	
10	0	1	0 Q9VAN0 Q9VAN0	Q9VAN0	CG11899
11	0	1	0 Q9VAN0 Q9VAN0	Q9VAN0	CG11899
12	2	1	0 D7FAM9;D7F D7FAM9	D7FAM9	gr97a;Gr97a-
13	1	1	1 P28668;H8F4 P28668	P28668	Aats-glupro;A
14	1	1	1 P28668;H8F4 P28668	P28668	Aats-glupro;A
15	1	1	1 P28668;H8F4 P28668	P28668	Aats-glupro;A
16	1	1	2 Q7KTG2 Q7KTG2	Q7KTG2	Apolt
17	0	2	2 A0A0C4DHG6 A0A0C4DHG6 A0A0C4DHG6 Gel		
18	0	1	0 Q8SYN6;Q9V\ Q8SYN6	Q8SYN6	CG8209
19	0	1	0 Q9VNH5 Q9VNH5	Q9VNH5	
20	0	1	0 Q9VNH5 Q9VNH5	Q9VNH5	
21	0	1	0 Q9VNH5 Q9VNH5	Q9VNH5	
22	0	1	1 Q9VP27;M9P Q9VP27	Q9VP27	Glg1
23	0	2	2 O61380;A8D\ O61380	O61380	eIF4G
24	0	1	1 Q9VHR8-2;Q\ Q9VHR8-2	Q9VHR8-2	DppIII;CG561
25	0	2	0 M9NGE4;M9\ M9NGE4	M9NGE4	mud
26	0	1	1 Q8T410;Q0K\ Q8T410	Q8T410	Cnx99A;Cnx1\
27	0	1	1 Q9V9Z1 Q9V9Z1	Q9V9Z1	mRpL32
28	0	1	0 Q9XZ34;Q4V\ Q9XZ34	Q9XZ34	Rif1;CG30085
29	0	2	1 P91875 P91875	P91875	Rpl1
30	0	1	1 Q0PQ31;Q0P Q0PQ31	Q0PQ31	Klp61F
31	0	1	1 M9PBL3;P02\ M9PBL3	M9PBL3	Hsp83
32	1	1	0 Q9VUB8 Q9VUB8	Q9VUB8	endos
33	1	1	0 Q9VUB8 Q9VUB8	Q9VUB8	endos
34	1	1	0 Q9VUB8 Q9VUB8	Q9VUB8	endos
35	1	1	1 Q8IA36;Q9W Q8IA36	Q8IA36	mRpS29
36	0	2	1 Q6V6U1;Q6V Q6V6U1	Q6V6U1	nec
37	0	2	1 Q9U6X3;Q9V Q9U6X3	Q9U6X3	MTA1-like
38	0	1	1 Q9VRQ4 Q9VRQ4	Q9VRQ4	
39	0	1	1 Q9VRQ4 Q9VRQ4	Q9VRQ4	
40	0	1	1 Q9VRQ4 Q9VRQ4	Q9VRQ4	
41	1	1	1 Q9VSM8;Q95 Q9VSM8	Q9VSM8	GAPsec
42	1	1	2 Q9VH81 Q9VH81	Q9VH81	PpD3
43	1	1	0 Q0E9E2;Q86\ Q0E9E2;Q7K\ Q7KN97		BcDNA:GH06.
44	0	1	0 B4F4Z1;Q9W\ B4F4Z1	B4F4Z1	CG12681
45	0	1	0 B4F4Z1;Q9W\ B4F4Z1	B4F4Z1	CG12681
46	0	1	0 COMJ66;P235 COMJ66	COMJ66	CG5363;cdc2
47					
48					
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2	0	1	0 CON__P0076	CON__P0076	CON__P00761
3	0	1	0 CON__P0076	CON__P0076	CON__P00761
4	1	2	1 Q9VVI1	Q9VVI1	Q9VVI1
5	1	1	1	REV__Q95S3	REV__Q95S34
6	1	1	1	REV__Q95S3	REV__Q95S34
7	1	1	1	REV__Q95S3	REV__Q95S34
8	1	1	1	REV__Q95S3	REV__Q95S34
9	1	1	1	REV__Q95S3	REV__Q95S34
10	1	1	1	REV__Q95S3	REV__Q95S34
11	1	1	1	REV__Q95S3	REV__Q95S34
12	1	1	1	REV__Q95S3	REV__Q95S34
13	0	2	0	REV__Q9VPU	REV__Q9VPU CG13950
14	0	2	0	REV__Q9VPU	REV__Q9VPU CG13950
15	1	1	1 Q961E0;Q5BI	Q961E0	Cul4
16	1	1	1 M9PBI9;M9P	M9PBI9	sls
17	1	1	1 M9PBI9;M9P	M9PBI9	sls
18	0	1	1 M9PBI9;M9P	M9PBI9	sls
19	0	3	0 P35875;P358	P35875	Parp
20	1	2	2 A8JV07;B4F5I	A8JV07	CG9915;CG95
21	1	1	1 Q867Z4-3	Q867Z4-3	Iola
22	0	1	2 A0A0B4LFD2;A0A0B4LFD2	A0A0B4LFD2	Hsc70-5
23	1	1	1 B7FNN6;P05E	B7FNN6	RpLP2-RB;RpI
24	1	1	1 B7FNN6;P05E	B7FNN6	RpLP2-RB;RpI
25	1	1	1 B7FNN6;P05E	B7FNN6	RpLP2-RB;RpI
26	0	1	1 M9NG39;P41	M9NG39	Pep
27	0	1	2 P05205	P05205	Su(var)205
28	0	1	2 P05205	P05205	Su(var)205
29	0	1	2 P05205	P05205	Su(var)205
30	0	1	2 P05205	P05205	Su(var)205
31	0	1	2 CON__P0266	CON__P0266	CON__P02666
32	0	1	2 CON__P0266	CON__P0266	CON__P02666
33	1	2	2 M9PBK5;P08!	M9PBK5	RpLP1
34	1	2	2 M9PBK5;P08!	M9PBK5	RpLP1
35	1	2	2 M9PBK5;P08!	M9PBK5	RpLP1
36	1	1	2 M9PBK5;P08!	M9PBK5	RpLP1
37	0	1	2 Q9VCC0	Q9VCC0	CHORD
38	0	1	1 M9PE74;Q9V	M9PE74	nocte
39	0	1	1 Q7PLP4;A8Y5	Q7PLP4	CG41099;CG1
40	0	1	1 Q9VTI8	Q9VTI8	chrb
41	0	2	2 Q9VFR0	Q9VFR0	CG9286
42	0	1	2 Q6IHK8	Q6IHK8	HDC02276
43	0	1	1 Q9I7K6	Q9I7K6	CG8223
44	0	1	1 Q9I7K6	Q9I7K6	CG8223
45	0	1	1 Q9I7K6	Q9I7K6	CG8223
46	0	1	1 Q9I7K6	Q9I7K6	CG8223
47	0	1	1 Q9I7K6	Q9I7K6	CG8223
48	0	1	1 Q9I7K6	Q9I7K6	CG8223
49	0	1	1 Q9I7K6	Q9I7K6	CG8223
50	0	1	1 Q9I7K6	Q9I7K6	CG8223
51	0	1	1 Q9I7K6	Q9I7K6	CG8223
52	0	2	2 Q9VFR0	Q9VFR0	CG9286
53	0	1	2 Q6IHK8	Q6IHK8	HDC02276
54	0	1	1 Q9I7K6	Q9I7K6	CG8223
55	0	1	1 Q9I7K6	Q9I7K6	CG8223
56	0	1	1 Q9I7K6	Q9I7K6	CG8223
57	0	1	1 Q9I7K6	Q9I7K6	CG8223
58	0	1	1 Q9I7K6	Q9I7K6	CG8223
59	0	1	1 Q9I7K6	Q9I7K6	CG8223
60	0	1	1 Q9I7K6	Q9I7K6	CG8223
61	0	1	1 Q9I7K6	Q9I7K6	CG8223

1					
2					
3	0	1	1 Q9I7K6	Q9I7K6	Q9I7K6 CG8223
4	0	1	1 Q9VCC0	Q9VCC0	Q9VCC0 CHORD
5	0	1	1 REV__D4G7E	REV__D4G7E0	
6	0	2	2 Q9VAA9	Q9VAA9	Q9VAA9
7	0	2	1 Q9W1H4	Q9W1H4	Q9W1H4 DNA-ligl
8	0	1	1 X2JF19;Q9NB	X2JF19	X2JF19 hiw
9	0	1	1 Q8IR12;Q9VX	Q8IR12	Q8IR12 Cap;Cap-RA
10	0	2	1 Q9VZ30	Q9VZ30	Q9VZ30
11	1	2	1 Q9Y162	Q9Y162	Q9Y162 Vps4
12	0	2	0 A8DYI1;Q7K5	A8DYI1	A8DYI1 CG5544
13	0	1	1 Q9VIF0	Q9VIF0	Q9VIF0 CG9246
14	0	1	0 Q9NH11;Q9V	Q9NH11	Q9NH11 RecQ4
15	0	2	2 T2FFB7;Q9VL	T2FFB7	T2FFB7 Aats-ala-RB;A
16	0	2	1 Q95RH7;F0JA	Q95RH7	Q95RH7 Rab35
17	0	1	0 Q7KUA4;Q7K	Q7KUA4	Q7KUA4 Uba2
18	1	1	0 Q9V4M2	Q9V4M2	Q9V4M2 wech
19	1	1	0 Q9V4M2	Q9V4M2	Q9V4M2 wech
20	1	1	0 Q9GP67;Q7K	Q9GP67	Q9GP67 Ret
21	1	1	0 D5AEK6;Q95F	D5AEK6	D5AEK6 CG9795-RA
22	1	1	0 D5AEK6;Q95F	D5AEK6	D5AEK6 CG9795-RA
23	1	1	0 Q6IKG0	Q6IKG0	Q6IKG0
24	2	1	1 REV__Q8IN09	REV__Q8IN09	
25	1	2	0 Q9VWH1	Q9VWH1	Q9VWH1
26	1	1	0 H1UUN5;Q9V	H1UUN5	H1UUN5 CG14043-RA;
27	1	1	0 H1UUN5;Q9V	H1UUN5	H1UUN5 CG14043-RA;
28	1	1	0 Q9VR91	Q9VR91	Q9VR91 HERC2
29	1	1	0 Q9VIH1;Q8SX	Q9VIH1	Q9VIH1 RPA2;CG9273
30	1	1	1 Q6IIC4	Q6IIC4	Q6IIC4 HDC19000
31	1	1	1 Q6IIC4	Q6IIC4	Q6IIC4 HDC19000
32	1	1	1 Q6IIC4	Q6IIC4	Q6IIC4 HDC19000
33	1	1	1 Q6IIC4	Q6IIC4	Q6IIC4 HDC19000
34	1	1	1 AOA0B4LEV8;AOA0B4LEV8	AOA0B4LEV8	AOA0B4LEV8 coil
35	0	1	1 Q8IGR0;P153	Q8IGR0	Q8IGR0 aru;RpS27A;R
36	0	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
37	0	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
38	0	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
39	0	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
40	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
41	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
42	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
43	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
44	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
45	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
46	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
47	0	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
48	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
49	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
50	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
51	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
52	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
53	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
54	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
55	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
56	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
57	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
58	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
59	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
60	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
61	1	1	1 X2JDR1;Q8IR	X2JDR1	X2JDR1 CG9413-RB
62					
63					
64					
65					

1					
2					
3	1	1	1 X2JDR1;Q8IR <sup>4</sup> X2JDR1	X2JDR1	CG9413-RB
4	1	1	1 X2JDR1;Q8IR <sup>4</sup> X2JDR1	X2JDR1	CG9413-RB
5	1	1	1 X2JDR1;Q8IR <sup>4</sup> X2JDR1	X2JDR1	CG9413-RB
6	1	1	1 X2JDR1;Q8IR <sup>4</sup> X2JDR1	X2JDR1	CG9413-RB
7	1	1	1 X2JDR1;Q8IR <sup>4</sup> X2JDR1	X2JDR1	CG9413-RB
8	1	1	0 Q6IJT9 Q6IJT9	Q6IJT9	HDC14233
9	1	1	1 T2GFF4 T2GFF4	T2GFF4	
10	1	1	0 Q9W1X7 Q9W1X7	Q9W1X7	MED23
11	2	1	0 Q7KSW3 Q7KSW3	Q7KSW3	
12	0	1	0 Q9V3W0 Q9V3W0	Q9V3W0	UK114
13	0	2	1 CON__P2093 CON__P2093 CON__P20930		
14	1	1	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc;tacc-RA
15	1	1	0 Q9VA95 Q9VA95	Q9VA95	Bet5
16	1	1	0 B7YZZ9;P278(B7YZZ9	B7YZZ9	Rrp1
17	1	1	0 B7YZZ9;P278(B7YZZ9	B7YZZ9	Rrp1
18	1	1	0 B7YZZ9;P278(B7YZZ9	B7YZZ9	Rrp1
19	0	1	1 Q8IHE7;C9QF Q8IHE7	Q8IHE7	CG6664
20	0	1	1 Q8IHE7;C9QF Q8IHE7	Q8IHE7	CG6664
21	0	1	1 Q9VYV4 Q9VYV4	Q9VYV4	Amun
22	0	1	1 Q9VYV4 Q9VYV4	Q9VYV4	Amun
23	0	1	1 Q9VYV4 Q9VYV4	Q9VYV4	Amun
24	0	1	1 Q9VYV4 Q9VYV4	Q9VYV4	Amun
25	0	1	2 Q9VYV4 Q9VYV4	Q9VYV4	Amun
26	0	1	2 Q9VYV4 Q9VYV4	Q9VYV4	Amun
27	0	1	1 Q9VGZ3;Q9N Q9VGZ3;Q9V Q9VGZ3	Q9VGZ3	Irp-1B;Irp-1A
28	0	1	2 E1NZC8;H8F4 E1NZC8	E1NZC8	MED1-RA;ME
29	0	1	2 Q7KKI0;A1Z8(Q7KKI0	Q7KKI0	Cct5;Cct5-RB
30	0	1	2 Q9VIE7;Q8W(Q9VIE7	Q9VIE7	bur
31	0	1	1 REV__A0A0B <sup>4</sup> REV__A0A0B4KEZ8		
32	1	2	2 Q967T2 Q967T2	Q967T2	pol
33	0	1	0 Q8INI3;Q86N Q8INI3	Q8INI3	CG31347-RA;
34	0	1	0 Q8INI3;Q86N Q8INI3	Q8INI3	CG31347-RA;
35	0	1	2 Q8IRG6;Q8IR Q8IRG6	Q8IRG6	dre4
36	1	2	2 Q8IRG6;Q8IR Q8IRG6	Q8IRG6	dre4
37	0	1	2 Q8IRG6;Q8IR Q8IRG6	Q8IRG6	dre4
38	0	1	0 Q4V3L7;Q4V(Q4V3L7	Q4V3L7	BcDNA:GH10(
39	0	1	0 E2QCZ8;Q0KI E2QCZ8	E2QCZ8	CG43427
40	0	1	0 E2QCZ8;Q0KI E2QCZ8	E2QCZ8	CG43427
41	0	1	0 Q7KNF3;Q8IF Q7KNF3	Q7KNF3	Trap1
42	2	1	0 E2QCZ8;Q0KI E2QCZ8	E2QCZ8	CG43427
43	0	2	0 E2QCZ8;Q0KI E2QCZ8	E2QCZ8	CG43427
44	0	2	1 A0A0B4LFL3;A0A0B4LFL3	A0A0B4LFL3	Ef1beta
45	0	1	0 Q9VIV2;B1NL Q9VIV2	Q9VIV2	swm
46					
47					
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2					
3	1	1	0 Q9VIV2;B1NL Q9VIV2	Q9VIV2	swm
4	0	1	0 Q9VIV2;B1NL Q9VIV2	Q9VIV2	swm
5	0	1	0 Q6IGL3 Q6IGL3	Q6IGL3	HDC05999
6	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
7	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
8	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
9	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
10	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
11	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
12	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
13	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
14	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
15	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
16	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
17	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
18	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
19	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
20	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
21	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
22	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
23	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
24	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
25	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
26	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
27	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
28	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
29	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
30	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
31	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
32	0	1	0 A4UZZ4;Q9X1A4UZZ4	A4UZZ4	GlyP
33	0	1	0 A4UZZ4;Q9X1A4UZZ4	A4UZZ4	GlyP
34	0	1	1 A4UZZ4;Q9X1A4UZZ4	A4UZZ4	GlyP
35	0	1	1 A4UZZ4;Q9X1A4UZZ4	A4UZZ4	GlyP
36	0	1	0 Q9VY84 Q9VY84	Q9VY84	
37	0	1	1 A0ZWT4;A0Z\ A0ZWT4	A0ZWT4	TepII;Tep2
38	0	1	1 M9PBI9;M9P M9PBI9	M9PBI9	sls
39	1	1	0 AOA0B4JD95; AOA0B4JD95	AOA0B4JD95	zip
40	0	1	0 AOA0B4JD95; AOA0B4JD95	AOA0B4JD95	zip
41	0	1	1 Q1RKX3;A0A( Q1RKX3	Q1RKX3	
42	0	1	0 Q9VV82;Q8S\ Q9VV82	Q9VV82	CG18861;CG3
43	1	1	0 Q95RK9;Q6A\ Q95RK9	Q95RK9	Cap-G
44	0	1	0 Q95RK9;Q6A\ Q95RK9	Q95RK9	Cap-G
45	0	1	0 Q95RK9;Q6A\ Q95RK9	Q95RK9	Cap-G
46	0	1	0 Q9VQ76;M9F Q9VQ76	Q9VQ76	tho2
47	0	1	0 C0PUW8;Q9\ C0PUW8	C0PUW8	CG3305-RA;L:
48	1	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
49	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
50	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
51	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
52	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
53	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
54	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
55	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
56	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
57	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
58	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
59	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
60	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
61	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
62					
63					
64					
65					

1					
2					
3	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
4	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
5	0	1	0 Q8MYL1      Q8MYL1	Q8MYL1	Fancd2
6	0	1	0 Q8MYL1      Q8MYL1	Q8MYL1	Fancd2
7	0	1	0 Q8MYL1      Q8MYL1	Q8MYL1	Fancd2
8	0	1	0 Q8MYL1      Q8MYL1	Q8MYL1	Fancd2
9	0	1	0 Q8MYL1      Q8MYL1	Q8MYL1	Fancd2
10	0	1	0 Q8MYL1      Q8MYL1	Q8MYL1	Fancd2
11	0	1	0 Q8MYL1      Q8MYL1	Q8MYL1	Fancd2
12	1	1	0 C9QPJ3;Q9VCC9QPJ3	C9QPJ3	pps-RA;pps
13	0	1	0	REV_Q961N	REV_Q961M1
14	0	1	0	REV_Q961N	REV_Q961M1
15	0	1	0 Q9VV74      Q9VV74	Q9VV74	Smn
16	0	1	0 Q9VV74      Q9VV74	Q9VV74	Smn
17	0	1	0 Q9VV74      Q9VV74	Q9VV74	Smn
18	0	1	0 Q9VV74      Q9VV74	Q9VV74	Smn
19	0	1	0 Q9VV74      Q9VV74	Q9VV74	Smn
20	0	1	1 Q9VZW4;A8V Q9VZW4	Q9VZW4	CG32487
21	0	1	1 Q9VZW4;A8V Q9VZW4	Q9VZW4	CG32487
22	0	1	1 Q9VZW4;A8V Q9VZW4	Q9VZW4	CG32487
23	0	1	1 Q9VZW4;A8V Q9VZW4	Q9VZW4	CG32487
24	0	2	0 A0A0B4KFB8;A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
25	0	2	0 A0A0B4KFB8;A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
26	0	2	0 A0A0B4KFB8;A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
27	0	2	0 A0A0B4KFB8;A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
28	0	1	1 Q7KK51;Q9W Q7KK51	Q7KK51	BcDNA.GH04f
29	0	1	0 M9PCD7;M9f M9PCD7	M9PCD7	
30	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
31	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
32	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
33	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
34	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
35	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
36	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
37	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
38	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
39	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
40	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
41	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
42	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
43	0	1	2 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
44	1	1	0 Q8MNR4      Q8MNR4	Q8MNR4	gag-pol
45	0	1	0 O02195      O02195	O02195	Trip1
46	0	1	0 O02195      O02195	O02195	Trip1
47	0	1	1 Q86BM5;Q9v Q86BM5;Q9v Q86BM5	Akap200	
48	0	1	1 Q86BM5;Q9v Q86BM5;Q9v Q86BM5	Akap200	
49	0	1	1 Q86BM5;Q9v Q86BM5;Q9v Q86BM5	Akap200	
50	0	1	1 Q86BM5;Q9v Q86BM5;Q9v Q86BM5	Akap200	
51	0	1	1 Q86BM5;Q9v Q86BM5;Q9v Q86BM5	Akap200	
52	0	1	1 Q86BM5;Q9v Q86BM5;Q9v Q86BM5	Akap200	
53	0	1	1 Q86BM5;Q9v Q86BM5;Q9v Q86BM5	Akap200	
54	0	1	1 Q86BM5;Q9v Q86BM5;Q9v Q86BM5	Akap200	
55	0	1	0 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
56	0	1	0 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
57	0	1	0 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
58	0	1	0 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
59	0	1	0 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
60	0	1	0 Q9I7K6      Q9I7K6	Q9I7K6	CG8223
61	0	1	0 Q9I7K6      Q9I7K6	Q9I7K6	CG8223

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3	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
4	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
5	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
6	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
7	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
8	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
9	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
10	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
11	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
12	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
13	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
14	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
15	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
16	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
17	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
18	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
19	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
20	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
21	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
22	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
23	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
24	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
25	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
26	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
27	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
28	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
29	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
30	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
31	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
32	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
33	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
34	1	1	0 B9ER03	B9ER03	B9ER03	CG10597-RB
35	0	1	0 Q4AB54;P022	Q4AB54	Q4AB54	His1:CG3386:
36	0	1	0 Q4AB54;P022	Q4AB54	Q4AB54	His1:CG3386:
37	0	1	0 Q4AB54;P022	Q4AB54	Q4AB54	His1:CG3386:
38	0	1	0 Q4AB54;P022	Q4AB54	Q4AB54	His1:CG3386:
39	0	4	0 Q9VNH5	Q9VNH5	Q9VNH5	
40	0	1	0 Q95RN0-2	Q95RN0-2	Q95RN0-2	CG10038
41	0	1	0 Q9VZS3	Q9VZS3	Q9VZS3	CG17737
42	0	1	0 Q9VZS3	Q9VZS3	Q9VZS3	CG17737
43	0	1	0 Q8INM3;Q8INM3	Q8INM3	Q8INM3	sle
44	0	1	0 Q8INM3;Q8INM3	Q8INM3	Q8INM3	sle
45	1	2	1 A0A0H4Y1G5	A0A0H4Y1G5	A0A0H4Y1G5	hyd
46	2	2	1 A0A0H4Y1G5	A0A0H4Y1G5	A0A0H4Y1G5	hyd
47	2	2	1 A0A0H4Y1G5	A0A0H4Y1G5	A0A0H4Y1G5	hyd
48	0	2	2 Q9VPR5;Q4V	Q9VPR5	Q9VPR5	CG2807
49	1	1	0 Q9W5W8	Q9W5W8	Q9W5W8	
50	0	1	0 Q9W401	Q9W401	Q9W401	kdn
51	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
52	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
53	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
54	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
55	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
56	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
57	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
58	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
59	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
60	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
61	0	1	0 Q9XZL7;A0AC	Q9XZL7	Q9XZL7	tacc
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3	0	1	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc
4	0	2	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc
5	0	2	0 M9PDK5;Q9v M9PDK5	M9PDK5	VhaSFD
6	0	1	2 Q4V3Z6 Q4V3Z6	Q4V3Z6	
7	0	2	0 A0A0C5K8A0 A0A0C5K8A0 A0A0C5K8A0 lds		
8	0	2	1 M9NDM4;Q9 M9NDM4	M9NDM4	wds
9	0	1	0 Q86BJ3-3 Q86BJ3-3	Q86BJ3-3	
10	0	1	0 P81900;A8DY P81900	P81900	Pka-R2
11	0	1	0 Q9V6U8 Q9V6U8	Q9V6U8	Uba3
12	0	1	0 Q9V6U8 Q9V6U8	Q9V6U8	Uba3
13	0	1	0 Q9V6U8 Q9V6U8	Q9V6U8	Uba3
14	0	1	0 Q9V6U8 Q9V6U8	Q9V6U8	Uba3
15	0	1	0 Q9V6U8 Q9V6U8	Q9V6U8	Uba3
16	0	1	2 Q9V рХ4 Q9V рХ4	Q9V рХ4	CG31510-RA
17	0	2	2 C7LAH9;C9QF C7LAH9	C7LAH9	Moe;Moe-RA
18	0	2	2 Q967T2 Q967T2	Q967T2	pol
19	0	1	0 A1Z968;Q5KTA1Z968	A1Z968	NAT1
20	0	3	0 Q9VKW5 Q9VKW5	Q9VKW5	
21	0	1	0 Q29QZ8 Q29QZ8	Q29QZ8	
22	1	1	0 Q9VIS5 Q9VIS5	Q9VIS5	
23	0	2	2 A8E774;P250 A8E774	A8E774	Cyp1;CG9916
24	0	1	2 Q9W335 Q9W335	Q9W335	I(1)G0320
25	0	1	2 Q9W335 Q9W335	Q9W335	I(1)G0320
26	0	2	1 A1A6R3;Q9VIA1A6R3	A1A6R3	
27	0	1	1 Q9VWF8 Q9VWF8	Q9VWF8	
28	0	1	0 COMJE4;Q24E COMJE4	COMJE4	CG4236;Caf1
29	0	1	0 COMJE4;Q24E COMJE4	COMJE4	CG4236;Caf1
30	0	1	0 COMJE4;Q24E COMJE4	COMJE4	CG4236;Caf1
31	0	1	1 A0A0B4K7G4 A0A0B4K7G4 A0A0B4K7G4 mod		
32	0	1	0 Q9VL18 Q9VL18	Q9VL18	eEF1delta
33	0	1	0 Q9VL18 Q9VL18	Q9VL18	eEF1delta
34	1	1	1 Q95SA9 Q95SA9	Q95SA9	spoon
35	1	1	1 Q95SA9 Q95SA9	Q95SA9	spoon
36	1	1	1 Q95SA9 Q95SA9	Q95SA9	spoon
37	0	1	0 P20240 P20240	P20240	Ote
38	0	1	0 P20240 P20240	P20240	Ote
39	0	1	0 P20240 P20240	P20240	Ote
40	0	1	1 A0A0B4K7G4 A0A0B4K7G4 A0A0B4K7G4 mod		
41	0	1	0 Q9VL18 Q9VL18	Q9VL18	eEF1delta
42	0	1	0 Q9VL18 Q9VL18	Q9VL18	eEF1delta
43	0	1	1 X2JIN0;M9M! X2JIN0	X2JIN0	
44	0	2	2 Q24574-2;Q2 Q24574-2	Q24574-2	Ubp64E
45	0	2	2 Q24574-2;Q2 Q24574-2	Q24574-2	Ubp64E
46	0	1	1 A0A0B4K7Z5;A0A0B4K7Z5 A0A0B4K7Z5 Rpn6		
47	0	1	0 M9PFS8;Q9V M9PFS8	M9PFS8	CG9705
48	0	1	0 M9PFS8;Q9V M9PFS8	M9PFS8	CG9705
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3       0       2       0 B7Z0G1;Q02E B7Z0G1       B7Z0G1       hay  
4       1       1       1 CON\_\_P0266 CON\_\_P0266 CON\_\_P02662  
5       1       1       1 CON\_\_P0266 CON\_\_P0266 CON\_\_P02662  
6       0       1       0 Q9VE98       Q9VE98       Q9VE98  
7       0       1       0 Q9VE98       Q9VE98       Q9VE98  
8       0       1       0 Q9VIS5       Q9VIS5       Q9VIS5  
9       0       1       1 Q9V3U0       Q9V3U0       Q9V3U0       CG4500  
10      0       2       1 E1JI68       E1JI68       E1JI68  
11      0       1       1 Q9VRV7       Q9VRV7       Q9VRV7       CG13298  
12      0       1       0 Q8MSA2;Q8M Q8MSA2       Q8MSA2       CG14730  
13      0       1       0 Q9VPW4       Q9VPW4       Q9VPW4       mtRNAPol  
14      1       1       1 A1ZBT6;Q96C A1ZBT6       A1ZBT6  
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1	2	3	Protein Name	Type	Labeling State	Raw file	Fraction	Experiment	MS/MS m/z
4	Zinc finger pr	MULTI-MSMS			PT5722-2		2 B1		761.34
5	Zinc finger pr	ISO-MSMS			0 PT5722-32		32 B3		761.67
6	Zinc finger pr	ISO-MSMS			0 PT5722-2		2 B1		735.02
7	Zinc finger pr	ISO-MSMS			0 PT5722-32		32 B3		734.69
8	Zinc finger pr	ISO-MSMS			0 PT5722-2		2 B1		777.72
9	Zinc finger pr	ISO-MSMS			0 PT5722-7		7 B1 SCX		777.38
10	Zinc finger pr	ISO-MSMS			0 PT5722-2		2 B1		804.37
11	Zinc finger pr	ISO-MSMS			0 PT5722-32		32 B3		804.38
12	1	MULTI-MSMS			PT5722-58		58 H/H TiO2		767.35
13	Polycomb prc	ISO-MSMS			1 PT5722-40		40 B3 SCX		913.44
14	26S proteaso	ISO-MSMS			0 PT5722-51		51 H/H SCX		631.25
15	Hsc70-interact	MULTI-MSMS			PT5722-23		23 B2 SCX		516.59
16	Hsc70-interact	MULTI-MSMS			PT5722-23		23 B2 SCX		774.39
17	<e-RA	ISO-MSMS			0 PT5722-7		7 B1 SCX		757.02
18	Odorant bind	MSMS			1 PT5722-3		3 B1		753.86
19		MSMS			1 PT5722-19		19 B2		753.85
20	Multidrug-res	MSMS			1 PT5722-48		48 H/H		489.94
21	Phosphogluc	MULTI-MSMS			PT5722-7		7 B1 SCX		782.38
22	Phosphogluc	MULTI-MSMS			PT5722-8		8 B1 SCX		782.38
23	Phosphogluc	MULTI-MSMS			PT5722-23		23 B2 SCX		782.05
24	Phosphogluc	ISO-MSMS			0 PT5722-33		33 B3		782.38
25	Phosphogluc	MULTI-MSMS			PT5722-38		38 B3 SCX		782.38
26	Phosphogluc	MULTI-MSMS			PT5722-38		38 B3 SCX		1173.07
27	Phosphogluc	ISO-MSMS			0 PT5722-51		51 H/H SCX		782.05
28	Phosphogluc	MULTI-MSMS			PT5722-53		53 H/H SCX		782.05
29	Phosphogluc	MULTI-MATCH			PT5722-6		6 B1 SCX		
30	Phosphogluc	MULTI-MATCH			PT5722-21		21 B2 SCX		
31	Phosphogluc	MULTI-MATCH			PT5722-22		22 B2 SCX		
32	Phosphogluc	ISO-MSMS			0 PT5722-38		38 B3 SCX		782.71
33	Protein purity	MSMS			1 PT5722-32		32 B3		687.36
34	Glycogen [sta	MULTI-MSMS			PT5722-2		2 B1		1106.52
35	Glycogen [sta	MULTI-MSMS			PT5722-7		7 B1 SCX		1106.02
36	Glycogen [sta	ISO-MSMS			0 PT5722-37		37 B3 SCX		1106.03
37	Glycogen [sta	MULTI-MSMS			PT5722-47		47 H/H		1106.52
38	Glycogen [sta	MULTI-MSMS			PT5722-57		57 H/H TiO2		1106.52
39	Glycogen [sta	MULTI-MATCH			PT5722-56		56 H/H TiO2		
40	Glycogen [sta	MULTI-MSMS			PT5722-57		57 H/H TiO2		1146.5
41	Glycogen [sta	MULTI-MSMS			PT5722-57		57 H/H TiO2		764.67
42	Tripeptidyl-p	ISO-MSMS			0 PT5722-6		6 B1 SCX		943.2
43	Tripeptidyl-p	ISO-MSMS			0 PT5722-7		7 B1 SCX		943.2
44	Tripeptidyl-p	ISO-MSMS			0 PT5722-21		21 B2 SCX		943.2
45	Tripeptidyl-p	ISO-MSMS			0 PT5722-37		37 B3 SCX		943.2

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2	Tripeptidyl-p <sub>ε</sub> MULTI-MSMS	PT5722-51	51 H/H SCX	942.95
3	Transcription MULTI-MSMS	PT5722-1	1 B1	812.4
4	MULTI-MSMS	PT5722-3	3 B1	954.97
5	MULTI-SECPEP	PT5722-3	3 B1	954.97
6	MULTI-MATCH	PT5722-2	2 B1	
7	Ubiquitin-cor MULTI-MSMS	PT5722-20	20 B2	862.37
8	MSMS	1 PT5722-19	19 B2	547.28
9	MSMS	1 PT5722-20	20 B2	547.28
10	MSMS	1 PT5722-6	6 B1 SCX	956.93
11	MSMS	1 PT5722-6	6 B1 SCX	956.93
12	MSMS	1 PT5722-7	7 B1 SCX	956.93
13	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-2	2 B1	841.84
14	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-6	6 B1 SCX	841.34
15	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-7	7 B1 SCX	841.34
16	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-11	11 B1 TIO2	841.34
17	Eukaryotic tr <sub>c</sub> ISO-MSMS	0 PT5722-22	22 B2 SCX	841.34
18	Eukaryotic tr <sub>c</sub> ISO-MSMS	0 PT5722-27	27 B2 TIO2	841.34
19	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-36	36 B3 SCX	841.33
20	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-37	37 B3 SCX	841.34
21	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-41	41 B3 TIO2	841.34
22	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-51	51 H/H SCX	841.34
23	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-52	52 H/H SCX	841.83
24	Eukaryotic tr <sub>c</sub> MULTI-MATCH	PT5722-42	42 B3 TIO2	
25	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-5	5 B1	622.77
26	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-15	15 B1 TIO2	622.77
27	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-16	16 B2	626.77
28	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-20	20 B2	622.77
29	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-30	30 B2 TIO2	622.77
30	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-32	32 B3	626.77
31	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-34	34 B3	622.76
32	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-49	49 H/H	622.77
33	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-50	50 H/H	626.77
34	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-60	60 H/H TIO2	622.76
35	Cofilin/actin- $\alpha$ MULTI-MATCH	PT5722-33	33 B3	
36	MSMS	1 PT5722-48	48 H/H	729.36
37	NADH-ubiqui ISO-MSMS	1 PT5722-7	7 B1 SCX	817.71
38	1,2-dihydroxy MULTI-MSMS	PT5722-51	51 H/H SCX	659.82
39	1,2-dihydroxy MULTI-MATCH	PT5722-52	52 H/H SCX	
40	MULTI-MSMS	PT5722-8	8 B1 SCX	619.25
41	MULTI-MSMS	PT5722-23	23 B2 SCX	619.25
42	Protein split $\epsilon$ MSMS	0 PT5722-18	18 B2	671.34
43	ISO-MSMS	1 PT5722-24	24 B2 SCX	774.37
44	FACT comple ISO-MSMS	0 PT5722-6	6 B1 SCX	822.02

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3	FACT comple	MULTI-MSMS	PT5722-7	7 B1 SCX
4	FACT comple	MULTI-MSMS	PT5722-22	22 B2 SCX
5	FACT comple	MULTI-MSMS	PT5722-36	36 B3 SCX
6	FACT comple	MULTI-MSMS	PT5722-51	51 H/H SCX
7	FACT comple	MULTI-MSMS	PT5722-52	52 H/H SCX
8	Akap200	ISO-MSMS	0 PT5722-32	32 B3
9	Probable pho	MULTI-MSMS	PT5722-7	7 B1 SCX
10	Probable pho	MULTI-SECPEP	PT5722-37	37 B3 SCX
11	Putative gust	MULTI-MSMS	PT5722-8	8 B1 SCX
12	Bifunctional $\epsilon$	ISO-MSMS	0 PT5722-21	21 B2 SCX
13	Bifunctional $\epsilon$	ISO-MSMS	0 PT5722-37	37 B3 SCX
14	Bifunctional $\epsilon$	MULTI-MSMS	PT5722-51	51 H/H SCX
15	Gelsolin	ISO-MSMS	0 PT5722-32	32 B3
16		MULTI-MSMS	1 PT5722-18	18 B2
17		ISO-MSMS	PT5722-58	58 H/H TIO2
18		ISO-MSMS	0 PT5722-23	23 B2 SCX
19		ISO-MSMS	0 PT5722-38	38 B3 SCX
20		ISO-MSMS	0 PT5722-53	53 H/H SCX
21		MSMS	0 PT5722-48	48 H/H
22		ISO-MSMS	0 PT5722-5	5 B1
23	Dipeptidyl pe	MULTI-MSMS	PT5722-22	22 B2 SCX
24		MSMS	0 PT5722-28	28 B2 TIO2
25	4D	ISO-MSMS	0 PT5722-22	22 B2 SCX
26	39S ribosoma	MULTI-MSMS	PT5722-34	34 B3
27		ISO-MSMS	1 PT5722-4	4 B1
28	DNA-directed	MSMS	1 PT5722-39	39 B3 SCX
29		ISO-MSMS	1 PT5722-40	40 B3 SCX
30	Heat shock p $\iota$	MULTI-MSMS	PT5722-17	17 B2
31		ISO-MSMS	1 PT5722-10	10 B1 SCX
32		MULTI-MSMS	PT5722-40	40 B3 SCX
33		MULTI-MSMS	PT5722-55	55 H/H SCX
34		MSMS	0 PT5722-1	1 B1
35		MSMS	0 PT5722-49	49 H/H
36		MSMS	0 PT5722-39	39 B3 SCX
37		ISO-MSMS	0 PT5722-18	18 B2
38		MULTI-MSMS	PT5722-48	48 H/H
39		MULTI-MSMS	PT5722-58	58 H/H TIO2
40		MULTI-MSMS	PT5722-36	36 B3 SCX
41		MSMS	1 PT5722-48	48 H/H
42	Pyruvate cark	MULTI-SECPEP	PT5722-37	37 B3 SCX
43		ISO-MSMS	0 PT5722-36	36 B3 SCX
44		MULTI-MSMS	PT5722-37	37 B3 SCX
45	Cyclin-depen	MULTI-MSMS	PT5722-34	34 B3
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1		MULTI-MSMS	PT5722-3	3 B1	792.38
2		MULTI-MSMS	PT5722-18	18 B2	789.36
3		MSMS	0 PT5722-22	22 B2 SCX	1287.06
4		MULTI-SECPEP	PT5722-3	3 B1	913.45
5		MULTI-MSMS	PT5722-39	39 B3 SCX	908.94
6		MULTI-MATCH	PT5722-2	2 B1	
7		MULTI-MATCH	PT5722-38	38 B3 SCX	
8		MULTI-MATCH	PT5722-40	40 B3 SCX	
9		MULTI-MSMS	PT5722-10	10 B1 SCX	837.71
10		MULTI-SECPEP	PT5722-10	10 B1 SCX	837.71
11		ISO-MSMS	1 PT5722-7	7 B1 SCX	924.41
12	Titin	ISO-MSMS	0 PT5722-33	33 B3	864.91
13	Titin	ISO-MSMS	0 PT5722-38	38 B3 SCX	864.91
14	Titin	MSMS	0 PT5722-37	37 B3 SCX	856.91
15	Poly [ADP-rib	MULTI-SECPEP	PT5722-48	48 H/H	713.99
16	15-RB	ISO-MSMS	0 PT5722-5	5 B1	911.95
17	Longitudinals	ISO-MSMS	0 PT5722-10	10 B1 SCX	721.68
18	Heat shock 70	MSMS	0 PT5722-32	32 B3	496.93
19	60S acidic rib	MULTI-MSMS	PT5722-25	25 B2 SCX	1037.38
20	60S acidic rib	ISO-MSMS	0 PT5722-45	45 B3 TIO2	1037.38
21	60S acidic rib	MULTI-MSMS	PT5722-55	55 H/H SCX	1037.38
22	Zinc finger pr	MSMS	1 PT5722-8	8 B1 SCX	491.23
23	Heterochrom	ISO-MSMS	0 PT5722-9	9 B1 SCX	727.32
24	Heterochrom	MULTI-MSMS	PT5722-39	39 B3 SCX	969.42
25	Heterochrom	MULTI-MSMS	PT5722-39	39 B3 SCX	727.32
26	Heterochrom	ISO-MSMS	0 PT5722-54	54 H/H SCX	727.32
27		ISO-MSMS	0 PT5722-10	10 B1 SCX	854.39
28		ISO-MSMS	0 PT5722-39	39 B3 SCX	854.39
29	60S acidic rib	MSMS	0 PT5722-6	6 B1 SCX	1184.42
30	60S acidic rib	MSMS	0 PT5722-36	36 B3 SCX	789.95
31	60S acidic rib	MSMS	0 PT5722-40	40 B3 SCX	789.95
32	60S acidic rib	MULTI-MSMS	PT5722-55	55 H/H SCX	763.63
33	Cysteine and	MULTI-MSMS	PT5722-38	38 B3 SCX	732.32
34		MULTI-MSMS	PT5722-37	37 B3 SCX	728.65
35	7419	ISO-MSMS	1 PT5722-23	23 B2 SCX	671.36
36	Protein chary	MULTI-MSMS	PT5722-23	23 B2 SCX	847.4
37	Protein BCCIF	ISO-MSMS	0 PT5722-22	22 B2 SCX	915.96
38		ISO-MSMS	0 PT5722-39	39 B3 SCX	714.86
39	Protein NASP	ISO-MSMS	0 PT5722-7	7 B1 SCX	632.94
40	Protein NASP	MULTI-MSMS	PT5722-18	18 B2	632.61
41	Protein NASP	MULTI-MSMS	PT5722-32	32 B3	632.61
42	Protein NASP	ISO-MSMS	0 PT5722-36	36 B3 SCX	632.94
43	Protein NASP	ISO-MSMS	0 PT5722-38	38 B3 SCX	632.61

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3	Protein NASP MULTI-MSMS	PT5722-52	52 H/H SCX	632.61
4	Cysteine and MULTI-MSMS	PT5722-23	23 B2 SCX	1033.93
5	MULTI-MSMS	PT5722-32	32 B3	758.05
6	ISO-MSMS	0 PT5722-55	55 H/H SCX	765.87
7	DNA ligase 1 ISO-MSMS	1 PT5722-27	27 B2 TiO2	790.89
8	E3 ubiquitin- $\gamma$ MSMS	0 PT5722-54	54 H/H SCX	586.95
9	MULTI-MSMS	PT5722-33	33 B3	739.02
10	ISO-MSMS	1 PT5722-34	34 B3	968.12
11	MULTI-MSMS	PT5722-38	38 B3 SCX	777.4
12	MULTI-SECPEP	PT5722-48	48 H/H	905.45
13	Nucleolar cor ISO-MSMS	0 PT5722-37	37 B3 SCX	1108.79
14	ISO-MSMS	0 PT5722-35	35 B3	758.35
15	Alanine--tRN $\gamma$ MSMS	1 PT5722-3	3 B1	990.81
16	MSMS	0 PT5722-18	18 B2	690.97
17	ISO-MSMS	0 PT5722-32	32 B3	468.23
18	Protein wech ISO-MSMS	0 PT5722-8	8 B1 SCX	991.94
19	Protein wech ISO-MSMS	0 PT5722-51	51 H/H SCX	991.94
20	MSMS	0 PT5722-38	38 B3 SCX	764.41
21	MULTI-MSMS	PT5722-38	38 B3 SCX	567.61
22	ISO-MSMS	0 PT5722-38	38 B3 SCX	850.9
23	MULTI-MSMS	PT5722-40	40 B3 SCX	835.39
24	ISO-MSMS	1 PT5722-34	34 B3	913.48
25	MULTI-MSMS	PT5722-10	10 B1 SCX	745.02
26	Protein KBP h MULTI-MSMS	PT5722-36	36 B3 SCX	859.41
27	Protein KBP h MULTI-MATCH	PT5722-37	37 B3 SCX	
28	Probable E3 t MULTI-MSMS	PT5722-33	33 B3	760.74
29	MULTI-MSMS	PT5722-34	34 B3	837.68
30	ISO-MSMS	1 PT5722-23	23 B2 SCX	818.4
31	ISO-MSMS	1 PT5722-24	24 B2 SCX	818.4
32	ISO-MSMS	1 PT5722-38	38 B3 SCX	817.9
33	ISO-MSMS	1 PT5722-49	49 H/H	817.9
34	MULTI-MSMS	PT5722-33	33 B3	632.61
35	Ubiquitin-40S MSMS	0 PT5722-16	16 B2	694.8
36	MULTI-MSMS	PT5722-10	10 B1 SCX	909.43
37	MULTI-MSMS	PT5722-24	24 B2 SCX	609.63
38	MULTI-MATCH	PT5722-23	23 B2 SCX	
39	MULTI-MATCH	PT5722-25	25 B2 SCX	
40	MULTI-MSMS	PT5722-23	23 B2 SCX	597.63
41	MULTI-MSMS	PT5722-24	24 B2 SCX	896.44
42	MULTI-MATCH	PT5722-23	23 B2 SCX	
43	MULTI-MATCH	PT5722-25	25 B2 SCX	
44	sobremesa ISO-MSMS	1 PT5722-8	8 B1 SCX	911.43
45	sobremesa ISO-MSMS	1 PT5722-9	9 B1 SCX	911.43

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2	sobremesa	ISO-MSMS	1 PT5722-10	10 B1 SCX	911.44
3	sobremesa	ISO-MSMS	1 PT5722-26	26 B2 TIO2	911.43
4	sobremesa	ISO-MSMS	1 PT5722-38	38 B3 SCX	911.43
5	sobremesa	ISO-MSMS	1 PT5722-40	40 B3 SCX	911.44
6		ISO-MSMS	0 PT5722-49	49 H/H	793.86
7		ISO-MSMS	0 PT5722-35	35 B3	801.37
8		Mediator of F ISO-MSMS	0 PT5722-53	53 H/H SCX	824.38
9			0 PT5722-52	52 H/H SCX	905.45
10		MULTI-SECPEP	PT5722-10	10 B1 SCX	497.28
11		ISO-MSMS	1 PT5722-38	38 B3 SCX	830.09
12		ISO-MSMS	0 PT5722-41	41 B3 TIO2	930.46
13		MULTI-SECPEP	PT5722-10	10 B1 SCX	750.85
14	Recombinatic	ISO-MSMS	0 PT5722-12	12 B1 TIO2	914.74
15	Recombinatic	ISO-MSMS	0 PT5722-32	32 B3	914.41
16	Recombinatic	MULTI-MSMS	PT5722-57	57 H/H TIO2	914.74
17		ISO-MSMS	1 PT5722-10	10 B1 SCX	635.32
18		ISO-MSMS	1 PT5722-55	55 H/H SCX	634.82
19		MULTI-MSMS	PT5722-2	2 B1	555.27
20		MULTI-MSMS	PT5722-22	22 B2 SCX	832.41
21		MULTI-MSMS	PT5722-36	36 B3 SCX	555.27
22		MULTI-MSMS	PT5722-37	37 B3 SCX	832.4
23		MULTI-MATCH	PT5722-36	36 B3 SCX	
24		MULTI-MSMS	PT5722-2	2 B1	597.97
25		MULTI-MSMS	PT5722-7	7 B1 SCX	597.97
26		MULTI-MSMS	PT5722-52	52 H/H SCX	694.33
27		Mediator of F MSMS	0 PT5722-3	3 B1	719.36
28		ISO-MSMS	0 PT5722-3	3 B1	766.07
29		MSMS	0 PT5722-38	38 B3 SCX	883.43
30		ISO-MSMS	1 PT5722-4	4 B1	799.37
31		ISO-MSMS	1 PT5722-3	3 B1	799.4
32	CG31347	MULTI-MSMS	PT5722-33	33 B3	482.89
33	CG31347	MULTI-MATCH	PT5722-34	34 B3	
34	FACT comple:	MULTI-MSMS	PT5722-21	21 B2 SCX	754.67
35	FACT comple:	MULTI-MSMS	PT5722-22	22 B2 SCX	754.33
36	FACT comple:	MULTI-MSMS	PT5722-36	36 B3 SCX	754.33
37	614;BcDNA.GI	ISO-MSMS	-1 PT5722-35	35 B3	563.71
38	smallish, sma	MULTI-MSMS	PT5722-24	24 B2 SCX	558.59
39	smallish, sma	ISO-MSMS	0 PT5722-39	39 B3 SCX	558.58
40		MULTI-MSMS	PT5722-39	39 B3 SCX	936.46
41	smallish, sma	MULTI-SECPEP	PT5722-16	16 B2	958.48
42	smallish, sma	MULTI-SECPEP	PT5722-33	33 B3	958.48
43	Probable elor	ISO-MSMS	0 PT5722-24	24 B2 SCX	926.15
44		MULTI-MSMS	PT5722-20	20 B2	615.25

1		MULTI-MSMS	PT5722-40	40 B3 SCX	615.25
2		MULTI-MSMS	PT5722-50	50 H/H	602.75
3		MULTI-SECPEP	PT5722-50	50 H/H	425.52
4		ISO-MSMS	0 PT5722-6	6 B1 SCX	678.86
5		ISO-MSMS	0 PT5722-7	7 B1 SCX	678.86
6		ISO-MSMS	0 PT5722-8	8 B1 SCX	678.86
7		ISO-MSMS	0 PT5722-19	19 B2	678.86
8		ISO-MSMS	0 PT5722-20	20 B2	678.86
9		ISO-MSMS	0 PT5722-21	21 B2 SCX	678.86
10		ISO-MSMS	0 PT5722-22	22 B2 SCX	678.86
11		ISO-MSMS	0 PT5722-24	24 B2 SCX	678.86
12		ISO-MSMS	0 PT5722-31	31 B3	678.86
13		ISO-MSMS	0 PT5722-32	32 B3	678.86
14		ISO-MSMS	0 PT5722-36	36 B3 SCX	678.86
15		ISO-MSMS	0 PT5722-37	37 B3 SCX	678.86
16		ISO-MSMS	0 PT5722-39	39 B3 SCX	678.86
17		ISO-MSMS	0 PT5722-46	46 H/H	678.86
18		ISO-MSMS	0 PT5722-47	47 H/H	678.86
19		ISO-MSMS	0 PT5722-50	50 H/H	678.86
20		ISO-MSMS	0 PT5722-51	51 H/H SCX	678.86
21		ISO-MSMS	0 PT5722-54	54 H/H SCX	678.86
22		Phosphorylas ISO-MSMS	0 PT5722-36	36 B3 SCX	931.47
23		Phosphorylas MULTI-MSMS	PT5722-37	37 B3 SCX	931.98
24		Phosphorylas MULTI-MSMS	PT5722-37	37 B3 SCX	664.02
25		Phosphorylas MULTI-MATCH	PT5722-36	36 B3 SCX	
26		MULTI-MSMS	PT5722-25	25 B2 SCX	589.8
27		MSMS	0 PT5722-38	38 B3 SCX	707.81
28		Titin MSMS	1 PT5722-8	8 B1 SCX	806.39
29		Myosin heavy ISO-MSMS	0 PT5722-10	10 B1 SCX	613.29
30		Myosin heavy ISO-MSMS	0 PT5722-55	55 H/H SCX	613.29
31		ISO-MSMS	0 PT5722-4	4 B1	689.38
32	32164-RA	ISO-MSMS	1 PT5722-25	25 B2 SCX	613.28
33		ISO-MSMS	0 PT5722-37	37 B3 SCX	814.89
34		ISO-MSMS	0 PT5722-50	50 H/H	814.89
35		ISO-MSMS	0 PT5722-51	51 H/H SCX	814.89
36		MULTI-SECPEP	PT5722-19	19 B2	908.98
37	amp1	MULTI-MSMS	PT5722-35	35 B3	620.77
38		Vitellogenin-1 ISO-MSMS	0 PT5722-8	8 B1 SCX	717.63
39		Vitellogenin-1 ISO-MSMS	0 PT5722-18	18 B2	717.3
40		Vitellogenin-1 MULTI-MSMS	PT5722-33	33 B3	717.63
41		Vitellogenin-1 MULTI-MSMS	PT5722-38	38 B3 SCX	717.63
42		Vitellogenin-1 ISO-MSMS	0 PT5722-40	40 B3 SCX	717.63
43		Vitellogenin-1 MULTI-MSMS	PT5722-48	48 H/H	720.63

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2	Vitellogenin-`	MULTI-MSMS	PT5722-53	53 H/H SCX	717.29
3	Vitellogenin-`	ISO-MSMS	0 PT5722-55	55 H/H SCX	717.63
4		MULTI-MSMS	PT5722-4	4 B1	990.98
5		MULTI-MSMS	PT5722-18	18 B2	990.98
6		MULTI-MSMS	PT5722-23	23 B2 SCX	990.98
7		MULTI-MATCH	PT5722-24	24 B2 SCX	
8		MULTI-MATCH	PT5722-25	25 B2 SCX	
9		MULTI-MSMS	PT5722-33	33 B3	887.1
10		MULTI-MSMS	PT5722-55	55 H/H SCX	715.84
11		MULTI-MATCH	PT5722-54	54 H/H SCX	
12	Survival motc	ISO-MSMS	0 PT5722-24	24 B2 SCX	1072.48
13	Survival motc	ISO-MSMS	0 PT5722-39	39 B3 SCX	1072.47
14	Survival motc	ISO-MSMS	0 PT5722-40	40 B3 SCX	1072.47
15		ISO-MSMS	0 PT5722-2	2 B1	753.05
16		ISO-MSMS	0 PT5722-22	22 B2 SCX	752.72
17		ISO-MSMS	0 PT5722-36	36 B3 SCX	753.05
18	31367-RA	MULTI-MSMS	PT5722-23	23 B2 SCX	670.97
19	31367-RA	MULTI-MATCH	PT5722-21	21 B2 SCX	
20	31367-RA	MULTI-MATCH	PT5722-22	22 B2 SCX	
21	537;BcDNA:GI	MSMS	0 PT5722-24	24 B2 SCX	469.58
22		MSMS	0 PT5722-49	49 H/H	629.31
23	Protein NASP	ISO-MSMS	0 PT5722-3	3 B1	727.67
24	Protein NASP	MULTI-MSMS	PT5722-7	7 B1 SCX	546.01
25	Protein NASP	MULTI-MSMS	PT5722-18	18 B2	727.68
26	Protein NASP	ISO-MSMS	0 PT5722-18	18 B2	545.76
27	Protein NASP	ISO-MSMS	0 PT5722-23	23 B2 SCX	546.01
28	Protein NASP	ISO-MSMS	0 PT5722-32	32 B3	545.76
29	Protein NASP	MULTI-MSMS	PT5722-36	36 B3 SCX	728.01
30	Protein NASP	ISO-MSMS	0 PT5722-36	36 B3 SCX	546.01
31	Protein NASP	ISO-MSMS	0 PT5722-37	37 B3 SCX	727.68
32		ISO-MSMS	0 PT5722-35	35 B3	953.43
33	Eukaryotic tr`	MULTI-MSMS	PT5722-36	36 B3 SCX	1016.01
34	Eukaryotic tr`	MULTI-MATCH	PT5722-37	37 B3 SCX	
35	Akap200	ISO-MSMS	0 PT5722-9	9 B1 SCX	738
36	Akap200	MULTI-MSMS	PT5722-37	37 B3 SCX	737.66
37	Akap200	MULTI-MSMS	PT5722-39	39 B3 SCX	737.67
38	Akap200	ISO-MSMS	0 PT5722-47	47 H/H	737.66
39	Akap200	MULTI-MSMS	PT5722-54	54 H/H SCX	743.68
40	Protein NASP	MULTI-MSMS	PT5722-3	3 B1	1029.47
41	Protein NASP	MULTI-MSMS	PT5722-12	12 B1 TIO2	1028.97
42	Protein NASP	MULTI-MSMS	PT5722-13	13 B1 TIO2	1028.97
43	Protein NASP	MULTI-MSMS	PT5722-14	14 B1 TIO2	1028.97
44	Protein NASP	MULTI-MSMS	PT5722-18	18 B2	1029.47

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2				
3	Protein NASP ISO-MSMS	0 PT5722-23	23 B2 SCX	1028.97
4	Protein NASP MULTI-MSMS	PT5722-27	27 B2 TIO2	1028.97
5	Protein NASP MULTI-MSMS	PT5722-28	28 B2 TIO2	1028.97
6	Protein NASP MULTI-MSMS	PT5722-29	29 B2 TIO2	1028.97
7	Protein NASP MULTI-MSMS	PT5722-32	32 B3	1029.47
8	Protein NASP MULTI-MSMS	0 PT5722-32	32 B3	686.65
9	Protein NASP ISO-MSMS	PT5722-33	33 B3	1028.97
10	Protein NASP MULTI-MSMS	PT5722-33	33 B3	686.32
11	Protein NASP ISO-MSMS	0 PT5722-38	38 B3 SCX	1028.98
12	Protein NASP MULTI-MSMS	PT5722-42	42 B3 TIO2	1033.48
13	Protein NASP MULTI-MSMS	PT5722-42	42 B3 TIO2	686.65
14	Protein NASP MULTI-MSMS	PT5722-43	43 B3 TIO2	1029.47
15	Protein NASP MULTI-MSMS	PT5722-44	44 B3 TIO2	1028.96
16	Protein NASP ISO-MSMS	0 PT5722-44	44 B3 TIO2	686.65
17	Protein NASP ISO-MSMS	0 PT5722-45	45 B3 TIO2	1028.98
18	Protein NASP MULTI-MSMS	PT5722-47	47 H/H	1029.47
19	Protein NASP MULTI-MSMS	PT5722-48	48 H/H	1028.96
20	Protein NASP MULTI-MSMS	PT5722-52	52 H/H SCX	1028.96
21	Protein NASP MULTI-MSMS	PT5722-57	57 H/H TIO2	1029.47
22	Protein NASP MULTI-MSMS	PT5722-58	58 H/H TIO2	1028.97
23	Protein NASP MSMS	0 PT5722-58	58 H/H TIO2	686.32
24	Protein NASP MULTI-MSMS	PT5722-59	59 H/H TIO2	1028.97
25	Protein NASP MULTI-MATCH	PT5722-2	2 B1	
26	MULTI-MSMS	PT5722-4	4 B1	671.68
27	Histone H1 ISO-MSMS	0 PT5722-4	4 B1	693.66
28	Histone H1 ISO-MSMS	0 PT5722-19	19 B2	1039.49
29	Histone H1 MULTI-MSMS	PT5722-49	49 H/H	693.33
30	MSMS	1 PT5722-23	23 B2 SCX	732.71
31	UPF0528 prot ISO-MSMS	0 PT5722-14	14 B1 TIO2	700.65
32	Protein transl MULTI-MSMS	PT5722-40	40 B3 SCX	963.46
33	Protein transl ISO-MSMS	0 PT5722-45	45 B3 TIO2	963.47
34	Protein slend MULTI-MSMS	PT5722-57	57 H/H TIO2	845.37
35	Protein slend MULTI-MATCH	PT5722-58	58 H/H TIO2	
36	E3 ubiquitin- $\gamma$ MULTI-MSMS	PT5722-19	19 B2	785.71
37	E3 ubiquitin- $\gamma$ MULTI-MSMS	PT5722-24	24 B2 SCX	791.04
38	E3 ubiquitin- $\gamma$ MULTI-MATCH	PT5722-25	25 B2 SCX	
39	ISO-MSMS	0 PT5722-12	12 B1 TIO2	844.38
40	MSMS	1 PT5722-33	33 B3	655.32
41	Probable citr: MULTI-SECPEP	PT5722-23	23 B2 SCX	608.32
42	tacc ISO-MSMS	0 PT5722-7	7 B1 SCX	826.91
43	MULTI-MSMS	PT5722-41	41 B3 TIO2	826.91
44	ISO-MSMS	0 PT5722-51	51 H/H SCX	826.9
45	MULTI-MSMS	PT5722-54	54 H/H SCX	826.9

1		MULTI-MSMS	PT5722-57	57 H/H TIO2	826.4
2		MULTI-MSMS	PT5722-57	57 H/H TIO2	866.39
3		V-type proton MSMS	1 PT5722-31	31 B3	895.9
4		MSMS	1 PT5722-38	38 B3 SCX	679.38
5		Transcription MSMS	0 PT5722-56	56 H/H TIO2	755.73
6		Protein will d MSMS	0 PT5722-49	49 H/H	749.34
7		ISO-MSMS	1 PT5722-4	4 B1	982.46
8		cAMP-depenMULTI-MSMS	PT5722-58	58 H/H TIO2	876.03
9		Nedd8-activa MULTI-MSMS	PT5722-11	11 B1 TIO2	799.9
10		Nedd8-activa MULTI-MSMS	PT5722-28	28 B2 TIO2	799.9
11		Nedd8-activa MULTI-MSMS	PT5722-57	57 H/H TIO2	799.9
12		Nedd8-activa MULTI-MSMS	PT5722-58	58 H/H TIO2	799.9
13		ISO-MSMS	0 PT5722-38	38 B3 SCX	988.49
14		Moesin/ezrin ISO-MSMS	0 PT5722-18	18 B2	410.24
15		MSMS	0 PT5722-34	34 B3	696.01
16		MULTI-MSMS	PT5722-2	2 B1	861.78
17		MULTI-MSMS	PT5722-55	55 H/H SCX	1073.18
18		ISO-MSMS	0 PT5722-2	2 B1	717.84
19		MULTI-SECPEP	PT5722-22	22 B2 SCX	926.46
20		Peptidyl-prolyl ISO-MSMS	1 PT5722-39	39 B3 SCX	747.37
21		MULTI-MSMS	PT5722-19	19 B2	440.23
22		MULTI-MSMS	PT5722-34	34 B3	440.56
23		ISO-MSMS	1 PT5722-39	39 B3 SCX	988.48
24		MULTI-MSMS	PT5722-22	22 B2 SCX	651.83
25		Probable hist ISO-MSMS	0 PT5722-3	3 B1	1008.44
26		Probable hist MULTI-MSMS	PT5722-38	38 B3 SCX	1008.44
27		Probable hist MULTI-MSMS	PT5722-53	53 H/H SCX	1008.77
28	Otefin	ISO-MSMS	0 PT5722-3	3 B1	954.95
29	Otefin	ISO-MSMS	0 PT5722-33	33 B3	954.96
30	Otefin	ISO-MSMS	0 PT5722-38	38 B3 SCX	954.96
31	DNA-binding	ISO-MSMS	0 PT5722-32	32 B3	588.95
32	Probable elavl	MULTI-MSMS	PT5722-24	24 B2 SCX	628.31
33	Probable elavl	MULTI-MSMS	PT5722-54	54 H/H SCX	627.97
34		MULTI-MSMS	PT5722-4	4 B1	672.02
35		MULTI-MSMS	PT5722-18	18 B2	672.02
36		MULTI-MSMS	PT5722-32	32 B3	671.69
37	Bap111 Brahma	ISO-MSMS	0 PT5722-34	34 B3	903.72
38		MULTI-MSMS	PT5722-54	54 H/H SCX	622.65
39	Ubiquitin carl	MULTI-MSMS	PT5722-37	37 B3 SCX	766.07
40	Ubiquitin carl	MULTI-MATCH	PT5722-36	36 B3 SCX	
41	26S proteasome	MSMS	0 PT5722-48	48 H/H	623.31
42	Cold shock dc	MULTI-MSMS	PT5722-40	40 B3 SCX	767.82
43	Cold shock dc	MULTI-MSMS	PT5722-55	55 H/H SCX	772.32

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1	DNA excision	MULTI-MSMS	PT5722-39	39 B3 SCX	874.37
2		ISO-MSMS	0 PT5722-23	23 B2 SCX	641.82
3		ISO-MSMS	0 PT5722-48	48 H/H	642.07
4		MULTI-MSMS	PT5722-37	37 B3 SCX	671.85
5		MULTI-MATCH	PT5722-36	36 B3 SCX	
6		MSMS	0 PT5722-20	20 B2	705.34
7	Long-chain-fa	ISO-MSMS	0 PT5722-54	54 H/H SCX	720.38
8		ISO-MSMS	0 PT5722-33	33 B3	738.86
9	Splicing facto	ISO-MSMS	0 PT5722-52	52 H/H SCX	557.25
10		MULTI-MSMS	PT5722-22	22 B2 SCX	710.36
11	DNA-directed	MULTI-MSMS	PT5722-39	39 B3 SCX	821.92
12		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

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3	4	942699453	376676871	43554.6	-0.24396	-0.00022998
4	3	812069803	243318758	47351.67	-0.33769	-0.00027423
5	2	954971699	190792885	42136.86	0.16333	0.00015598
6	2	954971699	190792885	42136.86	0.16333	0.00015598
7	2	954971699	190792885	43141.78	-0.34128	-0.00032592
8	2	862367787	172272102	45493.23	-15807	-0.0013632
9	2	543273182	108453181	NaN	NaN	NaN
10	2	543273182	108453181	NaN	NaN	NaN
11	2	948917758	189582096	NaN	NaN	NaN
12	2	948917758	189582096	NaN	NaN	NaN
13	2	948917758	189582096	NaN	NaN	NaN
14	2	948917758	189582096	NaN	NaN	NaN
15	2	948917758	189582096	NaN	NaN	NaN
16	2	948917758	189582096	NaN	NaN	NaN
17	2	84133509	168065563	45027.15	-0.89245	-0.00075085
18	2	84133509	168065563	44767.33	-0.58062	-0.0004885
19	2	84133509	168065563	44982.43	-0.63029	-0.00053029
20	2	84133509	168065563	45711.25	0	0
21	2	84133509	168065563	NaN	NaN	0.69875
22	2	84133509	168065563	NaN	NaN	-0.11447
23	2	84133509	168065563	43560.81	-0.47621	-0.00040065
24	2	84133509	168065563	45250.93	-0.87036	-0.00073227
25	2	84133509	168065563	45688.7	-0.94427	-0.00079445
26	2	84133509	168065563	46313.07	-0.57953	-0.00048758
27	2	84133509	168065563	45818.69	-0.70187	-0.0005905
28	2	84133509	168065563	46058.67	-0.88319	-0.00074306
29	2	622765061	124351557	49666.66	-11675	-0.00072709
30	2	622765061	124351557	53750.39	0	0
31	2	622765061	124351557	53765.87	-0.68807	-0.00042851
32	2	622765061	124351557	49223.58	-0.70701	-0.0004403
33	2	622765061	124351557	53622.12	0	0
34	2	622765061	124351557	52022.43	-0.23251	-0.0001448
35	2	622765061	124351557	53283.96	-0.8521	-0.00053066
36	2	622765061	124351557	54265.55	-0.51174	-0.0003187
37	2	622765061	124351557	54265.55	-0.35894	-0.00022353
38	2	622765061	124351557	49801.67	-0.50061	0.1143
39	2	622765061	124351557	53179.15	-0.31982	-0.00031176
40	2	622765061	124351557	54084.26	-0.00019917	0.29178
41	3	72669461	2177062	NaN	NaN	NaN
42	3	812032628	243307605	NaN	NaN	-0.43446
43	2	651301613	130058867	48959.03	-0.26603	-0.00017327
44	2	651301613	130058867	50046.32	-0.73326	-0.00047757
45	2	619254852	123649515	53106.32	-0.21324	-0.00013205
46	2	619254852	123649515	51842.47	-0.24336	-0.0001507
47	2	671344678	13406748	NaN	NaN	NaN
48	3	768697134	230306957	NaN	NaN	10683
49	3	821683108	246202749	NaN	NaN	0.72795
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3	3	821683108	246202749	46390.55	-0.52842	-0.00043419	0.18359
4	3	821683108	246202749	46712.96	-0.49176	-0.00040407	-0.048026
5	3	821683108	246202749	46631.54	-0.5666	-0.00046556	0.12942
6	3	821683108	246202749	46837.07	-0.46708	-0.00038379	-0.087081
7	3	821683108	246202749	46733.58	-0.54819	-0.00045044	-0.36846
8	2	905411329	180880811	NaN	NaN	NaN	0.84056
9	4	385940632	153973342	66420.11	0.018018	0.069539	-13849
10	4	385940632	153973342	66350.92	-0.27129	-0.0001047	-13766
11	2	926902094	185178963	44362.79	-0.85174	-0.00078948	-23454
12	3	9094124	272521537	NaN	NaN	NaN	0.53441
13	3	9094124	272521537	NaN	NaN	NaN	0.7078
14	3	9094124	272521537	44209.95	-0.57909	-0.00052663	0.11881
15	3	74103403	222008026	NaN	NaN	NaN	-0.96098
16	3	676307141	202589959	NaN	NaN	NaN	13318
17	3	788043977	23611101	47177.56	0	0	-0.95449
18	3	105211134	315331218	NaN	NaN	NaN	0.088838
19	3	105211134	315331218	NaN	NaN	NaN	-0.079777
20	3	105211134	315331218	NaN	NaN	NaN	0.38664
21	2	901935928	18018573	NaN	NaN	NaN	NaN
22	2	811864979	16217154	NaN	NaN	NaN	-17282
23	3	542593843	16247597	56848.63	-0.085335	-0.46302	16839
24	2	697759845	139350514	NaN	NaN	NaN	NaN
25	2	612797218	122357988	NaN	NaN	NaN	0.87587
26	3	785378079	235311241	47347.99	-0.69284	-0.00054414	-18986
27	3	788036934	236108897	NaN	NaN	NaN	0.63878
28	2	839405956	167679736	NaN	NaN	NaN	NaN
29	3	913090604	273624998	NaN	NaN	NaN	13904
30	2	730277241	145853993	49649.55	0.0087363	0.063799	-0.4595
31	2	702762518	140351048	NaN	NaN	NaN	-14181
32	2	702762518	140351048	49509.86	-0.77163	-0.00054227	-0.70452
33	2	702762518	140351048	50982.97	-0.46099	-0.00032397	0.016504
34	2	948935405	189585626	NaN	NaN	NaN	NaN
35	3	500897748	149967141	NaN	NaN	NaN	NaN
36	2	84188116	168174777	NaN	NaN	NaN	NaN
37	2	64230521	128259587	NaN	NaN	NaN	0.85034
38	2	64230521	128259587	51321.98	-0.39844	-0.00025592	-0.30627
39	2	64230521	128259587	52150.46	0	0	-0.43276
40	2	692867121	138371969	50168.29	-0.27966	-0.00019377	-0.18817
41	2	894436096	178685764	NaN	NaN	NaN	NaN
42	2	620306364	123859818	49206.27	-0.79259	-0.00049165	-0.50163
43	3	821402721	246118633	NaN	NaN	NaN	0.32563
44	3	821402721	246118633	46888.1	-0.66651	-0.00054747	-0.93131
45	2	633294311	126457407	51009.8	-0.71716	-0.00045417	0.79737

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3	3	789043031	236410726	47036.24	-0.52761	-0.00041631	-0.89262
4	3	789043031	236410726	46820.52	-0.33946	-0.00026785	-1513
5	2	128704259	257207063	NaN	NaN	NaN	NaN
6	2	908943753	181587295	43925.27	-0.15097	-0.00013722	-14113
7	2	908943753	181587295	43245.38	-0.87631	-0.00079652	0.13465
8	2	908943753	181587295	44846.23	-0.85025	-0.00077283	-0.24021
9	2	908943753	181587295	43456.12	-0.87947	-0.00079939	-0.30722
10	2	908943753	181587295	44681.04	-15423	-0.0014018	0.61805
11	3	83770283	251008666	44966.19	-0.54529	-0.00045679	13236
12	3	83770283	251008666	44966.19	-0.54529	-0.00045679	13236
13	2	915894989	182977542	NaN	NaN	NaN	18622
14	2	864915527	17278165	NaN	NaN	NaN	0.92292
15	2	864915527	17278165	NaN	NaN	NaN	0.22132
16	2	85691807	171182159	NaN	NaN	NaN	NaN
17	3	714652181	214093471	49880.31	-11474	-0.00082	-16852
18	2	911952217	182188988	NaN	NaN	NaN	-16267
19	3	721690041	216204829	NaN	NaN	NaN	11152
20	3	496928497	148776366	NaN	NaN	NaN	NaN
21	2	103737957	207274458	41426.96	-0.80348	-0.00083351	-0.3003
22	2	103737957	207274458	NaN	NaN	NaN	0.01813
23	2	103737957	207274458	41640.52	-0.73718	-0.00076473	-0.066447
24	2	483220615	964426677	NaN	NaN	NaN	NaN
25	4	727068215	290424375	NaN	NaN	NaN	10117
26	3	969088528	290424375	42884.98	-11746	-0.0011383	-0.24134
27	4	727068215	290424375	49911.34	-0.99858	-0.00072604	-0.1016
28	4	727068215	290424375	NaN	NaN	NaN	0.51106
29	3	8540532	255913777	NaN	NaN	NaN	0.60084
30	3	8540532	255913777	NaN	NaN	NaN	0.29601
31	2	118441603	23668175	NaN	NaN	NaN	NaN
32	3	789946443	23668175	NaN	NaN	NaN	NaN
33	3	789946443	23668175	NaN	NaN	NaN	NaN
34	3	763290999	228685117	47898.98	-0.71276	-0.00054404	-0.16419
35	3	732319107	219393549	49921.53	-0.59548	-0.00043608	0.32665
36	3	728314467	218192157	51794.11	-10257	-0.00074707	0.90945
37	2	66333925	132466395	NaN	NaN	NaN	15429
38	2	846904963	169179537	43777	-0.61085	-0.00051733	12207
39	2	914957825	18279011	NaN	NaN	NaN	-10979
40	2	71385613	142569771	NaN	NaN	NaN	10855
41	3	632607934	189480197	NaN	NaN	NaN	10578
42	3	632607934	189480197	52561.09	-0.94823	-0.00059985	-0.19406
43	3	632607934	189480197	54769.45	-0.55402	-0.00035048	0.0018982
44	3	632607934	189480197	NaN	NaN	NaN	0.58237
45	3	632607934	189480197	NaN	NaN	NaN	0.64711

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3	3	632607934	189480197	52791.61	-0.51669	-0.00032686 -0.51163
4	2	103392754	206584053	40415.86	-0.79586	-0.00082286 0.25047
5	3	757710721	227011033	47473.69	-0.41805	-0.00031676 0.90588
6	2	76537244	152873033	NaN	NaN	NaN -17092
7	2	782872804	156373105	NaN	NaN	NaN -0.173
8	3	586953594	175783895	NaN	NaN	NaN NaN
9	3	733013906	219601989	48116.09	-0.36865	-0.00027023 0.19886
10	3	962450349	288432922	NaN	NaN	NaN 0.46048
11	3	777065113	232817351	47861.34	-0.74969	-0.00058255 -20764
12	2	901931716	180184888	47012.53	-0.15586	-0.00014058 15503
13	3	110845052	332232973	NaN	NaN	NaN 0.45608
14	2	758352554	151469056	NaN	NaN	NaN -0.029571
15	3	982795507	294536469	NaN	NaN	NaN NaN
16	3	690976337	206990718	NaN	NaN	NaN NaN
17	2	468233525	934452498	NaN	NaN	NaN 0.41775
18	2	991439898	198086524	NaN	NaN	NaN 0.23051
19	2	991439898	198086524	NaN	NaN	NaN 0.56887
20	3	764403789	229018954	NaN	NaN	NaN NaN
21	3	567603685	169978922	56402.93	-0.56275	-0.00031942 0.77722
22	2	850901889	169978922	NaN	NaN	NaN 12041
23	2	830881291	165974803	44962.62	-0.60138	-0.00049967 -0.045227
24	2	904967374	18079202	NaN	NaN	NaN 12742
25	3	741017596	222003096	47644.57	-11412	-0.00084565 0.4771
26	2	859406284	171679801	45496.41	-0.79204	-0.00068069 17602
27	2	859406284	171679801	46122.58	-0.6682	-0.00057426 22269
28	3	760406638	227819809	45270.59	-0.7434	-0.00056529 0.6408
29	3	837675847	251000571	46192.75	0.27528	0.0002306 -10232
30	2	809886573	161775859	NaN	NaN	NaN -13628
31	2	809886573	161775859	NaN	NaN	NaN -0.79476
32	2	809886573	161775859	NaN	NaN	NaN -11434
33	2	809886573	161775859	NaN	NaN	NaN -15373
34	3	6326071	189479947	55347.39	-0.66669	-0.00042175 10897
35	2	694848396	138768224	NaN	NaN	NaN NaN
36	2	909435761	181685697	43696.7	-18642	-0.0016954 0.0030465
37	3	606626266	181685697	52622.78	-0.53676	-0.00032561 -11913
38	3	606626266	181685697	53944.11	-0.10199	-0.61868 -12749
39	3	606626266	181685697	53182.92	-0.37484	-0.00022739 -10728
40	3	597626378	17898573	52584.19	-0.2817	-0.00016835 -0.85859
41	2	895935928	17898573	42945.04	-0.27722	-0.00024837 -17824
42	2	895935928	17898573	43884.54	-11219	-0.0010051 -0.50313
43	3	597626378	17898573	51025.32	-0.64456	-0.00038521 -0.27575
44	2	903419923	180482529	NaN	NaN	NaN 0.48176
45	2	903419923	180482529	NaN	NaN	NaN 12271

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3	2	903419923	180482529	NaN	NaN	NaN	17114
4	2	903419923	180482529	NaN	NaN	NaN	0.061222
5	2	903419923	180482529	NaN	NaN	NaN	13955
6	2	903419923	180482529	NaN	NaN	NaN	14456
7	2	793855273	158569599	NaN	NaN	NaN	-40766
8	2	801371287	160072802	NaN	NaN	NaN	-0.58927
9	2	824379735	164674492	NaN	NaN	NaN	14386
10	2	904952444	180789034	NaN	NaN	NaN	-15692
11	2	497713261	993411969	63181.4	-0.47068	-0.00023426	0.38491
12	3	824410832	247021067	NaN	NaN	NaN	-1.47
13	3	930129053	278736533	NaN	NaN	NaN	0.60166
14	2	750845854	149967715	47822.81	-10651	-0.00079971	12842
15	3	914401501	274018267	NaN	NaN	NaN	-0.36446
16	3	914401501	274018267	NaN	NaN	NaN	0.40981
17	3	914401501	274018267	43868.11	-0.60547	-0.00055364	-0.39734
18	2	626806	125159745	NaN	NaN	NaN	-13851
19	2	626806	125159745	NaN	NaN	NaN	-17886
20	3	555273215	166279782	57588.13	-0.64389	-0.00035753	-0.39201
21	2	832406184	166279782	45805.02	-0.90136	-0.0007503	-0.30556
22	3	555273215	166279782	57856	-0.18944	-0.00010519	-0.24905
23	2	832406184	166279782	45675.85	-0.69867	-0.00058158	0.5334
24	2	832406184	166279782	47421.39	-0.78716	-0.00065524	-0.099439
25	3	597971536	179089278	53542.4	-0.51142	-0.00030581	-11847
26	3	597971536	179089278	52488.26	-0.45983	-0.00027496	-13331
27	2	68832562	137463669	49598.84	-0.7459	-0.00051342	-14928
28	2	719360517	143670648	NaN	NaN	NaN	NaN
29	3	765739171	229419569	NaN	NaN	NaN	0.65819
30	3	883435756	264728544	NaN	NaN	NaN	NaN
31	2	790848806	157968306	NaN	NaN	NaN	-0.89867
32	3	791391554	237115283	NaN	NaN	NaN	-12631
33	3	482892334	144565517	60270.27	-0.078487	-0.37901	0.29151
34	3	482892334	144565517	56998.14	-0.33879	-0.0001636	10269
35	3	754333416	225997842	48501.36	-12935	-0.00097576	0.59531
36	3	754333416	225997842	48648.12	-0.68361	-0.00051567	0.44713
37	3	754333416	225997842	47620.15	-0.6986	-0.00052698	0.019261
38	2	563212456	112441036	NaN	NaN	NaN	13213
39	3	558251534	167173277	52879.02	-0.43009	-0.0002401	0.60775
40	3	558579539	167271679	NaN	NaN	NaN	10397
41	2	935956338	186989812	42893.06	-0.22415	-0.0002098	0.46973
42	2	958475759	191493696	42446.84	-10427	-0.00099945	14035
43	2	958475759	191493696	42782.33	-0.13625	-0.0001306	10331
44	4	925648089	369856325	NaN	NaN	NaN	0.99947
45	2	610743263	121947197	52952.65	-0.76413	-0.00046669	-12932
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3	2	610743263	121947197	52520.14	-0.41241	-0.00025187
4	2	602745805	120347706	53745.4	-0.83504	-0.00050332
5	3	425186859	127253875	64696.68	0.35045	0.00014901
6	2	678862361	135571017	NaN	NaN	-0.15588
7	2	678862361	135571017	NaN	NaN	-0.50484
8	2	678862361	135571017	NaN	NaN	-0.68469
9	2	678862361	135571017	NaN	NaN	-0.20306
10	2	678862361	135571017	NaN	NaN	-0.24851
11	2	678862361	135571017	NaN	NaN	-0.2432
12	2	678862361	135571017	NaN	NaN	-10303
13	2	678862361	135571017	NaN	NaN	-0.52289
14	2	678862361	135571017	NaN	NaN	-0.85876
15	2	678862361	135571017	NaN	NaN	-0.46929
16	2	678862361	135571017	NaN	NaN	-0.22617
17	2	678862361	135571017	NaN	NaN	-0.41926
18	2	678862361	135571017	NaN	NaN	-0.37923
19	2	678862361	135571017	NaN	NaN	-10336
20	2	678862361	135571017	NaN	NaN	-0.5864
21	2	678862361	135571017	NaN	NaN	-0.89777
22	2	678862361	135571017	NaN	NaN	-0.80944
23	2	678862361	135571017	NaN	NaN	-0.39322
24	2	931474598	186093464	NaN	NaN	11623
25	2	931474598	186093464	45039.56	-0.80878	-0.00075335 0.064491
26	3	664017145	198902961	52663.82	-0.50236	-0.00033357 0.087416
27	3	664017145	198902961	52017.14	-0.36311	-0.00024111 0.31241
28	2	585296323	116857809	54610.31	-0.32262	-0.00018883 -11838
29	2	707816139	141361773	NaN	NaN	NaN
30	3	80104169	240010324	NaN	NaN	NaN
31	3	612950689	183583024	NaN	NaN	17737
32	3	612950689	183583024	NaN	NaN	16463
33	2	68937871	137674287	NaN	NaN	-0.18966
34	3	610281047	182782131	NaN	NaN	-0.9206
35	2	814893244	162777193	NaN	NaN	-20437
36	2	814893244	162777193	NaN	NaN	-11287
37	2	814893244	162777193	NaN	NaN	-1196
38	2	909436338	181685812	43061.84	-13698	-0.0012458 -11923
39	2	620769615	123952468	54836.2	0.78559	0.00048767 -0.43215
40	3	71729563	214886506	NaN	NaN	10651
41	3	71729563	214886506	NaN	NaN	0.96299
42	3	71729563	214886506	50576.19	-0.81753	-0.00058641 -0.5649
43	3	71729563	214886506	48931.68	-11873	-0.00085165 -0.36907
44	3	71729563	214886506	NaN	NaN	0.82332
45	3	71729563	214886506	48935.83	-0.89124	-0.00063928 -0.42935

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3	3	71729563	214886506	48589.26	-0.93498	-0.00067066	-0.48078
4	3	71729563	214886506	NaN	NaN	NaN	0.61346
5	2	990473732	197893291	41371.02	-0.13943	-0.0001381	1129
6	2	990473732	197893291	41700.63	-0.8848	-0.00087637	17107
7	2	990473732	197893291	41721.6	-0.71732	-0.00071049	15135
8	2	990473732	197893291	41596.73	-0.78942	-0.0007819	10194
9	2	990473732	197893291	41791.86	-0.78107	-0.00077363	1597
10	2	990473732	197893291	41791.86	-0.78107	-0.00077363	1597
11	3	883441965	264730407	43202.57	-0.69887	-0.00061741	-12377
12	2	711337239	142065992	46830.41	-0.42617	-0.00030315	-15062
13	2	711337239	142065992	48552.99	-0.28408	-0.00020208	-2123
14	3	107214017	321339869	NaN	NaN	NaN	10075
15	3	107214017	321339869	NaN	NaN	NaN	11244
16	3	107214017	321339869	NaN	NaN	NaN	0.064241
17	3	752716813	225512861	NaN	NaN	NaN	0.39857
18	3	752716813	225512861	NaN	NaN	NaN	0.6837
19	3	752716813	225512861	NaN	NaN	NaN	0.95028
20	3	670304899	200789287	50782.59	-12919	-0.00086598	-14228
21	3	670304899	200789287	50413.44	-0.92069	-0.00061714	-23988
22	3	670304899	200789287	49867.72	-0.80455	-0.00053929	-22151
23	3	46957791	14057119	NaN	NaN	NaN	NaN
24	2	629315578	12566166	NaN	NaN	NaN	NaN
25	3	727339959	217899805	NaN	NaN	NaN	0.67973
26	4	545756788	217899805	55200.6	-0.47673	-0.00026018	-11118
27	3	727339959	217899805	47298.66	-1453	-0.0010568	-0.28561
28	4	545756788	217899805	NaN	NaN	NaN	10085
29	4	545756788	217899805	NaN	NaN	NaN	0.51477
30	4	545756788	217899805	NaN	NaN	NaN	0.43893
31	3	727339959	217899805	49461.57	-0.8152	-0.00059293	-0.26477
32	4	545756788	217899805	NaN	NaN	NaN	0.29208
33	3	727339959	217899805	NaN	NaN	NaN	0.67912
34	2	953429864	190484518	NaN	NaN	NaN	16975
35	2	101600828	203000201	42507.05	-0.96301	-0.00097843	-13997
36	2	101600828	203000201	41054.1	-0.99274	-0.0010086	-20601
37	3	737665277	2209974	NaN	NaN	NaN	0.7087
38	3	737665277	2209974	48021.57	-0.81164	-0.00059872	-1022
39	3	737665277	2209974	49666.97	-0.73257	-0.00054039	-0.59356
40	3	737665277	2209974	NaN	NaN	NaN	0.063042
41	3	737665277	2209974	48325.57	-0.67641	-0.00049896	-0.688
42	2	102896974	205592493	40445.55	-0.72577	-0.0007468	-0.46537
43	2	102896974	205592493	40108.64	0	0	-17689
44	2	102896974	205592493	40719.98	0	0	-16878
45	2	102896974	205592493	42294.86	0	0	-15537
46	2	102896974	205592493	40144.92	-0.4439	-0.00045676	-10553

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3	2	102896974	205592493	NaN	NaN	NaN	0.40686
4	2	102896974	205592493	40656.43	0	0	-17644
5	2	102896974	205592493	40637.25	0	0	-16164
6	2	102896974	205592493	41381.46	0	0	-11285
7	2	102896974	205592493	40644.64	-0.15679	-0.00016133	-12504
8							
9	3	686315585	205592493	NaN	NaN	NaN	0.93733
10	2	102896974	205592493	41106.15	-0.72335	-0.0007443	-0.40616
11	3	686315585	205592493	50304.32	-0.18577	-0.0001275	-0.72788
12	2	102896974	205592493	NaN	NaN	NaN	0.12316
13	2	102896974	205592493	40951.85	-0.88397	-0.00090958	-0.59491
14	3	686315585	205592493	50827.29	-0.88301	-0.00060602	0.062175
15	2	102896974	205592493	40977.51	0	0	-14647
16	2	102896974	205592493	41019.25	0	0	-13648
17	3	686315585	205592493	NaN	NaN	NaN	0.036765
18	2	102896974	205592493	NaN	NaN	NaN	-0.070952
19	2	102896974	205592493	41467.31	-0.1204	-0.00012389	-0.57332
20	2	102896974	205592493	41073.05	-0.52115	-0.00053625	0.11019
21	2	102896974	205592493	42349.81	-0.25346	-0.0002608	-0.58571
22	2	102896974	205592493	41294.95	-0.6056	-0.00062315	-0.12905
23	2	102896974	205592493	41438.02	0	0	-0.67687
24	3	686315585	205592493	NaN	NaN	NaN	NaN
25	2	102896974	205592493	41382.49	0	0	-0.21612
26	2	102896974	205592493	40875.37	-0.67242	-0.0006919	-0.46279
27	3	671690264	201204896	51096.34	-0.04967	-0.33363	-18587
28	3	693327825	207696165	NaN	NaN	NaN	0.95663
29	2	10394881	207696165	NaN	NaN	NaN	0.78001
30	3	693327825	207696165	51124.58	-0.24826	-0.00017213	-0.90324
31	2	728702169	145538978	NaN	NaN	NaN	NaN
32	3	700653767	209893947	NaN	NaN	NaN	-0.27695
33	2	962961855	192390916	42497.58	-1186	-0.0011421	-0.19763
34	2	962961855	192390916	NaN	NaN	NaN	-0.18423
35	2	84536639	168871823	46651.53	-0.60604	-0.00051233	0.0019643
36	2	84536639	168871823	46361.82	0	0	-0.24501
37	3	785376455	235310754	47188.41	-0.56286	-0.00044205	-0.18373
38	3	790708094	236910245	46846.98	-0.63925	-0.00050546	-13783
39	3	790708094	236910245	46786.05	-0.61018	-0.00048247	-0.9336
40	2	844389487	168676442	NaN	NaN	NaN	-11825
41	2	651312178	13006098	NaN	NaN	NaN	NaN
42	2	608315912	121461727	53822.03	-0.50827	-0.00030919	-15834
43	2	826402579	16507906	NaN	NaN	NaN	19666
44	2	826402579	16507906	44413.07	-0.71751	-0.00059296	-0.17386
45	2	826402579	16507906	NaN	NaN	NaN	20438
46	2	826402579	16507906	44639.39	-0.90043	-0.00074412	0.59597

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2	2	826402579	16507906	45362.56	-0.6055	-0.00050038	0.23264
3	2	866385744	173075693	46475.25	-0.60516	-0.0005243	0.48461
4	2	891894799	178177504	NaN	NaN	NaN	NaN
5	2	667353026	13326915	NaN	NaN	NaN	NaN
6	2	755736567	150945858	NaN	NaN	NaN	NaN
7	2	749335523	149665649	NaN	NaN	NaN	NaN
8	2	978457133	195489971	NaN	NaN	NaN	-0.84486
9	3	875689928	262404795	46945.66	0	0	-0.25452
10	2	799900538	159778652	45334.03	0	0	-14209
11	2	799900538	159778652	49691.38	0	0	-0.59866
12	2	799900538	159778652	47238.11	-0.60566	-0.00048447	0.065684
13	2	799900538	159778652	46978.66	0	0	-0.66459
14	3	988155981	296144611	NaN	NaN	NaN	-0.4279
15	3	410244091	122771044	NaN	NaN	NaN	-11645
16	3	696003393	208498835	NaN	NaN	NaN	NaN
17	3	86144196	258130405	45295.8	-0.52496	-0.00045222	0.18813
18	3	106950427	320549098	40548.52	-0.22543	-0.0002411	-0.015594
19	2	717842491	143367043	NaN	NaN	NaN	-12811
20	2	926900409	185178626	42856.25	-10051	-0.00093167	-0.69765
21	2	739356789	147669903	NaN	NaN	NaN	0.43958
22	3	440230399	131766937	62752.88	-0.20477	-0.90147	-0.60419
23	3	440230399	131766937	62672.29	-0.27832	-0.00012253	0.42741
24	3	982802767	294538647	NaN	NaN	NaN	14222
25	2	65182631	130163807	53177.34	-0.078739	-0.51324	13658
26	3	100810317	302128768	NaN	NaN	NaN	0.81854
27	3	100810317	302128768	41498.1	-0.1923	-0.00019385	-0.69867
28	3	100810317	302128768	41709.66	-0.69225	-0.00069786	-0.24163
29	4	954455923	381379459	NaN	NaN	NaN	-0.43112
30	4	954455923	381379459	NaN	NaN	NaN	0.51079
31	4	954455923	381379459	NaN	NaN	NaN	0.73047
32	3	58895203	176383426	NaN	NaN	NaN	0.42039
33	3	627975057	188090334	52572.27	-0.7764	-0.00048756	0.44512
34	3	627975057	188090334	53267.84	-0.11549	-0.72523	-0.59607
35	3	67168786	201204175	51096.34	-0.04967	-0.33363	17197
36	3	67168786	201204175	50391.08	0.0094576	0.063526	19131
37	3	67168786	201204175	47925.68	0.24981	0.0001678	13833
38	1	903418304	902411027	NaN	NaN	NaN	32655
39	3	616635936	184688598	53442.93	-0.70568	-0.00043514	-0.78204
40	3	765738599	229419397	47979.82	-0.85582	-0.00065534	0.29911
41	3	765738599	229419397	49532.86	-0.70076	-0.0005366	0.056787
42	2	623309961	124460537	NaN	NaN	NaN	NaN
43	2	767816139	153361773	47355.37	-0.91422	-0.00070196	0.32816
44	2	767816139	153361773	47850.7	-0.59703	-0.00045841	0.23351

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3       2 874372637 174673072 45399.33 -0.94238 -0.00082399 0.8373  
4       4 64181992 256325057 NaN       NaN       NaN       0.80509  
5       4 64181992 256325057 NaN       NaN       NaN       0.58357  
6       2 671854536 134169452 51400.14 -0.34084 -0.00022899 -0.88366  
7       2 671854536 134169452 51149.23 -0.83208 -0.00055903 -0.96309  
8       2 705334302 140865405 NaN       NaN       NaN       NaN  
9       2 719871544 143772854 NaN       NaN       NaN       0.67791  
10      2 738856418 147569828 NaN       NaN       NaN       -17285  
11      2 55724683 111247911 NaN       NaN       NaN       -0.94221  
12      3 707352305 211903509 50088.56 -0.81337 -0.00057534 0.54251  
13      2 821919262 164182397 46434.6 -0.73217 -0.00060178 -11055  
14      3 912426655 273425814 NaN       NaN       NaN       14577  
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	Mass Error [D]	Uncalibrated	Uncalibrated	Max intensity	Max intensity	Retention tir	Retention len
1	-0.03119	-0.67506	-0.00051395	7.6168E+14	7.6468E+14	73595	0.60837
2	0.00011031	NaN	NaN	NaN	NaN	78863	0.81698
3	0.00066902	NaN	NaN	NaN	NaN	67212	0.58141
4	0.00016907	NaN	NaN	NaN	NaN	71066	10799
5	0.00066715	NaN	NaN	NaN	NaN	58525	0.57363
6	0.0006082	NaN	NaN	NaN	NaN	63039	0.88077
7	0.00038378	NaN	NaN	NaN	NaN	63152	0.58234
8	0.0002275	NaN	NaN	NaN	NaN	67438	0.67523
9	-0.00076819	-10011	-0.00076819	7.6769E+14	7.7036E+14	70.19	0.49585
10	0.0012503	NaN	NaN	NaN	NaN	93.17	11154
11	-0.00018593	NaN	NaN	NaN	NaN	78.78	0.98734
12	-0.00030454	-0.43728	-0.0002259	5.1659E+14	5.196E+14	88265	0.5152
13	-0.00053259	-12064	-0.0009342	7.7438E+14	7.7889E+14	88249	13346
14	-0.00013134	NaN	NaN	NaN	NaN	75278	0.52748
15	NaN	NaN	NaN	NaN	NaN	73177	1
16	NaN	NaN	NaN	NaN	NaN	73417	1
17	NaN	NaN	NaN	NaN	NaN	89034	1
18	-0.00017778	-0.53768	-0.00042049	7.8238E+14	7.8506E+14	103.41	0.57672
19	-0.0006593	-15044	-0.0011765	7.8238E+14	7.8539E+13	100.42	0.85462
20	-0.0002705	-10055	-0.00078632	7.8205E+14	7.8539E+14	97275	10631
21	0.00025218	NaN	NaN	NaN	NaN	102.37	19762
22	-0.00036016	-10411	-0.00081417	7.8238E+13	7.8539E+14	97438	0.64938
23	-0.00023058	-11317	-0.0013269	1.1731E+14	1.1781E+14	97415	0.58425
24	-0.00047476	NaN	NaN	NaN	NaN	102.5	13302
25	-0.00055074	-11336	-0.0008865	7.8238E+14	7.8505E+14	97.99	10517
26	-0.00027068	-1197	-0.00093614	7.8238E+14	7.8539E+14	105.34	0.73146
27	-0.00074711	-19164	-0.0014987	7.8238E+14	7.8572E+13	100.21	0.42425
28	-0.00033472	-10915	-0.00085358	7.8238E+14	7.8539E+14	98.64	0.56222
29	0.00010427	NaN	NaN	NaN	NaN	98032	0.47295
30	NaN	NaN	NaN	NaN	NaN	83069	1
31	0.00019739	-0.75963	-0.00084016	1.1065E+14	1.1115E+14	116.29	0.62392
32	0.07116	-0.66506	-0.00073556	1.1065E+14	1.111E+14	119.5	0.31782
33	0.00049847	NaN	NaN	NaN	NaN	126.64	0.47802
34	0.00012997	-0.36938	-0.00040854	1.1065E+14	1.111E+14	136.54	0.56355
35	0.51479	-0.55911	-0.00061838	1.1065E+14	1.111E+14	116.89	0.64877
36	-0.00053448	-0.48324	-0.00053448	1.1065E+14	1.111E+14	117.13	0.53051
37	0.45817	-0.56565	-0.00064824	1.1465E+14	1.151E+14	126.86	0.8235
38	-0.00010878	-0.74786	-0.00057162	7.6467E+14	7.6767E+14	126.92	0.62176
39	0.00069741	NaN	NaN	NaN	NaN	79829	0.67028
40	0.00041604	NaN	NaN	NaN	NaN	78767	0.8231
41	0.00053748	NaN	NaN	NaN	NaN	77134	0.60345
42	0.00059228	NaN	NaN	NaN	NaN	81341	14287

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2							
3	-0.0011118	-14233	-0.0013418	9.4295E+13	9.4746E+14	78.16	10275
4	0.00061522	0.4199	0.00034099	8.1241E+14	8.1541E+14	127.2	15163
5	-0.0012163	-11103	-0.0010603	9.5547E+14	9.5998E+14	97553	13201
6	-0.0012163	-11103	-0.0010603	9.5547E+14	9.5998E+14	97553	13201
7	-0.00025871	-0.61219	-0.00058463	9.5497E+14	9.5948E+14	97.7	0.46027
8	-0.00024759	-18678	-0.0016107	8.6237E+14	8.6738E+14	53491	0.71414
9							
10	NaN	NaN	NaN	NaN	NaN	68544	1
11	NaN	NaN	NaN	NaN	NaN	118.05	1
12	NaN	NaN	NaN	NaN	NaN	149.53	1
13	NaN	NaN	NaN	NaN	NaN	151.95	1
14	NaN	NaN	NaN	NaN	NaN	145.85	1
15							
16	0.00035223	-0.47379	-0.00039862	8.4134E+14	8.4584E+14	81717	0.60141
17	-0.00032288	-0.9644	-0.00081138	8.4184E+14	8.4584E+14	85461	0.54626
18	0.00020634	-0.38504	-0.00032395	8.4134E+14	8.4584E+14	84705	0.659
19	-0.00098804	-11744	-0.00098804	8.4133E+14	8.4634E+14	81916	0.5723
20							
21	0.00058788	NaN	NaN	NaN	NaN	83036	0.60281
22	-0.96311	NaN	NaN	NaN	NaN	81405	0.53769
23	-0.00028568	-0.81577	-0.00068633	8.4134E+14	8.4634E+14	95193	0.4995
24	-0.39236	-0.917	-0.0007715	8.4134E+14	8.4584E+14	94723	0.63361
25	-0.00023838	-12276	-0.0010328	8.4134E+14	8.4634E+14	82131	0.55059
26	-0.00030253	-0.93911	-0.00079011	8.4134E+14	8.4584E+14	84447	0.58243
27	-0.46825	-0.75752	-0.00063733	8.4134E+14	8.4634E+14	83209	0.60301
28	0.74163	-0.79504	-0.00066889	8.4184E+14	8.4684E+14	81927	0.48901
29							
30	0.00044878	-0.44689	-0.00027831	6.2277E+14	6.2677E+14	76755	15688
31	-0.00022485	-0.36105	-0.00022485	6.2277E+14	6.2677E+14	76205	0.73231
32	-0.60297	-0.78489	-0.0004888	6.2277E+13	6.2677E+14	76587	0.50031
33	0.00013403	-0.4918	-0.00030627	6.2277E+14	6.2727E+14	77517	13885
34	-0.00020821	-0.33432	-0.00020821	6.2277E+14	6.2677E+11	77719	0.58629
35	-0.00017696	-0.51667	-0.00032176	6.2277E+14	6.2677E+14	87667	0.53617
36	-0.16273	-0.87823	-0.00054693	6.2277E+11	6.2677E+14	87765	0.65209
37							
38	0.00029792	-0.033363	-0.20777	6.2277E+14	6.2677E+14	78112	0.86717
39	0.71185	-0.24463	-0.00015235	6.2277E+14	6.2677E+14	76455	16749
40	0.00018171	-0.20884	-0.00013006	6.2277E+14	6.2677E+14	78722	0.7103
41	-0.00027057	-0.75428	-0.00046974	6.2277E+14	6.2727E+14	87866	0.6384
42							
43	NaN	NaN	NaN	NaN	NaN	122.52	1
44	-0.0009661	NaN	NaN	NaN	NaN	68.89	0.65425
45	0.00076365	0.90647	0.00059039	6.513E+14	6.5982E+14	51208	0.58456
46	0.00095766	0.73712	0.00048009	6.513E+13	6.5932E+14	48669	0.51516
47	0.000807	10899	0.00067495	6.1926E+14	6.2376E+14	94877	0.67711
48	0.00098824	13525	0.00083754	6.1926E+14	6.2376E+14	94214	0.52608
49							
50	NaN	NaN	NaN	NaN	NaN	103.34	1
51	0.00082118	NaN	NaN	NaN	NaN	105.6	0.71088
52	0.00059814	NaN	NaN	NaN	NaN	103.01	0.75828
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3	0.00015085	-0.34483	-0.00028334	8.2202E+14	8.2502E+14	101.81	0.72246
4	-0.39462	-0.53978	-0.00044353	8.2202E+14	8.2502E+14	100.02	0.75243
5	0.00010634	-0.43717	-0.00035922	8.2202E+13	8.2502E+14	110.97	10815
6	-0.71553	-0.55416	-0.00045534	8.2202E+14	8.2502E+13	102.64	0.68706
7	-0.00030275	-0.91665	-0.0007532	8.2202E+14	8.2502E+13	101.37	0.67909
8	0.00076105	NaN	NaN	NaN	NaN	92142	0.93179
9	-0.00053448	-13669	-0.00052752	3.8594E+14	3.8819E+14	51006	0.59747
10	-0.0005313	-16479	-0.000636	3.8594E+14	3.8819E+14	57204	0.60443
11	-0.002174	-31971	-0.0029634	9.274E+14	9.3141E+14	100.08	0.38492
12	0.000486	NaN	NaN	NaN	NaN	78509	0.36842
13	0.00064369	NaN	NaN	NaN	NaN	87301	0.7648
14	0.00010804	-0.46028	-0.00041858	9.0975E+14	9.1509E+14	79768	0.59363
15	-0.00071212	NaN	NaN	NaN	NaN	112.8	27081
16	0.00090068	NaN	NaN	NaN	NaN	82156	0.76271
17	-0.00075218	-0.95449	-0.00075218	7.8838E+14	7.9172E+14	74365	0.92761
18	0.93468	NaN	NaN	NaN	NaN	88133	0.81361
19	-0.83934	NaN	NaN	NaN	NaN	88.65	0.6924
20	0.00040679	NaN	NaN	NaN	NaN	88.85	0.88759
21	NaN	NaN	NaN	NaN	NaN	99695	1
22	-0.0014031	NaN	NaN	NaN	NaN	112.33	18711
23	0.0009137	15986	0.0008674	5.426E+14	5.4827E+14	95334	11889
24	NaN	NaN	NaN	NaN	NaN	156.79	1
25	0.00053673	NaN	NaN	NaN	NaN	36951	0.46461
26	-0.0014911	-25914	-0.0020352	7.8571E+13	7.9139E+14	104.25	35964
27	0.00050338	NaN	NaN	NaN	NaN	131.49	14676
28	NaN	NaN	NaN	NaN	NaN	108.81	1
29	0.0012696	NaN	NaN	NaN	NaN	107.43	0.63021
30	-0.00033556	-0.45077	-0.00032918	7.3028E+14	7.3879E+14	19983	0.60118
31	-0.00099659	NaN	NaN	NaN	NaN	70489	0.52867
32	-0.00049511	-14762	-0.0010374	7.0276E+14	7.0727E+14	71545	0.62837
33	0.11598	-0.44449	-0.00031237	7.0276E+14	7.0677E+12	70618	0.64713
34	NaN	NaN	NaN	NaN	NaN	145.58	1
35	NaN	NaN	NaN	NaN	NaN	132.72	1
36	NaN	NaN	NaN	NaN	NaN	46769	1
37	0.00054618	NaN	NaN	NaN	NaN	68143	0.7126
38	-0.00019672	-0.70471	-0.00045264	6.4231E+14	6.5032E+13	68025	0.55331
39	-0.00027796	-0.43276	-0.00027796	6.4231E+14	6.5032E+13	66.38	0.4973
40	-0.00013037	-0.46783	-0.00032414	6.9337E+14	7.0088E+14	112.85	0.64781
41	NaN	NaN	NaN	NaN	NaN	99768	1
42	-0.00031116	-12942	-0.00080281	6.2031E+14	6.2481E+14	81608	0.42968
43	0.00026747	NaN	NaN	NaN	NaN	114.86	21124
44	-0.00076498	-15978	-0.0013125	8.2174E+14	8.2507E+13	113.95	19634
45	0.00050497	0.080209	0.50796	6.3329E+14	6.378E+14	73482	0.64719
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3	-0.00070432	-14202	-0.0011206	7.8938E+14	7.9238E+14	101.55	2301
4	-0.0011938	-18524	-0.0014616	7.8904E+13	7.9238E+14	103.25	3909
5	NaN	NaN	NaN	NaN	NaN	158.33	1
6	-0.0012828	-15622	-0.00142	9.0894E+14	9.1345E+14	84287	23439
7	0.00012239	-0.74165	-0.00067412	9.0894E+14	9.1345E+14	86972	31512
8	-0.00021834	-10905	-0.00099116	9.0894E+14	9.1345E+14	85118	0.52312
9	-0.00027925	-11867	-0.0010786	9.0894E+14	9.1345E+14	87125	23323
10	0.00056178	-0.92422	-0.00084006	9.0894E+14	9.1295E+14	86615	0.70896
11	0.0011088	0.77828	0.00065197	8.3771E+14	8.4104E+14	94719	0.92674
12	0.0011088	0.77828	0.00065197	8.3771E+14	8.4104E+14	94719	0.92674
13	0.0017056	NaN	NaN	NaN	NaN	102.66	0.65705
14	0.00079825	NaN	NaN	NaN	NaN	95975	0.4333
15	0.00019143	NaN	NaN	NaN	NaN	87746	0.45703
16	NaN	NaN	NaN	NaN	NaN	103.55	1
17	-0.0012044	-28326	-0.0020244	7.1465E+14	7.1766E+14	44389	0.89149
18	-0.0014835	NaN	NaN	NaN	NaN	136.11	0.47278
19	0.00080481	NaN	NaN	NaN	NaN	87788	0.47366
20	NaN	NaN	NaN	NaN	NaN	83317	1
21	-0.00031152	-11038	-0.001145	1.0374E+14	1.0424E+13	108.15	0.59637
22	0.18808	NaN	NaN	NaN	NaN	108.99	0.44384
23	-0.68931	-0.80363	-0.00083366	1.0374E+14	1.0424E+14	108.84	0.54576
24	NaN	NaN	NaN	NaN	NaN	47106	1
25	0.00073559	NaN	NaN	NaN	NaN	66421	0.63902
26	-0.00023388	-1416	-0.0013722	9.6942E+14	9.7844E+14	64623	0.91163
27	-0.73872	-11002	-0.00079991	7.2732E+14	7.3383E+14	64653	0.91163
28	0.00037158	NaN	NaN	NaN	NaN	64588	0.61862
29	0.00051315	NaN	NaN	NaN	NaN	56769	0.68841
30	0.00025281	NaN	NaN	NaN	NaN	55167	0.62209
31	NaN	NaN	NaN	NaN	NaN	94476	1
32	NaN	NaN	NaN	NaN	NaN	113.66	1
33	NaN	NaN	NaN	NaN	NaN	101.06	1
34	-0.00012533	-0.87695	-0.00066937	7.6363E+14	7.693E+14	87498	0.53297
35	0.00023921	-0.26883	-0.00019687	7.3232E+13	7.4067E+14	87227	0.6408
36	0.00066237	-0.1163	-8.47E-05	7.2865E+14	7.3399E+14	61.07	0.54445
37	0.0010234	NaN	NaN	NaN	NaN	75437	0.8054
38	0.0010338	0.60982	0.00051646	8.4741E+14	8.5592E+14	88247	0.58873
39	-0.0010046	NaN	NaN	NaN	NaN	97.45	0.86969
40	0.00077487	NaN	NaN	NaN	NaN	85368	13406
41	0.00066917	NaN	NaN	NaN	NaN	57495	0.41724
42	-0.00012276	-11423	-0.00072262	6.3261E+14	6.3862E+14	53759	0.55851
43	0.012008	-0.55212	-0.00034928	6.3261E+14	6.3828E+14	63476	0.71551
44	0.00036841	NaN	NaN	NaN	NaN	66.49	0.72619
45	0.00040937	NaN	NaN	NaN	NaN	57738	0.36544
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1	-0.00032366	-10283	-0.00065052	6.3261E+14	6.3828E+14	55677	0.57108
2	0.00025897	-0.54539	-0.00056389	1.0339E+14	1.0424E+13	98.44	0.51672
3	0.00068639	0.48783	0.00036963	7.5771E+14	7.6339E+14	121.46	18293
4	-0.0013081	NaN	NaN	NaN	NaN	71685	20642
5	-0.00013544	NaN	NaN	NaN	NaN	45.23	0.52084
6	NaN	NaN	NaN	NaN	NaN	71708	1
7	0.00014577	-0.16979	-0.00012446	7.3335E+14	7.3902E+14	104.82	14964
8	0.00044319	NaN	NaN	NaN	NaN	135.41	0.67035
9	-0.0016135	-28261	-0.0021961	7.774E+14	7.8307E+14	86374	10412
10	0.0013983	13945	0.0012577	9.0193E+14	9.0644E+14	95482	11019
11	0.00050554	NaN	NaN	NaN	NaN	121.3	0.4834
12	-0.22425	NaN	NaN	NaN	NaN	147.46	0.71451
13	NaN	NaN	NaN	NaN	NaN	129.23	1
14	NaN	NaN	NaN	NaN	NaN	49.11	1
15	0.00019561	NaN	NaN	NaN	NaN	57966	0.90657
16	0.00022854	NaN	NaN	NaN	NaN	92568	0.82124
17	0.000564	NaN	NaN	NaN	NaN	95027	0.59917
18	NaN	NaN	NaN	NaN	NaN	121.25	1
19	0.00044116	0.21447	0.00012174	5.676E+14	5.7094E+14	93914	0.86501
20	0.0010246	NaN	NaN	NaN	NaN	93985	0.59921
21	-0.37578	-0.6466	-0.00053725	8.3138E+14	8.3539E+14	104.81	0.75336
22	0.0011531	NaN	NaN	NaN	NaN	124.65	27934
23	0.00035354	-0.6641	-0.00049211	7.4102E+14	7.4469E+14	87759	0.98688
24	0.0015127	0.96818	0.00083206	8.5941E+14	8.6392E+13	108.02	0.7541
25	0.0019138	15587	0.0013395	8.5991E+14	8.6342E+14	106.82	0.74968
26	0.00048727	-0.10261	-0.78022	7.6074E+14	7.6341E+14	125.55	11819
27	-0.00085709	-0.74789	-0.00062649	8.3801E+14	8.4101E+14	103.81	0.70619
28	-0.0011037	NaN	NaN	NaN	NaN	59949	0.91953
29	-0.00064366	NaN	NaN	NaN	NaN	59764	0.9465
30	-0.00092598	NaN	NaN	NaN	NaN	61765	1128
31	-0.0012451	NaN	NaN	NaN	NaN	123.93	0.76739
32	0.00068932	0.42296	0.00026757	6.3261E+14	6.3862E+14	63899	0.77814
33	NaN	NaN	NaN	NaN	NaN	92513	1
34	0.027706	-18612	-0.0016926	9.0994E+14	9.1394E+14	88764	0.6004
35	-0.00072269	-17281	-0.0010483	6.0663E+14	6.0996E+14	89718	14088
36	-0.00077341	-13769	-0.00083528	6.0663E+14	6.0963E+14	89.86	11759
37	-0.0006508	-14476	-0.00087818	6.0663E+14	6.0963E+14	89509	0.76118
38	-0.00051312	-11403	-0.00068147	5.9763E+14	6.0063E+14	68206	19744
39	-0.0015969	-20596	-0.0018453	8.9644E+14	9.0094E+14	74517	0.44894
40	-0.00045077	-1625	-0.0014559	8.9594E+14	8.9994E+14	74981	0.66922
41	-0.00016479	-0.92031	-0.00055	5.9763E+13	6.0063E+14	67525	0.73146
42	0.00043523	NaN	NaN	NaN	NaN	86999	0.7193
43	0.0011086	NaN	NaN	NaN	NaN	85962	0.63573

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3	0.0015461	NaN	NaN	NaN	NaN	84968	0.63683
4	0.05531	NaN	NaN	NaN	NaN	82974	0.69716
5	0.0012608	NaN	NaN	NaN	NaN	84321	0.64992
6	0.001306	NaN	NaN	NaN	NaN	83.74	0.96486
7	-0.0032362	NaN	NaN	NaN	NaN	136.11	0.6861
8	-0.00047223	NaN	NaN	NaN	NaN	148.56	0.90619
9	0.001186	NaN	NaN	NaN	NaN	96381	0.94798
10	-0.00142	NaN	NaN	NaN	NaN	90.9	0.50488
11	0.00019157	-0.085767	-0.42687	4.9771E+14	5.0172E+14	84455	0.5863
12	-0.0012119	NaN	NaN	NaN	NaN	134.05	0.67351
13	0.00055962	NaN	NaN	NaN	NaN	114.39	0.52245
14	0.00096424	0.21912	0.00016453	7.5085E+13	7.5535E+14	90274	11238
15	-0.00033326	NaN	NaN	NaN	NaN	95998	0.73493
16	0.00037473	NaN	NaN	NaN	NaN	105	0.64604
17	-0.00036333	-10028	-0.00091697	9.1474E+14	9.1841E+14	95819	0.87028
18	-0.00086817	NaN	NaN	NaN	NaN	76414	0.88351
19	-0.00112111	NaN	NaN	NaN	NaN	73243	10119
20	-0.00021767	-10359	-0.00057521	5.5527E+14	5.6095E+14	55913	0.41409
21	-0.00025435	-12069	-0.0010046	8.3241E+14	8.4142E+14	57181	0.44668
22	-0.00013829	-0.43849	-0.00024348	5.5527E+14	5.6128E+14	65694	0.53619
23	0.000444	-0.16528	-0.00013758	8.3241E+14	8.4092E+14	64475	0.49722
24	-0.82773	-0.8866	-0.00073801	8.3241E+14	8.4142E+14	65717	0.48075
25	-0.0007084	-16961	-0.0010142	5.9797E+14	6.0665E+14	46122	0.3931
26	-0.00079715	-17929	-0.0010721	5.9797E+14	6.0632E+14	52587	0.64492
27	-0.0010275	-22387	-0.001541	6.8833E+14	6.9283E+14	85365	14531
28	NaN	NaN	NaN	NaN	NaN	72982	1
29	0.000504	NaN	NaN	NaN	NaN	117.77	12158
30	NaN	NaN	NaN	NaN	NaN	88941	1
31	-0.00071071	NaN	NaN	NaN	NaN	105.25	16989
32	-0.00099964	NaN	NaN	NaN	NaN	124.28	12887
33	0.00014077	0.21302	0.00010287	4.8289E+14	4.859E+13	45681	0.70065
34	0.00049587	0.68809	0.00033227	4.8289E+14	4.859E+14	45763	0.59803
35	0.00044906	-0.69823	-0.00052669	7.5467E+13	7.6268E+14	71015	0.46674
36	0.00033729	-0.23648	-0.00017839	7.5467E+14	7.6301E+14	69722	0.74473
37	0.14529	-0.67934	-0.00051245	7.5467E+14	7.6268E+14	81242	0.67423
38	0.00074417	NaN	NaN	NaN	NaN	115.73	0.92355
39	0.00033928	0.17765	0.99176	5.5825E+14	5.6126E+14	46373	13627
40	0.00058073	NaN	NaN	NaN	NaN	48931	0.67912
41	0.00043965	0.24558	0.00022985	9.3596E+14	9.4097E+14	116.18	0.55276
42	0.0013452	0.36076	0.00034578	9.5848E+14	9.6298E+13	130.53	1487
43	0.00099024	0.89689	0.00085964	9.5898E+14	9.6349E+14	132	15108
44	0.00092516	NaN	NaN	NaN	NaN	82967	0.77986
45	-0.00078979	-20573	-0.0012565	6.1074E+14	6.1475E+14	116.71	0.92902
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3	-0.00089042	-18703	-0.0011423	6.1074E+13	6.1475E+14	46818	0.65672
4	-0.00071657	-20239	-0.0012199	6.0275E+14	6.0725E+14	126.59	17975
5	0.00083546	23154	0.00098447	4.2519E+13	4.2786E+14	127.92	23453
6							
7	-0.00010582	NaN	NaN	NaN	NaN	73446	0.85529
8	-0.00034272	NaN	NaN	NaN	NaN	71689	0.95847
9							
10	-0.00046481	NaN	NaN	NaN	NaN	68475	0.57893
11	-0.00013785	NaN	NaN	NaN	NaN	63488	0.81966
12	-0.0001687	NaN	NaN	NaN	NaN	128.62	23097
13	-0.0001651	NaN	NaN	NaN	NaN	68041	0.80257
14	-0.00069943	NaN	NaN	NaN	NaN	66515	11619
15	-0.00035497	NaN	NaN	NaN	NaN	64425	1019
16	-0.00058298	NaN	NaN	NaN	NaN	121.77	39073
17	-0.00031859	NaN	NaN	NaN	NaN	71122	0.53815
18	-0.00015354	NaN	NaN	NaN	NaN	77373	10956
19	-0.00028462	NaN	NaN	NaN	NaN	75968	12429
20	-0.00025744	NaN	NaN	NaN	NaN	64014	10419
21	-0.00070165	NaN	NaN	NaN	NaN	118.8	25957
22	-0.00039808	NaN	NaN	NaN	NaN	125.72	29955
23	-0.00060946	NaN	NaN	NaN	NaN	129.27	2961
24	-0.0005495	NaN	NaN	NaN	NaN	69.77	10571
25	-0.00026694	NaN	NaN	NaN	NaN	63333	0.77888
26	0.0010827	NaN	NaN	NaN	NaN	114.04	0.57431
27	0.60072	-0.74429	-0.00069328	9.3147E+14	9.3598E+14	113.71	0.57819
28	0.58046	-0.41494	-0.00027553	6.6435E+14	6.7003E+13	100.49	0.50895
29	0.00020745	-0.050695	-0.33663	6.6402E+14	6.6969E+14	101.5	0.65757
30	-0.00069289	-15065	-0.00088172	5.853E+14	5.893E+14	86224	11847
31	NaN	NaN	NaN	NaN	NaN	73341	1
32	NaN	NaN	NaN	NaN	NaN	116.91	1
33	0.0010872	NaN	NaN	NaN	NaN	76655	2995
34	0.0010091	NaN	NaN	NaN	NaN	73568	31739
35	-0.00013075	NaN	NaN	NaN	NaN	116.05	28391
36	-0.00056183	NaN	NaN	NaN	NaN	75235	29744
37	-0.0016654	NaN	NaN	NaN	NaN	87.75	0.77527
38	-0.00091974	NaN	NaN	NaN	NaN	124.53	14063
39	-0.00097463	NaN	NaN	NaN	NaN	80879	0.96615
40	-0.0010843	-25621	-0.0023301	9.0994E+14	9.1394E+14	100.58	17367
41	-0.00026826	0.35344	0.00021941	6.2077E+14	6.2528E+14	119.83	12677
42	0.00076401	NaN	NaN	NaN	NaN	54759	0.54944
43	0.00069075	NaN	NaN	NaN	NaN	52031	0.43327
44	-0.0004052	-13824	-0.00099161	7.1763E+14	7.2097E+14	62327	11715
45	-0.00026473	-15564	-0.0011164	7.173E+14	7.2063E+14	56364	0.55442
46	0.00059057	NaN	NaN	NaN	NaN	52195	0.50599
47	-0.00030797	-13206	-0.00094725	7.173E+14	7.2063E+13	51827	0.88256
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1	-0.00034486	-14158	-0.0010155	7.1763E+14	7.2063E+14	52567	0.85705
2	0.00044003	NaN	NaN	NaN	NaN	50.78	0.51909
3	0.0011183	0.98959	0.00098016	9.9048E+14	9.9498E+14	130.2	14043
4	0.0016944	0.82589	0.00081803	9.9048E+14	9.9548E+14	101.65	2687
5	0.0014991	0.79621	0.00078863	9.9098E+14	9.9548E+14	102.56	18499
6	0.0010097	0.22998	0.00022779	9.9048E+14	9.9548E+14	102.36	0.76945
7	0.0015818	0.81593	0.00080816	9.9048E+14	9.9548E+14	102.16	0.55981
8	-0.0010935	-19366	-0.0017109	8.8378E+14	8.8678E+14	133.99	17068
9	-0.0010714	-19323	-0.0013745	7.1134E+14	7.1584E+14	90056	0.66355
10	-0.0015102	-24071	-0.0017122	7.1134E+14	7.1584E+14	90591	10372
11	0.0010802	NaN	NaN	NaN	NaN	81284	13858
12	0.0012056	NaN	NaN	NaN	NaN	81377	16813
13	0.68876	NaN	NaN	NaN	NaN	81158	0.85651
14	0.00030001	NaN	NaN	NaN	NaN	111.95	0.94267
15	0.00051464	NaN	NaN	NaN	NaN	114.19	0.63842
16	0.00071529	NaN	NaN	NaN	NaN	123.38	0.5867
17	-0.00095371	-27147	-0.0018197	6.7064E+14	6.7331E+14	63084	0.72208
18	-0.001608	-33195	-0.0022251	6.703E+14	6.7331E+14	66.67	0.38632
19	-0.0014848	-30196	-0.0020241	6.703E+13	6.7331E+14	64794	0.56033
20	NaN	NaN	NaN	NaN	NaN	41	1
21	NaN	NaN	NaN	NaN	NaN	127.06	1
22	0.00049439	NaN	NaN	NaN	NaN	42096	0.57529
23	-0.00060678	-15885	-0.00086696	5.4601E+14	5.5227E+14	50042	0.65393
24	-0.00020773	-17386	-0.0012645	7.2767E+14	7.3602E+14	42335	0.72315
25	0.00055042	NaN	NaN	NaN	NaN	42336	0.93044
26	0.00028094	NaN	NaN	NaN	NaN	43609	10889
27	0.00023955	NaN	NaN	NaN	NaN	50433	0.32283
28	-0.00019258	-1.08	-0.00078551	7.2734E+14	7.3569E+14	57465	0.65966
29	0.00015941	NaN	NaN	NaN	NaN	57517	0.85898
30	0.00049395	NaN	NaN	NaN	NaN	55509	0.62685
31	0.0016185	NaN	NaN	NaN	NaN	116.77	12049
32	-0.0014221	-23627	-0.0024005	1.0165E+14	1.021E+14	94386	0.5759
33	-0.0020931	-30528	-0.0031017	1.0165E+14	1.0205E+14	93092	0.70579
34	0.00052278	NaN	NaN	NaN	NaN	54745	0.51048
35	-0.00075392	-18337	-0.0013526	7.38E+14	7.4367E+14	64875	0.77584
36	-0.00043785	-13261	-0.00097824	7.3767E+14	7.4401E+14	53482	0.68179
37	0.46504	NaN	NaN	NaN	NaN	106.88	10294
38	-0.00050752	-13644	-0.0010065	7.3767E+14	7.4367E+14	52.9	0.56873
39	-0.00047885	-11911	-0.0012256	1.029E+14	1.034E+13	120.16	12281
40	-0.0018201	-17689	-0.0018201	1.0295E+14	1.034E+14	119.81	11799
41	-0.0017367	-16878	-0.0017367	1.029E+14	1.034E+14	119.92	1068
42	-0.0015987	-15537	-0.0015987	1.0295E+14	1.0335E+14	119.98	0.58934
43	-0.0010859	-14992	-0.0015427	1.0295E+14	1.034E+14	120.5	10766

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3	0.00041865	NaN	NaN	NaN	NaN	120.4	0.50204
4	-0.0018155	-17644	-0.0018155	1.029E+14	1.0335E+14	120.97	0.6772
5	-0.0016632	-16164	-0.0016632	1.0295E+14	1.034E+14	121.12	13278
6	-0.0011612	-11285	-0.0011612	1.0295E+13	1.034E+14	121.39	0.68147
7	-0.0012866	-14072	-0.001448	1.0295E+14	1.034E+14	133.17	0.95207
8	0.0006433	NaN	NaN	NaN	NaN	133.21	0.64886
9	-0.00041792	-11295	-0.0011622	1.029E+14	1.034E+14	133.07	1098
10	-0.00049955	-0.91365	-0.00062705	6.8632E+14	6.8965E+14	133.09	0.57579
11	0.00012673	NaN	NaN	NaN	NaN	121.19	0.82292
12	-0.00061214	-14789	-0.0015217	1.029E+14	1.0335E+13	121.83	0.82023
13	0.42672	-0.82083	-0.00056335	6.8665E+14	6.8965E+14	121.79	0.83508
14	-0.0015071	-14647	-0.0015071	1.029E+14	1.0335E+14	121.84	0.78532
15	-0.0014044	-13648	-0.0014044	1.0295E+13	1.034E+14	121.85	0.75122
16	0.25233	NaN	NaN	NaN	NaN	121.87	0.56217
17	-0.73007	NaN	NaN	NaN	NaN	122.13	0.63235
18	-0.00058993	-0.69372	-0.00071382	1.029E+14	1.0335E+14	123.85	24877
19	0.00011339	-0.41096	-0.00042286	1.029E+14	1.0335E+14	121.54	0.76222
20	-0.00060268	-0.83917	-0.00086349	1.0295E+14	1.0335E+14	120.81	0.62215
21	-0.00013279	-0.73465	-0.00075593	1.029E+14	1.034E+14	121.92	18693
22	-0.00069648	-0.67687	-0.00069648	1.0295E+14	1.034E+14	122.16	0.78681
23	NaN	NaN	NaN	NaN	NaN	122.13	1
24	-0.00022238	-0.21612	-0.00022238	1.0295E+14	1.0335E+14	122.46	0.56194
25	-0.0004762	-11352	-0.0011681	1.0295E+14	1.034E+12	120.15	0.95764
26	-0.0012485	-19084	-0.0012818	6.7202E+14	6.7503E+14	136.58	0.83658
27	0.00066326	NaN	NaN	NaN	NaN	82514	0.82999
28	0.00081082	NaN	NaN	NaN	NaN	83068	0.49942
29	-0.00062624	-11515	-0.00079837	6.9366E+14	6.97E+14	84379	0.89329
30	NaN	NaN	NaN	NaN	NaN	155.72	1
31	-0.00019404	NaN	NaN	NaN	NaN	89253	0.60728
32	-0.00019031	-13837	-0.0013324	9.6346E+14	9.6797E+14	104.82	0.48682
33	-0.00017741	NaN	NaN	NaN	NaN	103.7	0.42697
34	0.016606	-0.60408	-0.00051067	8.4537E+14	8.4987E+14	103.23	0.55985
35	-0.00020713	-0.24501	-0.00020713	8.4537E+13	8.4937E+14	103.35	0.45023
36	-0.0001443	-0.74659	-0.00058635	7.8571E+14	7.9139E+14	109.22	40656
37	-0.0010898	-20175	-0.0015953	7.9071E+14	7.9705E+14	97.26	0.6924
38	-0.00073821	-15438	-0.0012207	7.9104E+13	7.9672E+14	97048	0.50105
39	-0.00099851	NaN	NaN	NaN	NaN	145.57	0.78989
40	NaN	NaN	NaN	NaN	NaN	75723	1
41	-0.00096319	-20916	-0.0012724	6.0832E+14	6.1282E+14	46869	10154
42	0.0016252	NaN	NaN	NaN	NaN	105.61	0.69661
43	-0.00014368	-0.89137	-0.00073663	8.264E+14	8.3141E+14	100.9	0.40081
44	0.001689	NaN	NaN	NaN	NaN	105.18	0.58349
45	0.00049251	-0.30446	-0.00025161	8.2691E+14	8.3091E+14	101.02	0.55649
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1	2	3	0.00019225	-0.37286	-0.00030813	8.264E+14	8.3091E+14	99569	0.63045
4	5	6	0.00041986	-0.12055	-0.00010444	8.6639E+14	8.7089E+14	116.48	0.51491
7	8	9	NaN	NaN	NaN	NaN	NaN	121.67	1
10	11	12	NaN	NaN	NaN	NaN	NaN	113.28	1
13	14	15	NaN	NaN	NaN	NaN	NaN	151.58	1
16	17	18	NaN	NaN	NaN	NaN	NaN	125.85	1
19	20	21	-0.00082665	NaN	NaN	NaN	NaN	136.98	0.261
22	23	24	-0.00022288	-0.25452	-0.00022288	8.7602E+14	8.7903E+14	110.07	0.51246
25	26	27	-0.0011366	-14209	-0.0011366	7.999E+14	8.0441E+14	87404	0.47132
28	29	30	-0.00047887	-0.59866	-0.00047887	7.999E+14	8.0441E+14	85976	0.56593
31	32	33	0.52541	-0.53997	-0.00043193	7.999E+14	8.0441E+14	85818	0.46095
34	35	36	-0.00053161	-0.66459	-0.00053161	7.999E+14	8.0441E+14	85572	0.62428
37	38	39	-0.00042284	NaN	NaN	NaN	NaN	109.96	0.50768
40	41	42	-0.00047773	NaN	NaN	NaN	NaN	58598	0.60669
43	44	45	NaN	NaN	NaN	NaN	NaN	101.36	1
46	47	48	0.00016206	-0.33683	-0.00029016	8.6178E+14	8.6478E+14	131.49	0.4763
49	50	51	-0.16677	-0.24102	-0.00025778	1.0702E+14	1.0732E+14	94485	0.76564
52	53	54	-0.00091965	NaN	NaN	NaN	NaN	51407	0.58632
55	56	57	-0.00064665	-17028	-0.0015783	9.269E+14	9.3191E+14	99424	0.74223
58	59	60	0.00032501	NaN	NaN	NaN	NaN	128.19	0.34515
61	62	63	-0.00026598	-0.80896	-0.00035613	4.4023E+14	4.4858E+14	18285	0.77988
64	65	66	0.00018816	0.14909	0.65632	4.4023E+14	4.4824E+14	23095	0.53612
67	68	69	0.0013978	NaN	NaN	NaN	NaN	102.31	11992
70	71	72	0.00089024	1287	0.00083892	6.5183E+14	6.6084E+14	75395	0.5929
73	74	75	0.00082517	NaN	NaN	NaN	NaN	100.73	0.78802
76	77	78	-0.00070433	-0.89096	-0.00089818	1.0084E+14	1.0118E+14	101.71	0.80127
79	80	81	-0.00024359	-0.93389	-0.00094145	1.0088E+14	1.0114E+14	102.32	0.64181
82	83	84	-0.00041149	NaN	NaN	NaN	NaN	109.77	12359
85	86	87	0.00048753	NaN	NaN	NaN	NaN	123.32	24183
88	89	90	0.00069721	NaN	NaN	NaN	NaN	110.69	0.79527
91	92	93	0.00024759	NaN	NaN	NaN	NaN	50314	0.50629
94	95	96	0.00027953	-0.33127	-0.00020803	6.2798E+14	6.3098E+14	65335	0.6929
97	98	99	-0.00037432	-0.71156	-0.00044684	6.2831E+14	6.3098E+14	64578	0.70169
100	101	102	0.0011551	24473	0.0011217	6.7202E+14	6.7503E+14	136.58	0.83658
103	104	105	0.001285	19226	0.0012914	6.7202E+14	6.7469E+14	123.02	49787
106	107	108	0.00092914	16331	0.0010969	6.7202E+14	6.7469E+14	130.28	13125
109	110	111	0.0029501	NaN	NaN	NaN	NaN	133.41	0.23895
112	113	114	-0.00048223	-14877	-0.00091738	6.1664E+14	6.2231E+13	60817	1302
115	116	117	0.00022904	-0.55671	-0.00042629	7.6607E+14	7.7409E+14	99489	0.72061
118	119	120	0.43484	-0.64397	-0.00049312	7.6607E+13	7.7442E+14	101.06	0.71611
121	122	123	NaN	NaN	NaN	NaN	NaN	73008	1
124	125	126	0.00025197	-0.58606	-0.00044999	7.6782E+14	7.7282E+13	85163	0.63515
127	128	129	0.0001793	-0.36352	-0.00027911	7.6782E+14	7.7232E+14	84.24	0.67552

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3 0.00073212 -0.10507 -0.91872 8.7437E+14 8.7938E+14 74512 0.9054  
4 0.00051672 NaN NaN NaN NaN 76323 10375  
5 0.00037455 NaN NaN NaN NaN 76021 0.9187  
6 -0.00059369 -12245 -0.00082269 6.7185E+14 6.7586E+14 127.35 0.49883  
7 -0.00064706 -17952 -0.0012061 6.7185E+14 6.7636E+14 127.88 0.40822  
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10 NaN NaN NaN NaN NaN 130.09 1  
11 0.00048801 NaN NaN NaN NaN 85346 0.61977  
12 -0.0012771 NaN NaN NaN NaN 67162 0.75741  
13 -0.00052504 NaN NaN NaN NaN 71933 0.7854  
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15 0.00038374 -0.27086 -0.00019159 7.0735E+13 7.1036E+14 90903 0.60856  
16 -0.00090867 -18377 -0.0015104 8.2192E+14 8.2643E+14 79004 0.57461  
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18 0.00133 NaN NaN NaN NaN 86106 16299  
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	Calibrated rel	Calibrated rel	Calibrated rel	Retention time	Match time	m/z	Match q-value
1	88682	88396	89005	15086			
2	86296	85.84	86657	7433			
3	82298	82.03	82611	15086			
4	78199	77715	78795	71326			
5	73611	73316	73.89	15086			
6	70516	70158	71039	74774			
7	78238	78026	78608	15086			
8	74.77	74446	75121	73329			
9	77147	76906	77402	69571			
10	101.1	100.56	101.67	7932			
11	87514	86958	87945	87342			
12	93396	93101	93616	51308			
13	93.38	92952	94286	51308			
14	82656	82348	82875	73776			
15	89428	88928	89928	16251			
16	89.57	89.07	90.07	16153			
17	94385	93885	94885	53507			
18	104.38	104.12	104.7	0.96355			
19	104.58	104.14	104.99	4162			
20	104.8	104.24	105.3	75276			
21	103.74	103.3	105.28	13625			
22	104.52	104.19	104.84	7082			
23	104.53	104.22	104.81	71179			
24	104.52	103.97	105.3	20194			
25	104.5	104.11	105.16	65146			
26	104.15	103.85	104.58	-11905 -0.2187	0.00029497	NaN	
27	104.86	104.64	105.06	46491 -0.0084508	-0.00093103	NaN	
28	104.94	104.7	105.26	6304 0.074542	0.00030615	NaN	
29	105.27	104.99	105.47	72397			
30	90302	89802	90802	72328			
31	135.39	135.12	135.75	19095			
32	132.19	132.02	132.34	12687			
33	134.08	133.79	134.27	74366			
34	128.76	128.37	128.94	-7775			
35	100.99	100.72	101.37	-15894			
36	101.36	101.13	101.66	-15771 0.183	-0.0006071	NaN	
37	110.96	110.53	111.36	-15894			
38	111.02	110.62	111.24	-15894			
39	85153	84797	85467	5324			
40	86045	85642	86465	72776			
41	88198	87942	88546	11064			
42	84867	84016	85445	35258			

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2						
3		86894	86285	87312	87342	
4	127.2	126.54	128.06	-0.076294		
5	106.59	105.91	107.23	90348		
6	106.59	105.91	107.23	90348		
7	106.27	105.98	106.44	85719 -0.158	0.0012713	NaN
8						
9						
10	57524	57252	57966	40333		
11	84797	84297	85297	16253		
12	126.94	126.44	127.44	8889		
13	154.65	154.15	155.15	51221		
14	157.07	156.57	157.57	51221		
15	154.53	154.03	155.03	86792		
16	100.91	100.66	101.26	19196		
17						
18						
19	90685	90438	90985	5224		
20	91882	91522	92181	71776		
21	95804	95551	96123	13888		
22	95855	95.55	96152	12818		
23	88706	88454	88991	73008		
24						
25	100.46	100.21	100.71	52721		
26	101.56	101.28	101.91	68355		
27						
28	97518	97303	97853	15387		
29	93081	92.79	93372	86341		
30	95115	94.78	95383	11906		
31						
32	97608	97316	97805	15681 0.045101	0.00031363	NaN
33	83294	82811	84379	65389		
34	74634	74321	75054	-15717		
35	92495	92273	92774	15908		
36	81551	81135	82523	40333		
37	85429	85159	85746	26115		
38						
39	94.9	94616	95153	72329		
40	96211	95907	96559	84453		
41						
42	88911	88.57	89437	10799		
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	Match score	Number of d <sub>c</sub>	Number of sc	Number of is <sub>c</sub>	PIF	Fraction of to Base peak fra
1		51	13	7	0	0
2					0	0
3					0	0
4					0	0
5					0	0
6					0	0
7					0	0
8					0	0
9					0	0
10					0	0
11					0	0
12					0	0
13					0	0
14					0	0
15		182	32	9	0	0
16					0	0
17					0	0
18					0	0
19		32	6	7	0	0
20					0	0
21		46	17	8	0	0
22					0	0
23					0	0
24					0	0
25					0	0
26					0	0
27					0	0
28		54	7	12	0	0
29		74	11	12	0	0
30		79	13	13	0	0
31					0	0
32					0	0
33		89	9	14	0	0
34					0	0
35		49	8	10	0	0
36					0	0
37		91	14	13	0	0
38	76533	72	12	13	NaN	NaN
39	87352	152	21	11	NaN	NaN
40	87352	75	13	11	NaN	NaN
41					0	0
42					0	0
43					0	0
44					0	0
45		138	22	12	0	0
46					0	0
47		96	21	6	0	0
48					0	0
49					0	0
50		42	7	10	0	0
51		338	43	11	0	0
52	63883	203	35	9	NaN	NaN
53		337	55	9	0	0
54		171	41	7	0	0
55					0	0
56					0	0
57					0	0
58					0	0
59					0	0
60					0	0
61					0	0
62					0	0
63					0	0
64					0	0
65					0	0

1						
2						
3		102	14	16	0	0
4		95	22	8	0	0
5		171	18	13	0	0
6		171	18	13	0	0
7						
8	94911	55	16	6 NaN	NaN	NaN
9		286	45	10	0	0
10					0	0
11					0	0
12					0	0
13					0	0
14					0	0
15					0	0
16					0	0
17					0	0
18		128	23	9	0	0
19		40	7	9	0	0
20		40	8	8	0	0
21		248	38	9	0	0
22					0	0
23					0	0
24					0	0
25					0	0
26		33	6	9	0	0
27		49	8	10	0	0
28		228	36	9	0	0
29		44	7	9	0	0
30		61	8	10	0	0
31					0	0
32					0	0
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34		633	102	9	0	0
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36		135	33	6	0	0
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38		167	39	6	0	0
39		72	17	6	0	0
40		61	16	7	0	0
41		218	57	6	0	0
42		594	111	9	0	0
43		221	48	7	0	0
44	48532	25	8	5 NaN	NaN	NaN
45					0	0
46					0	0
47					0	0
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49					0	0
50					0	0
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52		151	38	6	0	0
53	43635	98	31	5 NaN	NaN	NaN
54		36	8	6	0	0
55		21	6	5	0	0
56					0	0
57					0	0
58					0	0
59					0	0
60					0	0
61					0	0
62					0	0
63					0	0
64					0	0
65					0	0

1						
2						
3	45	9	7	0	0	0
4	240	32	12	0	0	0
5	109	14	13	0	0	0
6	76	11	11	0	0	0
7	297	33	12	0	0	0
8				0	0	0
9						
10						
11	158	32	7	0	0	0
12	103	22	7	0	0	0
13	22	5	6	0	0	0
14				0	0	0
15						
16						
17				0	0	0
18	45	7	9	0	0	0
19				0	0	0
20						
21				0	0	0
22	456	61	11	0	0	0
23				0	0	0
24						
25				0	0	0
26						
27				0	0	0
28						
29				0	0	0
30	115	28	9	0	0	0
31				0	0	0
32						
33				0	0	0
34	534	64	13	0	0	0
35				0	0	0
36						
37				0	0	0
38						
39				0	0	0
40	155	38	6	0	0	0
41				0	0	0
42						
43	74	16	7	0	0	0
44	39	14	5	0	0	0
45				0	0	0
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47				0	0	0
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49				0	0	0
50						
51	25	8	6	0	0	0
52	140	32	6	0	0	0
53	32	8	7	0	0	0
54						
55				0	0	0
56	15	5	4	0	0	0
57						
58				0	0	0
59	196	32	11	0	0	0
60	102	32	5	0	0	0
61						
62						
63						
64						
65						

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3						
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5		382	50	12	0	0
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7		179	32	13	0	0
8		144	44	12	0	0
9				0	0	0
10	44511	27	15	4 NaN	NaN	NaN
11	58658	218	35	12 NaN	NaN	NaN
12	58658	51	9	9 NaN	NaN	NaN
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14		257	22	15	0	0
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22		175	39	10	0	0
23				0	0	0
24				0	0	0
25				0	0	0
26				0	0	0
27		149	34	8	0	0
28				0	0	0
29		190	32	10	0	0
30				0	0	0
31				0	0	0
32				0	0	0
33				0	0	0
34		124	13	15	0	0
35		114	13	13	0	0
36				0	0	0
37				0	0	0
38				0	0	0
39				0	0	0
40				0	0	0
41				0	0	0
42				0	0	0
43				0	0	0
44				0	0	0
45		73	15	7	0	0
46		70	9	11	0	0
47		42	10	6	0	0
48				0	0	0
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50		32	7	7	0	0
51				0	0	0
52				0	0	0
53				0	0	0
54				0	0	0
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59				0	0	0
60				0	0	0
61				0	0	0
62						
63						
64						
65						

1						
2						
3		208	31	10	0	0
4		30	6	6	0	0
5		90	24	6	0	0
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8				0	0	0
9				0	0	0
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11		121	20	14	0	0
12				0	0	0
13				0	0	0
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15		68	14	9	0	0
16				0	0	0
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20				0	0	0
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22				0	0	0
23				0	0	0
24				0	0	0
25				0	0	0
26				0	0	0
27				0	0	0
28		63	12	10	0	0
29				0	0	0
30		76	17	7	0	0
31				0	0	0
32				0	0	0
33		135	16	14	0	0
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35				0	0	0
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38		57	12	9	0	0
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43				0	0	0
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46				0	0	0
47				0	0	0
48		62	11	8	0	0
49		170	23	11	0	0
50				0	0	0
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52	41621	127	25	9 NaN	NaN	NaN
53		194	28	10	0	0
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55				0	0	0
56	43.69	49	8	10 NaN	NaN	NaN
57	44246	164	38	7 NaN	NaN	NaN
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62				0	0	0
63				0	0	0
64				0	0	0
65				0	0	0

1						
2					0	0
3					0	0
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5					0	0
6					0	0
7					0	0
8					0	0
9					0	0
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13					0	0
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15				0	0	0
16				0	0	0
17				0	0	0
18	90	20	8	0	0	0
19				0	0	0
20				0	0	0
21				0	0	0
22	488	58	12	0	0	0
23				0	0	0
24				0	0	0
25				0	0	0
26	138	25	8	0	0	0
27				0	0	0
28	44	9	8	0	0	0
29	42	12	6	0	0	0
30	24	6	6	0	0	0
31				0	0	0
32	72316	32	10	7 NaN	NaN	NaN
33		163	24	9	0	0
34		160	30	11	0	0
35		184	26	12	0	0
36				0	0	0
37				0	0	0
38				0	0	0
39				0	0	0
40				0	0	0
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42				0	0	0
43				0	0	0
44		105	16	10	0	0
45	68536	145	29	8 NaN	NaN	NaN
46		104	21	9	0	0
47		42	10	8	0	0
48		50	8	10	0	0
49				0	0	0
50				0	0	0
51				0	0	0
52		497	80	15	0	0
53				0	0	0
54				0	0	0
55		37	10	5	0	0
56		701	98	10	0	0
57		157	20	9	0	0
58				0	0	0
59				0	0	0
60		58	14	8	0	0
61				0	0	0
62						
63						
64						
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1						
2						
3	179	40	6	0	0	0
4	173	77	4	0	0	0
5	369	111	5	0	0	0
6				0	0	0
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8				0	0	0
9				0	0	0
10				0	0	0
11				0	0	0
12				0	0	0
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15				0	0	0
16				0	0	0
17				0	0	0
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28				0	0	0
29				0	0	0
30				0	0	0
31				0	0	0
32				0	0	0
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34	32	6	8	0	0	0
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45					0	0
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47					0	0
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52	197	83	5	0	0	0
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57	56	7	12	0	0	0
58					0	0
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60	239	30	12	0	0	0
61						
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14						
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17					0	0
18					0	0
19					0	0
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22					0	0
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29					0	0
30					0	0
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32					0	0
33		287	34	12	0	0
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35					0	0
36					0	0
37					0	0
38					0	0
39					0	0
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43					0	0
44					0	0
45		41	7	10	0	0
46					0	0
47	40432	52	9	10 NaN	NaN	NaN
48					0	0
49					0	0
50		86	10	13	0	0
51		61	10	9	0	0
52					0	0
53					0	0
54		235	30	12	0	0
55		130	15	14	0	0
56		752	79	15	0	0
57		709	71	15	0	0
58		190	39	8	0	0
59		130	13	14	0	0
60					0	0
61					0	0
62						
63						
64						
65						

1						
2						
3						
4						
5		282	45	10	0	0
6		865	89	14	0	0
7		211	45	7	0	0
8		135	15	13	0	0
9					0	0
10					0	0
11		109	15	13	0	0
12		41	7	9	0	0
13					0	0
14					0	0
15		442	54	12	0	0
16		170	55	6	0	0
17		421	52	11	0	0
18		428	50	11	0	0
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20					0	0
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22					0	0
23		834	147	10	0	0
24		48	9	8	0	0
25		214	42	8	0	0
26		1043	126	15	0	0
27		391	55	10	0	0
28					0	0
29					0	0
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31		194	38	8	0	0
32		128.33	556	63	12 NaN	NaN
33			93	12	15	NaN
34					0	0
35					0	0
36					0	0
37					0	0
38		342	59	9	0	0
39					0	0
40					0	0
41					0	0
42					0	0
43		45	9	8	0	0
44					0	0
45		203	37	8	0	0
46		86179	128	30	6 NaN	NaN
47			513	53	15	NaN
48			71	11	10	NaN
49		40177	93	22	7 NaN	NaN
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55		280	52	9	0	0
56					0	0
57					0	0
58		88	27	5	0	0
59					0	0
60					0	0
61		81	21	7	0	0
62					0	0
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64					0	0
65					0	0

1						
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3	154	42	7	0	0	0
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10				0	0	0
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12				0	0	0
13	181	35	8	0	0	0
14	172	31	9	0	0	0
15	147	37	7	0	0	0
16	152	30	7	0	0	0
17	255	41	9	0	0	0
18				0	0	0
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20				0	0	0
21				0	0	0
22				0	0	0
23	162	31	7	0	0	0
24	278	26	17	0	0	0
25				0	0	0
26				0	0	0
27				0	0	0
28	131	18	11	0	0	0
29				0	0	0
30	258	50	7	0	0	0
31	112	37	6	0	0	0
32				0	0	0
33				0	0	0
34	22	7	5	0	0	0
35				0	0	0
36				0	0	0
37	92	10	13	0	0	0
38	76	10	11	0	0	0
39				0	0	0
40				0	0	0
41				0	0	0
42				0	0	0
43				0	0	0
44				0	0	0
45	191	27	10	0	0	0
46	179	31	9	0	0	0
47	93	12	15	0	0	0
48	510	76	10	0	0	0
49	72	17	7	0	0	0
50				0	0	0
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53	559	75	10	0	0	0
54	22	9	4	0	0	0
55				0	0	0
56	53551	26	9	6 NaN	NaN	NaN
57				0	0	0
58				0	0	0
59	48	8	9	0	0	0
60	65	12	8	0	0	0
61				0	0	0
62						
63						
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1						
2						
3		56	12	7	0	0
4					0	0
5					0	0
6					0	0
7		65	16	6	0	0
8	77288	81	22	6	NaN	NaN
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11					0	0
12					0	0
13					0	0
14					0	0
15		33	7	8	0	0
16		25	7	5	0	0
17					0	0
18					0	0
19						
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	PEP	MS/MS Coun	MS/MS Scan	Score	Delta score	Combinatoric Ratio	H/L
1	0.0024998	1	8758	50873	36926	10	0.32364
2	0.00066166	2	9811	63937	45532	10	0.39827
3	0.011114	1	7485	56.48	27381	5	0.189
4	0.015999	1	8380	54047	32371	5	0.27281
5	0.013065	1	5937	41615	26992	5	0.25025
6	0.0012876	1	6660	53625	31949	5	0.14797
7	0.00037934	1	6747	55302	26579	10	0.2281
8	0.0045661	1	7721	42209	20086	10	0.37424
9	0.014163	1	4648	48579	48579	5	0.31534
10	0.012897	1	13576	48467	20106	3	65582
11	0.01963	1	9065	80688	35.32	1	Nan
12	0.0063079	1	13327	73.36	51447	1	0.3703
13	0.033103	1	13329	80596	56065	1	0.58594
14	0.0053695	1	9268	50827	18461	1	Nan
15	0.02807	1	10887	45433	82528	1	
16	0.014498	1	7441	57149	22.38	1	
17	0.027538	1	14169	61344	22898	2	
18	0.0025375	3	15318	67396	61087	2	0.54438
19	0.0010496	2	15421	76533	55254	2	0.49769
20	0.98785	1	15234	87352	62871	2	0.49671
21	0.0093801	1	17999	56.48	28389	2	0.34323
22	0.0030875	1	15853	58796	39861	2	0.49439
23	2.2007E-11	1	15878	118.67	103.82	2	11087
24	0.011985	1	14078	54.15	28274	2	0.16628
25	0.0013892	1	14879	99409	80404	2	0.46245
26	NaN	0	NaN	NaN		0	0.55402
27	NaN	0	NaN	NaN		0	12755
28	NaN	0	NaN	NaN		0	0.57747
29	0.022911	1	16018	47603	15.25	4	0.51852
30	0.0359	1	10643	44612	89015	1	
31	0.0096279	1	16802	83.31	83.31	5	0.62157
32	0.038931	1	18314	65207	45627	5	0.53203
33	0.02059	1	20557	96391	63022	5	0.43102
34	0.001369	1	12202	95444	95444	5	0.63294
35	0.044014	1	8067	63883	44861	5	0.59556
36	NaN	0	NaN	NaN		0	0.43797
37	0.0004661	2	8847	90.78	72.2	10	0.51119
38	0.019791	1	8859	43794	43794	10	0.47973
39	0.0023691	1	9284	56099	33977	9	0.1246
40	0.0054448	1	10051	51264	31511	9	0.081331
41	0.00031051	1	7891	42301	20735	9	0.12181
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15	0.033141	1	21255	45207	17983
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28	0.40851	1	13835	125.51	65422
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8	0.021213	1	12473	82267	42362
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29	0.020133	1	5593	41257	18627	6 0.25871
30	0.016457	1	8863	43091	25076	6 NaN
31	0.0021378	1	5542	50358	21809	6 0.46976
32	0.024512	1	23661	47187	14.62	1
33	0.00060368	1	6010	71685	39494	3 0.39278
34	0.0045191	2	15975	68676	44269	2 0.63431
35	0.0027084	2	7149	66041	33.95	2 0.37721
36	0.024744	1	7074	86179	86179	2 0.7238
37	NaN	0	NaN	NaN		0 0.53294
38	0.0041788	1	13639	40798	79401	42 0.33531
39	0.013928	1	14309	40177	20.83	21 0.48278
40	NaN	0	NaN	NaN		0 0.48512
41	0.026924	1	10724	45357	12927	3 NaN
42	0.016234	1	12035	52579	65772	3
43	0.029975	1	4702	65465	14213	3 0.18581
44	0.030294	1	15787	88283	41486	3 0.17475
45	0.021733	2	7087	90385	63123	3 0.27006
46	0.035888	1	14615	87676	60413	3 0.24707
47	0.0061697	1	13851	100.77	84926	3 0.8397
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3	0.0022498	1	6811 104.88	89939	3 0.30248
4	0.0065927	1	8043 69581	69581	3 0.27591
5	0.031	1	11864 52008	67278	18
6	0.018399	1	19406 58592	17598	1
7	0.030004	1	11763 45653	22293	15
8	0.030708	1	9603 46.89	75515	10
9	0.005004	1	13742 95429	50989	80 NaN
10	0.0097054	2	7441 51104	31948	3 0.33058
11	0.86601	1	5983 106.31	85721	3 0.96199
12	0.18711	1	5785 113.86	97118	3 0.26731
13	0.0017519	1	5830 89913	69677	3 0.38826
14	0.0023236	2	5682 85046	67418	3 0.50712
15	0.0045983	1	18690 47.05	21126	45 NaN
16	0.038563	1	7996 41427	17195	2 0.20728
17	0.011363	1	15517 59884	33112	3
18	0.011712	1	18688 51469	32533	7 0.51866
19	0.0043264	1	12296 40986	12895	35 0.35024
20	0.032187	1	4718 45115	14257	3 NaN
21	0.0060348	1	15472 63181	13847	2 13046
22	0.039321	1	24020 58172	87241	6 NaN
23	0.011627	1	1240 42629	30571	4 0.58787
24	0.0021129	2	1671 58274	47348	4 0.48042
25	0.0020297	1	18544 49497	75857	30 39007
26	0.003254	1	10400 61161	85827	2 0.60011
27	0.00011073	1	17054 63925	39718	3 0.47343
28	0.00041089	2	16830 82942	82942	3 NaN
29	0.0030549	1	15804 47.05	27121	3 0.61585
30	1.0221E-08	2	18995 75416	53565	2 0.1746
31	1.2654E-08	1	22592 73603 49.58		2 0.30054
32	0.040158	2	18880 57629	41819	2 0.2115
33	0.03597	1	4781 48907	25916	3 0.29631
34	0.0090881	1	7651 65887	46124	5 0.2541
35	0.013697	1	6573 62002	48379	5 0.44899
36	0.0025483	1	13644 47548 16.41		4 0.5026
37	0.0068367	1	20960 42314	13982	4 0.32278
38	0.0070169	1	20592 42095	26493	4 0.57424
39	0.03068	1	22205 40103	12983	5 NaN
40	0.0033688	1	5888 52966	67171	6 0.4069
41	0.00066613	1	14867 53551	37967	15 0.24014
42	NaN	0	NaN NaN		0 0.34407
43	0.024356	1	10768 61765	20656	2
44	0.028584	1	11840 86803	67506	3 0.4286
45	0.024336	1	10297 89.44	42378	3 0.3455
46					
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3	0.0069893	1	12360	45084	19102	1 0.43579
4	0.0025547	1	10770	54103	27742	3 0.73698
5	0.0028601	1	11365	52814	24459	3 0.032076
6	0.02981	1	20702	77288 51.17		2 0.49286
7						
8	NaN	0	NaN	NaN		0 0.47535
9						
10	0.025826	1	10358	56916	14705	3
11	0.0068009	1	10752	63624	24	6 NaN
12	0.004607	1	10195	70942	7761	2 NaN
13	0.034442	1	8310	57047	21603	2 0.044587
14	0.0095447	1	13692	62077	26979	16 29426
15	0.0075079	1	13370	53377	86432	2 0.19195
16						
17	0.010466	1	14965	47726	61113	8 NaN
18						
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	Ratio H/L nor Ratio H/L shif	Intensity	Intensity L	Intensity H	Reverse	Potential con
1	0.57984	0	119240	84688	34548	
2	0.73098	0	88880	65772	23108	
3	0.35155	0	247460	209250	38214	
4	0.53892	0	229620	176360	53258	
5	0.51506	0	164080	137950	26132	
6	0.28614	0	192690	172720	19962	
7	0.44277	0	84864	78384	6480.6	
8	0.25798	0	90922	75426	15496	
9	0.38091	0	67903	46479	21424	
10	12628	0	173700	12556	161150	
11	NaN	0	142390	141990	407.64	
12	0.94138	0	313510	204840	108670	
13	14614	0	218980	132170	86805	
14	NaN	0	105780	98411	7367.4	
15						
16						
17						
18	10247	0	313690	179890	133790	
19	0.86522	0	578820	331790	247040	
20	12257	0	756200	447440	308760	
21	0.65471	0	401910	277420	124490	
22	0.90773	0	4876900	2849900	2027100	
23	21426	0	813590	481360	332230	
24	0.45693	0	129650	112250	17405	
25	0.97177	0	707250	476140	231110	
26	0.90304	0	339740	185380	154350	
27	1655	0	114740	45031	69710	
28	13952	0	156460	80831	75629	
29	10078	0	359240	234560	124680	
30						
31						
32						
33	11573	0	242390	145890	96503	
34	0.93693	0	80759	49713	31047	
35	0.87588	0	137250	112380	24868	
36	13616	0	599260	339050	260210	
37	13431	0	273570	164130	109440	
38	0.49196	0	90726	55894	34831	
39	11528	0	132120	81066	51050	
40	10819	0	65880	44312	21569	
41	0.21051	0	289450	271610	17837	
42	0.15605	0	231540	220620	10918	
43	0.18851	0	101150	97603	3548.5	
44	0.38686	0	439390	388300	51092	
45						
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2					
3	NaN	0	948710	618890	329820
4	0.65032	0	533560	408580	124980
5	10214	0	7382900	3846400	3536400 +
6	10214	0	7382900	3846400	3536400 +
7	12928	0	63270	43570	19700 +
8					
9	0.69503	0	91083	60678	30406
10					
11					
12					
13					
14					
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16					
17					
18	0.50367	0	255820	208970	46851
19	0.68522	0	120480	85761	34715
20	0.36672	0	195370	160860	34513
21	0.57834	0	215610	156630	58975
22	0.29314	0	165720	146660	19056
23	0.11562	0	61337	54770	6566.9
24	0.78028	0	309790	261000	48791
25	0.67052	0	567380	403460	163920
26	1057	0	122240	78061	44174
27	0.76923	0	259970	200520	59452
28	10578	0	255800	185350	70457
29	0.37952	0	90624	68113	22511
30	0.68932	0	1099700	782150	317510
31	0.32049	0	288330	210060	78265
32	0.85198	0	92724	53318	39407
33	0.47149	0	1000500	723220	277270
34	0.38078	0	175680	126400	49279
35	12283	0	226430	135120	91304
36	0.92394	0	245390	165200	80189
37	0.56326	0	91162	73823	17339
38	0.67576	0	1507900	1142600	365350
39	0.67518	0	313510	226040	87470
40	0.9039	0	216730	144730	72005
41					
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51	NaN	0	175250	2451.8	172800
52	0.70272	0	141990	90082	51908
53	0.42025	0	65000	39535	25465
54	1205	0	249100	134730	114360
55	0.71817	0	101870	78338	23527
56					
57					
58					
59	NaN	0	49661	0	49661
60	0.29435	0	222970	194040	28930
61					
62					
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2					
3	0.44968	0	563920	450140	113770
4	0.29647	0	412880	368280	44599
5	0.38264	0	677870	528810	149060
6	1103	0	233860	170080	63786
7	0.99748	0	348080	237670	110410
8	10496	0	233940	157990	75949
9	0.71628	0	290030	203570	86459
10	0.96139	0	334750	215590	119160
11	0.94173	0	155670	108410	47258
12	NaN	0	46427	46427	0
13	0.42529	0	224170	173460	50716
14	0.49948	0	144360	94052	50313
15	0.1674	0	583050	492700	90355
16	NaN	0	169030	7818.4	161210
17	0.46507	0	141240	93405	47837
18	0.50514	0	566310	504650	61657
19	0.51941	0	3542300	3076600	465680
20	0.8704	0	940910	803650	137260
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29	NaN	0	127550	127550	0
30	1118	0	225000	141650	83349
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33	21855	0	129210	66144	63070
34	0.43474	0	781810	449920	331890
35	69727	0	673200	126020	547180
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37					
38	43778	0	405010	21418	383590
39	0.31421	0	51616	38672	12944
40	56773	0	61882	10820	51062
41	23934	0	141910	51627	90278
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43					
44	0.72155	0	59383	43312	16070
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50	0.44605	0	52323	47569	4753.8
51	10384	0	63053	37972	25081
52	0.41515	0	48416	32483	15933
53	13198	0	257740	168290	89450
54					
55					
56	10617	0	82681	54727	27953
57	0.80221	0	267730	199900	67833
58	11831	0	235780	146960	88819
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61	0.62867	0	192830	140670	52161
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3	0.872	0	1201900	614420	587520	+
4	11019	0	382440	233280	149170	+
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6						
7	12567	0	4788200	2287400	2500800	+
8	0.60287	0	5225400	3739200	1486200	+
9						
10	0.73885	0	40278	24927	15351	+
11	0.95139	0	17833000	10411000	7421600	+
12	0.47429	0	269230	216790	52439	+
13						
14	20359	0	1336400	547220	789140	+
15	20359	0	1336400	547220	789140	+
16						
17	NaN	0	75545 3620.3		71925	
18	NaN	0	118170	113950 4228.6		
19	0.47712	0	704450	583790	120660	
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22	19572	0	80164	43221	36943	
23	20773	0	549530	258330	291210	
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25	NaN	0	118510	117450 1068.2		
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28	0.68091	0	81763	56657	25106	
29	NaN	0	38095	38095	0	
30	10889	0	88606	56127	32479	
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33	0.25037	0	92069	79289	12781	
34	NaN	0	2094800	1472500	622330	
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36	0.36563	0	1630400	1123800	506620	
37	0.32395	0	109120	94661	14462	
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39	0.43446	0	113860	98979	14883	+
40	NaN	0	224060	210040	14027	+
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45	0.8344	0	107580	74859	32725	
46	0.42549	0	1130200	837440	292760	
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48	0.41441	0	131510	106460	25052	
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50	58018	0	262860 9999.3		252860	
51	0.72226	0	612300	522560	89737	
52	0.081851	0	248790	226140	22648	
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54	10226	0	2609100	1567300	1041800	
55	0.83063	0	70607	51988	18619	
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57	1167	0	85966	59484	26482	
58	0.17394	0	142560	96229	46327	
59	0.61909	0	112590	76884	35704	
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61	0.51276	0	145510	109250	36260	
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3	0.74773	0	259730	179230	80499
4	14503	0	124760	77149	47611
5	0.35248	0	596300	456280	140020 +
6					
7	0.010883	0	1484100	1470600	13541
8	NaN	0	47083	0	47083
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11	12824	0	3488800	2057200	1431700
12	NaN	0	111000	0	111000
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14	0.060171	0	3534500	3438100	96399
15	22121	0	307820	146820	161000
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17	0.40595	0	202890	179410	23481
18	NaN	0	186780	184800	1975.3
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21					
22	0.59997	0	126640	90471	36171
23	NaN	0	320330	320330	0
24	NaN	0	100890	95525	5365.8
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27	0.76132	0	644980	482650	162320
28	0.69286	0	477550	373400	104150
29					
30	12879	0	190470	103230	87242
31					
32	0.37879	0	1415900	1036800	379070 +
33	11306	0	1152000	692920	459080
34					
35	13769	0	140760	85807	54957
36	0.88871	0	138730	80715	58018
37					
38	10384	0	908070	538680	369390
39	0.73671	0	158880	119960	38917
40	NaN	0	579630	0	579630
41	NaN	0	1413400	5969.9	1407400
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43	NaN	0	1577100	2660.6	1574400
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45	16106	0	1761700	199790	1561900
46	0.69084	0	152640	91267	61377
47					
48	13636	0	222500	143610	78888
49	0.99817	0	747460	411250	336210
50	0.71009	0	2616300	1958600	657700
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52	12681	0	157470	77181	80285
53					
54	0.67044	0	588100	436040	152060
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56	11169	0	64518	45510	19007
57	0.64895	0	231730	175970	55754
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59	16839	0	75448	41623	33824
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61	10579	0	177870	20506	157370
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63	NaN	0	141500	3165.4	138330
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3	29139	0	155890	6584.4	149300
4	12805	0	245330	6144.9	239180
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7	NaN	0	557620	8397	549220
8	10329	0	387120	326370	60754
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10	NaN	0	150110	150110	0
11	0.071051	0	458210	447510	10695
12	NaN	0	44137	44137	0
13					
14	11035	0	54728	33299	21429
15	14984	0	159940	9393.4	150550
16					+
17	0.61664	0	119030	88874	30154
18	0.69043	0	232280	168040	64239
19	0.13002	0	68358	62946	5411.8
20					
21	NaN	0	82502	76424	6077.1
22	0.81089	0	187560	116680	70873
23					
24	41549	0	259330	8189.1	251140
25	66059	0	458870	19718	439150
26	0.85524	0	125600	83931	41672
27					
28	10192	0	79361	56407	22954
29	0.73437	0	148100	96002	52094
30	0.77457	0	121610	85316	36293
31					
32	0.74515	0	86893	58523	28370
33	0.7399	0	145970	95549	50423
34					
35	0.57051	0	169540	106950	62587
36	13895	0	3667900	2133300	1534600
37					
38					
39	NaN	0	313750	311870	1886.5
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41					
42	NaN	0	48021	0	48021 +
43	32448	0	117830	5923.9	111900
44	13252	0	611770	421080	190690
45					
46	0.83229	0	365160	284700	80454
47	0.32425	0	98676	80919	17757
48	0.10636	0	177240	151810	25433
49					
50	0.4312	0	397460	267310	130150
51					
52	0.33156	0	2454400	2047800	406530
53	0.62262	0	187470	133590	53884
54					
55	14833	0	202480	113830	88643
56					
57	0.4546	0	225420	165180	60239
58	0.8017	0	2313800	1693400	620410
59					
60	0.32468	0	341520	318030	23491
61	13087	0	521720	258180	263540
62					
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3        14326            0        108750            61541            47204  
4        0.77004            0        171740            103250            68490  
5        0.92008            0        211480            134120            77361  
6        NaN                0        577970            576350 1613.4  
7        NaN                0        653230            653230            0  
8        0.1509            0        555960            531660            24302  
9        NaN                0        161320            161320            0  
10      0.15305            0        144570            125540            19027  
11      0.014556            0        428150            424920 3227.6  
12      0.030196            0        1422400          1411100          11342  
13      0.029208            0        891850            884880 6971.7  
14      0.36952            0        262100            211230            50870  
15      0.088132            0        236880            231360 5519.7  
16      NaN                0        1002300          1002300          0  
17      0.0317            0        2060000          2043500          16450  
18      NaN                0        2216100          2162400          53705  
19      0.1905            0        91803              87186            4617  
20      0.25369            0        133890            120940            12953  
21      0.10484            0        239590            221720            17874  
22      0.017454            0        1062000          1053200 8798.7  
23      0.051932            0        335180            326930 8245.6  
24      0.4968            0        69172              54664            14508  
25      0.79754            0        113370            80653            32720  
26      0.65676            0        139310            108980            30327  
27      0.76525            0        181360            123370            57998  
28      10179              0        1443800          819400          624370  
29  
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41      0.0064642        0        3335500          3323200          12336  
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47      NaN                0        233020            229570 3453.5  
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8	14941	0	706560	347160	359400
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11	0.85365	0	116440	74135	42301 +
12	0.81982	0	406320	289960	116360 +
13	0.57508	0	237170	210870	26301
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35	13021	0	251520	141240	110280
36	0.6305	0	114300	70632	43672
37	0.79741	0	82466	60394	22072
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42	13324	0	228190	140540	87655
43	15523	0	219220	135430	83788
44	0.29128	0	89001	74059	14942
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46	0.66225	0	654380	444330	210050
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7	156		716	11	15	236	236
8	157		716	11	16	237	237
9	158		716	11	16	238	238
10	910		197	91	106	1571	1571
11	1035		1779	110	128	1731	1731
12	1247		105	134	154	2088	2088
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26	4272		1952	452	522	6927	6927
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37	47125	416	5686	6378		
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54                              342  
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Sequence	Length	K Count	Modification	Modified	Deamidation	Oxidation
			s	sequence	(NQ)	(M)
AAAPAAAVASP	25	1	2 Phospho (S`_AAAPAAAVAS(ph)PAAAATSADASPS(ph)PA			
AAAPAAAVASP	25	1	2 Phospho (S`_AAAPAAAVAS(ph)PAAAATSADASPS(ph)PA			
AAAPAAAVASP	25	1	Phospho (STY_AAAPAAAVASPAAAATSADASPS(ph)PAK_			
AAAPAAAVASP	25	1	Phospho (STY_AAAPAAAVASPAAAATSADASPS(ph)PAK_			
AAAPAAAVASP	26	2	Phospho (STY_AAAPAAAVASPAAAATS(ph)ADASPSPAKK_			
AAAPAAAVASP	26	2	Phospho (STY_AAAPAAAVASPAAAATSADASPS(ph)PAKK_			
AAAPAAAVASP	26	2	2 Phospho (S`_AAAPAAAVAS(ph)PAAAATSADASPS(ph)PA			
AAAPAAAVASP	26	2	2 Phospho (S`_AAAPAAAVAS(ph)PAAAATSADAS(ph)PSPA			
ALDLLMSYRLI	11		1 Oxidation (M_ALDLLM(ox)S(ph)Y(ph)RLK ALDLLM(1)SY			
ALDLLMSYRLI	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(ph)ASHNPGGPENDFGIK_			
ALQAVYPDYY	19	1	Phospho (STY_ALQAVYPDYYDESLYGS(ph)K_			
ALQAVYPDYY	19	1	Phospho (STY_ALQAVYPDYYDESLYGS(ph)K_			
ALQAVYPDYY	19	1	Phospho (STY_ALQAVYPDYYDESLYGS(ph)K_			
ALQAVYPDYY	19	1	Phospho (STY_ALQAVYPDYYDESLYGS(ph)K_			
ALQAVYPDYY	19	1	Phospho (STY_ALQAVYPDYYDESLYGS(ph)K_			
ALQAVYPDYY	19	1	Phospho (STY_ALQAVYPDYYDESLYGS(ph)K_			
ALQAVYPDYY	19	1	Phospho (STY_ALQAVYPDYYDESLYGS(ph)K_			
ALQAVYPDYY	19	1	2 Phospho (S`_ALQAVYPDYYDELS(ph)LYGS(ph)K_			
ALQAVYPDYY	19	1	2 Phospho (S`_ALQAVYPDYYDELS(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			

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2 APATPQAATS 39 2 Phospho (STY\_APATPQAATSVTNPAAGDGISVQNDPPVD  
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6 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
7 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
8 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
9 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
10 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
11 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
12 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
13 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
14 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
15 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
16 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
17 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
18 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
19 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
20 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
21 ASAFAQSDDE 14 1 Phospho (STY\_ASAFAQFS(ph)DDEEEVK\_  
22

23  
24 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
25 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
26 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
27 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
28 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
29 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
30 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
31 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
32 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)ASGVT(ph)VSDVCK\_  
33 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
34 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
35 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
36 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)AS(ph)GVTVSDVCK\_  
37 ASGVTVSDVC 11 1 Acetyl (Protei\_(ac)ASGVT(ph)VSDVCK\_  
38

39  
40 DLEYFNNLK 9 1 Phospho (STY\_DLEY(ph)FN|DLEYFN(1)N(1)LK  
41 DLEYFNNLK 9 1 Phospho (STY\_DLEY(ph)FN|DLEYFN(1)N(1)LK  
42

43  
44 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_  
45 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_  
46 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_  
47 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_  
48 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_  
49 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_  
50 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_  
51 DVDFGDSNDI 21 1 Phospho (STY\_DVDFGDS(ph)DNENEPDAYLARLK\_  
52

53  
54 EAAQYGTVN/ 14 1 Phospho (STY\_EAAQY(ph)GTVNAVLPK\_  
55 EAAQYGTVN/ 14 1 Phospho (STY\_EAAQY(ph)GTVNAVLPK\_  
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57  
58  
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61 EASPVSMASP 25 2 Oxidation (M\_EASPVSM(ox)AS(ph)PAKD|EASPVSM(1)^A  
62  
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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)A
ELPDSDSLNV/	27	1 Phospho (STY_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_
ELPDSDSLNV/	27	1 Phospho (STY_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_
ELPDSDSLNV/	27	1 Phospho (STY_ELPDSDSLNVAPPEGFS(ph)DEEPEERQCK_
FFDSGDYQM/	11	1 Oxidation (M_FFDSD(ph)GDYQM(ox)AK_ FFDSGDYQM(
FFDSGDYQM/	11	1 Oxidation (M_FFDSD(ph)GDYQM(ox)AK_ FFDSGDYQM(
FFDSGDYQM/	11	1 Oxidation (M_FFDSD(ph)GDYQM(ox)AK_ FFDSGDYQM(
KEESEEDDDI	17	1 Oxidation (M_KEESES(ph)EDDDM(ox)GF.KEESEEDDDI
KEESEEDDDI	17	1 Oxidation (M_KEESES(ph)EDDDM(ox)GF.KEESEEDDDI
KEESEEDDDI	17	1 Oxidation (M_KEESES(ph)EDDDM(ox)GF.KEESEEDDDI
KIDNPESAK\	25	3 Phospho (STY_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_
KIDNPESAK\	25	3 Phospho (STY_KIDNPESAKVS(ph)DAEEEEEEYAVEK_
KIDNPESAK\	25	3 Phospho (STY_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_
KIDNPESAK\	25	3 Phospho (STY_KIDNPES(ph)SAKVSDAEEEEEEYAVEK_
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
KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
KPEDPSSEAE/	17	2 Phospho (STY_KPEDPSSEAEALCS(ph)PAK_
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
MQLILSYLQSC	14	1 Acetyl (Protei_(ac)MQLILS( MQ(0.212)LILSYLQ(0.848)S
MQLILSYLQSC	14	1 Acetyl (Protei_(ac)MQLILS\ MQ(0.007)LILSYLQ(0.996)S
MQLILSYLQSC	14	1 Acetyl (Protei_(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_
MQLILSYLQSC	14	1 Acetyl (Protei_(ac)MQLILSY(ph)LQ(de)SQ(de)Q(de)IK_
MQLILSYLQSC	14	1 Oxidation (M_M(ox)Q(de)I MQ(0.844)LIL M(1)QLILSYLC

1	MQLILSYLQSC	14	1 Oxidation (M _M(ox)QLILS\ MQ(0.066)LIL M(1)QLILSYLC
2	MQLILSYLQSC	14	1 Oxidation (M _M(ox)QLILSYLQ(de)S(ph)Q(de)QIK_
3	MQLILSYLQSC	14	1 Oxidation (M _M(ox)Q(de)LILS(ph)YLQSQQ(de)IK_
4			
5	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
6	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
7	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
8	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
9	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
10	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
11	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
12	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
13	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
14	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.0 M(1)RDKISQL
15	MRDKISQLFC	13	2 Acetyl (Protei_(ac)M(ox)RD MRDKISQ(0.2 M(1)RDKISQL
16			
17	MVEPSPETVC	24	1 Oxidation (M _M(ox)VEPSPETVGDFQSVQ M(1)VEPSPET
18	MVEPSPETVC	24	1 Oxidation (M _M(ox)VEPSPETVGDFQSVQ M(1)VEPSPET
19	MVEPSPETVC	24	1 Oxidation (M _M(ox)VEPSPETVGDFQSVQ M(1)VEPSPET
20			
21	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
22	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
23	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
24	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
25	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
26	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
27	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
28	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
29	NAGGVGVGV	17	2 Phospho (STY_NAGGVGVGVGEKS(ph)PDLK_
30	NAGGVGVGV	18	3 Phospho (STY_NAGGVGVGVGEKS(ph)PDLKK_
31	NAGGVGVGV	18	3 Phospho (STY_NAGGVGVGVGEKS(ph)PDLKK_
32	NAGGVGVGV	18	3 Phospho (STY_NAGGVGVGVGEKS(ph)PDLKK_
33			
34	NVGIFIKDDSE	19	3 Phospho (STY_NVGIFIKDDS(ph)DEEDVDDKK_
35	NVGIFIKDDSE	19	3 Phospho (STY_NVGIFIKDDS(ph)DEEDVDDKK_
36	NVGIFIKDDSE	19	3 Phospho (STY_NVGIFIKDDS(ph)DEEDVDDKK_
37	NVGIFIKDDSE	19	3 Phospho (STY_NVGIFIKDDS(ph)DEEDVDDKK_
38			
39	PCNLYQTAQE	13	1 Phospho (STY_PCNLY(ph)QTAQEQLK_
40	PCNLYQTAQE	13	1 Phospho (STY_PCN(de)LY(\p PCN(0.992)LYQ(0.004)TAQ(
41			
42	PLPSGRIPQITI	17	1 2 Phospho (S_PLPS(ph)GRIPQIT(ph)PPASPK_
43	PLPSGRIPQITI	17	1 2 Phospho (S_PLPS(ph)GRIPQIT(ph)PPASPK_
44			
45	QELLQSYM	9	1 Oxidation (M_(gl)Q(de)ELL Q(1)ELLQ(1)S QELLQSYM(1)
46	QELLQSYM	9	1 Oxidation (M_(gl)Q(de)ELL Q(1)ELLQ(1)S QELLQSYM(1)
47	QELLQSYM	9	1 Phospho (STY_(gl)Q(de)ELL Q(1)ELLQ(1)SYM
48			
49	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
50	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
51	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
52	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
53	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
54	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
55	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
56	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
57	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
58	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
59	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
60	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
61	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
62	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
63			
64			
65			

1			
2			
3	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
4	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
5	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
6	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
7	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
8	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
9	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
10	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
11	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
12	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
13	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
14	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
15	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
16	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
17	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
18	QISIGIYELLK	11	1 Phospho (STY_QISIGIY(ph)ELLK_
19			
20			
21	QSSYHGVHQ\	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
22	QSSYHGVHQ\	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
23	QSSYHGVHQ\	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
24	QSSYHGVHQ\	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
25	QSSYHGVHQ\	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
26	QSSYHGVHQ\	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
27	QSSYHGVHQ\	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
28	QSSYHGVHQ\	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
29	QSSYHGVHQ\	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
30	QSSYHGVHQ\	18	1 Phospho (STY_(gl)QSSYHGVHQAWNTNQDS(ph)K_
31			
32			
33	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(\u21d3Q(0.987)SVPQ(0.987)LAN(0
34	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(\u21d3Q(0.962)SVPQ(0.972)LAN(0
35	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(\u21d3Q(0.942)SVPQ(0.985)LAN(0
36	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_
37	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_
38	QSVPQLANLT	16	1 Phospho (STY_Q(de)SVPQ(de)LAN(de)LT(ph)FQYFLK_
39			
40			
41			
42	REEENAAAAAE	31	1 Phospho (STY_REEENAAAAEEEAGEISATGGATS(ph)PEP\
43	REEENAAAAAE	31	1 Phospho (STY_REEENAAAAEEEAGEISATGGAT(ph)SPEP\
44	REEENAAAAAE	31	1 Phospho (STY_REEENAAAAEEEAGEISATGGAT(ph)SPEP\
45			
46			
47	RGCQILGLNK\	18	2 Phospho (STY_RGCQ(de)IL(RGCQ(0.965)ILGLN(0.024)K
48	RGCQILGLNK\	18	2 Phospho (STY_RGCQ(de)IL(RGCQ(0.838)ILGLN(0.155)K
49	RGCQILGLNK\	18	2 Phospho (STY_RGCQ(de)IL(RGCQ(0.999)ILGLNKYGIQQ\
50			
51			
52			
53	RGPPPPPPTAS\	17	1 2 Phospho (S_RGPPPPPPTA:RGPPPPPPTASESTRRN(1)K
54	RGPPPPPPTAS\	17	1 2 Phospho (S_RGPPPPPPTASES(ph)T(ph)RRN(de)K_
55	RGPPPPPPTAS\	17	1 2 Phospho (S_RGPPPPPPTASES(ph)T(ph)RRN(de)K_
56			
57			
58			
59	RKKPEDPSSE\	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
60	RKKPEDPSSE\	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
61	RKKPEDPSSE\	19	3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
62			
63			
64			
65			

1		
2	RKKPEDPSSE/	19
3	RKKPEDPSSE/	19
4	RKKPEDPSSE/	19
5	RKKPEDPSSE/	19
6	RKKPEDPSSE/	19
7	RKKPEDPSSE/	19
8	RKKPEDPSSE/	19
9	RKKPEDPSSE/	19
10	RKKPEDPSSE/	19
11		3 Phospho (STY_RKKPEDPSSEAEALCS(ph)PAK_
12	SAAVAEGGD/	23
13	SAAVAEGGD/	23
14	SAAVAEGGD/	23
15	SAAVAEGGD/	23
16	SAAVAEGGD/	23
17	SAAVAEGGD/	23
18	SAAVAEGGD/	23
19		2 Phospho (STY_SAAVAEGGDAVAET(ph)AKGEEGSPK_
20	SAAEAIVTTA	20
21	SAAEAIVTTA	20
22	SAAEAIVTTA	20
23	SAAEAIVTTA	20
24	SAAEAIVTTA	20
25	SAAEAIVTTA	20
26	SAAEAIVTTA	20
27	SAAEAIVTTA	20
28	SAAEAIVTTA	20
29	SAAEAIVTTA	20
30	SAAEAIVTTA	20
31	SAAEAIVTTA	20
32	SAAEAIVTTA	20
33	SAAEAIVTTA	20
34	SAAEAIVTTA	20
35	SAAEAIVTTA	20
36	SAAEAIVTTA	20
37	SAAEAIVTTA	20
38	SAAEAIVTTA	20
39	SAAEAIVTTA	20
40	SAAEAIVTTA	20
41	SAAEAIVTTA	20
42	SAAEAIVTTA	20
43	SAAEAIVTTA	20
44	SAAEAIVTTA	20
45	SAAEAIVTTA	20
46	SAAEAIVTTA	20
47	SAAEAIVTTA	20
48	SAAEAIVTTA	20
49	SAAEAIVTTA	20
50	SAAEAIVTTA	20
51	SAAEAIVTTA	20
52	SAAEAIVTTA	20
53	SAAEAIVTTA	20
54	SAAEAIVTTA	20
55	SAAEAIVTTA	20
56	SAAEAIVTTA	20
57	SAAEAIVTTA	20
58	SAAEAIVTTA	20
59		1 Acetyl (Protei_(ac)SAEAEAIVTTATADVSS(ph)PSK_
60	SDSAVATSASI	21
61		1 Acetyl (Protei_(ac)SDSAVAT(ph)SASPVAAPPATVEK_
62		
63		
64		
65		

1		
2		
3	SDSAVATSASI	21
4	SDSAVATSASI	21
5		1 Acetyl (Protei_(ac)SDSAVATS(ph)ASPVAAPPATVEK_
6		1 Acetyl (Protei_(ac)SDSAVAT(ph)SASPVAAPPATVEK_
7		
8	SPIVFELTQPSI	14
9	SPIVFELTQPSI	14
10	SPIVFELTQPSI	14
11	SPIVFELTQPSI	14
12	SPIVFELTQPSI	14
13	SPIVFELTQPSI	14
14	SPIVFELTQPSI	14
15		1 Phospho (STY_SPIVFELTQPS(ph)PEK_
16		1 Phospho (STY_SPIVFELTQPS(ph)PEK_
17		1 Phospho (STY_SPIVFELTQPS(ph)PEK_
18		1 Phospho (STY_SPIVFELTQPS(ph)PEK_
19		1 Phospho (STY_SPIVFELTQPS(ph)PEK_
20		1 Phospho (STY_SPIVFELTQPS(ph)PEK_
21		1 Phospho (STY_SPIVFELTQPS(ph)PEK_
22		1 2 Phospho (S_S(ph)PIVFELTQPS(ph)PEK_
23		
24	SVHSPNPGLIL	14
25	SVHSPNPGLIL	14
26	SVHSPNPGLIL	14
27	SVHSPNPGLIL	14
28	SVHSPNPGLIL	14
29		1 Acetyl (Protei_(ac)SVHS(ph)PNPGLILQSK_
30		1 Acetyl (Protei_(ac)SVHS(ph)PNPGLILQSK_
31		1 Acetyl (Protei_(ac)SVHS(ph)PNPGLILQSK_
32		1 Acetyl (Protei_(ac)SVHS(ph)PNPGLILQSK_
33		
34	TSPKPTKPASF	12
35	TSPKPTKPASF	12
36		3 Phospho (STY_TSPKPTKPAS(ph)PK_
37		3 Phospho (STY_TSPKPTKPAS(ph)PK_
38		
39	VDRSDNAAES	25
40	VDRSDNAAES	25
41	VDRSDNAAES	25
42	VDRSDNAAES	25
43		1 Acetyl (Protei_(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI
44		1 Acetyl (Protei_(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI
45		1 Acetyl (Protei_(ac)VDRSDNAAES(ph)FDDAVEERVINEEYI
46		
47	VNSLIVLESDE	33
48	VNSLIVLESDE	33
49	VNSLIVLESDE	33
50	VNSLIVLESDE	33
51		1 Phospho (STY_VNSLIVLES(ph)DEEEDEQLVQAADLVEQEDE
52		1 Phospho (STY_VNSLIVLES(ph)DEEEDEQLVQAADLVEQEDE
53		1 Phospho (STY_VNSLIVLES(ph)DEEEDEQLVQAADLVEQEDE
54		
55	VTILWMGGSC	19
56	VTILWMGGSC	19
57	VTILWMGGSC	19
58		1 Oxidation (M_VT(ph)ILWM(ox)GGSGSIV(VTILWM(1)G)
59		1 Oxidation (M_VT(ph)ILWM(ox)GGSGSIV(VTILWM(1)G)
60		1 Oxidation (M_VT(ph)ILWM(ox)GGSGSIV(VTILWM(1)G)
61		
62		
63		
64		
65		

Phospho (STY)	Deamidation (NQ) Score	Oxidation (M) Score	Phospho (STY)	Acetyl (Protein N- term)	Deamidation (NQ)	Gln->pyro- Glu
Probabilities	Diff	Diff	Diff			
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
<hr/>						
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
<hr/>						
ALGGIVLT(0.066)AS(0.934)HNPGGPENDF ALGGIVLT(-11				0	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK ALGGIVLT(0)A				0	0	0
ALGGIVLT(0.5)AS(0.5)HNPGGPENDFGIK ALGGIVLT(0)A				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)A				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)PGGF ALGGIVLT(0.6				0	1	0
<hr/>						
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
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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

1	APATPQAATSVTNPAAGDGIS(0.004)VQNC APAT(-44.28)	0	0	0
2				
3	ASAFQFS(1)DDEEEVK	AS(-64.04)AFI	0	0
4	ASAFQFS(1)DDEEEVK	AS(-48.64)AFI	0	0
5	ASAFQFS(1)DDEEEVK	AS(-75.24)AFI	0	0
6	ASAFQFS(1)DDEEEVK	AS(-54.82)AFI	0	0
7	ASAFQFS(1)DDEEEVK	AS(-61.47)AFI	0	0
8	ASAFQFS(1)DDEEEVK	AS(-59.12)AFI	0	0
9	ASAFQFS(1)DDEEEVK	AS(-56.8)AFQ	0	0
10	ASAFQFS(1)DDEEEVK	AS(-42.65)AFI	0	0
11	ASAFQFS(1)DDEEEVK	AS(-66.2)AFQ	0	0
12	ASAFQFS(1)DDEEEVK	AS(-67.24)AFI	0	0
13	ASAFQFS(1)DDEEEVK	AS(-96.36)AFI	0	0
14			0	0
15				
16	AS(1)GVTVSDVCK	AS(39.82)GV1	1	0
17	AS(1)GVTVSDVCK	AS(38.57)GV1	1	0
18	AS(1)GVTVSDVCK	AS(40.23)GV1	1	0
19	AS(1)GVTVSDVCK	AS(38.02)GV1	1	0
20	AS(0.977)GVT(0.022)VSDVCK	AS(16.42)GV1	1	0
21	AS(0.997)GVT(0.003)VSDVCK	AS(25.59)GV1	1	0
22	AS(0.42)GVT(0.568)VS(0.012)DVCK	AS(-1.31)GVT	1	0
23	AS(0.998)GVT(0.002)VSDVCK	AS(26.02)GV1	1	0
24	AS(1)GVTVSDVCK	AS(35.02)GV1	1	0
25	AS(0.976)GVT(0.023)VS(0.001)DVCK	AS(16.37)GV1	1	0
26			1	0
27				
28	DLEY(1)FNNL DLEYFN(65.22)N(65.22)LK	DLEY(65.22)F	0	2
29	DLEY(1)FNNL DLEYFN(54.07)N(54.07)LK	DLEY(54.07)F	0	2
30				
31				
32	DVDFGDS(1)DNENEPDAYLARLK	DVDFGDS(53.	0	0
33	DVDFGDS(1)DNENEPDAYLARLK	DVDFGDS(67.	0	0
34	DVDFGDS(1)DNENEPDAYLARLK	DVDFGDS(43.	0	0
35	DVDFGDS(1)DNENEPDAYLARLK	DVDFGDS(56.	0	0
36	DVDFGDS(0.994)DNENEPDAY(0.006)LARI DVDFGDS(22.	0	0	0
37	DVDFGDS(0.999)DNENEPDAY(0.001)LARI DVDFGDS(31.	0	0	0
38				
39				
40	EAAQY(0.933)GT(0.067)VNAVLPK	EAAQY(11.44	0	0
41	EAAQY(0.799)GT(0.201)VNAVLPK	EAAQY(6)GT(	0	0
42				
43				
44				
45	EAS(0.012)PVS(0.157)MAS( EASPVSM(53. EAS(-18.36)P\	0	0	0
46				
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1	EAS(0.014)PVS(0.221)MAS( EASPVSM(53. EAS(-17.37)PV)	0	0	0
2	EAS(0.127)PVS(0.465)MAS( EASPVSM(40. EAS(-5.65)PV)	0	0	0
3				
4	ELPDSDSLNVAPPEGFS(1)DEEPEERQCK	ELPDS(-46.35	0	0
5	ELPDSDSLNVAPPEGFS(1)DEEPEERQCK	ELPDS(-49.23	0	0
6	ELPDSDS(0.001)LNVAPPEGFS(0.999)DEEP	ELPDS(-38.75	0	0
7				
8	FFDS(1)GDYQMAK	FFDSGDYQM  FFDS(40.97)G	0	0
9	FFDS(0.994)GDY(0.006)QM	FFDSGDYQM  FFDS(22.15)G	0	0
10	FFDS(1)GDYQMAK	FFDSGDYQM  FFDS(36.09)G	0	0
11				
12	KEES(0.181)ES(0.819)EDDD KEESESEDDDI KEES(-6.55)ES	0	0	0
13	KEES(0.209)ES(0.791)EDDD KEESESEDDDI KEES(-5.78)ES	0	0	0
14	KEES(0.074)ES(0.926)EDDD KEESESEDDDI KEES(-10.98)E	0	0	0
15				
16	KIDNPES(0.333)S(0.333)AKVS(0.333)DAEI KIDNPES(0)S(	0	0	0
17	KIDNPES(0.012)S(0.022)AKVS(0.966)DAEI KIDNPES(-19.	0	0	0
18	KIDNPES(0.489)S(0.489)AKVS(0.022)DAEI KIDNPES(0)S(	0	0	0
19	KIDNPES(0.567)S(0.41)AKVS(0.023)DAEEI KIDNPES(1.41	0	0	0
20				
21	KKEEES(1)DQS(1)DDDMGF KKKEEESDQSD  KKEEES(46.14	0	0	0
22	KKEEES(1)DQS(1)DDDMGF KKKEEESDQSD  KKEEES(46.7)	0	0	0
23	KKEEES(1)DQS(1)DDDMGF KKKEEESDQSD  KKEEES(42.09	0	0	0
24	KKEEES(0.035)DQS(0.965)D KKKEEESDQSD  KKEEES(-14.3	0	0	0
25				
26	KPEDPSSEAEALCS(1)PAK	KPEDPS(-47.0	0	0
27	KPEDPSSEAEALCS(1)PAK	KPEDPS(-37.5	0	0
28	KPEDPSSEAEALCS(1)PAK	KPEDPS(-41.9	0	0
29	KPEDPSSEAEALCS(1)PAK	KPEDPS(-51.7	0	0
30	KPEDPSSEAEALCS(1)PAK	KPEDPS(-69.7	0	0
31	KPEDPSSEAEALCS(1)PAK	KPEDPS(-49.5	0	0
32				
33	MPNLQS(0.857)S(0.121)IPF M(56.2)PNLQ MPNLQS(8.45	1	0	0
34	MPNLQS(0.492)S(0.492)IPF M(40.24)PNL MPNLQS(0)S(	1	0	0
35	MPNLQS(0.778)S(0.175)IPF M(47.71)PNL MPNLQS(6.47	1	0	0
36	MPNLQS(0.497)S(0.497)IPF M(58.89)PNL MPNLQS(0)S(	1	0	0
37				
38	MQLILS(0.694 MQ(-7.66)LILSYLQ(7.66)SQ  MQLILS(7.66	1	3	0
39	MQLILS(0.244 MQ(-25.8)LILSYLQ(25.8)SQ  MQLILS(-4.01	1	3	0
40				
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61				
62	MQLILS(0.974 MQ(7.74)LILS M(44.25)QLIL MQLILS(19.37	0	2	0
63				
64				
65				

1	MQLILS(0.201)MQ(-13.61)LI M(43.69)QLIL MQLILS(-5.35	0	2	0
2		0	2	0
3		0	2	0
4				
5	MRDKIS(1)QL MRDKISQ(-15 M(62.09)RDK MRDKIS(62.0	1	1	0
6	MRDKIS(1)QL MRDKISQ(-15 M(54.34)RDK MRDKIS(54.3	1	1	0
7	MRDKIS(1)QL MRDKISQ(-10 M(56.2)RDKIS MRDKIS(56.2	1	1	0
8	MRDKIS(1)QL MRDKISQ(-17 M(51.13)RDK MRDKIS(51.1	1	1	0
9	MRDKIS(1)QL MRDKISQ(-12 M(51.46)RDK MRDKIS(51.4	1	1	0
10	MRDKIS(1)QL MRDKISQ(-4. M(43.8)RDKIS MRDKIS(43.8	1	1	0
11				
12	MVEPSPETVGDFQS VQEEVE M(86.56)VEP! MVEPS(-69.6	0	0	0
13	MVEPSPETVGDFQS(0.245)\ M(50.26)VEP! MVEPS(-41.7	0	0	0
14	MVEPSPETVGDFQS(0.001)\ M(50.32)VEP! MVEPS(-37.1	0	0	0
15				
16	NAGGVGVGVGEKS(1)PDLK	NAGGVGVGV	0	0
17	NAGGVGVGVGEKS(1)PDLK	NAGGVGVGV	0	0
18	NAGGVGVGVGEKS(1)PDLK	NAGGVGVGV	0	0
19	NAGGVGVGVGEKS(1)PDLK	NAGGVGVGV	0	0
20	NAGGVGVGVGEKS(1)PDLK	NAGGVGVGV	0	0
21	NAGGVGVGVGEKS(1)PDLK	NAGGVGVGV	0	0
22	NAGGVGVGVGEKS(1)PDLKK	NAGGVGVGV	0	0
23	NAGGVGVGVGEKS(1)PDLKK	NAGGVGVGV	0	0
24				
25	NVGIFIKDDS(1)DEEDVDDKK	NVGIFIKDDS(	0	0
26	NVGIFIKDDS(1)DEEDVDDKK	NVGIFIKDDS(	0	0
27	NVGIFIKDDS(1)DEEDVDDKK	NVGIFIKDDS(	0	0
28				
29	PCNLY(0.854)QT(0.146)AQEQLK	PCNLY(7.67)C	0	0
30	PCNLY(0.962) PCN(24.93)LYQ(-24.93)TAQ PCNLY(14.07)	0	1	0
31				
32	PLPS(1)GRIPQIT(0.999)PPAS(0.001)PK	PLPS(41.55)G	0	0
33	PLPS(1)GRIPQIT(0.997)PPAS(0.004)PK	PLPS(33.2)GR	0	0
34				
35	QELLQS(0.87; Q(51.95)ELLC QELLQSYM(5: QELLQS(8.31	0	2	1
36	QELLQS(0.84; Q(41.43)ELLC QELLQSYM(4: QELLQS(7.5)Y	0	2	1
37	QELLQS(0.24; Q(45.02)ELLQ(45.02)SYM K QELLQS(-4.96	0	2	1
38				
39	QISIGIY(1)ELLK	QIS(-47.73)IG	0	0
40	QISIGIY(1)ELLK	QIS(-48.31)IG	0	0
41	QISIGIY(1)ELLK	QIS(-46.94)IG	0	0
42	QIS(0.001)IGIY(0.999)ELLK	QIS(-32.34)IG	0	0
43	QISIGIY(1)ELLK	QIS(-55.01)IG	0	0
44	QISIGIY(1)ELLK	QIS(-38.47)IG	0	0
45				

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2					
3	QISIGIY(1)ELLK	QIS(-43.94)IG	0	0	0
4	QISIGIY(1)ELLK	QIS(-39.86)IG	0	0	0
5	QISIGIY(1)ELLK	QIS(-57.55)IG	0	0	0
6	QISIGIY(1)ELLK	QIS(-35.76)IG	0	0	0
7	QISIGIY(1)ELLK	QIS(-50.69)IG	0	0	0
8	QISIGIY(1)ELLK	QIS(-47.93)IG	0	0	0
9	QISIGIY(1)ELLK	QIS(-49.83)IG	0	0	0
10	QISIGIY(1)ELLK	QIS(-53)IGIY(1)	0	0	0
11	QISIGIY(1)ELLK	QIS(-39.44)IG	0	0	0
12	QISIGIY(1)ELLK	QIS(-55.72)IG	0	0	0
13	QISIGIY(1)ELLK	QIS(-52.88)IG	0	0	0
14	QISIGIY(1)ELLK	QIS(-36.23)IG	0	0	0
15					
16					
17					
18					
19					
20					
21	QSSYHGVHQAWNT(0.042)NQDS(0.957)K QS(-41.5)S(-4	0	0	1	
22	QSSYHGVHQAWNT(0.028)NQDS(0.972)K QS(-47.65)S(-	0	0	1	
23	QSSYHGVHQAWNT(0.042)NQDS(0.958)K QS(-80.23)S(-	0	0	1	
24	QSSYHGVHQAWNT(0.001)NQDS(0.999)K QS(-87.48)S(-	0	0	1	
25	QSSYHGVHQAWNT(0.01)NQDS(0.99)K QS(-52.27)S(-	0	0	1	
26	QSSYHGVHQAWNT(0.025)NQDS(0.975)K QS(-60.4)S(-6	0	0	1	
27	QSSYHGVHQAWNT(0.005)NQDS(0.995)K QS(-73.94)S(-	0	0	1	
28	QSSYHGVHQAWNT(0.128)NQDS(0.872)K QS(-48.42)S(-	0	0	1	
29					
30					
31					
32					
33	QS(0.014)VPC Q(21.8)SVPQ(21.8)LAN(20.: QS(-21.8)VPC	0	3	0	
34	QS(0.005)VPC Q(13.41)SVPQ(14.75)LAN(5 QS(-25.08)VP	0	3	0	
35	QS(0.006)VPC Q(11.59)SVPQ(18.04)LAN(6 QS(-24.64)VP	0	3	0	
36		0	3	0	
37		0	3	0	
38		0	3	0	
39		0	3	0	
40					
41					
42	REEENAAAAEEEAGEISAT(0.01)GGAT(0.21 REEENAAAAE	0	0	0	
43	REEENAAAAEEEAGEISAT(0.001)GGAT(0.4 REEENAAAAE	0	0	0	
44	REEENAAAAEEEAGEIS(0.005)AT(0.02)GG/REEENAAAAE	0	0	0	
45					
46					
47	RGCQILGLNK' RGCQ(16.13)ILGLN(-16.13)I RGCQILGLNK'	0	1	0	
48	RGCQILGLNK' RGCQ(7.33)ILGLN(-7.33)KY( RGCQILGLNK'	0	1	0	
49	RGCQILGLNK' RGCQ(33.24)ILGLN(-33.24)I RGCQILGLNK'	0	1	0	
50					
51					
52					
53	RGPPPPPT(0.1 RGPPPPPTASESTRN(43.11 RGPPPPPT(-2	0	1	0	
54		0	1	0	
55		0	1	0	
56		0	1	0	
57					
58					
59	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-5)	0	0	0
60	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-4)	0	0	0
61	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-4)	0	0	0
62					
63					
64					
65					

1	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-3)	0	0	0
2	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-4)	0	0	0
3	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-3)	0	0	0
4	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-4)	0	0	0
5	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-4)	0	0	0
6	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-4)	0	0	0
7	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-5)	0	0	0
8	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-4)	0	0	0
9	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-5)	0	0	0
10	RKKPEDPSSEAEALCS(1)PAK	RKKPEDPS(-5)	0	0	0
11					
12	SAAVAEGGDAVAET(0.733)AKGEEGS(0.26 S(-42.23)AAV		0	0	0
13	SAAVAEGGDAVAET(0.901)AKGEEGS(0.09 S(-58.47)AAV		0	0	0
14	SAAVAEGGDAVAET(0.614)AKGEEGS(0.38 S(-39.38)AAV		0	0	0
15	S(0.001)AAVAEGGDAVAET(0.702)AKGEEGS(-28.94)AAV		0	0	0
16	SAAVAEGGDAVAET(0.209)AKGEEGS(0.79 S(-48.44)AAV		0	0	0
17					
18	SAAEAIVTTATADVS(0.307)S(0.514)PS(0..S(-107.65)AE	1	0	0	0
19	SAAEAIVTTATADVS(0.034)S(0.483)PS(0..S(-78.78)AEA	1	0	0	0
20	SAAEAIVTTATADVS(0.051)S(0.77)PS(0.1 S(-102.74)AE	1	0	0	0
21	SAAEAIVTTATADVS(0.007)S(0.496)PS(0..S(-76.49)AEA	1	0	0	0
22	SAAEAIVT(0.022)T(0.02)AT(0.067)ADVS(S(-61.37)AEA	1	0	0	0
23	SAAEAIVTTADVS(0.01)S(0.495)PS(0.4!S(-54.67)AEA	1	0	0	0
24	SAAEAIVT(0.001)AT(0.004)ADVS(0.046 S(-61.79)AEA	1	0	0	0
25	SAAEAIVTTATADVS(0.019)S(0.957)PS(0..S(-108.85)AE	1	0	0	0
26	SAAEAIVTTATADVS(0.041)S(0.479)PS(0..S(-81.76)AEA	1	0	0	0
27	SAAEAIVTTATADVS(0.047)S(0.743)PS(0..S(-102.8)AEA	1	0	0	0
28	SAAEAIVTTATADVS(0.48)S(0.329)PS(0.1!S(-50.28)AEA	1	0	0	0
29	SAAEAIVTTATADVS(0.045)S(0.421)PS(0..S(-119.63)AE	1	0	0	0
30	SAAEAIVTTAT(0.001)ADVS(0.035)S(0.37 S(-66.49)AEA	1	0	0	0
31	SAAEAIVTTATADVS(0.007)S(0.783)PS(0..S(-112.12)AE	1	0	0	0
32	SAAEAIVTTATADVS(0.052)S(0.762)PS(0..S(-82.71)AEA	1	0	0	0
33	SAAEAIVT(0.01)T(0.012)AT(0.04)ADVS(0 S(-39.1)AEAE	1	0	0	0
34	SAAEAIVTTATADVS(0.067)S(0.467)PS(0..S(-77.93)AEA	1	0	0	0
35	SAAEAIVTTATADVS(0.021)S(0.489)PS(0..S(-77.91)AEA	1	0	0	0
36	SAAEAIVT(0.002)AT(0.006)ADVS(0.174 S(-40.69)AEA	1	0	0	0
37	SAAEAIVTTATADVS(0.035)S(0.71)PS(0.2!S(-81.87)AEA	1	0	0	0
38	SAAEAIVTTATADVS(0.175)S(0.771)PS(0..S(-108.29)AE	1	0	0	0
39	SAAEAIVTTATADVS(0.035)S(0.813)PS(0..S(-91.77)AEA	1	0	0	0
40	SAAEAIVTTATADVS(0.008)S(0.158)PS(0..S(-76.74)AEA	1	0	0	0
41	SAAEAIVTTATADVS(0.066)S(0.717)PS(0..S(-108.3)AEA	1	0	0	0
42	SAAEAIVTTATADVS(0.185)S(0.408)PS(0..S(-80.53)AEA	1	0	0	0
43	SAAEAIVTTATADVS(0.018)S(0.396)PS(0..S(-55.82)AEA	1	0	0	0
44	SAAEAIVTTATADVS(0.068)S(0.878)PS(0..S(-89.55)AEA	1	0	0	0
45		1	0	0	0
46					
47	S(0.015)DS(0.015)AVAT(0.71)S(0.194)AS( S(-16.63)DS(-	1	0	0	0
48					
49					
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1	S(0.01)DS(0.01)AVAT(0.112)S(0.693)AS(0 S(-18.26)DS(-	1	0	0
2	SDSAVAT(0.333)S(0.333)AS(0.333)PVAAP S(-34.71)DS(-	1	0	0
3				
4	SPIVFELT(0.001)QPS(0.999)PEK	S(-54.97)PIVF	0	0
5	SPIVFELT(0.001)QPS(0.999)PEK	S(-67.16)PIVF	0	0
6	SPIVFELT(0.001)QPS(0.999)PEK	S(-63.62)PIVF	0	0
7	SPIVFELTQPS(1)PEK	S(-86.11)PIVF	0	0
8	SPIVFELTQPS(1)PEK	S(-70.03)PIVF	0	0
9	S(1)PIVFELT(0.009)QPS(0.991)PEK	S(40.41)PIVFE	0	0
10				
11	S(0.06)VHS(0.94)PNPGLILQSK	S(-11.98)VHSI	1	0
12	S(0.003)VHS(0.997)PNPGLILQSK	S(-25.47)VHSI	1	0
13	S(0.002)VHS(0.998)PNPGLILQSK	S(-27.48)VHSI	1	0
14	S(0.008)VHS(0.992)PNPGLILQSK	S(-21.15)VHSI	1	0
15				
16	TSPKPT(0.028)KPAS(0.972)PK	T(-33.19)S(-3)	0	0
17	TSPKPT(0.079)KPAS(0.921)PK	T(-51.25)S(-4)	0	0
18				
19	VDRS(0.006)DNAAES(0.994)FDDAVEERVII VDRS(-22.51)	1	0	0
20	VDRS(0.003)DNAAES(0.997)FDDAVEERVII VDRS(-24.86)	1	0	0
21	VDRS(0.007)DNAAES(0.993)FDDAVEERVII VDRS(-21.63)	1	0	0
22				
23	VNS(0.002)LIVLES(0.998)DEEEDEQLVQAA VNS(-28.14)L	0	0	0
24	VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA VNS(-29.34)L	0	0	0
25	VNS(0.001)LIVLES(0.999)DEEEDEQLVQAA VNS(-31.63)L	0	0	0
26				
27				
28				
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34				
35				
36				
37				
38				
39	VT(0.996)ILWMGGS(0.003) VTILWM(47.5 VT(24.72)ILW	0	0	0
40	VT(0.996)ILWMGGS(0.002) VTILWM(42.3 VT(27.11)ILW	0	0	0
41	VT(0.999)ILWMGGS(0.001) VTILWM(42.0 VT(32.61)ILW	0	0	0
42				
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65				

Oxidation (M)	Phospho (STY)	Missed cleavages	Proteins	Leading Proteins	Leading Razor Protein	Gene Names
0	0	2	0 M9NG39;P41 M9NG39	M9NG39	Pep	
0	0	2	0 M9NG39;P41 M9NG39	M9NG39	Pep	
0	0	1	0 M9NG39;P41 M9NG39	M9NG39	Pep	
0	0	1	0 M9NG39;P41 M9NG39	M9NG39	Pep	
0	0	1	1 M9NG39;P41 M9NG39	M9NG39	Pep	
0	0	1	1 M9NG39;P41 M9NG39	M9NG39	Pep	
0	0	2	1 M9NG39;P41 M9NG39	M9NG39	Pep	
0	0	2	1 M9NG39;P41 M9NG39	M9NG39	Pep	
<hr/>						
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1	1	2	0 Q4V3Q5;Q8N Q4V3Q5	Q4V3Q5	CG31941	Obp22a
1	1	2	0 Q4V3Q5;Q8N Q4V3Q5	Q4V3Q5	Obp22a	Obp22a
<hr/>						
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	1	0 Q9VUY9	Q9VUY9	Q9VUY9	Pgm
0	0	2	0 AOA0B4KHJ5;AOA0B4KHJ5	AOA0B4KHJ5	CG6904-RA;G	
0	0	1	0 AOA0B4KHJ5;AOA0B4KHJ5	AOA0B4KHJ5	CG6904-RA;G	
0	0	1	0 AOA0B4KHJ5;AOA0B4KHJ5	AOA0B4KHJ5	CG6904-RA;G	
0	0	1	0 AOA0B4KHJ5;AOA0B4KHJ5	AOA0B4KHJ5	CG6904-RA;G	
0	0	1	0 AOA0B4KHJ5;AOA0B4KHJ5	AOA0B4KHJ5	CG6904-RA;G	
0	0	1	0 AOA0B4KHJ5;AOA0B4KHJ5	AOA0B4KHJ5	CG6904-RA;G	
0	0	2	0 AOA0B4KHJ5;AOA0B4KHJ5	AOA0B4KHJ5	CG6904-RA;G	
0	0	2	0 AOA0B4KHJ5;AOA0B4KHJ5	AOA0B4KHJ5	CG6904-RA;G	
<hr/>						
<hr/>						
0	0	1	1 AOA0B4LGC0,A0A0B4LGC0	AOA0B4LGC0	TppII	
0	0	1	1 AOA0B4LGC0,A0A0B4LGC0	AOA0B4LGC0	TppII	
0	0	1	1 AOA0B4LGC0,A0A0B4LGC0	AOA0B4LGC0	TppII	
0	0	1	1 AOA0B4LGC0,A0A0B4LGC0	AOA0B4LGC0	TppII	

1	0	1	1	A0A0B4LGC0;A0A0B4LGC0	A0A0B4LGC0	TppII
2	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
3	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
4	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
5	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
6	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
7	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
8	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
9	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
10	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
11	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
12	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
13	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
14	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
15	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
16	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
17	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
18	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
19	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
20	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
21	0	1	0	A0A0B4LFL2;A0A0B4LFL2	A0A0B4LFL2	elf3-S8
22						
23	0	1	0	P45594	P45594	tsr
24	0	1	0	P45594	P45594	tsr
25	0	1	0	P45594	P45594	tsr
26	0	1	0	P45594	P45594	tsr
27	0	1	0	P45594	P45594	tsr
28	0	1	0	P45594	P45594	tsr
29	0	1	0	P45594	P45594	tsr
30	0	1	0	P45594	P45594	tsr
31	0	1	0	P45594	P45594	tsr
32	0	1	0	P45594	P45594	tsr
33	0	1	0	P45594	P45594	tsr
34	0	1	0	P45594	P45594	tsr
35	0	1	0	P45594	P45594	tsr
36	0	1	0	P45594	P45594	tsr
37	0	1	0	P45594	P45594	tsr
38						
39						
40	0	1	0	Q9V5R2;A1Z8Q9V5R2	Q9V5R2	Pex6
41	0	1	0	Q9V5R2;A1Z8Q9V5R2	Q9V5R2	Pex6
42						
43						
44	0	1	0	B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
45	0	1	0	B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
46	0	1	0	B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
47	0	1	0	B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
48	0	1	0	B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
49	0	1	0	B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
50	0	1	0	B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
51	0	1	0	B5RJ65;Q053 B5RJ65	B5RJ65	Ssrp-RA;Ssrp
52						
53						
54	0	1	0	Q9VAN0	Q9VAN0	CG11899
55	0	1	0	Q9VAN0	Q9VAN0	CG11899
56						
57						
58						Aats-
59						glupro;Aats-
60						glupro-RB
61	1	1	1	P28668;H8F4 P28668	P28668	
62						
63						
64						
65						

1					
2					
3	1	1	1 P28668;H8F4 P28668	P28668	Aats-glupro;A
4	1	1	1 P28668;H8F4 P28668	P28668	Aats-glupro;A
5					
6					
7	0	1	0 Q9VNH5	Q9VNH5	Q9VNH5
8	0	1	0 Q9VNH5	Q9VNH5	Q9VNH5
9	0	1	0 Q9VNH5	Q9VNH5	Q9VNH5
10					
11					
12	1	1	0 Q9VUB8	Q9VUB8	Q9VUB8 endos
13	1	1	0 Q9VUB8	Q9VUB8	Q9VUB8 endos
14	1	1	0 Q9VUB8	Q9VUB8	Q9VUB8 endos
15					
16					
17					
18	1	1	1 B7FNN6;P053 B7FNN6	B7FNN6	RpLP2-RB;RpI
19	1	1	1 B7FNN6;P053 B7FNN6	B7FNN6	RpLP2-RB;RpI
20	1	1	1 B7FNN6;P053 B7FNN6	B7FNN6	RpLP2-RB;RpI
21					
22					
23					
24	0	1	2 P05205	P05205	P05205 Su(var)205
25	0	1	2 P05205	P05205	P05205 Su(var)205
26	0	1	2 P05205	P05205	P05205 Su(var)205
27	0	1	2 P05205	P05205	P05205 Su(var)205
28					
29					
30					
31	1	2	2 M9PBK5;P08! M9PBK5	M9PBK5	RpLP1
32	1	2	2 M9PBK5;P08! M9PBK5	M9PBK5	RpLP1
33	1	2	2 M9PBK5;P08! M9PBK5	M9PBK5	RpLP1
34	1	1	2 M9PBK5;P08! M9PBK5	M9PBK5	RpLP1
35					
36					
37					
38	0	1	1 Q9I7K6	Q9I7K6	CG8223
39	0	1	1 Q9I7K6	Q9I7K6	CG8223
40	0	1	1 Q9I7K6	Q9I7K6	CG8223
41	0	1	1 Q9I7K6	Q9I7K6	CG8223
42	0	1	1 Q9I7K6	Q9I7K6	CG8223
43	0	1	1 Q9I7K6	Q9I7K6	CG8223
44	0	1	1 Q9I7K6	Q9I7K6	CG8223
45	0	1	1 Q9I7K6	Q9I7K6	CG8223
46					
47					
48					
49	1	1	1 Q6IIC4	Q6IIC4	Q6IIC4 HDC19000
50	1	1	1 Q6IIC4	Q6IIC4	Q6IIC4 HDC19000
51	1	1	1 Q6IIC4	Q6IIC4	Q6IIC4 HDC19000
52	1	1	1 Q6IIC4	Q6IIC4	Q6IIC4 HDC19000
53	1	1	1 Q6IIC4	Q6IIC4	Q6IIC4 HDC19000
54					
55					
56	0	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
57	0	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
58	0	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
59	0	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
60	0	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
61	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
62					
63					
64					
65					

1					
2					
3	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
4	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
5	1	1	0 B7Z0H3	B7Z0H3	B7Z0H3 RhoGEF3
6					
7					
8					
9	1	1	1 X2JDR1;Q8IR\ X2JDR1	X2JDR1	CG9413-RB
10	1	1	1 X2JDR1;Q8IR\ X2JDR1	X2JDR1	CG9413-RB
11	1	1	1 X2JDR1;Q8IR\ X2JDR1	X2JDR1	CG9413-RB
12	1	1	1 X2JDR1;Q8IR\ X2JDR1	X2JDR1	CG9413-RB
13	1	1	1 X2JDR1;Q8IR\ X2JDR1	X2JDR1	CG9413-RB
14	1	1	1 X2JDR1;Q8IR\ X2JDR1	X2JDR1	CG9413-RB
15	1	1	1 X2JDR1;Q8IR\ X2JDR1	X2JDR1	CG9413-RB
16					
17					
18	1	1	0 B7YZZ9;P278\ B7YZZ9	B7YZZ9	Rrp1
19	1	1	0 B7YZZ9;P278\ B7YZZ9	B7YZZ9	Rrp1
20	1	1	0 B7YZZ9;P278\ B7YZZ9	B7YZZ9	Rrp1
21					
22					
23					
24	0	1	1 Q9VYV4	Q9VYV4	Amun
25	0	1	1 Q9VYV4	Q9VYV4	Amun
26	0	1	1 Q9VYV4	Q9VYV4	Amun
27	0	1	1 Q9VYV4	Q9VYV4	Amun
28	0	1	1 Q9VYV4	Q9VYV4	Amun
29	0	1	1 Q9VYV4	Q9VYV4	Amun
30	0	1	2 Q9VYV4	Q9VYV4	Amun
31	0	1	2 Q9VYV4	Q9VYV4	Amun
32	0	1	2 Q9VYV4	Q9VYV4	Amun
33					
34					
35	0	1	2 Q8IRG6;Q8IR\ Q8IRG6	Q8IRG6	dre4
36	0	1	2 Q8IRG6;Q8IR\ Q8IRG6	Q8IRG6	dre4
37	0	1	2 Q8IRG6;Q8IR\ Q8IRG6	Q8IRG6	dre4
38					
39					
40	0	1	0 E2QCZ8;Q0KI E2QCZ8	E2QCZ8	CG43427
41	0	1	0 E2QCZ8;Q0KI E2QCZ8	E2QCZ8	CG43427
42					
43					
44					
45	0	2	0 E2QCZ8;Q0KI E2QCZ8	E2QCZ8	CG43427
46	0	2	0 E2QCZ8;Q0KI E2QCZ8	E2QCZ8	CG43427
47					
48					
49	1	1	0 Q9VIV2;B1NL Q9VIV2	Q9VIV2	swm
50	1	1	0 Q9VIV2;B1NL Q9VIV2	Q9VIV2	swm
51	0	1	0 Q9VIV2;B1NL Q9VIV2	Q9VIV2	swm
52					
53					
54					
55	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
56	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
57	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
58	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
59	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
60	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
61	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
62					

1					
2					
3	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
4	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
5	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
6	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
7	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
8	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
9	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
10	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
11	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
12	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
13	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
14	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
15	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
16	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
17	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
18	0	1	0 A1Z8W9;A0A A1Z8W9	A1Z8W9	garz
19					
20					
21	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
22	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
23	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
24	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
25	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
26	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
27	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
28	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
29	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
30	0	1	0 X2JD55;Q29C X2JD55	X2JD55	Yp1
31					
32					
33	0	1	0 Q8MYL1	Q8MYL1	Fancd2
34	0	1	0 Q8MYL1	Q8MYL1	Fancd2
35	0	1	0 Q8MYL1	Q8MYL1	Fancd2
36	0	1	0 Q8MYL1	Q8MYL1	Fancd2
37	0	1	0 Q8MYL1	Q8MYL1	Fancd2
38	0	1	0 Q8MYL1	Q8MYL1	Fancd2
39	0	1	0 Q8MYL1	Q8MYL1	Fancd2
40					
41					
42	0	1	0 Q9VV74	Q9VV74	Smn
43	0	1	0 Q9VV74	Q9VV74	Smn
44	0	1	0 Q9VV74	Q9VV74	Smn
45					
46					
47	0	1	1 Q9VZW4;A8V Q9VZW4	Q9VZW4	CG32487
48	0	1	1 Q9VZW4;A8V Q9VZW4	Q9VZW4	CG32487
49	0	1	1 Q9VZW4;A8V Q9VZW4	Q9VZW4	CG32487
50	0	1	1 Q9VZW4;A8V Q9VZW4	Q9VZW4	CG32487
51					
52					
53	0	2	0 A0A0B4KFB8; A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
54	0	2	0 A0A0B4KFB8; A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
55	0	2	0 A0A0B4KFB8; A0A0B4KFB8	A0A0B4KFB8	CG15187;CG3
56					
57					
58					
59	0	1	2 Q9I7K6	Q9I7K6	CG8223
60	0	1	2 Q9I7K6	Q9I7K6	CG8223
61	0	1	2 Q9I7K6	Q9I7K6	CG8223
62					
63					
64					
65					

1	0	1	2 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
2	0	1	2 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
3	0	1	2 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
4	0	1	2 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
5	0	1	2 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
6	0	1	2 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
7	0	1	2 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
8	0	1	2 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
9	0	1	2 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
10	0	1	2 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
11	<hr/>					
12	0	1	1 Q86BM5;Q9\ Q86BM5;Q9\ Q86BM5	Akap200		
13	0	1	1 Q86BM5;Q9\ Q86BM5;Q9\ Q86BM5	Akap200		
14	0	1	1 Q86BM5;Q9\ Q86BM5;Q9\ Q86BM5	Akap200		
15	0	1	1 Q86BM5;Q9\ Q86BM5;Q9\ Q86BM5	Akap200		
16	0	1	1 Q86BM5;Q9\ Q86BM5;Q9\ Q86BM5	Akap200		
17	0	1	1 Q86BM5;Q9\ Q86BM5;Q9\ Q86BM5	Akap200		
18	0	1	1 Q86BM5;Q9\ Q86BM5;Q9\ Q86BM5	Akap200		
19	<hr/>					
20	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
21	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
22	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
23	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
24	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
25	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
26	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
27	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
28	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
29	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
30	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
31	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
32	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
33	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
34	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
35	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
36	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
37	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
38	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
39	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
40	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
41	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
42	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
43	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
44	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
45	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
46	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
47	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
48	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
49	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
50	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
51	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
52	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
53	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
54	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
55	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
56	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
57	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
58	0	1	0 Q9I7K6	Q9I7K6	Q9I7K6	CG8223
59	<hr/>					
60	0	1	0 Q4AB54;P02\ Q4AB54	Q4AB54	His1:CG3386:	
61	<hr/>					
62						
63						
64						
65						

1					
2					
3	0	1	0 Q4AB54;P022 Q4AB54	Q4AB54	His1:CG3386:
4	0	1	0 Q4AB54;P022 Q4AB54	Q4AB54	His1:CG3386:
5					
6					
7	0	1	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc
8	0	1	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc
9	0	1	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc
10	0	1	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc
11	0	1	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc
12	0	1	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc
13	0	1	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc
14	0	2	0 Q9XZL7;A0AC Q9XZL7	Q9XZL7	tacc
15					
16					
17	0	1	0 Q9V6U8	Q9V6U8	Uba3
18	0	1	0 Q9V6U8	Q9V6U8	Uba3
19	0	1	0 Q9V6U8	Q9V6U8	Uba3
20	0	1	0 Q9V6U8	Q9V6U8	Uba3
21	0	1	0 Q9V6U8	Q9V6U8	Uba3
22					
23					
24	0	1	2 Q9W335	Q9W335	I(1)G0320
25	0	1	2 Q9W335	Q9W335	I(1)G0320
26					
27					
28	0	1	0 COMJE4;Q245 COMJE4	COMJE4	CG4236;Caf1
29	0	1	0 COMJE4;Q245 COMJE4	COMJE4	CG4236;Caf1
30	0	1	0 COMJE4;Q245 COMJE4	COMJE4	CG4236;Caf1
31					
32					
33					
34	0	1	0 P20240	P20240	Ote
35	0	1	0 P20240	P20240	Ote
36	0	1	0 P20240	P20240	Ote
37					
38					
39	1	1	1 Q95SA9	Q95SA9	spoon
40	1	1	1 Q95SA9	Q95SA9	spoon
41	1	1	1 Q95SA9	Q95SA9	spoon
42					

44  
45  
46  
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Protein	Labeling					
Names	Type	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
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Odorant bind MSMS		1	PT5722-3		3 B1	753.86
MSMS		1	PT5722-19		19 B2	753.85
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Phosphogluc MULT-MSMS			PT5722-7		7 B1 SCX	782.38
Phosphogluc MULT-MSMS			PT5722-8		8 B1 SCX	782.38
Phosphogluc MULT-MSMS			PT5722-23		23 B2 SCX	782.05
Phosphogluc ISO-MSMS		0	PT5722-33		33 B3	782.38
Phosphogluc MULT-MSMS			PT5722-38		38 B3 SCX	782.38
Phosphogluc MULT-MSMS			PT5722-38		38 B3 SCX	1173.07
Phosphogluc ISO-MSMS		0	PT5722-51		51 H/H SCX	782.05
Phosphogluc MULT-MSMS			PT5722-53		53 H/H SCX	782.05
Phosphogluc MULT-MATCH			PT5722-6		6 B1 SCX	
Phosphogluc MULT-MATCH			PT5722-21		21 B2 SCX	
Phosphogluc MULT-MATCH			PT5722-22		22 B2 SCX	
Phosphogluc ISO-MSMS		0	PT5722-38		38 B3 SCX	782.71
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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
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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

1	Tripeptidyl-p <sub>c</sub> MULTI-MSMS	PT5722-51	51 H/H SCX	942.95
2	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-2	2 B1	841.84
3	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-6	6 B1 SCX	841.34
4	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-7	7 B1 SCX	841.34
5	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-11	11 B1 TIO2	841.34
6	Eukaryotic tr <sub>c</sub> ISO-MSMS	0 PT5722-22	22 B2 SCX	841.34
7	Eukaryotic tr <sub>c</sub> ISO-MSMS	0 PT5722-27	27 B2 TIO2	841.34
8	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-36	36 B3 SCX	841.33
9	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-37	37 B3 SCX	841.34
10	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-41	41 B3 TIO2	841.34
11	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-51	51 H/H SCX	841.34
12	Eukaryotic tr <sub>c</sub> MULTI-MSMS	PT5722-52	52 H/H SCX	841.83
13	Eukaryotic tr <sub>c</sub> MULTI-MATCH	PT5722-42	42 B3 TIO2	
14	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-5	5 B1	622.77
15	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-15	15 B1 TIO2	622.77
16	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-16	16 B2	626.77
17	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-20	20 B2	622.77
18	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-30	30 B2 TIO2	622.77
19	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-32	32 B3	626.77
20	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-34	34 B3	622.76
21	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-49	49 H/H	622.77
22	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-50	50 H/H	626.77
23	Cofilin/actin- $\alpha$ MULTI-MSMS	PT5722-60	60 H/H TIO2	622.76
24	Cofilin/actin- $\alpha$ MULTI-MATCH	PT5722-33	33 B3	
25	MULTI-MSMS	PT5722-8	8 B1 SCX	619.25
26	MULTI-MSMS	PT5722-23	23 B2 SCX	619.25
27	FACT comple: ISO-MSMS	0 PT5722-6	6 B1 SCX	822.02
28	FACT comple: MULTI-MSMS	PT5722-7	7 B1 SCX	822.02
29	FACT comple: MULTI-MSMS	PT5722-22	22 B2 SCX	821.69
30	FACT comple: MULTI-MSMS	PT5722-36	36 B3 SCX	822.02
31	FACT comple: MULTI-MSMS	PT5722-51	51 H/H SCX	822.02
32	FACT comple: MULTI-MSMS	PT5722-52	52 H/H SCX	822.02
33	Probable pho MULTI-MSMS	PT5722-7	7 B1 SCX	388.19
34	Probable pho MULTI-SECPEP	PT5722-37	37 B3 SCX	388.46
35	Bifunctional $\xi$ ISO-MSMS	0 PT5722-21	21 B2 SCX	909.75

1	Bifunctional $\xi$ ISO-MSMS	0 PT5722-37	37 B3 SCX	909.75
2	Bifunctional $\xi$ MULTI-MSMS	PT5722-51	51 H/H SCX	909.75
3				
4				
5				
6				
7	ISO-MSMS	0 PT5722-23	23 B2 SCX	1052.44
8	ISO-MSMS	0 PT5722-38	38 B3 SCX	1052.78
9	ISO-MSMS	0 PT5722-53	53 H/H SCX	1052.78
10				
11				
12				
13	ISO-MSMS	1 PT5722-10	10 B1 SCX	707.27
14	MULTI-MSMS	PT5722-40	40 B3 SCX	707.27
15	MULTI-MSMS	PT5722-55	55 H/H SCX	702.76
16				
17				
18	60S acidic rib MULTI-MSMS	PT5722-25	25 B2 SCX	1037.38
19	60S acidic rib ISO-MSMS	0 PT5722-45	45 B3 TIO2	1037.38
20	60S acidic rib MULTI-MSMS	PT5722-55	55 H/H SCX	1037.38
21				
22				
23				
24	Heterochrom ISO-MSMS	0 PT5722-9	9 B1 SCX	727.32
25	Heterochrom MULTI-MSMS	PT5722-39	39 B3 SCX	969.42
26	Heterochrom MULTI-MSMS	PT5722-39	39 B3 SCX	727.32
27	Heterochrom ISO-MSMS	0 PT5722-54	54 H/H SCX	727.32
28				
29				
30				
31	60S acidic rib MSMS	0 PT5722-6	6 B1 SCX	1184.42
32	60S acidic rib MSMS	0 PT5722-36	36 B3 SCX	789.95
33	60S acidic rib MSMS	0 PT5722-40	40 B3 SCX	789.95
34	60S acidic rib MULTI-MSMS	PT5722-55	55 H/H SCX	763.63
35				
36				
37				
38	Protein NASP ISO-MSMS	0 PT5722-7	7 B1 SCX	632.94
39	Protein NASP MULTI-MSMS	PT5722-18	18 B2	632.61
40	Protein NASP MULTI-MSMS	PT5722-32	32 B3	632.61
41	Protein NASP ISO-MSMS	0 PT5722-36	36 B3 SCX	632.94
42	Protein NASP ISO-MSMS	0 PT5722-38	38 B3 SCX	632.61
43	Protein NASP MULTI-MSMS	PT5722-52	52 H/H SCX	632.61
44				
45				
46				
47				
48				
49	ISO-MSMS	1 PT5722-23	23 B2 SCX	818.4
50	ISO-MSMS	1 PT5722-24	24 B2 SCX	818.4
51	ISO-MSMS	1 PT5722-38	38 B3 SCX	817.9
52	ISO-MSMS	1 PT5722-49	49 H/H	817.9
53				
54				
55				
56	MULTI-MSMS	PT5722-10	10 B1 SCX	909.43
57	MULTI-MSMS	PT5722-24	24 B2 SCX	609.63
58	MULTI-MATCH	PT5722-23	23 B2 SCX	
59	MULTI-MATCH	PT5722-25	25 B2 SCX	
60	MULTI-MSMS	PT5722-23	23 B2 SCX	597.63
61				
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1		MULTI-MSMS	PT5722-24	24 B2 SCX	896.44
2		MULTI-MATCH	PT5722-23	23 B2 SCX	
3		MULTI-MATCH	PT5722-25	25 B2 SCX	
4					
5		sobremesa ISO-MSMS	1 PT5722-8	8 B1 SCX	911.43
6		sobremesa ISO-MSMS	1 PT5722-9	9 B1 SCX	911.43
7		sobremesa ISO-MSMS	1 PT5722-10	10 B1 SCX	911.44
8		sobremesa ISO-MSMS	1 PT5722-26	26 B2 TIO2	911.43
9		sobremesa ISO-MSMS	1 PT5722-38	38 B3 SCX	911.43
10		sobremesa ISO-MSMS	1 PT5722-40	40 B3 SCX	911.44
11					
12		Recombinatic ISO-MSMS	0 PT5722-12	12 B1 TIO2	914.74
13		Recombinatic ISO-MSMS	0 PT5722-32	32 B3	914.41
14		Recombinatic MULTI-MSMS	PT5722-57	57 H/H TIO2	914.74
15					
16		Amun MULTI-MSMS	PT5722-2	2 B1	555.27
17		MULTI-MSMS	PT5722-22	22 B2 SCX	832.41
18		MULTI-MSMS	PT5722-36	36 B3 SCX	555.27
19		MULTI-MSMS	PT5722-37	37 B3 SCX	832.4
20		MULTI-MATCH	PT5722-36	36 B3 SCX	
21		MULTI-MSMS	PT5722-2	2 B1	597.97
22		MULTI-MSMS	PT5722-7	7 B1 SCX	597.97
23					
24		FACT comple: MULTI-MSMS	PT5722-21	21 B2 SCX	754.67
25		FACT comple: MULTI-MSMS	PT5722-22	22 B2 SCX	754.33
26		FACT comple: MULTI-MSMS	PT5722-36	36 B3 SCX	754.33
27					
28		smallish, sma MULTI-MSMS	PT5722-24	24 B2 SCX	558.59
29		smallish, sma ISO-MSMS	0 PT5722-39	39 B3 SCX	558.58
30					
31		smallish, sma MULTI-SECPEP	PT5722-16	16 B2	958.48
32		smallish, sma MULTI-SECPEP	PT5722-33	33 B3	958.48
33					
34		swm MULTI-MSMS	PT5722-20	20 B2	615.25
35		MULTI-MSMS	PT5722-40	40 B3 SCX	615.25
36		MULTI-MSMS	PT5722-50	50 H/H	602.75
37					
38		garz ISO-MSMS	0 PT5722-6	6 B1 SCX	678.86
39		ISO-MSMS	0 PT5722-7	7 B1 SCX	678.86
40		ISO-MSMS	0 PT5722-8	8 B1 SCX	678.86
41		ISO-MSMS	0 PT5722-19	19 B2	678.86
42		ISO-MSMS	0 PT5722-20	20 B2	678.86
43		ISO-MSMS	0 PT5722-21	21 B2 SCX	678.86
44					

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3	ISO-MSMS	0 PT5722-22	22 B2 SCX	678.86	
4	ISO-MSMS	0 PT5722-24	24 B2 SCX	678.86	
5	ISO-MSMS	0 PT5722-31	31 B3	678.86	
6	ISO-MSMS	0 PT5722-32	32 B3	678.86	
7	ISO-MSMS	0 PT5722-36	36 B3 SCX	678.86	
8	ISO-MSMS	0 PT5722-37	37 B3 SCX	678.86	
9	ISO-MSMS	0 PT5722-39	39 B3 SCX	678.86	
10	ISO-MSMS	0 PT5722-46	46 H/H	678.86	
11	ISO-MSMS	0 PT5722-47	47 H/H	678.86	
12	ISO-MSMS	0 PT5722-50	50 H/H	678.86	
13	ISO-MSMS	0 PT5722-51	51 H/H SCX	678.86	
14	ISO-MSMS	0 PT5722-54	54 H/H SCX	678.86	
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21	Vitellogenin-1 ISO-MSMS	0 PT5722-8	8 B1 SCX	717.63	
22	Vitellogenin-1 ISO-MSMS	0 PT5722-18	18 B2	717.3	
23	Vitellogenin-1 MULTI-MSMS	PT5722-33	33 B3	717.63	
24	Vitellogenin-1 MULTI-MSMS	PT5722-38	38 B3 SCX	717.63	
25	Vitellogenin-1 ISO-MSMS	0 PT5722-40	40 B3 SCX	717.63	
26	Vitellogenin-1 MULTI-MSMS	PT5722-48	48 H/H	720.63	
27	Vitellogenin-1 MULTI-MSMS	PT5722-53	53 H/H SCX	717.29	
28	Vitellogenin-1 ISO-MSMS	0 PT5722-55	55 H/H SCX	717.63	
29					
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33	Fancd2	MULTI-MSMS	PT5722-4	4 B1	990.98
34		MULTI-MSMS	PT5722-18	18 B2	990.98
35		MULTI-MSMS	PT5722-23	23 B2 SCX	990.98
36		MULTI-MATCH	PT5722-24	24 B2 SCX	
37		MULTI-MATCH	PT5722-25	25 B2 SCX	
38					
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42	Survival motc	ISO-MSMS	0 PT5722-24	24 B2 SCX	1072.48
43	Survival motc	ISO-MSMS	0 PT5722-39	39 B3 SCX	1072.47
44	Survival motc	ISO-MSMS	0 PT5722-40	40 B3 SCX	1072.47
45					
46					
47	CG32487	ISO-MSMS	0 PT5722-2	2 B1	753.05
48		ISO-MSMS	0 PT5722-22	22 B2 SCX	752.72
49		ISO-MSMS	0 PT5722-36	36 B3 SCX	753.05
50					
51					
52					
53	B1367-RA	MULTI-MSMS	PT5722-23	23 B2 SCX	670.97
54	B1367-RA	MULTI-MATCH	PT5722-21	21 B2 SCX	
55	B1367-RA	MULTI-MATCH	PT5722-22	22 B2 SCX	
56					
57					
58					
59	Protein NASP	ISO-MSMS	0 PT5722-3	3 B1	727.67
60	Protein NASP	MULTI-MSMS	PT5722-7	7 B1 SCX	546.01
61	Protein NASP	MULTI-MSMS	PT5722-18	18 B2	727.68
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1	Protein NASP ISO-MSMS	0 PT5722-18	18 B2	545.76
2	Protein NASP ISO-MSMS	0 PT5722-23	23 B2 SCX	546.01
3	Protein NASP ISO-MSMS	0 PT5722-32	32 B3	545.76
4	Protein NASP MULTI-MSMS	PT5722-36	36 B3 SCX	728.01
5	Protein NASP ISO-MSMS	0 PT5722-36	36 B3 SCX	546.01
6	Protein NASP ISO-MSMS	0 PT5722-37	37 B3 SCX	727.68
7				
8	Akap200 ISO-MSMS	0 PT5722-9	9 B1 SCX	738
9	Akap200 MULTI-MSMS	PT5722-37	37 B3 SCX	737.66
10	Akap200 MULTI-MSMS	PT5722-39	39 B3 SCX	737.67
11	Akap200 ISO-MSMS	0 PT5722-47	47 H/H	737.66
12	Akap200 MULTI-MSMS	PT5722-54	54 H/H SCX	743.68
13				
14	Protein NASP MULTI-MSMS	PT5722-3	3 B1	1029.47
15	Protein NASP MULTI-MSMS	PT5722-12	12 B1 TIO2	1028.97
16	Protein NASP MULTI-MSMS	PT5722-13	13 B1 TIO2	1028.97
17	Protein NASP MULTI-MSMS	PT5722-14	14 B1 TIO2	1028.97
18	Protein NASP MULTI-MSMS	PT5722-18	18 B2	1029.47
19	Protein NASP ISO-MSMS	0 PT5722-23	23 B2 SCX	1028.97
20	Protein NASP MULTI-MSMS	PT5722-27	27 B2 TIO2	1028.97
21	Protein NASP MULTI-MSMS	PT5722-28	28 B2 TIO2	1028.97
22	Protein NASP MULTI-MSMS	PT5722-29	29 B2 TIO2	1028.97
23	Protein NASP MULTI-MSMS	PT5722-32	32 B3	1029.47
24	Protein NASP ISO-MSMS	0 PT5722-32	32 B3	686.65
25	Protein NASP MULTI-MSMS	PT5722-33	33 B3	1028.97
26	Protein NASP MULTI-MSMS	PT5722-33	33 B3	686.32
27	Protein NASP ISO-MSMS	0 PT5722-38	38 B3 SCX	1028.98
28	Protein NASP MULTI-MSMS	PT5722-42	42 B3 TIO2	1033.48
29	Protein NASP MULTI-MSMS	PT5722-42	42 B3 TIO2	686.65
30	Protein NASP MULTI-MSMS	PT5722-43	43 B3 TIO2	1029.47
31	Protein NASP MULTI-MSMS	PT5722-44	44 B3 TIO2	1028.96
32	Protein NASP ISO-MSMS	0 PT5722-44	44 B3 TIO2	686.65
33	Protein NASP ISO-MSMS	0 PT5722-45	45 B3 TIO2	1028.98
34	Protein NASP MULTI-MSMS	PT5722-47	47 H/H	1029.47
35	Protein NASP MULTI-MSMS	PT5722-48	48 H/H	1028.96
36	Protein NASP MULTI-MSMS	PT5722-52	52 H/H SCX	1028.96
37	Protein NASP MULTI-MSMS	PT5722-57	57 H/H TIO2	1029.47
38	Protein NASP MULTI-MSMS	PT5722-58	58 H/H TIO2	1028.97
39	Protein NASP MSMS	0 PT5722-58	58 H/H TIO2	686.32
40	Protein NASP MULTI-MSMS	PT5722-59	59 H/H TIO2	1028.97
41	Protein NASP MULTI-MATCH	PT5722-2	2 B1	
42				
43	Histone H1 ISO-MSMS	0 PT5722-4	4 B1	693.66
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1	Histone H1	ISO-MSMS	0 PT5722-19	19 B2	1039.49
2	Histone H1	MULTI-MSMS	PT5722-49	49 H/H	693.33
3	tacc	ISO-MSMS	0 PT5722-7	7 B1 SCX	826.91
4		MULTI-MSMS	PT5722-41	41 B3 TIO2	826.91
5		ISO-MSMS	0 PT5722-51	51 H/H SCX	826.9
6		MULTI-MSMS	PT5722-54	54 H/H SCX	826.9
7		MULTI-MSMS	PT5722-57	57 H/H TIO2	826.4
8		MULTI-MSMS	PT5722-57	57 H/H TIO2	866.39
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34	Otefin	ISO-MSMS	0 PT5722-3	3 B1	1008.44
35	Otefin	ISO-MSMS	0 PT5722-33	33 B3	954.96
36	Otefin	ISO-MSMS	0 PT5722-38	38 B3 SCX	954.96
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Charge	m/z	Mass	Resolution	Uncalibrated m/z [ppm]	Uncalibrated 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

1	4	942,699,453	376,676,871	43554.6	-0.24396	-0.00022998	-11,793
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2	2	84,133,509	168,065,563	45027.15	-0.89245	-0.00075085	0.41865
3	2	84,133,509	168,065,563	44767.33	-0.58062	-0.0004885	-0.38377
4	2	84,133,509	168,065,563	44982.43	-0.63029	-0.00053029	0.24525
5	2	84,133,509	168,065,563	45711.25	0	0	-11,744
6	2	84,133,509	168,065,563	NaN	NaN	NaN	0.69875
7	2	84,133,509	168,065,563	NaN	NaN	NaN	-0.11447
8	2	84,133,509	168,065,563	43560.81	-0.47621	-0.00040065	-0.33956
9	2	84,133,509	168,065,563	45250.93	-0.87036	-0.00073227	-0.046635
10	2	84,133,509	168,065,563	45688.7	-0.94427	-0.00079445	-0.28334
11	2	84,133,509	168,065,563	46313.07	-0.57953	-0.00048758	-0.35958
12	2	84,133,509	168,065,563	45818.69	-0.70187	-0.0005905	-0.055655
13	2	84,133,509	168,065,563	46058.67	-0.88319	-0.00074306	0.088149

22	2	622,765,061	124,351,557	49666.66	-11,675	-0.00072709	0.72062
23	2	622,765,061	124,351,557	53750.39	0	0	-0.36105
24	2	622,765,061	124,351,557	53765.87	-0.68807	-0.00042851	-0.096821
25	2	622,765,061	124,351,557	49223.58	-0.70701	-0.0004403	0.21521
26	2	622,765,061	124,351,557	53622.12	0	0	-0.33432
27	2	622,765,061	124,351,557	52022.43	-0.23251	-0.0001448	-0.28415
28	2	622,765,061	124,351,557	53283.96	-0.8521	-0.00053066	-0.026131
29	2	622,765,061	124,351,557	54265.55	-0.51174	-0.0003187	0.47838
30	2	622,765,061	124,351,557	49801.67	-0.35894	-0.00022353	0.1143
31	2	622,765,061	124,351,557	53179.15	-0.50061	-0.00031176	0.29178
32	2	622,765,061	124,351,557	54084.26	-0.31982	-0.00019917	-0.43446

39	2	619,254,852	123,649,515	53106.32	-0.21324	-0.00013205	13,032
40	2	619,254,852	123,649,515	51842.47	-0.24336	-0.0001507	15,959

44	3	821,683,108	246,202,749	NaN	NaN	NaN	0.72795
45	3	821,683,108	246,202,749	46390.55	-0.52842	-0.00043419	0.18359
46	3	821,683,108	246,202,749	46712.96	-0.49176	-0.00040407	-0.048026
47	3	821,683,108	246,202,749	46631.54	-0.5666	-0.00046556	0.12942
48	3	821,683,108	246,202,749	46837.07	-0.46708	-0.00038379	-0.087081
49	3	821,683,108	246,202,749	46733.58	-0.54819	-0.00045044	-0.36846

54	4	385,940,632	153,973,342	66420.11	0.018018	6.95E-02	-13,849
55	4	385,940,632	153,973,342	66350.92	-0.27129	-0.0001047	-13,766

61	3	9,094,124	272,521,537	NaN	NaN	NaN	0.53441
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1	3	9,094,124	272,521,537	NaN	NaN	0.7078
2	3	9,094,124	272,521,537	44209.95	-0.57909	-0.00052663
3	3	105,211,134	315,331,218	NaN	NaN	0.088838
4	3	105,211,134	315,331,218	NaN	NaN	-0.079777
5	3	105,211,134	315,331,218	NaN	NaN	0.38664
6	2	702,762,518	140,351,048	NaN	NaN	-14,181
7	2	702,762,518	140,351,048	49509.86	-0.77163	-0.00054227
8	2	702,762,518	140,351,048	50982.97	-0.46099	-0.00032397
9	2	103,737,957	207,274,458	41426.96	-0.80348	-0.00083351
10	2	103,737,957	207,274,458	NaN	NaN	0.01813
11	2	103,737,957	207,274,458	41640.52	-0.73718	-0.00076473
12	4	727,068,215	290,424,375	NaN	NaN	10,117
13	3	969,088,528	290,424,375	42884.98	-11,746	-0.0011383
14	4	727,068,215	290,424,375	49911.34	-0.99858	-0.00072604
15	4	727,068,215	290,424,375	NaN	NaN	0.51106
16	2	118,441,603	23,668,175	NaN	NaN	NaN
17	3	789,946,443	23,668,175	NaN	NaN	NaN
18	3	789,946,443	23,668,175	NaN	NaN	NaN
19	3	763,290,999	228,685,117	47898.98	-0.71276	-0.00054404
20	2	632,607,934	189,480,197	NaN	NaN	10,578
21	3	632,607,934	189,480,197	52561.09	-0.94823	-0.00059985
22	3	632,607,934	189,480,197	54769.45	-0.55402	-0.00035048
23	3	632,607,934	189,480,197	NaN	NaN	0.58237
24	3	632,607,934	189,480,197	NaN	NaN	0.64711
25	3	632,607,934	189,480,197	52791.61	-0.51669	-0.00032686
26	2	809,886,573	161,775,859	NaN	NaN	-13,628
27	2	809,886,573	161,775,859	NaN	NaN	-0.79476
28	2	809,886,573	161,775,859	NaN	NaN	-11,434
29	2	809,886,573	161,775,859	NaN	NaN	-15,373
30	2	909,435,761	181,685,697	43696.7	-18,642	-0.0016954
31	3	606,626,266	181,685,697	52622.78	-0.53676	-0.00032561
32	3	606,626,266	181,685,697	53944.11	-0.10199	-6.19E-01
33	3	606,626,266	181,685,697	53182.92	-0.37484	-0.00022739
34	3	597,626,378	17,898,573	52584.19	-0.2817	-0.00016835
35	3	597,626,378	17,898,573	52584.19	-0.2817	-0.85859

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3	2	895,935,928	17,898,573	42945.04	-0.27722	-0.00024837
4	2	895,935,928	17,898,573	43884.54	-11,219	-0.0010051
5	3	597,626,378	17,898,573	51025.32	-0.64456	-0.00038521
6						-0.27575
7						
8						
9	2	903,419,923	180,482,529	NaN	NaN	0.48176
10	2	903,419,923	180,482,529	NaN	NaN	12,271
11	2	903,419,923	180,482,529	NaN	NaN	17,114
12	2	903,419,923	180,482,529	NaN	NaN	0.061222
13	2	903,419,923	180,482,529	NaN	NaN	13,955
14	2	903,419,923	180,482,529	NaN	NaN	14,456
15	2	903,419,923	180,482,529	NaN	NaN	
16						
17						
18	3	914,401,501	274,018,267	NaN	NaN	-0.36446
19	3	914,401,501	274,018,267	NaN	NaN	0.40981
20	3	914,401,501	274,018,267	43868.11	-0.60547	-0.00055364
21						-0.39734
22						
23						
24	3	555,273,215	166,279,782	57588.13	-0.64389	-0.00035753
25	2	832,406,184	166,279,782	45805.02	-0.90136	-0.0007503
26	3	555,273,215	166,279,782	57856	-0.18944	-0.00010519
27	2	832,406,184	166,279,782	45675.85	-0.69867	-0.00058158
28	2	832,406,184	166,279,782	47421.39	-0.78716	-0.00065524
29	3	597,971,536	179,089,278	53542.4	-0.51142	-0.00030581
30	3	597,971,536	179,089,278	52488.26	-0.45983	-0.00027496
31						-11,847
32						-13,331
33						
34						
35	3	754,333,416	225,997,842	48501.36	-12,935	-0.00097576
36	3	754,333,416	225,997,842	48648.12	-0.68361	-0.00051567
37	3	754,333,416	225,997,842	47620.15	-0.6986	-0.00052698
38						0.019261
39						
40						
41	3	558,251,534	167,173,277	52879.02	-0.43009	-0.0002401
42	3	558,579,539	167,271,679	NaN	NaN	0.60775
43						10,397
44						
45	2	958,475,759	191,493,696	42446.84	-10,427	-0.00099945
46	2	958,475,759	191,493,696	42782.33	-0.13625	-0.0001306
47						14,035
48						10,331
49						
50	2	610,743,263	121,947,197	52952.65	-0.76413	-0.00046669
51	2	610,743,263	121,947,197	52520.14	-0.41241	-0.00025187
52	2	602,745,805	120,347,706	53745.4	-0.83504	-0.00050332
53						-12,932
54						-14,579
55	2	678,862,361	135,571,017	NaN	NaN	-0.15588
56	2	678,862,361	135,571,017	NaN	NaN	-0.50484
57	2	678,862,361	135,571,017	NaN	NaN	-0.68469
58	2	678,862,361	135,571,017	NaN	NaN	-0.20306
59	2	678,862,361	135,571,017	NaN	NaN	-0.24851
60	2	678,862,361	135,571,017	NaN	NaN	
61	2	678,862,361	135,571,017	NaN	NaN	-0.2432
62						
63						
64						
65						

1	2	3	2	678,862,361	135,571,017	NaN	NaN	NaN	-10,303
4	5	6	2	678,862,361	135,571,017	NaN	NaN	NaN	-0.52289
7	8	9	2	678,862,361	135,571,017	NaN	NaN	NaN	-0.85876
10	11	12	2	678,862,361	135,571,017	NaN	NaN	NaN	-0.46929
13	14	15	2	678,862,361	135,571,017	NaN	NaN	NaN	-0.22617
16	17	18	2	678,862,361	135,571,017	NaN	NaN	NaN	-0.41926
19	20	21	2	678,862,361	135,571,017	NaN	NaN	NaN	-0.37923
22	23	24	2	678,862,361	135,571,017	NaN	NaN	NaN	-10,336
25	26	27	2	678,862,361	135,571,017	NaN	NaN	NaN	-0.5864
28	29	30	2	678,862,361	135,571,017	NaN	NaN	NaN	-0.89777
31	32	33	2	678,862,361	135,571,017	NaN	NaN	NaN	-0.80944
34	35	36	3	71,729,563	214,886,506	NaN	NaN	NaN	-0.39322
37	38	39	3	71,729,563	214,886,506	NaN	NaN	NaN	10,651
40	41	42	3	71,729,563	214,886,506	NaN	NaN	NaN	0.96299
43	44	45	3	71,729,563	214,886,506	50576.19	-0.81753	-0.00058641	-0.5649
46	47	48	3	71,729,563	214,886,506	48931.68	-11,873	-0.00085165	-0.36907
49	50	51	3	71,729,563	214,886,506	48935.83	-0.89124	-0.00063928	-0.42935
52	53	54	3	71,729,563	214,886,506	48589.26	-0.93498	-0.00067066	-0.48078
55	56	57	3	71,729,563	214,886,506	NaN	NaN	NaN	0.61346
58	59	60	2	990,473,732	197,893,291	41371.02	-0.13943	-0.0001381	1,129
61	62	63	2	990,473,732	197,893,291	41700.63	-0.8848	-0.00087637	17,107
64	65	66	2	990,473,732	197,893,291	41721.6	-0.71732	-0.00071049	15,135
67	68	69	2	990,473,732	197,893,291	41596.73	-0.78942	-0.0007819	10,194
70	71	72	2	990,473,732	197,893,291	41791.86	-0.78107	-0.00077363	1,597
73	74	75	3	107,214,017	321,339,869	NaN	NaN	NaN	10,075
76	77	78	3	107,214,017	321,339,869	NaN	NaN	NaN	11,244
79	80	81	3	107,214,017	321,339,869	NaN	NaN	NaN	0.064241
82	83	84	3	752,716,813	225,512,861	NaN	NaN	NaN	0.39857
85	86	87	3	752,716,813	225,512,861	NaN	NaN	NaN	0.6837
88	89	90	3	752,716,813	225,512,861	NaN	NaN	NaN	0.95028
91	92	93	3	670,304,899	200,789,287	50782.59	-12,919	-0.00086598	-14,228
94	95	96	3	670,304,899	200,789,287	50413.44	-0.92069	-0.00061714	-23,988
97	98	99	3	670,304,899	200,789,287	49867.72	-0.80455	-0.00053929	-22,151
100	101	102	3	727,339,959	217,899,805	NaN	NaN	NaN	0.67973
103	104	105	4	545,756,788	217,899,805	55200.6	-0.47673	-0.00026018	-11,118
106	107	108	3	727,339,959	217,899,805	47298.66	-1,453	-0.0010568	-0.28561

1	4	545,756,788	217,899,805	NaN	NaN	NaN	10,085
2	4	545,756,788	217,899,805	NaN	NaN	NaN	0.51477
3	4	545,756,788	217,899,805	NaN	NaN	NaN	0.43893
4	3	727,339,959	217,899,805	49461.57	-0.8152	-0.00059293	-0.26477
5	4	545,756,788	217,899,805	NaN	NaN	NaN	0.29208
6	3	727,339,959	217,899,805	NaN	NaN	NaN	0.67912
7							
8							
9							
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11							
12	3	737,665,277	2,209,974	NaN	NaN	NaN	0.7087
13	3	737,665,277	2,209,974	48021.57	-0.81164	-0.00059872	-1,022
14	3	737,665,277	2,209,974	49666.97	-0.73257	-0.00054039	-0.59356
15	3	737,665,277	2,209,974	NaN	NaN	NaN	0.063042
16	3	737,665,277	2,209,974	48325.57	-0.67641	-0.00049896	-0.688
17							
18							
19							
20							
21	2	102,896,974	205,592,493	40445.55	-0.72577	-0.0007468	-0.46537
22	2	102,896,974	205,592,493	40108.64	0	0	-17,689
23	2	102,896,974	205,592,493	40719.98	0	0	-16,878
24	2	102,896,974	205,592,493	42294.86	0	0	-15,537
25	2	102,896,974	205,592,493	40144.92	-0.4439	-0.00045676	-10,553
26	2	102,896,974	205,592,493	NaN	NaN	NaN	0.40686
27	2	102,896,974	205,592,493	40656.43	0	0	-17,644
28	2	102,896,974	205,592,493	40637.25	0	0	-16,164
29	2	102,896,974	205,592,493	41381.46	0	0	-11,285
30	2	102,896,974	205,592,493	40644.64	-0.15679	-0.00016133	-12,504
31	3	686,315,585	205,592,493	NaN	NaN	NaN	0.93733
32	2	102,896,974	205,592,493	41106.15	-0.72335	-0.0007443	-0.40616
33	3	686,315,585	205,592,493	50304.32	-0.18577	-0.0001275	-0.72788
34	2	102,896,974	205,592,493	NaN	NaN	NaN	0.12316
35	2	102,896,974	205,592,493	40951.85	-0.88397	-0.00090958	-0.59491
36	3	686,315,585	205,592,493	50827.29	-0.88301	-0.00060602	0.062175
37	2	102,896,974	205,592,493	40977.51	0	0	-14,647
38	2	102,896,974	205,592,493	41019.25	0	0	-13,648
39	3	686,315,585	205,592,493	NaN	NaN	NaN	0.036765
40	2	102,896,974	205,592,493	NaN	NaN	NaN	-0.070952
41	2	102,896,974	205,592,493	41467.31	-0.1204	-0.00012389	-0.57332
42	2	102,896,974	205,592,493	41073.05	-0.52115	-0.00053625	0.11019
43	2	102,896,974	205,592,493	42349.81	-0.25346	-0.0002608	-0.58571
44	2	102,896,974	205,592,493	41294.95	-0.6056	-0.00062315	-0.12905
45	2	102,896,974	205,592,493	41438.02	0	0	-0.67687
46	3	686,315,585	205,592,493	NaN	NaN	NaN	NaN
47	2	102,896,974	205,592,493	41382.49	0	0	-0.21612
48	2	102,896,974	205,592,493	40875.37	-0.67242	-0.0006919	-0.46279
49							
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61	3	693,327,825	207,696,165	NaN	NaN	NaN	0.95663
62							
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2							
3	2	10,394,881	207,696,165	NaN	NaN	NaN	0.78001
4	3	693,327,825	207,696,165	51124.58	-0.24826	-0.00017213	-0.90324
5							
6							
7	2	826,402,579	16,507,906	NaN	NaN	NaN	19,666
8	2	826,402,579	16,507,906	44413.07	-0.71751	-0.00059296	-0.17386
9	2	826,402,579	16,507,906	NaN	NaN	NaN	20,438
10	2	826,402,579	16,507,906	44639.39	-0.90043	-0.00074412	0.59597
11	2	826,402,579	16,507,906	45362.56	-0.6055	-0.00050038	0.23264
12	2	866,385,744	173,075,693	46475.25	-0.60516	-0.0005243	0.48461
13							
14							
15							
16							
17	2	799,900,538	159,778,652	45334.03	0	0	-14,209
18	2	799,900,538	159,778,652	49691.38	0	0	-0.59866
19	2	799,900,538	159,778,652	47238.11	-0.60566	-0.00048447	0.065684
20	2	799,900,538	159,778,652	46978.66	0	0	-0.66459
21							
22							
23							
24	3	440,230,399	131,766,937	62752.88	-0.20477	-9.01E-01	-0.60419
25	3	440,230,399	131,766,937	62672.29	-0.27832	-0.00012253	0.42741
26							
27							
28	3	100,810,317	302,128,768	NaN	NaN	NaN	0.81854
29	3	100,810,317	302,128,768	41498.1	-0.1923	-0.00019385	-0.69867
30	3	100,810,317	302,128,768	41709.66	-0.69225	-0.00069786	-0.24163
31							
32							
33							
34	4	954,455,923	381,379,459	NaN	NaN	NaN	-0.43112
35	4	954,455,923	381,379,459	NaN	NaN	NaN	0.51079
36	4	954,455,923	381,379,459	NaN	NaN	NaN	0.73047
37							
38							
39	3	67,168,786	201,204,175	51096.34	-0.04967	-3.34E-01	17,197
40	3	67,168,786	201,204,175	50391.08	0.0094576	6.35E-02	19,131
41	3	67,168,786	201,204,175	47925.68	0.24981	0.0001678	13,833
42							
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Mass Error [Da]	Mass Error [ppm]	Uncalibrated [Da]	Uncalibrated 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

1  
2 -0.0011118 -14,233 -0.0013418 ##### ##### 78.16 10,275

3  
4  
5  
6 0.00035223 -0.47379 -0.00039862 ##### ##### 81,717 0.60141  
7 -0.00032288 -0.9644 -0.00081138 ##### ##### 85,461 0.54626  
8 0.00020634 -0.38504 -0.00032395 ##### ##### 84,705 0.659  
9 -0.00098804 -11,744 -0.00098804 ##### ##### 81,916 0.5723  
10 0.00058788 NaN NaN NaN NaN 83,036 0.60281  
11 -9.63E-01 NaN NaN NaN NaN 81,405 0.53769  
12 -0.00028568 -0.81577 -0.00068633 ##### ##### 95,193 0.4995  
13 -3.92E-01 -0.917 -0.0007715 ##### ##### 94,723 0.63361  
14 -0.00023838 -12,276 -0.0010328 ##### ##### 82,131 0.55059  
15 -0.00030253 -0.93911 -0.00079011 ##### ##### 84,447 0.58243  
16 -4.68E-01 -0.75752 -0.00063733 ##### ##### 83,209 0.60301  
17 7.42E-01 -0.79504 -0.00066889 ##### ##### 81,927 0.48901

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19  
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24 0.00044878 -0.44689 -0.00027831 ##### ##### 76,755 15,688  
25 -0.00022485 -0.36105 -0.00022485 ##### ##### 76,205 0.73231  
26 -6.03E-01 -0.78489 -0.0004888 ##### ##### 76,587 0.50031  
27 0.00013403 -0.4918 -0.00030627 ##### ##### 77,517 13,885  
28 -0.00020821 -0.33432 -0.00020821 ##### ##### 77,719 0.58629  
29 -0.00017696 -0.51667 -0.00032176 ##### ##### 87,667 0.53617  
30 -1.63E-01 -0.87823 -0.00054693 ##### ##### 87,765 0.65209  
31 0.00029792 -0.033363 -2.08E-01 ##### ##### 78,112 0.86717  
32 7.12E-01 -0.24463 -0.00015235 ##### ##### 76,455 16,749  
33 0.00018171 -0.20884 -0.00013006 ##### ##### 78,722 0.7103  
34 -0.00027057 -0.75428 -0.00046974 ##### ##### 87,866 0.6384

35  
36  
37  
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39  
40 0.000807 10,899 0.00067495 ##### ##### 94,877 0.67711  
41 0.00098824 13,525 0.00083754 ##### ##### 94,214 0.52608

42  
43  
44  
45 0.00059814 NaN NaN NaN 103.01 0.75828  
46 0.00015085 -0.34483 -0.00028334 ##### ##### 101.81 0.72246  
47 -3.95E-01 -0.53978 -0.00044353 ##### ##### 100.02 0.75243  
48 0.00010634 -0.43717 -0.00035922 ##### ##### 110.97 10,815  
49 -7.16E-01 -0.55416 -0.00045534 ##### ##### 102.64 0.68706  
50 -0.00030275 -0.91665 -0.0007532 ##### ##### 101.37 0.67909

51  
52  
53  
54 -0.00053448 -13,669 -0.00052752 ##### ##### 51,006 0.59747  
55 -0.0005313 -16,479 -0.000636 ##### ##### 57,204 0.60443

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61 0.000486 NaN NaN NaN 78,509 0.36842  
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1	0.00064369	NaN	NaN	NaN	NaN	87,301	0.7648
2	0.00010804	-0.46028	-0.00041858	#####	#####	79,768	0.59363
3							
4							
5							
6							
7	9.35E-01	NaN	NaN	NaN	NaN	88,133	0.81361
8	-8.39E-01	NaN	NaN	NaN	NaN	88.65	0.6924
9	0.00040679	NaN	NaN	NaN	NaN	88.85	0.88759
10							
11							
12							
13	-0.00099659	NaN	NaN	NaN	NaN	70,489	0.52867
14	-0.00049511	-14,762	-0.0010374	#####	#####	71,545	0.62837
15	1.16E-01	-0.44449	-0.00031237	#####	#####	70,618	0.64713
16							
17							
18	-0.00031152	-11,038	-0.001145	#####	#####	108.15	0.59637
19	1.88E-01	NaN	NaN	NaN	NaN	108.99	0.44384
20	-6.89E-01	-0.80363	-0.00083366	#####	#####	108.84	0.54576
21							
22							
23					Y		
24	0.00073559	NaN	NaN	NaN	NaN	66,421	0.63902
25	-0.00023388	-1,416	-0.0013722	#####	#####	64,623	0.91163
26	-7.39E-01	-11,002	-0.00079991	#####	#####	64,653	0.91163
27	0.00037158	NaN	NaN	NaN	NaN	64,588	0.61862
28							
29							
30							
31	NaN	NaN	NaN	NaN	NaN	94,476	1
32	NaN	NaN	NaN	NaN	NaN	113.66	1
33	NaN	NaN	NaN	NaN	NaN	101.06	1
34	-0.00012533	-0.87695	-0.00066937	#####	#####	87,498	0.53297
35							
36							
37							
38	0.00066917	NaN	NaN	NaN	NaN	57,495	0.41724
39	-0.00012276	-11,423	-0.00072262	#####	#####	53,759	0.55851
40	1.20E-02	-0.55212	-0.00034928	#####	#####	63,476	0.71551
41	0.00036841	NaN	NaN	NaN	NaN	66.49	0.72619
42	0.00040937	NaN	NaN	NaN	NaN	57,738	0.36544
43	-0.00032366	-10,283	-0.00065052	#####	#####	55,677	0.57108
44							
45							
46							
47							
48							
49	-0.0011037	NaN	NaN	NaN	NaN	59,949	0.91953
50	-0.00064366	NaN	NaN	NaN	NaN	59,764	0.9465
51	-0.00092598	NaN	NaN	NaN	NaN	61,765	1,128
52	-0.0012451	NaN	NaN	NaN	NaN	123.93	0.76739
53							
54							
55							
56	2.77E-02	-18,612	-0.0016926	#####	#####	88,764	0.6004
57	-0.00072269	-17,281	-0.0010483	#####	#####	89,718	14,088
58	-0.00077341	-13,769	-0.00083528	#####	#####	89.86	11,759
59	-0.0006508	-14,476	-0.00087818	#####	#####	89,509	0.76118
60	-0.00051312	-11,403	-0.00068147	#####	#####	68,206	19,744
61							
62							
63							
64							
65							

1	-0.0015969	-20,596	-0.0018453	#####	#####	74,517	0.44894
2	-0.00045077	-1,625	-0.0014559	#####	#####	74,981	0.66922
3	-0.00016479	-0.92031	-0.00055	#####	#####	67,525	0.73146
4							
5							
6							
7							
8	0.00043523	NaN	NaN	NaN	NaN	86,999	0.7193
9	0.0011086	NaN	NaN	NaN	NaN	85,962	0.63573
10	0.0015461	NaN	NaN	NaN	NaN	84,968	0.63683
11	5.53E-02	NaN	NaN	NaN	NaN	82,974	0.69716
12	0.0012608	NaN	NaN	NaN	NaN	84,321	0.64992
13	0.001306	NaN	NaN	NaN	NaN	83.74	0.96486
14							
15							
16							
17							
18	-0.00033326	NaN	NaN	NaN	NaN	95,998	0.73493
19	0.00037473	NaN	NaN	NaN	NaN	105	0.64604
20	-0.00036333	-10,028	-0.00091697	#####	#####	95,819	0.87028
21							
22							
23							
24	-0.00021767	-10,359	-0.00057521	#####	#####	55,913	0.41409
25	-0.00025435	-12,069	-0.0010046	#####	#####	57,181	0.44668
26	-0.00013829	-0.43849	-0.00024348	#####	#####	65,694	0.53619
27	0.000444	-0.16528	-0.00013758	#####	#####	64,475	0.49722
28	-8.28E-01	-0.8866	-0.00073801	#####	#####	65,717	0.48075
29	-0.0007084	-16,961	-0.0010142	#####	#####	46,122	0.3931
30	-0.00079715	-17,929	-0.0010721	#####	#####	52,587	0.64492
31							
32							
33							
34							
35	0.00044906	-0.69823	-0.00052669	#####	#####	71,015	0.46674
36	0.00033729	-0.23648	-0.00017839	#####	#####	69,722	0.74473
37	1.45E-01	-0.67934	-0.00051245	#####	#####	81,242	0.67423
38							
39							
40							
41	0.00033928	0.17765	9.92E-01	#####	#####	46,373	13,627
42	0.00058073	NaN	NaN	NaN	NaN	48,931	0.67912
43							
44							
45	0.0013452	0.36076	0.00034578	#####	#####	130.53	1,487
46	0.00099024	0.89689	0.00085964	#####	#####	132	15,108
47							
48							
49	-0.00078979	-20,573	-0.0012565	#####	#####	116.71	0.92902
50	-0.00089042	-18,703	-0.0011423	#####	#####	46,818	0.65672
51	-0.00071657	-20,239	-0.0012199	#####	#####	126.59	17,975
52							
53							
54							
55	-0.00010582	NaN	NaN	NaN	NaN	73,446	0.85529
56	-0.00034272	NaN	NaN	NaN	NaN	71,689	0.95847
57	-0.00046481	NaN	NaN	NaN	NaN	68,475	0.57893
58	-0.00013785	NaN	NaN	NaN	NaN	63,488	0.81966
59	-0.0001687	NaN	NaN	NaN	NaN	128.62	23,097
60	-0.0001651	NaN	NaN	NaN	NaN	68,041	0.80257
61							
62							
63							
64							
65							

1	-0.00069943	NaN	NaN	NaN	66,515	11,619
2	-0.00035497	NaN	NaN	NaN	64,425	1,019
3	-0.00058298	NaN	NaN	NaN	121.77	39,073
4	-0.00031859	NaN	NaN	NaN	71,122	0.53815
5	-0.00015354	NaN	NaN	NaN	77,373	10,956
6	-0.00028462	NaN	NaN	NaN	75,968	12,429
7	-0.00025744	NaN	NaN	NaN	64,014	10,419
8	-0.00070165	NaN	NaN	NaN	118.8	25,957
9	-0.00039808	NaN	NaN	NaN	125.72	29,955
10	-0.00060946	NaN	NaN	NaN	129.27	2,961
11	-0.0005495	NaN	NaN	NaN	69.77	10,571
12	-0.00026694	NaN	NaN	NaN	63,333	0.77888
13						
14	0.00076401	NaN	NaN	NaN	54,759	0.54944
15	0.00069075	NaN	NaN	NaN	52,031	0.43327
16	-0.0004052	-13,824	-0.00099161	#####	62,327	11,715
17	-0.00026473	-15,564	-0.0011164	#####	56,364	0.55442
18	0.00059057	NaN	NaN	NaN	52,195	0.50599
19	-0.00030797	-13,206	-0.00094725	#####	51,827	0.88256
20	-0.00034486	-14,158	-0.0010155	#####	52,567	0.85705
21	0.00044003	NaN	NaN	NaN	50.78	0.51909
22						
23	0.0011183	0.98959	0.00098016	#####	130.2	14,043
24	0.0016944	0.82589	0.00081803	#####	101.65	2,687
25	0.0014991	0.79621	0.00078863	#####	102.56	18,499
26	0.0010097	0.22998	0.00022779	#####	102.36	0.76945
27	0.0015818	0.81593	0.00080816	#####	102.16	0.55981
28						
29	0.0010802	NaN	NaN	NaN	81,284	13,858
30	0.0012056	NaN	NaN	NaN	81,377	16,813
31	6.89E-01	NaN	NaN	NaN	81,158	0.85651
32						
33	0.00030001	NaN	NaN	NaN	111.95	0.94267
34	0.00051464	NaN	NaN	NaN	114.19	0.63842
35	0.00071529	NaN	NaN	NaN	123.38	0.5867
36						
37	-0.00095371	-27,147	-0.0018197	#####	63,084	0.72208
38	-0.001608	-33,195	-0.0022251	#####	66.67	0.38632
39	-0.0014848	-30,196	-0.0020241	#####	64,794	0.56033
40						
41	0.00049439	NaN	NaN	NaN	42,096	0.57529
42	-0.00060678	-15,885	-0.00086696	#####	50,042	0.65393
43	-0.00020773	-17,386	-0.0012645	#####	42,335	0.72315
44						
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1	0.00055042	NaN	NaN	NaN	NaN	42,336	0.93044
2	0.00028094	NaN	NaN	NaN	NaN	43,609	10,889
3	0.00023955	NaN	NaN	NaN	NaN	50,433	0.32283
4	-0.00019258	-1.08	-0.00078551	#####	#####	57,465	0.65966
5	0.00015941	NaN	NaN	NaN	NaN	57,517	0.85898
6	0.00049395	NaN	NaN	NaN	NaN	55,509	0.62685
7							
8							
9							
10							
11							
12	0.00052278	NaN	NaN	NaN	NaN	54,745	0.51048
13	-0.00075392	-18,337	-0.0013526	#####	#####	64,875	0.77584
14	-0.00043785	-13,261	-0.00097824	#####	#####	53,482	0.68179
15	4.65E-01	NaN	NaN	NaN	106.88		10,294
16	-0.00050752	-13,644	-0.0010065	#####	#####	52.9	0.56873
17							
18							
19							
20	-0.00047885	-11,911	-0.0012256	#####	#####	120.16	12,281
21	-0.0018201	-17,689	-0.0018201	#####	#####	119.81	11,799
22	-0.0017367	-16,878	-0.0017367	#####	#####	119.92	1,068
23	-0.0015987	-15,537	-0.0015987	#####	#####	119.98	0.58934
24	-0.0010859	-14,992	-0.0015427	#####	#####	120.5	10,766
25	0.00041865	NaN	NaN	NaN	120.4	0.50204	
26	-0.0018155	-17,644	-0.0018155	#####	#####	120.97	0.6772
27	-0.0016632	-16,164	-0.0016632	#####	#####	121.12	13,278
28	-0.0011612	-11,285	-0.0011612	#####	#####	121.39	0.68147
29	-0.0012866	-14,072	-0.001448	#####	#####	133.17	0.95207
30	0.0006433	NaN	NaN	NaN	133.21	0.64886	
31	-0.00041792	-11,295	-0.0011622	#####	#####	133.07	1,098
32	-0.00049955	-0.91365	-0.00062705	#####	#####	133.09	0.57579
33	0.00012673	NaN	NaN	NaN	121.19	0.82292	
34	-0.00061214	-14,789	-0.0015217	#####	#####	121.83	0.82023
35	4.27E-01	-0.82083	-0.00056335	#####	#####	121.79	0.83508
36	-0.0015071	-14,647	-0.0015071	#####	#####	121.84	0.78532
37	-0.0014044	-13,648	-0.0014044	#####	#####	121.85	0.75122
38	2.52E-01	NaN	NaN	NaN	121.87	0.56217	
39	-7.30E-01	NaN	NaN	NaN	122.13	0.63235	
40	-0.00058993	-0.69372	-0.00071382	#####	#####	123.85	24,877
41	0.00011339	-0.41096	-0.00042286	#####	#####	121.54	0.76222
42	-0.00060268	-0.83917	-0.00086349	#####	#####	120.81	0.62215
43	-0.00013279	-0.73465	-0.00075593	#####	#####	121.92	18,693
44	-0.00069648	-0.67687	-0.00069648	#####	#####	122.16	0.78681
45	NaN	NaN	NaN	NaN	122.13	1	
46	-0.00022238	-0.21612	-0.00022238	#####	#####	122.46	0.56194
47	-0.0004762	-11,352	-0.0011681	#####	#####	120.15	0.95764
48							
49							
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51							
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56							
57							
58							
59							
60							
61	0.00066326	NaN	NaN	NaN	NaN	82,514	0.82999
62							
63							
64							
65							

1	0.00081082	NaN	NaN	NaN	NaN	83,068	0.49942
2	-0.00062624	-11,515	-0.00079837	#####	#####	84,379	0.89329
3							
4	0.0016252	NaN	NaN	NaN	NaN	105.61	0.69661
5	-0.00014368	-0.89137	-0.00073663	#####	#####	100.9	0.40081
6	0.001689	NaN	NaN	NaN	NaN	105.18	0.58349
7	0.00049251	-0.30446	-0.00025161	#####	#####	101.02	0.55649
8	0.00019225	-0.37286	-0.00030813	#####	#####	99,569	0.63045
9	0.00041986	-0.12055	-0.00010444	#####	#####	116.48	0.51491
10							
11	-0.0011366	-14,209	-0.0011366	#####	#####	87,404	0.47132
12	-0.00047887	-0.59866	-0.00047887	#####	#####	85,976	0.56593
13	5.25E-01	-0.53997	-0.00043193	#####	#####	85,818	0.46095
14	-0.00053161	-0.66459	-0.00053161	#####	#####	85,572	0.62428
15							
16							
17	-0.00026598	-0.80896	-0.00035613	#####	#####	18,285	0.77988
18	0.00018816	0.14909	6.56E-01	#####	#####	23,095	0.53612
19							
20							
21	0.00082517	NaN	NaN	NaN	NaN	100.73	0.78802
22	-0.00070433	-0.89096	-0.00089818	#####	#####	101.71	0.80127
23	-0.00024359	-0.93389	-0.00094145	#####	#####	102.32	0.64181
24							
25							
26	-0.00041149	NaN	NaN	NaN	NaN	109.77	12,359
27	0.00048753	NaN	NaN	NaN	NaN	123.32	24,183
28	0.00069721	NaN	NaN	NaN	NaN	110.69	0.79527
29							
30							
31	0.0011551	Jan-67	0.0011217	#####	#####	136.58	0.83658
32	0.001285	19,226	0.0012914	#####	#####	123.02	49,787
33	0.00092914	16,331	0.0010969	#####	#####	130.28	13,125
34							
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65							

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

1	86,894	86,285	87,312	87,342
2				
3	100.91	100.66	101.26	19,196
4	90,685	90,438	90,985	5,224
5	91,882	91,522	92,181	71,776
6	95,804	95,551	96,123	13,888
7	95,855	95.55	96,152	12,818
8	88,706	88,454	88,991	73,008
9	100.46	100.21	100.71	52,721
10	101.56	101.28	101.91	68,355
11	97,518	97,303	97,853	15,387
12	93,081	92.79	93,372	86,341
13	95,115	94.78	95,383	11,906
14	97,608	97,316	97,805	15,681 0.045101 0.00031363 NaN
15				
16	83,294	82,811	84,379	65,389
17	74,634	74,321	75,054	-15,717
18	92,495	92,273	92,774	15,908
19	81,551	81,135	82,523	40,333
20	85,429	85,159	85,746	Jul-71
21	94.9	94,616	95,153	72,329
22	96,211	95,907	96,559	84,453
23	88,911	88.57	89,437	10,799
24	93.44	93,001	94,676	16,985
25	104.69	104.38	105.09	25,969
26	96,344	96,047	96,686	84,784 0.066776 -0.00027052 NaN
27				
28	96,434	96,099	96,776	15,562
29	101.75	101.4	101.93	75,363
30				
31	101.92	101.66	102.42	-10,905
32	102.87	102.55	103.27	10,635
33	106.32	105.95	106.71	63,039
34	106.6	106.18	107.26	-43,689
35	104.66	104.32	105.01	20,194
36	106.06	105.76	106.44	46,915
37				
38	58,484	58,195	58,792	74,781
39	60.63	60,381	60,985	34,263
40				
41	89,573	89,404	89,773	11,064
42				

1	90,527	90.11	90,874	32,259
2	88,402		88,072	88,666
3				86,341
4				
5				
6				
7	93,264		92,876	93,689
8			93,163	51,308
9	93,584			93,855
10				49,337
11	93,358		92,951	93,838
12				45,084
13				
14	84.35		84,065	84,594
15			86,306	13,861
16	86,597			15,052
17			87,258	86,975
18				87,622 16.64
19	127.03		126.78	127.37
20			92,842	18,882
21	92,689			-16,152
22	127.99		127.68	128.23
23				19,151
24	78,645	78.34		78,979
25			79,931	12,223
26	79,545			80,457
27	79,961	79,545		15,308
28			80,457	15,308
29	80,397		80,116	80,734
30				15,809
31	104.01		103.51	104.51
32			90,539	95,334
33	91,039			-22.62
34	90,247		89,747	91,539
35				-10,808
36	93,917		93,654	94,187
37				64,188
38	64,873		64,649	65,066
39			70,036	73,776
40	69.74			70,298
41	70,984	71.7		16,277
42			71.41	79,337
43	67,525	67.14		67,866
44			70,325	10,349
45	70,505		70.69	12,767
46			67,784	68,086
47				12,107
48				
49	74,601		74,277	75,196
50			74.91	14,652
51	74,549			15,146
52			74,532	75,496
53	74,252	75.38		12,766
54	104.46		104.26	105.03
55				-19,476
56	92,904		92,636	93,236
57			94,746	41,393
58	94,091	95.5		50,272
59	94,791		94,313	49,305
60			94,602	-0.041153 -0.00017331
61	94,959		95,489	NaN
62			82,757	54,503 0.12724 0.00019452
63	81,481		83,455	NaN
64				14,552
65				

1	89,364	89,119	89,568	14,847			
2	89,433	89,182	89,851	14,452	0.034115	0.00081033	NaN
3	82,596	82,258	82.99	15,072	-0.024422	0.00039573	NaN
4							
5	101.78	101.32	102.04	14,786			
6	102.39	102.07	102.71	16,433			
7	102.64	102.25	102.89	17,669			
8	89,947	89,633	90.33	69,729			
9	102.68	102.23	102.88	18,364			
10	102.6	102.23	103.19	18,858			
11							
12	89,819	89,454	90,189	-61,797			
13	106.31	106.07	106.72	1,319			
14	102.66	102.21	103.08	68,448			
15							
16	70,999	70,781	71,195	15,086			
17	69,999	69.77	70,217	12,818			
18	66,729	66,453	66,989	10,349			
19	67,301	67,076	67,574	28,262			
20	66,751	66,453	66,934	10,349	-0.27472	-0.00060714	NaN
21	61,208	61,025	61,419	15,086			
22	60,065	59,868	60,513	74,781			
23							
24	82,279	82,057	82,523	11,264			
25	82.54	82,217	82,961	12,818			
26	83,176	82,873	83,547	19,343			
27							
28	61.82	61,491	62,854	15,446			
29	64,376	63,856	64,536	15,445			
30							
31	132.31	131.6	133.09	17,792			
32	138.47	137.36	138.88	64,748			
33							
34	125.7	125.43	126.36	89,881			
35	62,572	62,327	62,984	15,754			
36	110.3	109.5	111.29	-16,286			
37							
38	79.07	78,797	79,652	5,624			
39	79,267	78,869	79,828	75,776			
40	79,353	79,035	79,614	10,877			
41	79,841	79,541	80,361	16,353			
42	137.41	136.35	138.66	Aug-79			
43	79,605	79,349	80,152	11,564			
44							
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1	79,533	79.2	80,362	13,018
2	79,571	79,233	80,252	15,146
3	117.36	115.3	119.21	-4.41
4	78,254	78,052	78.59	71,326
5	78,607	78,338	79,434	12,349
6	78,795	78,468	79,711	28,264
7	79,322	78,967	80,009	15,308
8	117.33	115.93	118.52	-1,474
9	117.94	116.54	119.54	-7,775
10	112.99	111.61	114.57	-16,286
11	78,905	78,599	79,657	91,348
12	79,142	78,859	79,638	15,809
13	65,937	65.78	66,329	11,178
14	68,308	68.1	68,534	16,277
15	70,805	70,492	71,663	84,783
16	69,031	68,797	69,352	12,667
17	67,748	67,541	68,047	15,553
18	67,992	67,722	68,604	16,165
19	67,095	66,778	67,635	14,528
20	68,119	67,908	68,427	17,339
21	127.38	126.72	128.13	-28,205
22	91,871	91,424	94,111	-97,767
23	91,754	91,367	93,217	-10,805
24	91,648	91,276	92,046	-10,707 -0.045914 -0.00071351 NaN
25	91.68	91,441	92	-10,484 -0.014114 0.0004307 NaN
26	95,931	95,438	96,824	14,647
27	95,986	95,643	97,325	14,609
28	96,007	95.73	96,587	14,849
29	131.04	130.73	131.67	19,095
30	130.72	130.46	131.1	16,528
31	130.23	129.91	130.5	68,524
32	77,736	77,388	78.11	14,652
33	78,233	78.05	78,437	11,564 0.30605 -0.00075337 NaN
34	77,812	77,542	78,103	13,018 -0.11486 -0.00038386 NaN
35	58,848	58,649	59,224	16,752
36	57,547	57.25	57,904	75,053
37	59.31	58,947	59.67	16,975

1	59,312	58,829	59.76	16,975
2	58,862	58,414	59,503	15,253
3	58,767	58,553	58,876	83,342
4	59	58,688	59,348	15,351
5	59,052	58,547	59,406	15,351
6	58,935	58,636	59,263	34,263
7				
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11				
12	66,968	66.75	67,261	12,223
13	67,702	67,352	68,128	28,262
14	68,789	68,474	69,156	15,308
15	99,005	98,655	99,685	-78,752
16	69,009	68,747	69,316	16,109
17				
18				
19				
20				
21	134.91	134.46	135.69	14,748
22	95,223	94,798	95,978	-24,592
23	95,257	94,854	95,922	-24,667
24	96,836	96,597	97,186	-23,143
25				
26	134.77	134.35	135.43	14,277
27	132.85	132.62	133.12	12,449
28	101.21	100.93	101.61	-19,762
29	101.57	101.1	102.43	-19,551
30	101.9	101.6	102.28	-19.49
31	140.2	139.77	140.72	70,318
32	140.24	139.96	140.6	70,318
33	139.44	139	140.1	63,746
34	139.46	139.14	139.72	63,746
35	133.04	132.66	133.48	11,854
36	106.04	105.62	106.44	-15,786
37	106.01	105.69	106.53	-15,786
38	105.47	105.17	105.96	-16.37
39	110.64	110.29	111.05	-11,217
40	110.65	110.38	110.95	-11,217
41	107.67	107.41	108.04	-14,454
42	116.08	115.68	118.17	-7,775
43	133.51	133.11	133.87	11,971
44	131.31	131.05	131.67	10,506
45	106.02	105.52	107.39	-15,894
46	102.68	102.32	103.11	-19,482
47	102.65	102.15	103.15	-19,482
48	119.33	119.06	119.62	-31,306
49	134.43	134.07	135.03	14,285 -0.2373 2.57E-02 NaN
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1	103.13	102.89	103.39	20,062
2	95,077	94,701	95,594	10,699
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7	106.57	106.13	106.83	0.96355
8	89,438	89,273	89,673	-11,459
9	107.2	106.99	107.57	20,194
10	90,677	90,413	90,969	-10,344
11	106.41	106.01	106.64	68,448
12	100.59	100.37	100.88	-15,894
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17	93,802	93.59	94,061	6,398
18	93,687	93,465	94,031	77,113
19	90,358	90,157	90,618	45,403
20	92,529	92,252	92,877	69,571
<hr/>				
24	35,537	35.11	35.89	17,251
25	33,624	33,368	33,904	10,529
<hr/>				
28	91.62	91,221	92,009	-91,056
29	90,709	90,255	91,056	-11
30	90,794	90,466	91,107	-11,525
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34	129.53	129.05	130.29	19,759
35	134.2	132.87	135.29	10,886
36	128.26	127.84	128.64	17,564
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39	133.66	133.44	134.27	-29,207
40	137.09	135.07	140.05	14,078
41	137.31	136.42	137.73	70,318
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1	102	14	16	0	0	0
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5	248	38	9	0	0	0
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16	228	36	9	0	0	0
17	44	7	9	0	0	0
18	61	8	10	0	0	0
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24	252	48	8	0	0	0
25	135	33	6	0	0	0
26	539	91	9	0	0	0
27	167	39	6	0	0	0
28	72	17	6	0	0	0
29	61	16	7	0	0	0
30	218	57	6	0	0	0
31	594	111	9	0	0	0
32	221	48	7	0	0	0
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55	103	22	7	0	0	0
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149	34	8	0	0	0
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190	32	10	0	0	0
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114	13	13	0	0	0
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73	15	7	0	0	0
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88	33	6	0	0	0
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			0	0	0
208	31	10	0	0	0
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			0	0	0
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170	23	11	0	0	0
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41,621	127	9 NaN	NaN	NaN	
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5	43.69	38	7	7	0	0
6	44,246	49	8	10 NaN	NaN	NaN
7		164	38	7 NaN	NaN	NaN
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20					0	0
21		488	58	12	0	0
22					0	0
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25		44	9	8	0	0
26		42	12	6	0	0
27		24	6	6	0	0
28		72,316	32	10	7 NaN	NaN
29		163	24	9	0	0
30		160	30	11	0	0
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34					0	0
35		104	21	9	0	0
36		42	10	8	0	0
37		50	8	10	0	0
38					0	0
39					0	0
40		497	80	15	0	0
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45		701	98	10	0	0
46		157	20	9	0	0
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49		58	14	8	0	0
50		179	40	6	0	0
51		173	77	4	0	0
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	79	25	5	0	0
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	61	10	9	0	0
			0	0	0
	235	30	12	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	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	0
	109	15	13	0	0	0
	41	7	9	0	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
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	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	0
	194	38	8	0	0	0
58	128.33	556	63	12 NaN	NaN	NaN

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

	MS/MS	MS/MS Scan			Combinatori		
	PEP	Count	Number	Score	Delta score	cs	Ratio H/L
1	0.0024998	1	8758	50,873	36,926	10	0.32364
2	0.00066166	2	9811	63,937	45,532	10	0.39827
3	0.011114	1	7485	56.48	27,381	5	0.189
4	0.015999	1	8380	54,047	32,371	5	0.27281
5	0.013065	1	5937	41,615	26,992	5	0.25025
6	0.0012876	1	6660	53,625	31,949	5	0.14797
7	0.00037934	1	6747	55,302	26,579	10	0.2281
8	0.0045661	1	7721	42,209	20,086	10	0.37424
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21							
22	0.02807	1	10887	45,433	82,528	1	
23	0.014498	1	7441	57,149	22.38	1	
24							
25							
26							
27	0.0025375	3	15318	67,396	61,087	2	0.54438
28	0.0010496	2	15421	76,533	55,254	2	0.49769
29	9.88E-01	1	15234	87,352	62,871	2	0.49671
30							
31	0.0093801	1	17999	56.48	28,389	2	0.34323
32	0.0030875	1	15853	58,796	39,861	2	0.49439
33	2.20E-11	1	15878	118.67	103.82	2	11,087
34							
35	0.011985	1	14078	54.15	28,274	2	0.16628
36	1.39E-03	1	14879	99,409	80,404	2	0.46245
37							
38	NaN	0	NaN	NaN	NaN	0	0.55402
39							
40	NaN	0	NaN	NaN	NaN	0	12,755
41							
42	NaN	0	NaN	NaN	NaN	0	0.57747
43	0.022911	1	16018	47,603	15.25	4	0.51852
44							
45	0.0096279	1	16802	83.31	83.31	5	0.62157
46	0.038931	1	18314	65,207	45,627	5	0.53203
47	0.02059	1	20557	96,391	63,022	5	0.43102
48							
49	0.001369	1	12202	95,444	95,444	5	0.63294
50	0.044014	1	8067	63,883	44,861	5	0.59556
51							
52	NaN	0	NaN	NaN	NaN	0	0.43797
53							
54	0.0004661	2	8847	90.78	72.2	10	0.51119
55							
56							
57	0.019791	1	8859	43,794	43,794	10	0.47973
58							
59							
60	2.37E-03	1	9284	56,099	33,977	9	0.1246
61	5.44E-03	1	10051	51,264	31,511	9	0.081331
62	0.00031051	1	7891	42,301	20,735	9	0.12181
63	0.00078287	1	10748	40,129	24,923	9	0.18889
64							
65							

1	0.013428	1	8952	45,842	29,153	9 NaN
2	0.00011047	1	10305	114.99	71,032	2 0.27122
3	0.021028	1	10475	90,755	46,157	2 0.41465
4	2.74E-02	1	11305	128.79	86,731	2 0.19931
5	0.0087381	1	5589	98,077	44,682	2 0.42649
6	0.00059842	1	12030	103.99	70,796	2 0.12084
7	0.0099793	1	5466	94,973	53,491	2 0.12082
8	1.62E-01	1	13652	131.54	84,649	2 0.38566
9	4.09E-01	1	13835	125.51	65,422	2 0.35571
10	0.005735	1	5602	101.23	78	2 0.62417
11	7.66E-09	1	10295	154.48	111.1	2 0.27884
12	6.83E-03	2	10693	139.74	84,787	2 0.47856
13	NaN	0		NaN	NaN	0 0.21525
14						
15	0.0027448	3	5000	113.69	81,986	3 0.34725
16	0.0027173	1	5304	99,991	75,481	3 0.34253
17	0.022825	1	5646	64,313	50,913	3 0.74067
18	0.0024174	2	5047	112.42	75,976	3 0.31066
19	0.013363	1	5352	69,314	42,956	3 0.29144
20	0.012442	1	11571	70,438	43,549	3 0.62239
21	0.017913	1	12775	48,532	19,229	3 0.48128
22	0.0060641	1	5110	79,886	54,922	3 0.259
23	0.0034134	3	5036	91,307	61,303	3 0.29809
24	0.0036161	2	5500	86,803	58,598	3 0.2857
25	NaN	0		NaN	NaN	0 0.46249
26						
27	0.0057169	1	14238	65,224	65,947	1 0.70699
28	0.013013	1	14612	54,066	15,763	1 0.3297
29						
30	0.026132	1	14173	64,346	42,864	2 0.17971
31	0.00017333	1	14967	91,414	66,183	2 0.24866
32	0.0012865	1	15524	72,793	53.63	2 0.11958
33	0.0024762	1	17094	66,777	66,777	2 0.19281
34	0.0046037	1	14113	60,938	60,938	2 0.39613
35	0.016277	1	14290	50,722	31,033	2 0.4492
36						
37	0.0066911	1	4389	47,039	15,317	2 0.37845
38	0.023679	1	5542	40,767	24,827	2 0.47176
39						
40	0.0036427	1	8183	53,603	35,982	4 NaN
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1	0.0037112	1	12115	53,444	27,084	4 0.20669
2	0.0087212	1	9313	40,086	22,324	4 0.32137
3						
4	0.0053796	1	13274	55,588	34,365	3 0.20466
5	0.005144	1	13684	55,846	32.21	3 0.28266
6	0.0092671	1	12933	51,323	30,538	3 0.41583
7						
8	0.033384	1	7994	72,321	24,037	2 31,103
9	0.018663	1	8978	62,166	15.76	2 12,633
10	0.0037806	1	7516	80,632	50.02	2 0.33563
11						
12	0.01242	1	14018	46,099	26-May	2 0.43173
13	0.025403	1	7613	44,045	15,496	2 NaN
14	0.0075169	1	14614	49,326	27,441	2 0.4862
15						
16	0.0062369	1	7138	42,863	25,104	4 0.2213
17	1.63E-04	1	10094	80,664	58.9	4 NaN
18	3.58E-04	1	10118	76,807	57,114	4 0.26256
19	9.41E-01	1	6563	66,845	42.34	4 0.2477
20						
21	0.039708	1	12403	46,145	20,121	1
22	0.03181	1	17663	46,701	20,706	1
23	0.03593	1	15186	42,095	26,854	1
24	0.005205	1	10972	42,059	31,197	2 0.37748
25						
26	0.023872	1	5568	50,831	30,601	3 0.41778
27	0.018293	1	6974	40,602	27,181	3 0.5327
28	0.0056349	2	6932	48,711	27,745	3 0.2539
29	0.018465	1	7406	54,004	34,831	3 0.3153
30	0.0010818	1	6609	76,586	54,589	3 0.3185
31	0.0024738	3	5136	56,121	36,823	3 0.39543
32						
33	0.0055099	1	7239	56,205	11,358	3 NaN
34	0.020928	1	6553	40,242	88,942	3 NaN
35	0.011604	1	7470	47,712	97,173	3 NaN
36	0.0041436	1	9143	58,885	23,208	3 10,111
37						
38	0.014343	1	11748	44,252	11,745	12 0.74268
39	0.0099871	1	12753	41,621	41,621	12 0.64113
40	NaN	0	NaN	NaN	NaN	0 0.29793
41	NaN	0	NaN	NaN	NaN	0 0.83982
42	0.0093154	1	9040	44,246	15,175	18 0.26957
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1	0.035826	1	9568	43.69	19,606	18	0.60977
2	NaN	0		NaN	NaN	0	0.26093
3	NaN	0		NaN	NaN	0	10,618
4							
5	0.0055019	1	12566	62,088	Dec-79	2	60,165
6	0.011075	1	11100	54,343	26,289	2	NaN
7							
8	0.0094476	1	10950	56,205	22.94	2	14,999
9	0.013879	1	5804	51,135	13,958	2	11,805
10	0.013592	1	12656	51,463	18,198	2	7,004
11	0.028261	1	11531	43,798	68,534	2	NaN
12							
13	0.00034151	1	6543	86,557	67,693	4	0.14147
14	0.004696	1	15133	50,255	26,363	4	NaN
15	0.0096204	1	6510	50,323	22,645	4	0.35956
16							
17	0.011481	1	5455	44,468	27,256	1	0.42219
18	0.011523	1	6599	64,749	50,445	1	0.449
19	0.0026626	1	7257	55,575	38.65	1	0.36541
20	0.0058585	1	7079	72,316	72,316	1	0.39553
21	NaN	0		NaN	NaN	0	0.44217
22							
23	0.004046	1	3914	43.05	33.25	1	0.54788
24	0.0036301	1	4652	43,861	35,553	1	0.41072
25							
26	0.0040337	1	6817	41,446	19,745	1	0.22528
27	0.0010549	1	9182	50,178	14,686	1	0.093787
28	0.0023183	1	10573	45,363	26,499	1	0.34137
29							
30	0.0070692	1	4275	64,224	81,371	2	0.21532
31	0.0026817	1	6598	75,416	25,933	8	0.35198
32							
33	0.032575	1	14601	47,537	20,404	3	0.40559
34	0.040478	1	24658	43,861	43,861	3	0.41982
35							
36	0.010757	2	8200	51,949	37.48	2	0.84105
37	0.022437	1	4435	41,427	18,865	2	0.75432
38	0.041501	1	9477	45,022	20,768	2	0.34812
39							
40	0.0182	1	7944	61,815	21-Mar	2	NaN
41	0.011692	1	8473	67,214	18,266	2	NaN
42	0.011692	1	8462	67,214	11,235	2	0.086717
43							
44	0.041234	1	6118	51,998	16,961	2	NaN
45	0.0052422	1	10100	76,927	32,734	2	0.096784
46	0.0059889	1	6288	75,416	26,118	2	0.01201
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1	0.0081995	1	8492	70,942	25,289	2 0.013381
2	0.024685	1	7463	58,274	24,187	2 0.018572
3	0.0017384	1	11862	90,827	56,827	2 0.21213
4	0.038559	1	8382	53,013	68,068	2 0.044513
5	0.018769	1	9720	61,344	10,335	2 NaN
6	0.011692	1	9542	67,214	24,897	2 0.018412
7	0.0059149	1	9958	75,566	35,693	2 NaN
8	0.016684	1	9018	63,073	29,024	2 0.0723
9	0.011855	2	10057 67.08		39,166	2 0.11481
10	0.0076293	1	10005	72,096 31.62		2 0.047213
11	0.0068534	1	7195	73,666	32,283	2 0.0062677
12	0.031417	1	6332	55,721	20,953	2 0.024096
13						
14	0.024113	1	5678	41,703	21,943	5 NaN
15	0.0081741	1	6673	50,891	21,615	5 NaN
16	0.00022932	2	9121	80,314	49,982	5 0.43213
17	0.00015138	1	6309	89,043 56.69		5 0.68121
18	0.0052321	1	5346	55,844	30,942	5 0.24467
19	0.0011627	3	6431	60,761	37,535	5 0.61086
20	0.00029277	2	5360	75,703	50,748	5 0.59265
21	0.010752	1	4126	48,961	25,563	5 0.1266
22						
23	0.0044681	1	12023	49,066	20-Sep	12 0.69795
24	0.010474	1	16835	43,042	13,943	12 0.42738
25	0.0050612	1	16316	47,622	13,729	12 0.4548
26	NaN	0	NaN	NaN		0 0.96313
27	NaN	0	NaN	NaN		0 0.65978
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29	6.44E-02	1	11010	63,316	38,686	5 0.29767
30	3.57E-04	2	13917	76,109	52,094	5 0.18027
31	0.00044264	1	11006	49,912	30,606	5 0.27171
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33	0.027894	1	16020	40,187	12,661	4 0.083061
34	0.023762	1	17589	42,257	17,835	4 NaN
35	0.0047553	1	19634	56,872	35,513	4 0.052186
36						
37	0.014065	1	7899	43,115	65,234	6 0.5391
38	NaN	0	NaN	NaN		0 29,714
39	NaN	0	NaN	NaN		0 12,702
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41	0.0090328	1	4505	84,436	56,117	3 NaN
42	0.00050631	1	4212	54,004	54,004	3 0.66971
43	0.00014728	2	4879	70,316	41,689	3 0.60681
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1	0.017538	1	4864	44,391	99,957	3	0.78079
2	0.0061945	1	4148	52,172	23,545	3	0.42382
3	0.020574	1	4797	42,708	20,468	3	0.49494
4	0.00013482	2	5616	71,376	52,796	3	0.84281
5	0.0070897	1	5597	50,376	31,796	3	0.45843
6	0.029933	1	5209	71,929	46,772	3	0.38952
7							
8	0.026547	1	5129	44,029	24,268	3	0.15335
9	0.000655	1	7126	62,617	41,939	3	0.5177
10	0.016141	1	7635	42,639	22,609	3	0.35349
11	0.02124	1	7642	45,844	28,419	3	Nan
12	0.00062315	2	4701	56,748	39,862	3	0.63442
13							
14	4.37E-16	3	21272	128.33	90,339	7	0.62808
15	0.00048003	1	8209	84,249	66,015	7	0.74161
16	2.01E-04	1	8303	107.75	90,506	7	0.63761
17	0.00048098	1	8283	84,208	84,208	7	0.58945
18	0.00045259	3	20748	85,423	46,147	7	0.55036
19	0.0034012	1	19553	56,719	35.15	7	Nan
20	0.0016868	2	8222	69,361	69,361	7	0.75594
21	6.03E-16	2	8373	125.73	108.49	7	0.56281
22	0.00039938	1	8323	87,228	65,659	7	0.50359
23	3.58E-03	3	21145	105.91	55,867	7	0.6626
24	0.0034179	1	21208	53,327	24.25	7	0.28191
25	9.33E-10	3	24871	122.6	93,847	7	0.66951
26	0.00050727	1	24926	69,612	46,275	7	0.80047
27	3.01E-07	2	21071	127.49	89,834	7	0.42587
28	0.00026142	3	9741	90,581	70,893	7	0.66297
29	0.0043172	1	9764	47,942	22,119	7	0.52528
30	0.00061323	4	8707	78,552	57,309	7	0.62127
31	0.00044057	5	8523	85,937	64,364	7	0.62092
32	0.0043557	2	8539	50,226	29.26	7	0.35126
33	0.00029721	2	8791	85,177	60,509	7	0.18401
34	4.64E-06	9	9905	115.56	89,013	7	0.50312
35	9.48E-01	1	21020	94,632	76,316	7	0.49387
36	0.00046045	1	16782	85,087	70,065	7	0.39694
37	1.12E-04	5	8495	111.3	72,495	7	0.50955
38	0.00020613	4	8376	91,926	74,207	7	0.50597
39	0.0076101	1	8395	58,864	30,698	7	
40	2.29E-01	1	8671	97,271	82,391	7	0.35501
41	NaN	0	NaN	NaN	NaN	0	0.69868
42							
43	0.020133	1	5593	41,257	18,627	6	0.25871
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1	0.016457	1	8863	43,091	25,076	6 NaN
2	0.0021378	1	5542	50,358	21,809	6 0.46976
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7	0.030294	1	15787	88,283	41,486	3 0.17475
8	0.021733	2	7087	90,385	63,123	3 0.27006
9						
10	0.035888	1	14615	87,676	60,413	3 0.24707
11	0.0061697	1	13851	100.77	84,926	3 0.8397
12	0.0022498	1	6811	104.88	89,939	3 0.30248
13	0.0065927	1	8043	69,581	69,581	3 0.27591
14						
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16						
17	8.66E-01	1	5983	106.31	85,721	3 0.96199
18	1.87E-01	1	5785	113.86	97,118	3 0.26731
19						
20	0.0017519	1	5830	89,913	69,677	3 0.38826
21	0.0023236	2	5682	85,046	67,418	3 0.50712
22						
23						
24	0.011627	1	1240	42,629	30,571	4 0.58787
25	0.0021129	2	1671	58,274	47,348	4 0.48042
26						
27						
28	0.00011073	1	17054	63,925	39,718	3 0.47343
29	4.11E-04	2	16830	82,942	82,942	3 NaN
30						
31	0.0030549	1	15804	47.05	27,121	3 0.61585
32						
33						
34	1.02E-08	2	18995	75,416	53,565	2 0.1746
35	1.27E-08	1	22592	73,603	49.58	2 0.30054
36	4.02E-02	2	18880	57,629	41,819	2 0.2115
37						
38						
39	0.0025483	1	13644	47,548	16.41	4 0.5026
40	0.0068367	1	20960	42,314	13,982	4 0.32278
41	0.0070169	1	20592	42,095	26,493	4 0.57424
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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		
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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		
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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		
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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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1	NaN	0	948710	618890	329820
2					
3	0.50367	0	255820	208970	46851
4	0.68522	0	120480	85761	34715
5	0.36672	0	195370	160860	34513
6	0.57834	0	215610	156630	58975
7	0.29314	0	165720	146660	19056
8	0.11562	0	61337	54770	6566.9
9	0.78028	0	309790	261000	48791
10	0.67052	0	567380	403460	163920
11	1,057	0	122240	78061	44174
12	0.76923	0	259970	200520	59452
13	10,578	0	255800	185350	70457
14	0.37952	0	90624	68113	22511
15					
16	0.68932	0	1099700	782150	317510
17	0.32049	0	288330	210060	78265
18	0.85198	0	92724	53318	39407
19	0.47149	0	1000500	723220	277270
20	0.38078	0	175680	126400	49279
21	12,283	0	226430	135120	91304
22	0.92394	0	245390	165200	80189
23	0.56326	0	91162	73823	17339
24	0.67576	0	1507900	1142600	365350
25	0.67518	0	313510	226040	87470
26	0.9039	0	216730	144730	72005
27					
28	1,205	0	249100	134730	114360
29	0.71817	0	101870	78338	23527
30					
31	0.29435	0	222970	194040	28930
32	0.44968	0	563920	450140	113770
33	0.29647	0	412880	368280	44599
34	0.38264	0	677870	528810	149060
35	1,103	0	233860	170080	63786
36	0.99748	0	348080	237670	110410
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38	0.71628	0	290030	203570	86459
39	0.96139	0	334750	215590	119160
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41	NaN	0	46427	46427	0
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1	0.42529	0	224170	173460	50716
2	0.49948	0	144360	94052	50313
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7	0.50514	0	566310	504650	61657
8	0.51941	0	3542300	3076600	465680
9	0.8704	0	940910	803650	137260
10					
11					
12					
13	56,773	0	61882	10820	51062
14	23,934	0	141910	51627	90278
15	0.72155	0	59383	43312	16070
16					
17					
18	0.68091	0	81763	56657	25106
19	NaN	0	38095	38095	0
20					
21	10,889	0	88606	56127	32479
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23					
24	0.25037	0	92069	79289	12781
25	NaN	0	2094800	1472500	622330
26	0.36563	0	1630400	1123800	506620
27	0.32395	0	109120	94661	14462
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35	0.8344	0	107580	74859	32725
36					
37					
38	0.83063	0	70607	51988	18619
39	1,167	0	85966	59484	26482
40	0.17394	0	142560	96229	46327
41	0.61909	0	112590	76884	35704
42	0.51276	0	145510	109250	36260
43	0.74773	0	259730	179230	80499
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49	NaN	0	579630	0	579630
50	NaN	0	1413400	5969.9	1407400
51	NaN	0	1577100	2660.6	1574400
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53	16,106	0	1761700	199790	1561900
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56	13,636	0	222500	143610	78888
57	0.99817	0	747460	411250	336210
58	0.71009	0	2616300	1958600	657700
59	12,681	0	157470	77181	80285
60					
61	0.67044	0	588100	436040	152060
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3	11,169	0	64518	45510
4	0.64895	0	231730	175970
5	16,839	0	75448	41623
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9	10,579	0	177870	20506
10	NaN	0	141500 3165.4	138330
11	29,139	0	155890 6584.4	149300
12	12,805	0	245330 6144.9	239180
13	13,609	0	274210	11373
14	NaN	0	557620	262840
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18	0.13002	0	68358	62946 5411.8
19	NaN	0	82502	76424 6077.1
20	0.81089	0	187560	116680
21				70873
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24	0.85524	0	125600	83931
25	10,192	0	79361	56407
26	0.73437	0	148100	96002
27	0.77457	0	121610	85316
28	0.74515	0	86893	58523
29	0.7399	0	145970	95549
30	0.57051	0	169540	106950
31				62587
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35	0.32425	0	98676	80919
36	0.10636	0	177240	151810
37	0.4312	0	397460	267310
38				130150
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41	0.33156	0	2454400	2047800
42	0.62262	0	187470	133590
43				53884
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45	0.4546	0	225420	165180
46	0.8017	0	2313800	1693400
47				620410
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49	13,087	0	521720	258180
50	14,326	0	108750	61541
51	0.77004	0	171740	103250
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55	NaN	0	577970	576350 1613.4
56	NaN	0	653230	653230 0
57	0.1509	0	555960	531660
58	NaN	0	161320	161320 0
59	0.15305	0	144570	125540
60	0.014556	0	428150	424920 3227.6
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3	0.030196	0	1422400	1411100 11342
4	0.029208	0	891850	884880 6971.7
5	0.36952	0	262100	211230 50870
6	0.088132	0	236880	231360 5519.7
7	NaN	0	1002300	1002300 0
8	0.0317	0	2060000	2043500 16450
9	NaN	0	2216100	2162400 53705
10	0.1905	0	91803	87186 4617
11	0.25369	0	133890	120940 12953
12	0.10484	0	239590	221720 17874
13	0.017454	0	1062000	1053200 8798.7
14	0.051932	0	335180	326930 8245.6
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21	NaN	0	92543	77324 15219
22	NaN	0	60116	54471 5645.3
23	0.84281	0	878720	613020 265710
24	13,479	0	642750	380090 262660
25	0.42285	0	49295	41142 8152.9
26	1,242	0	505290	318400 186890
27	12,257	0	533460	308040 225410
28	0.26813	0	56813	52924 3888.9
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