Development and application of accurate mass measurements for large-scale protein interaction and proteome studies

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Abstract

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Traditionally and most commonly, accurate mass measurement is utilized to restrict peptide candidate search space on the precursor level to impart greater specificity in large peptide sequence databases. While use of accurate mass measurement is effective for discovery based proteomics, here we present novel applications of accurate mass measurement in proteomics to make further use of this expensive (monetarily and in time) acquisition attribute. This work began with the coupling and testing of a hybrid dual cell linear ion trap mass spectrometer (Velos) to a 7T Fourier transform ion cyclotron resonance (FTICR) mass spectrometer. This combination provides high speed, efficient ion accumulation with the high resolution and mass accuracy of FTICR. Using this mass spectrometer (Velos-FT) and an LTQ-Orbitrap it was shown theoretically and empirically that high resolution product ion spectra alone can be utilized to detect and quantify peptides. A DIA acquisition and data processing pipeline called, FT-All Reaction Monitoring (FT-ARM), was designed to exploit this observation. Direct similarities of FT-ARM to targeted proteomics data allow for discovery and targeted proteomics to be conducted in a single pass with little to no assay development. A search algorithm developed to score and assess data acquired using this strategy enabled quantitation into the attomole range and enabled identification within a complex background matrix. Specificity of the peptide assignment is attributed to the requirement of the simultaneous observation of a minimum number of product ions from the target peptide at a required mass measurement accuracy.

Real-time informatics analysis during mass spectrometry acquisition can serve to simplify post-acquisition analysis and more importantly, focus measurements on ions more likely to yield the desired information. Real-time informatics applied to engineered, cleavable cross-linkers allows known mass relationships to be used to direct subsequent experiments. Peptides released from cross-linked complexes can be directly targeted for MS^3 acquisition to obtain sequence information within a single LC/MS/MS acquisition. This new mass spectrometry method called Real-time Analysis for Cross-linked peptide Technology (ReACT) has been developed to enable assignment of cross-linked peptides "on-the-fly". Using ReACT, 708 unique cross-linked (<5% FDR) peptide pairs were identified from cross-linked *E. coli* cells. These data allow assembly of the first protein interaction network that also contains topological features of every interaction, as it existed in cells during cross-linker application.

TABLE OF CONTENTS

List of Figures..ii

List of Tables..iii

Acknowledgements...iv

Dedication..v

Introduction..1

Chapter I: The Velos-FT..12

Chapter II: Accurate Fragment Mass Analysis........................34

Chapter III: Real-time Analysis for Cross-linked peptides Technology.......64

Chapter IV: Directed Interrogation from Feature Ratios.............93

Conclusions...105

Appendix A: Supporting information for the Velos-FT...............108

Appendix B: Supporting information for FT-ARM.....................115

Appendix C: Supporting information for ReACT......................154

LIST OF FIGURES

Figure 1.1 Velos-FT conceptual diagram....................................19
Figure 1.2 Protein and peptide identification comparison..................20
Figure 1.3 Ion injection times...21
Figure 1.4 Tandem MS sampling dynamic range................................22
Figure 1.5 Top-down analysis of myoglobin..................................23
Figure 1.6 Dual cell fragmentation outline.................................25
Figure 1.7 Angiotensin tandem MS (CID vs. DCF).............................27
Figure 1.8 Q-value vs. fragmentation efficiency............................28
Figure 1.9 Identifications from yeast lysate digest........................29
Figure 2.1 FT-ARM conceptual workflow......................................47
Figure 2.2 FT-ARM experiment with peptide identification..................48
Figure 2.3 FT-ARM estimated false discovery................................51
Figure 2.4 FT-ARM performance compared to serial DDA.......................52
Figure 2.5 Identification of chimeric spectra and ID's per amu.............54
Figure 2.6 Quantification using FT-ARM.....................................56
Figure 3.1 ReACT conceptual and logical diagram............................74
Figure 3.2 Example of ReACT in labeled *E. coli* cells.......................76
Figure 3.3 Multiplexing cross-linkers with ReACT...........................78
Figure 3.4 Protein interaction network discovered in *E. coli*...............81
Figure 3.5 Inter-molecular protein interactions from *E. coli* ribosome......84
Figure 4.1 DIFR conceptual and logical diagram.............................96
Figure 4.2 Heavy isotope incorporation time-course monitored with DIFR....100
Figure 4.3 DIFR performance evaluation compared to conventional DDA.......101
Appendix Figure A.1 Velos-FT performance without AGC......................108
Appendix Figure A.2 LTQ-FT performance without AGC........................109
Appendix Figure A.3 Velos-FT performance with AGC.........................110
Appendix Figure A.4 LTQ-FT performance with AGC...........................111

Appendix Figure A.5 Spectral comparison of fragmentation using DCF........112

Appendix Figure B.1 The effect of MMA on FT-ARM search/scoring...........116

Appendix Figure B.2 The effect of match count on FT-ARM search/scoring....117

Appendix Figure B.3 Velos-FT performance with AGC.........................149

Appendix Figure B.4 LTQ-FT performance with AGC...........................150

Appendix Figure B.5 Spectral comparison of fragmentation using DCF........151

Appendix Figure B.6 Normalized *E. coli* quantification by FT-ARM...........152

Appendix Figure C.1 Various PIR cross-linkers used to demonstrate ReACT...156

Appendix Figure C.2 Targeting $[M+2H]^{2+}$ for cross-linked peptides 157

Appendix Figure C.3 Mass measurement accuracy using ReACT.................158

Appendix Figure C.4 ReACT reproducibility.................................159

Appendix Figure C.5 Inter and intra-molecular cross-links tally...........160

LIST OF TABLES

Appendix Table B.1 FT-ARM peptide identifications.....................118

Appendix Table B.2 Shotgun proteomics peptide identifications.........134

Appendix Table C.1 Purified protein cross-linked peptides.............161

Appendix Table C.2 Multiple cross-linkers applied to Ribonuclease A...162

Appendix Table C.3 High confidence *E. coli* cross-linked sites.........163

Appendix Table C.4 Low confidence *E. coli* cross-linked sites..........181

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DEDICATION

I dedicate this work to my father, Randal W. Weisbrod. At an early age, he promoted creative problem solving through engineering and science despite never having received formal education in either.

INTRODUCTION

The field of mass spectrometry has evolved to rely upon instrumentation capable of extraordinary resolution and mass measurement accuracy (MMA). MMA is effectively how well one is able to assign a measured m/z species or ion. MMA is defined by the following equation:

$$\mathrm{MMA} = \frac{\Delta m}{m} \qquad \text{(Eqn. 1)}$$

Where Δm refers to the difference between the theoretical mass and the measured mass. MMA is a unit less measure, although often conveniently referred to in parts-per-million (ppm) relative to Eqn. 1. For example, a 1000.000 *m/z* species with mass measurement accuracy of 1 ppm indicates a Δm value of 0.001 *m/z.* The relationship between MMA and measured mass is non-linear. This is concordant with the notion that resolution and mass accuracy are not uniformly measured across the m/z range within a single mass spectrum with Fourier transform based instruments(1, 2).

Mass spectrometry has become the primary analytical method for modern proteomics research. MMA has found its importance in proteomics primarily in the specificity imparted when attempting to identify proteins and peptides from extremely complex samples. Samples analyzed by modern proteomics approaches are complex due to the vast number of tryptic peptides generated from even simple organisms and the broad dynamic range over which proteins are expressed in cells and tissues(3). This complexity places high demand on the information contained within a mass spectrometry experiment aimed at peptide or protein identification/quantification(4). By far, the most common approach to peptide identification (and by inference protein identification) is shotgun proteomics(5).

Shotgun proteomics, also known as bottom-up proteomics, involves extraction and tryptic digestion of protein from a sample. Tryptic peptides are separated in-line prior to infusion into mass spectrometer via liquid chromatography (LC) electrospray ionization (ESI) interface(6). LC separation parameters and underlying sample complexity determine the flux of peptides observed by the mass spectrometer. The mass spectrometer is programmed to perform cycles of acquisition composed of a survey acquisition followed by a series of tandem MS acquisitions. The survey acquisition in this paradigm, usually acquired at high resolution, is used to determine the spectrum of intact m/z values for peptides presently eluting from the LC. Sequentially, the mass spectrometer isolates each individual peptide and performs MS/MS (or tandem MS) to obtain a spectrum containing fragment ions which are used to identify the peptide sequence. Because this process occurs sequentially or serially, only a single peptide is intended for tandem MS interrogation per acquisition. The nomenclature used to describe this intensity driven sampling process is data dependent acquisition (DDA). Although multiplexing is conceivable(7), at this step it is not widely utilized in contemporary proteomics research due to instrument hardware, downstream informatics, and other concerns. These data, the precursor m/z determined from the survey acquisition and the tandem MS spectrum obtained from isolation and fragmentation of the peptide, are supplied to database search algorithms(8-10) to provide peptide and protein identifications.

Peptide identification is carried out using database search algorithms such as Sequest(8, 9), Mascot(10), or others(11, 12). These algorithms differ in their underlying treatment of the data, but share two basic tenets. The first is that the precursor mass measurement, taken from the survey acquisition, is utilized to narrow the list of candidate peptides from a tryptic database. Typically, this is done with underlying knowledge of the MMA capable for a given instrument type. For instance, if an observed peptide had a precursor m/z of 1000.000 measured with 0 ppm average mass error with a standard deviation in mass error of 2 ppm, this peptide could be searched with a precursor m/z of 1000.000 ± 6 ppm. The mass tolerance for the search is designed to match the 99% confidence interval (CI) of the mass error distribution capable of the instrument. Any peptide in the tryptic database within the mass tolerance will now be considered further as a peptide sequence match candidate. Largely, MMA has been utilized to impart specificity to the shotgun proteomics data at the level of the search by limiting the number of peptide candidates considered for the second major tenet of the search, a correlation of theoretical and target tandem MS spectra. If the mass tolerance applied to the search is much greater than the achieved MMA(13), the general effect is that 'search space' for the target spectrum of interest is inflated. Inflated peptide candidate search space can result in lower peptide sequence assignment probability/score. If the mass tolerance applied to the search is much less than the actual MMA, the 'correct peptide' could be excluded from the search.

Correlation analysis in tandem MS spectra may take many forms, but most algorithms make use of a dot-product or cross-correlation derived calculation(8, 9, 11, 12, 14). Any such calculation is aimed at obtaining a quantity(s) which provide a measure of spectral similarity between the target and theoretical spectra (or any binary comparison between two vectors). This similarity "score" forms the basis for downstream transformations into p-values (or e-values)(15, 16). In addition, this score differentiates peptide candidates from one another. This score is typically what is used in estimation of sequence identification false discovery rate (FDR)(17, 18). Many post-scoring adjustments and correction factors have been developed to optimize the number of identifications which meet a given FDR threshold. However, the underlying correlation between empirically observed fragment ion peaks and theoretically determined fragment ion peaks remains at the foundation of peptide sequence identifications.

The bottom-up identification schema described above illustrates the most common role of MMA. It serves as a "filter" for peptide sequence candidates. While this has proven an effective and useful strategy in bottom-up proteomics, it also remains the most common application for the accurate mass measurement capabilities of modern high resolution mass spectrometers. However, there are seminal examples where others have leveraged mass measurement accuracy in novel approaches to further proteomics(19-22). Data independent acquisition, accurate mass and time approaches, and some emerging real-time acquisition methodologies rely heavily on mass accuracy and resolution in order to advance proteomics.

Data independent acquisition (DIA) is a newly emerging data acquisition strategy which has the promise of parallelizing mass spectrometry measurements and alleviating tandem MS sampling constraints observed within DDA shotgun proteomics. DIA as a paradigm in mass spectrometry can be found in proteomics literature at least as early as 2003(7, 23). Many different approaches have been suggested and explored since(20, 24-28) but any successful DIA strategy must have some mechanism for dealing with the inherently more complex tandem MS spectra resultant from simultaneous fragmentation of many peptides. Tandem MS spectra using DIA by design are chimeric superposition of many peptides. By contrast, using DDA it is assumed that each tandem MS contains fragment ions from a single peptide. This assumption is central to interpretation of the data following acquisition as described above. The informatics challenge associated with DIA data has been dealt with in one of two primary ways. The first involves clustering of precursor ions and fragment ions usually from chromatographic co-elution. The second more recently explored approach includes a hypothesis-driven identification schema.

Clustering or grouping product ions with their respective precursor is already assumed to occur during typical shotgun proteomics based on the physical constraints of the experiment. These constraints include relatively narrow precursor isolation (typically >3-5 Da) and chromatographic separation with high peak capacity. These two things coupled together serve to limit the occurrence of two or more peptides co-eluting and fragmenting to produce chimeric or mixed fragmentation patterns. DIA methods have been crafted with the acknowledgement that chimeric spectra exist and should be exploited to identify all peptides which comprise the chimera. In fact, the DIA paradigm provides the greatest promise of performance enhancement when multiplexing of peptide fragmentation is pushed to its utmost limit. To this end, clustering has been a tool which many DIA methods have exploited(20, 23-26, 29). Clustering in these methods is generally carried out through evaluation of co-elution between precursors and fragment ions. Temporal co-varying signal can be assessed through the use of Pierson's R and other correlations between expected Lorentzian/Gaussian peak profiles associated with liquid chromatography of peptides. Good agreement is expected between elution of precursor and product ions and serves as the basis utilized to direct clustering of the data intended for conventional proteomics pipelines (SEQUEST, Mascot, etc.). After clustering, the data can then be organized in the format of precursor m/z and corresponding product ions. In principal, this technique works and has been demonstrated. However, it's performance has never been capable of rivaling typical DDA proteomics workflows. This is in part due to the inherent complexity of the proteomics samples based on dynamic range and sheer number of co-eluting species. Mis-assignment of fragment ions during clustering serves to diminish the probability of obtaining a meaningful peptide sequence identity for the data.

The most recently developed methods to exploit DIA represent a paradigm shift away from forcibly packaging the data to fit existing search pipelines. These methods, aptly referred to by MacCoss et al. as hypothesis-driven proteomics, hold central the hypothesis that we expect to observe peptides from the proteome which we are analyzing. Each peptide we expect to observe represents a new hypothesis. Each hypothesized peptide is used to comb or mine the data for signal which constructively interferes with the expected theoretical spectrum for each given peptide in the proteome. In essence, DDA search pipelines ask, “Given the fragmentation pattern/data are there peptides which match?”, DIA searched within a hypothesis-driven paradigm asks, “Given the peptides expected from the proteome is there evidence that this peptide is in the sample?”. This may seem like a mere subtlety of wording, however, when translated to the logic required to search these data under each paradigm dramatically greater performance is observed with the latter(hypothesis-driven paradigm). Presently, only a handful of published accounts have demonstrated this approach(28, 30). Both of these methods require relatively high MMA in order to overcome the loss of specificity which accompanies co-isolation of multiple peptides in a single tandem MS spectrum. FT all reaction monitoring (FT-ARM) is one such method and is described in greater detail within Chapter II.

High mass measurement accuracy has allowed improved quantification via label-free, stable isotope labeling, and validation based experiments. Label-free MS^1 based quantification has become more reliable and readily practiced as a direct alternative to spectral counting based quantification approaches. This information is already a part of typical DDA workflows, however, reproducible chromatography, high MMA, and data analysis software are required to perform this approach. Recently, many software options have become available for this process both commercial and freely available (31, 32). While it remains challenging to perform these experiments on the bench side, the array of software with support for high resolution and MMA data has eliminated this as a barrier. It has been suggested that label-free quantification methods suffer from poor reproducibility, however, in a careful study presented at the ABRF a report showed that in the right hands label-free MS^1 quantification can eclipse the reproducibility of stable isotope labeled techniques. A related method which relies heavily on MMA, called Accurate mass and retention time tags (AMT), pioneered by the Smith et al.(21), has allowed for rapid identification and quantification of species previously identified by shotgun proteomics approaches. In the AMT approach, accurately defined peptide masses coupled with highly reproducible liquid chromatographic separations allows for unambiguous assignment of peptide sequences and presents the opportunity for quantification of all peptides within the AMT database.

With the availability of cheap, high-performance computers, incorporation of data-acquisition systems associated with mass spectrometry instruments has enabled more advanced data processing and informatics on-the-fly. Incorporation of simple logic, heuristics, or “smarter” data acquisition promotes the idea of the most efficient use of mass spectrometry resources in real-time, while data is being acquired. This promotes the instrument to have some degree of adaptability on a sample-to-sample, experiment-to-experiment basis. While the area of real-time approaches applied to mass spectrometry proteomics remains in its infancy, a few applications have been demonstrated. Coon et al. and Mann et al. have each successfully been able to show peptide identification in real-time. This allows them to predict what peptides may elute next, which peptides to focus on for quantification, perform targeted tandem MS re-sampling, etc. without the need for multiple LC-MS experiments. In an earlier report, Coon et al. demonstrated a simple decision tree based approach for phosphopeptide fragmentation. Here it was shown that based on a few simple peptide characteristics (charge, m/z, etc.) the analyte was directed for tandem ms fragmentation by either collision induced dissociation (CID) or electron transfer dissociation (ETD), based on empirical data to support the most favorable technique on a ion per ion basis. Therefore, at the least real-time efforts conserve sample and instrument time; but at the most, provide new information unobtainable within a single LC-MS experiment. In Chapter III and IV I investigate the use of real-time informatics to identify mass spectral features based on high MMA mass relationships.

Here novel roles for MMA in proteomics have been explored within the sub-context of instrumentation development, DIA, and real-time informatics strategies. This research was, in large part, conducted on a novel dual RF ion trap-7T Fourier transform ion cyclotron resonance mass spectrometer (FTICR-MS), which has been dubbed the Velos-FT. In Chapter I, I describe the construction and performance evaluation of this system. During normal operation, the magnetic field strength (7T) of this system permits average MMA on the sub-ppm level (~200-300 ppb) when applied to complex samples using external calibration. The MMA achievable with this system enabled testing the hypothesis that DIA spectra acquired with sufficiently high resolution and MMA enables unambiguous peptide assignment through a novel peptide centric search strategy. This process called FT all reaction monitoring (FT-ARM)is described in detail within Chapter II. The hybrid dual RF ion-trap FTICR-MS configuration of this system enables higher order mass spectrometry experiments ($\geq MS^2$). MMA is utilized as a primary discriminate in real-time informatics algorithms aimed at focusing instrument resources on performing higher order ms analysis on analytes of greatest importance. In Chapter III, a real-time algorithm for identification of cross-linked peptides can be achieved by identifying the mass relationship engineered within the collision induced dissociation (CID) cleavable cross-linker. Finally, Chapter IV is devoted to mass relationships among stable isotope labeled peptide pairs enable real-time filtering of all ions to direct MS/MS acquisitions to pairs with altered relative ratios. Assigning stable isotope pairs in real-time allows one to target only significantly altered peptide pairs for tandem MS acquisition, thus, targeting ions of greater interest to the use

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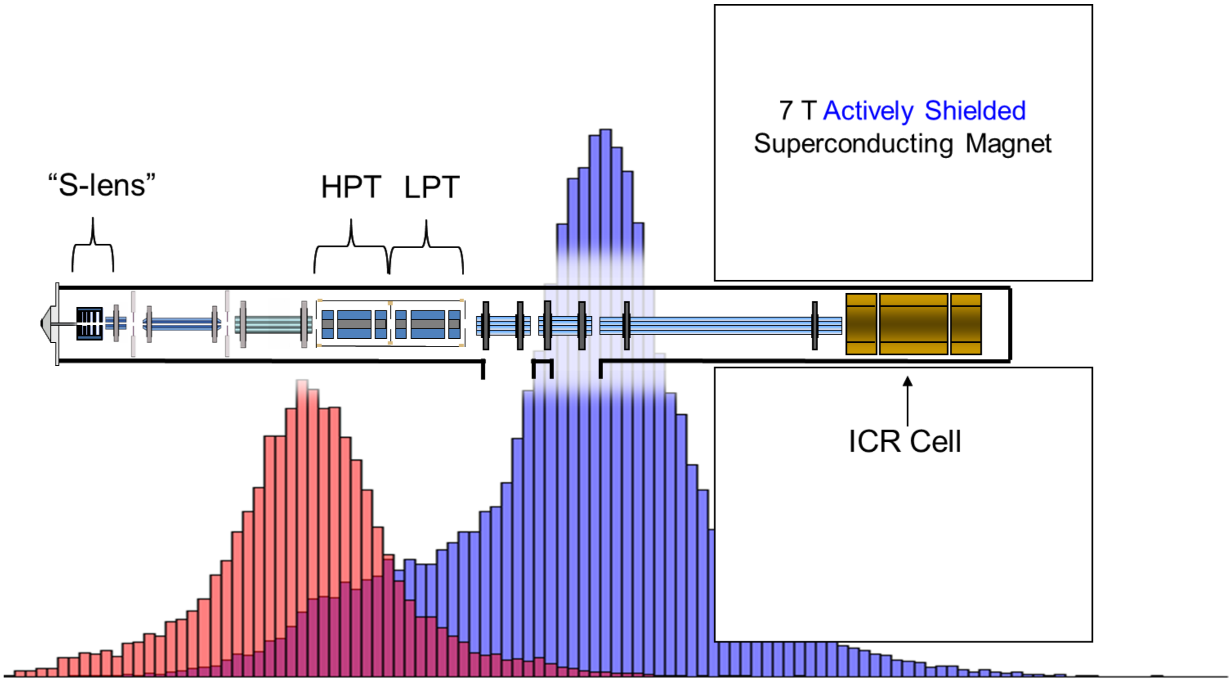
"S-lens"
HPT
LPT
7 T Actively Shielded
Superconducting Magnet
ICR Cell

Introduction:

The era of modern mass spectrometry has largely been dominated by advancements in instrumentation (1-6), sample handling (7-10), and database searching technologies (11-13). Innovations made in these areas have made possible incredible improvement in the analysis of complex samples. The drive to decipher information within the proteome (8, 10) has been a major force influencing technological development of mass spectrometry methods for biological applications. The current paradigm in proteome research involves shotgun (9) or bottom-up experiments in which protein samples (pure protein, cell lysates, tissue lysates, etc.) are enzymatically digested into peptide mixtures. The resulting peptide mixtures can have wide dynamic range in peptide concentration (14) and heterogeneity (15). In fact, the overall complexity of these peptide mixtures exceeds the sensitivity and efficiency in detection of all available modern instruments (4). The primary impediments to routine whole organism proteome measurements by mass spectrometry are acquisition speed, sensitivity, and dynamic range. Further development of instrumentation technology is required for routine high coverage, in-depth proteome analyses.

Mass spectrometry instrumentation (16) has evolved dramatically over the last twenty years. A current configuration for proteomics research today is a hybrid type and consists of two coupled mass analyzers, each capable of independent data acquisition. A conventional example combines a linear ion trap (LTQ) with a Fourier transform mass spectrometer (FTMS). In this case, the FTMS is either an ion cyclotron resonance mass spectrometer (LTQ-FT) or Orbitrap mass spectrometer. In general, hybrid mass analyzers benefit proteomics research by incorporating desired characteristics from each analyzer to yield unique capabilities.

Here we present results of our efforts to modify the LTQ-FT hybrid by combining a dual cell linear RF ion trap and FT-ICR mass spectrometer, referred to as a Velos-FT mass spectrometer. This instrument has many unique attributes such as the ability to rapidly accumulate ions, MS^n analysis at a higher repetition rate, and the ability to perform beam-type CID fragmentation between the dual cell linear RF ion traps. The Velos-FT has improved ability to accumulate ions, with observed ion accumulation time reduction of an order of magnitude or more (~3 ms vs. 40 ms) compared with conventional LTQ-FT instrumentation. When performing MS^n, selected ion monitoring (SIM), or data independent acquisition (DIA), this speed improvement can be very significant. Related to this, we show that with the Velos-FT, the number of peptide identifications per run is increased by 100% when compared with the LTQ-FT Ultra (50% on the protein group level). Top down proteomics (17) requires isolation and fragmentation prior to analysis. For top-down experiments, in many cases it is difficult to accumulate enough ions to achieve coherent cyclotron motion for the duration required to resolve high mass ions (18, 19). Here we show that the ability to accumulate large biomolecules with the custom Velos-FT is greatly improved over those with the LTQ-FT Ultra. The dual cell linear RF ion trap instrument configuration enables operation of a unique fragmentation method, which we call Dual Cell Fragmentation (DCF), performed by transferring ions between the two cells through the background gas using elevated DC potentials to accelerate and induce dissociation. This technique generates fragmentation patterns which share some similarities with spectra acquired on QTOF and triple quadrupole instruments. The so called “1/3 rule” which limits the lower mass limit for product ions generated by resonance excitation in RF based ion traps was shown to be reduced with DCF. The overall peptide identification rate was comparable to that obtained with resonance excitation CID, and many peptides were identified in both methods demonstrating the utility of DCF for peptide identification with spectra that also contain lower m/z ions. Furthermore, a distinct subset of peptides was identified with each method that may be a result of repeated analyses or subtle differences between the fragments observed in DCF and CID. Finally, with the cost of high performance instrumentation currently inflating much faster than available funds from most granting agencies that support mass spectrometry, the upgrade design of the Velos-FT presented here may present a useful option for other labs to consider.

Experimental:

Modification of the LTQ-FT Ultra

An LTQ-FT Ultra mass spectrometer (Thermo Fisher Scientific, Bremen, Germany) was modified to include an LTQ Velos mass spectrometer. The linear ion trap (LTQ) was removed and replaced with a dual cell linear radio frequency ion trap mass spectrometer(5) (Velos, Thermo Fisher Scientific, San Jose, CA). The two linear radio frequency ion traps will be referred to throughout the manuscript as the high pressure cell (HPC) and low pressure cell (LPC). No ion optic modifications were necessary for the coupling process as the flange designed to mate the LTQ and Velos to the Orbitrap or the FT mass spectrometer are identical. However, ion trap control software modifications were required for operation of the custom FT-ICR. Software in control of the LPC was modified so that it acts as a simple RF multipole during the transmission of ions from the HPC to the ICR cell for FT-MS acquisition mode. The standard FT ion transmission calibration script was modified to include the center lens, front, center and back sections of the LPC, along with the back lens of the dual cell trap assembly. Optimized DC voltages for each of these elements are applied during the transmission event of an FTMS acquisition. The ion transfer efficiency between the linear ion trap and ICR cell was determined to be similar for both the LTQ-FT Ultra and custom FT-ICR MS based upon unscaled total ion current measurements conducted using the same ion target value for both instruments (see Appendix A for details).

Ion-Trap Control Language (ITCL) DCF Program

Direct modification of factory installed ITCL code was performed in-house for the implementation of DCF. These modifications operate within the framework of the factory installed code for the LTQ-FT Ultra mass spectrometer. In short, CID collision energy setting of 1.0 in the user interface was used to enable DCF. This allows for the execution of DCF both directly from Tune as well as during method based operation. When DCF is enabled, ion accumulation and isolation proceed in the HPC without alteration of factory installed ITCL code. However, no resonance excitation is applied before initial transfer to the LPC. Ions are then transferred immediately back to the HPC. The HPC center section potential is adjusted to induce fragmentation through application of a large negative DC bias. This DC potential bias is determined as a function of precursor ion m/z, in a similar fashion as with beam-type CID collision cell experiments(20). This equation relating m/z to DC potential bias of the center section of the HPC was determined empirically to have a slope of -0.141 (V/Da) and an intercept of -20.00 (V) based upon collision energy optimization using a bovine serum albumin (BSA) digest. A q-value of 0.205 was used for fragmentation of Angiotensin I, which permitted detection of low mass fragment ions down to 25% of the precursor m/z.

Yeast Sample

Saccharomyces cerevisiae strain S288C (Baker's yeast) was grown in glucose rich media to mid-log phase. Cells were collected by centrifugation and resuspended in 100 mM ammonium bicarbonate buffer at an optical density (OD) of 0.90. The cells were lysed using a bead-beater(21). The lysate was centrifuged at 1000g for five minutes to remove debris (cell wall particles and unbroken cells). The lysate was centrifuged again for 30 minutes at 15,000g to separate the soluble and membrane protein fractions. The soluble fraction was assayed for protein concentration using Coomassie Plus Protein assay (Pierce, Rockford, IL) and found to be ~5.0 mg/mL. The insoluble fraction was not utilized in this experiment. The sample was reduced with 15 mM dithiothreitol (Sigma-Aldrich, St. Louis, MO) at room temperature for the duration of 30 minutes. The cysteine residues were blocked using iodoacetamide (Sigma-Aldrich, St. Louis, MO) 15 mM at room temperature for the duration of 30 minutes. The soluble fraction of the yeast lysate was digested using 1:250 ratio of sequencing grade trypsin (Promega, Madison, WI). The reaction was allowed to proceed for 2 hours at 37°C while under constant agitation via orbital shaking. The digest was quenched and frozen at -20°C. This sample was desalted using C18 Sepak (Waters Corporation, Milford, MA). The desalted peptides were lyophilized and redissolved in mobile phase A (99.9% ultrapure water, 0.1% formic acid). Injections of 1 μg of total protein were loaded for LC-MS/MS analysis.

Liquid Chromatography

Liquid chromatography was performed using a Waters NanoAcquity UPLC (Waters Corporation, Milford, MA). Pulled tip columns were constructed in-house using a laser-pulling device (Sutter Instrument Company, Novato, CA). A column of 30 cm in length was constructed with 75 um ID x 360 um OD fused silica capillary. The packing material used for peptide separation was 100 Å C18 magic beads (Microm Bioresources Inc., Auburn, CA). A fused silica trap column was constructed from 100 um ID x 360 um OD fused silica capillary. The frit was made on one end of the trap with Kasil (PQ Corporation, Valley Forge, PA) to contain C18 packing material. The packing material used in the trap was 200 Å C18 magic beads (Microm Bioresources Inc., Auburn, CA). A binary solvent gradient was used for peptide separation. Mobile phase A consisted of 99.9% water with 0.1% formic acid. Mobile phase B consisted of 95% acetonitrile with 0.1% formic acid. The gradient was setup as follows 5%-35% B in 30 minutes. Column washing was done with 80% B for 20 minutes, followed by re-equilibration for 30 minutes using 5% B.

Mass Spectrometry

All data were acquired on the LTQ-FT Ultra or the custom FT-ICR mass spectrometers (Thermo Fisher Scientific, San Jose, CA.). Data dependent acquisition (DDA) experiments for identification comparison were conducted using a "top 5" approach in which a high resolution FTMS acquisition (50,000 resolution at 400 *m/z*) was followed by 5 ion trap MS/MS acquisitions for the LTQ-FT Ultra or a "top 10" approach was used in the case of the custom FT-ICR MS with the same resolution settings. The AGC target value for the precursor scan was set to $1x10^6$ counts and for ion trap MS/MS scans to $1x10^4$ counts. All MS/MS targets were chosen from the high resolution FTMS scan. Charge state screening was applied with consideration of only 2+ and 3+ isotope distributions. Dynamic exclusion was used with the following parameters: one repeat count, 15 second repeat duration, 500 exclusion list size, and 90 second exclusion duration. Preview mode was enabled for all LC-MS/MS experiments which allowed both the ICR cell and the LTQ to acquire concomitantly.

Top down experiments

Myoglobin was used as received from Sigma-Aldrich (St. Louis, MO) and was dissolved in an electrospray ionization solution consists of HPLC grade methanol (Sigma-Aldrich, St. Louis, MO), 18 M Ohm water, and glacial acetic acid (Sigma-Aldrich, St. Louis, MO) in the ratio of 49:49:2. This solution was directly infused into the mass spectrometer at a flow rate of 0.500 uL/min. The myoglobin concentration of the infusion solution was 500 nM.

Data Handling and Searching

Data was extracted from the raw files and converted to mzXML format using ReAdW(ver 4.2.1). The mzXML2search (ver 4.1) was used to convert the data to Mascot generic format. All database searches were performed using Mascot Server (ver 2.2). The FASTA sequence database was downloaded from NCBI (*Saccharomyces cerevisiae*). Precursor mass tolerance of 25 ppm and fragment mass tolerance of 0.6 Da were used for data-dependent experiments. Protein groups were assigned within the latest version of the Mascot(11) or Sequest(12, 13) software and represent the simplest explanation of the proteins given the identified the peptide sequences. Reverse sequence searching was used as a strategy to estimate false discovery rate (FDR). Ion times and raw precursor ion intensities were extracted directly from the raw file headers utilizing the Thermo SDK. Maximum ion intensities for identified peptides were calculated from monoisotope peaks determined using Hardklör(22).

Results and Discussion:

The use of dual cell linear ion trap instrument configuration has gained popularity recently. The first of these instruments released was simply a stand-alone, bench-top dual cell linear ion trap(5) (Velos) and is currently available coupled to the Orbitrap mass spectrometer (4). This manuscript is the first published report of a dual cell linear ion trap-FT-ICR hybrid mass spectrometer and represents a useful reconfiguration option for existing LTQ-FT instruments. Other laboratories have subsequently adopted this technology(23). A conceptual diagram of the dual cell linear ion trap FT-ICR mass spectrometer reported in this manuscript is shown in Figure 1.1. The unique features of this instrument which provide significant performance enhancement are contained within the dual cell linear ion trap mass spectrometer. This instrument has been described in detail by Second(5) et al. In brief, the S-lens or stacked ring ion guide and the high pressure cell contribute to

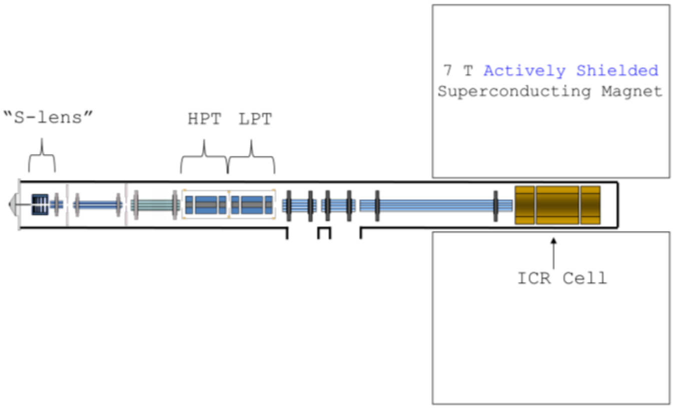

Figure 1.1: A conceptual diagram of the Velos-FT. This hybrid instrument consists of a dual linear ion trap "front end" coupled to a 7 Tesla FT-ICR high resolution mass spectrometer. Notable aspects include the stacked ring ion guide in the source, as well as the tandem linear ion trap arrangement.

increased ionization source transmission efficiency and increased trapping efficiency respectively. Operation of the LPC for mass scanning allows for faster MS/MS acquisition while the HPC allows for efficient accumulation and fragmentation of ions. The increased accumulation efficiency and faster scan speeds are manifest in faster MS/MS repetition rates. For example the predecessor to this instrument, the LTQ, could perform MS/MS at 4 Hz. With the dual cell linear RF ion trap front end, an MS/MS acquisition rate of ~10 Hz is achievable.

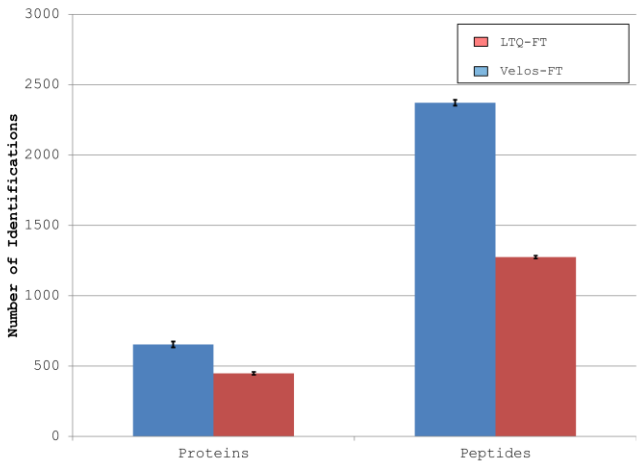

Figure 1.2: Comparison of the improvement in number of identifications achieved with the Velos-FT over the LTQ-FT Ultra. Both protein group and peptide identifications were made from three replicate analyses of yeast lysate digest. Mascot was used for protein group and peptide identification. The error bars represent one standard deviation.

Faster MS/MS acquisition rate should lead to more peptides being identified from complex samples. Yeast lysate digest(14, 24) provides a useful benchmark sample for mass spectrometry based proteomics because of its complexity and wide dynamic range of protein concentration. In this comparison, the custom FT-ICR MS and the LTQ-FT Ultra were set to operate in data-dependent acquisition mode. The top ten most abundant precursors were selected for MS/MS analysis in the Velos-FT, whereas, the top five most abundant precursors were selected in the LTQ-FT Ultra. The number of MS/MS events in each DDA experiment was selected based on the number of events which could be executed during the simultaneous high resolution precursor acquisition. This number is approximately two-fold larger for the Velos-FT due to the combination of shorter injection times and the higher linear trap scan rates. The results of three technical replicates, all searched with Mascot, are presented in Figure 1.2. The

Velos-FT identified an average of 653 +- 21 protein groups, which is a 46% increase over the 448 +- 10 protein groups identified with the LTQ FT Ultra. For unique peptides, 100% more identifications are observed for the Velos-FT. This can be rationalized by considering that the additional unique peptides are attributed to proteins which have already been identified, thus providing on average more complete sequence coverage. Similar gains were observed by Second et al.(5) and Olsen et al.(4) in initial experiments describing the Velos and the Velos-Orbitrap instruments.

The increase in number of identifications has been attributed partially to the increased ion transmission efficiency of the source of this instrument. The electrospray source of this instrument has been shown by others to be 5-10 times more efficient for ion transmission and accumulation(4, 5). This is attributed to the radio frequency stacked ring ion guide and the high pressure cell. For the yeast lysate, we observe average ion injection times of ~3 ms for the high resolution precursor mass measurement Figure 1.3. This is an order of magnitude lower than that of the LTQ-FT Ultra (~40 ms) for the same sample. Others have observed similar improvements for injection times when replacing the standard LTQ source optics with an ion funnel(25). Shorter ion accumulation times and faster analytical scan rates enable sampling depths not obtainable with the previous generation of instruments.

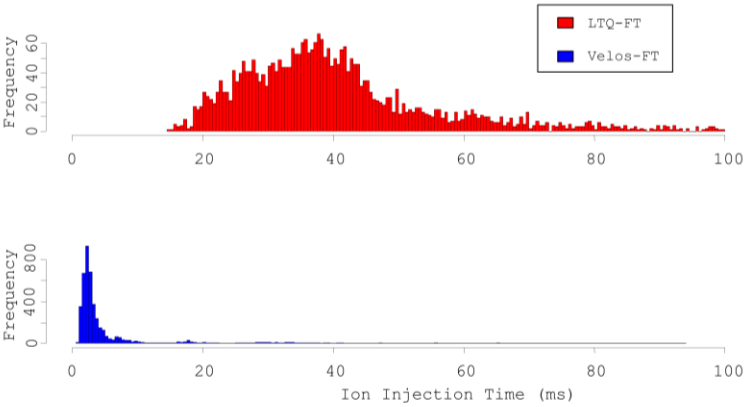

Figure 1.3: Histogram of ion injection times associated with the FT-MS precursor scans of a yeast lysate tryptic digest analysis. Average ion injection time for the LTQ-FT Ultra is ~40 ms whereas with the Velos-FT the average resides at <3 ms.

To allow demonstration of improved ion injection times possible with the custom FT-ICR MS, the maximum intensities for every precursor chosen for data-dependent MS/MS from the two instruments were extracted from data files and compared (Figure 1.4). Differences in the intensity distributions are due primarily to a 10-fold decrease in ion accumulation time for the Velos-FT, but also are influenced by other factors, such as ion transfer efficiency from the linear trap to ICR cell along with excitation and detection efficiencies. With automated gain control enabled, signal intensity is calculated by scaling inversely with the accumulation time in seconds (Figure 1.4A). To account for this difference, we normalized the data to the average peptide intensity (Figure 1.4B). Figure 1.4B illustrate the broader MS/MS sampling range, particularly the low intensity precursor tail, and increased overall sampling frequency achieved with the Velos-FT. These data indicate that when using the Velos-FT, an order of magnitude greater depth in sampling can be achieved over its predecessor. Although the Velos-FT is able to interrogate peptide species over a broader intensity range, this may not correspond with actual cellular protein and peptide abundance. In an effort to understand if peptide and protein identifications using the Velos-FT were extended to lower abundance species, proteins were mapped back to the yeast

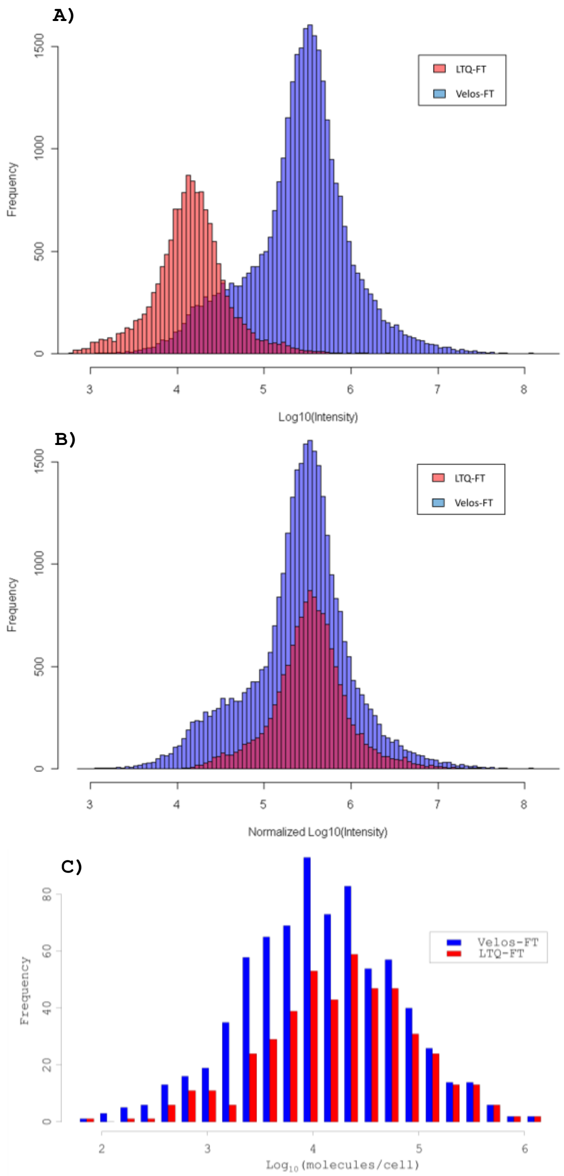

Figure 1.4: A) Comparison of distribution of the ion intensity of precursors selected for data-dependent MS/MS sequencing. B) Normalized comparison of ion intensity of precursors selected for data-dependent MS/MS sequencing. C) (Need explanation).

quantitative western blotting results of Ghaemmaghami *et al* .(Figure 1.4C). This analysis revealed an enhancement in the identification of lower abundance species using the Velos-FT relative to the LTQ-FT Ultra.

Top-down proteomics, the study of intact proteins, has been pursued by many as a method for a more complete protein characterization(26-28). This technique potentially allows one to not only identify proteins, but to also interrogate which isoforms, post-translational modifications, and other variants are present in the sample. Although top-down proteomics has great potential, intact protein analysis by mass spectrometry presents a unique set of challenges. One such challenge (29, 30) is increased susceptibility to systematic signal distribution. This is in part due to properties of large biomolecules, such as proteins, occupying a large number of charge states and isotopic forms. This charge state distribution effectively divides the analyte amongst the observed mass spectral peaks. Therefore, it becomes more likely for any single peak to

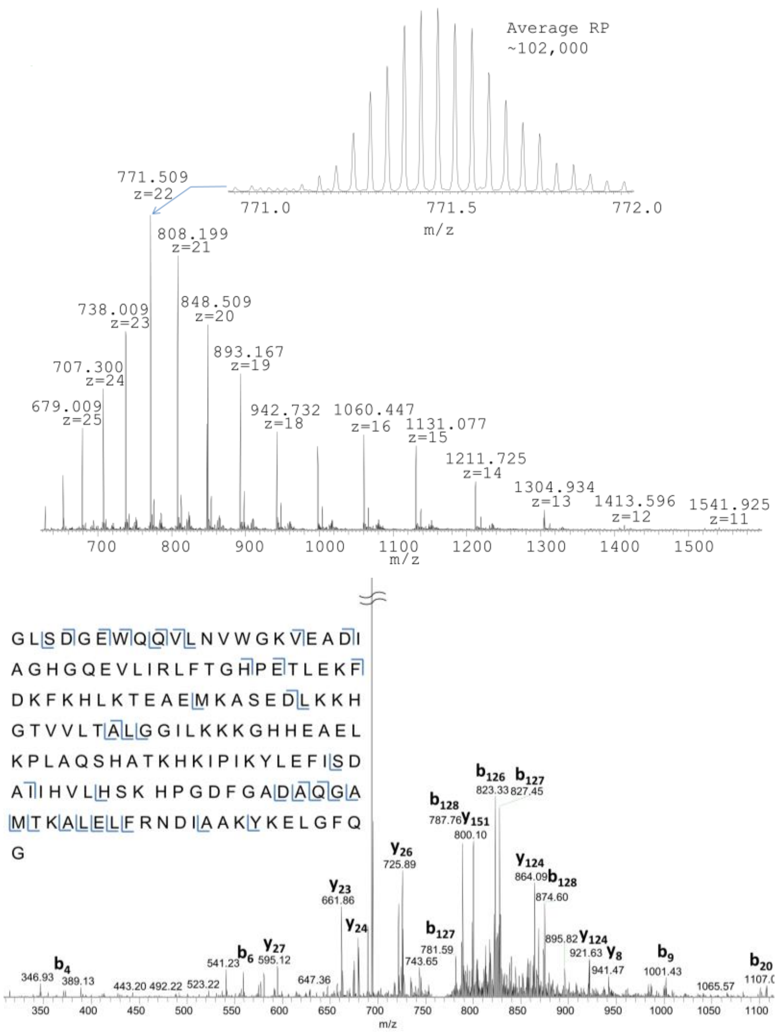

Figure 1.5: A) Full scan spectrum of myoglobin collected using the Velos-FT. The isotopic envelope is for myoglobin [M+H]22+ is shown in the inset. B) Annotated FT-MS/MS spectrum of myoglobin [M+H]^{22}+. The ion injection time required for this acquisition was 7.9 ms.

appear at or below the detection limit of the analyzer. Decreased ion injection times as observed using the Velos-FT are beneficial to all proteomics analyses, particularly for top-down MS/MS. In Fig. 5A, the phenomenon described above can be observed even for the relatively small, 17 kDa protein, myoglobin. Here charge states 11-27 are all simultaneously observed in the full spectrum along with greater than 15 isotope peaks for each charge state (isotope distribution shown in the inset of Figure 1.5A). Isolation and fragmentation of the most abundant charge state requires only 7.9 ms to accumulate 1,000,000 ion charges in the Velos-FT. Large targets such as this are typical for top-down experiments due to the numerous possible fragments along with the isotopic complexity for each of these fragments. Given the flow rate and concentration, this is corresponds to approximately 33 attomoles for this acquisition. In Figure 1.5B, the fragmentation pattern for myoglobin $[M+22H]^{22+}$ is shown. Upon deconvolution and searching using Mascot Top-down against the entire SwissProt database, myoglobin is the most probable identification with an E-value of 5.0×10^{-5} (73 of 897 possible *b* and *y* ion matches) demonstrating that useful and effective fragmentation of large biomolecules can be achieved in the HPC on the Velos-FT.

The configuration of two linear RF ion traps in series enables unique mass spectrometry experiments to be conducted with the Velos-FT. One such experiment, DCF, involves beam-type fragmentation of isolated precursor ions. A conceptual representation of DCF operation on the custom FT-ICR MS mass spectrometer is shown in Figure 1.6. During ion accumulation in the HPC, a DC potential barrier is applied to prevent ions from “leaking” from the HPC to the LPC. At this stage of a standard experiment, mass isolation and resonance excitation would be performed on the ion population in the HPC, followed by transfer to the LPC for mass analysis. In the DCF experiment, after accumulation in the HPC, isolation is performed but the resonance excitation is skipped, leaving the selected precursors. These precursors are transferred to the LPC, but then almost immediately transferred back to the HPC. Between transfers, the DC voltages applied to the HPC have been adjusted to create a large potential offset between the two cells. As the ion population is accelerated back to the HPC it encounters a much higher density of helium, with the higher energy collisions inducing collisional dissociation. Although collisional dissociation in an ion trap is not novel, DCF allows unique experimental capabilities previously unrealized with Velos, Velos Orbitrap, and Velos-FT instruments. During the preparation of this manuscript iHCD was described by McAlister et al.(31) to enable similar fragmentation utilizing the inlet of an LTQ. DCF was developed independently without the endorsement or support of Thermo Fisher Scientific. iHCD is different in that it is performed with air as the collision medium whereas DCF is performed primarily with helium. In iHCD ions are accumulated in the LTQ and transferred back to a multipole near the inlet to induce fragmentation subsequent to ion manipulation. Although collisions with nitrogen are more effective, DCF may benefit from reduced ion losses due to the short, simple ion path traversed during the activation process.

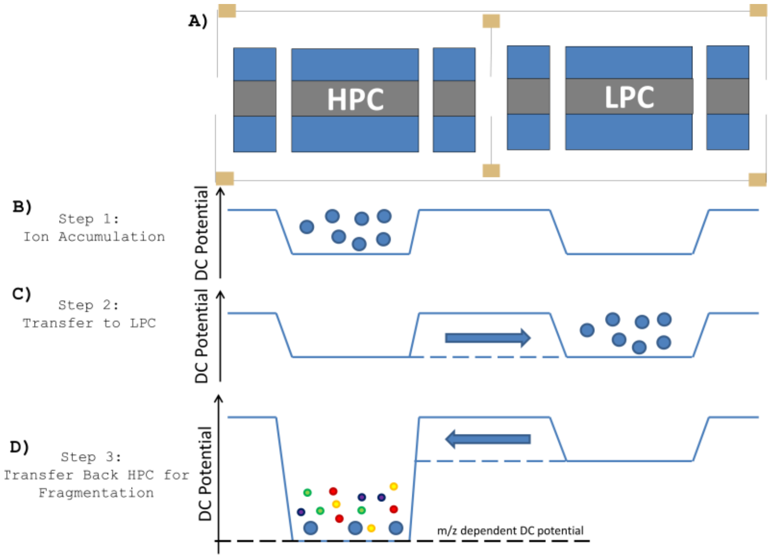

Figure 1.6 A) A conceptual representation of the dual cell linear ion traps used to enable fragmentation during transfer between the LPC and the HPC. B) DC potentials applied during ion accumulation in the HPC. C) DC potentials applied during transfer and trapping of the ion population in the LPC (solid lines = trapping potential, dashed lines = transfer potential). D) DC

Product ion scanning using CID in RF ion traps is a sensitive method for obtaining sequence information from peptides and proteins. CID fragmentation in RF ion traps is performed through application of a m/z dependent secular or “tickle” frequency which selectively excites the oscillatory motion of a particular m/z species. This excitation induces multiple collisions with the background gas in the trap until the peptide fragments. Although this technique has been shown to be highly efficient, usually a single bond is dissociated per peptide ion since as dissociation occurs, the applied frequency is non-resonant with most product ions. When the RF ion trap is operated with the default q of 0.25 product ions with m/z values less than 28% of the precursor m/z will not be stable. The default q represents a compromise between containing low m/z product ions and confining/inducing fragmentation of the parent. This cut-off is commonly rounded up and referred to as the “1/3 rule” and is the reason that small y1 fragment ions, immonium ions, iTRAQ(32) , and other low mass species are typically not observed in peptide MS/MS spectra with RF ion traps. DCF experiments are less dependent on the q-value applied during activation, and therefore are less susceptible to the low m/z limitation then resonant excitation CID. In Figure 1.7, two MS/MS fragmentation patterns of angiotensin I were acquired; one using resonant excitation CID (blue) with a q-value of 0.250 and the other using DCF(black) with a q-value of 0.205. The major differences between the two methods include the observance of more *a* ions (DCF), His immonium ion (DCF), amount of precursor remaining, and different relative b and y fragment ion intensity ratios (DCF vs. CID). The overall cycle times for each fragmentation method are comparable, however, DCF has a slightly shorter activation time (1 ms for DCF vs. 10 ms for CID). The dependence of the fragment ion yield from angiotensin I $[M+3H]^{3+}$ (y_4, b_5, and b_8 ions) on the q-value applied during fragmentation is shown in Figure 1.8. CID results in a q-value of 0.380 for optimum fragment ion yield. The optimum q-value for DCF fragmentation with the applied acceleration energy

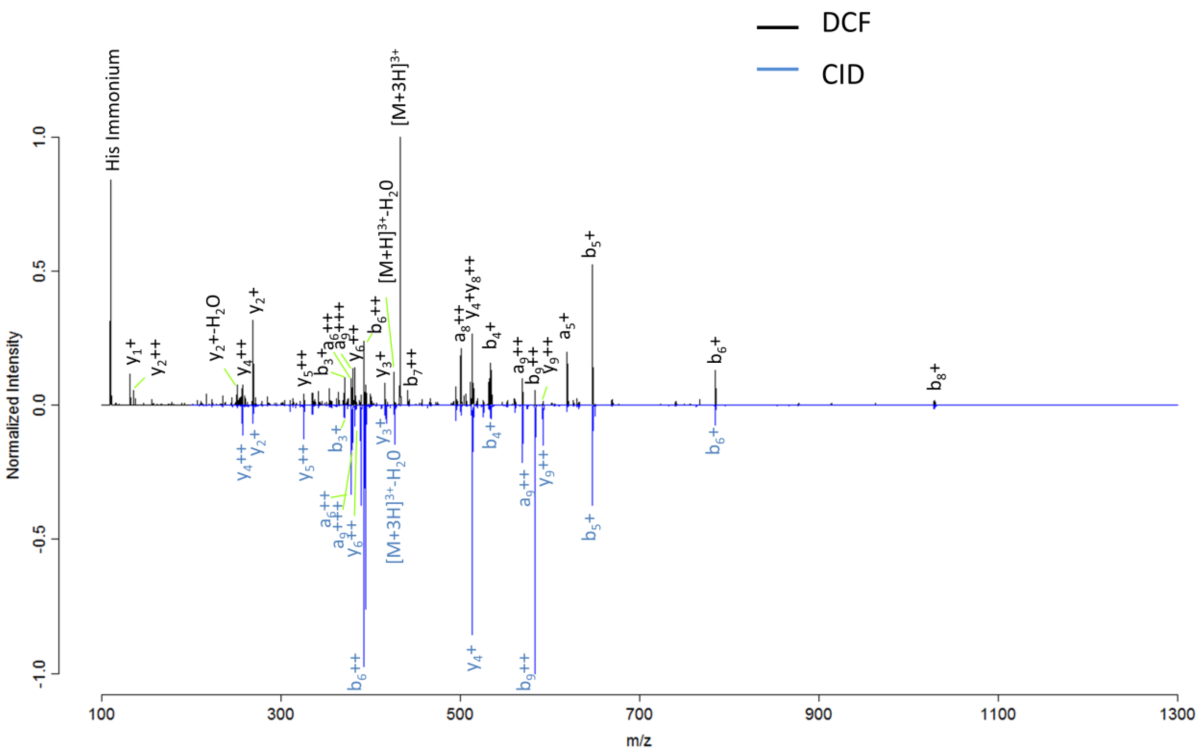

Figure 1.7 A comparison of MS/MS spectra acquired from fragmentation of angiotensin I $[M+3H]^{3+}$ using DCF (black) and CID (blue). Notably, the DCF spectrum contains more a ion series, y1, and histidine immonium ions.

was 0.320. In general, DCF can be operated at lower q-values, inaccessible to CID (see Fig. 8), without sacrificing fragment ion yield. The use of lower q-values permits observance of low m/z fragment ions. In theory, the use of low m/z ions characteristic of peptides with certain amino acids should increase the probability of peptide identifications in complex samples. These ions should be useful with database searching algorithms to optimize peptide identification rates, as suggested by McAllister et al(31). Differences between relative fragment ion ratios or fragment ion yields between CID and beam-type CID has long been known. This has presented significant difficulty in the transition between discovery based proteomic measurements on a trapping instrument to quantitative measurements using selected reaction monitoring (SRM) on quadrupole based instruments. We feel that b and y fragment ion intensity obtained with DCF may provide a more reliable selection of transitions when shifting to triple quadrupole SRM based quantitative proteomics(see Appendix A).

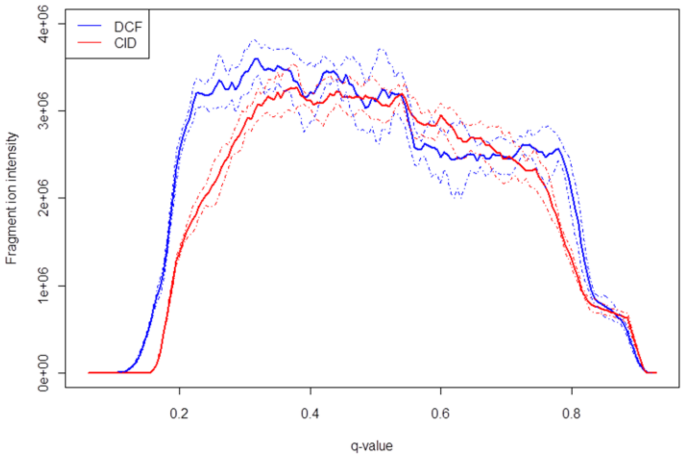

Figure 1.8 A plot of the fragment ion yield of angiotensin I $[M+3H]^{3+}$ as function of applied q-value during DCF and CID fragmentation. The solid traces represent an average of five technical replicates and the dashed traces above and below each solid trace represent ±σ.

The peptide identification rate for CID vs. DCF was evaluated using a tryptic digest of the soluble fraction of S. Cerviseae. The peptide identifications resulting from technical triplicate analyses using both Mascot(11) and Sequest(12, 13) database search algorithms are reported to show the capability of DCF compared to CID on a full-scale biological sample. No modification or tailoring of the search algorithms was performed in the case of DCF, although exploitation of unique fragmentation characteristics of DCF may improve scores and identification rates(31). All numbers reported reflect identifications made at <5% estimated FDR using a reverse database search strategy. Mascot search results produced 1743 unique peptides for DCF, a 22% increase relative to the 1433 unique peptides found for CID. Sequest search results produce 1495 unique peptides for DCF and 1709 unique peptides for CID. Optimization of each search algorithm parameters was not performed in either case, which may be the reason that CID data outperforms DCF data in the case of Sequest searches. The number of uniquely identified peptides between technical triplicates using the Sequest pipeline for each fragmentation type was found to be 215 +/- 14 peptides using CID and 201 +/- 19 peptides using DCF. In addition, these two means were not found to be significantly different by

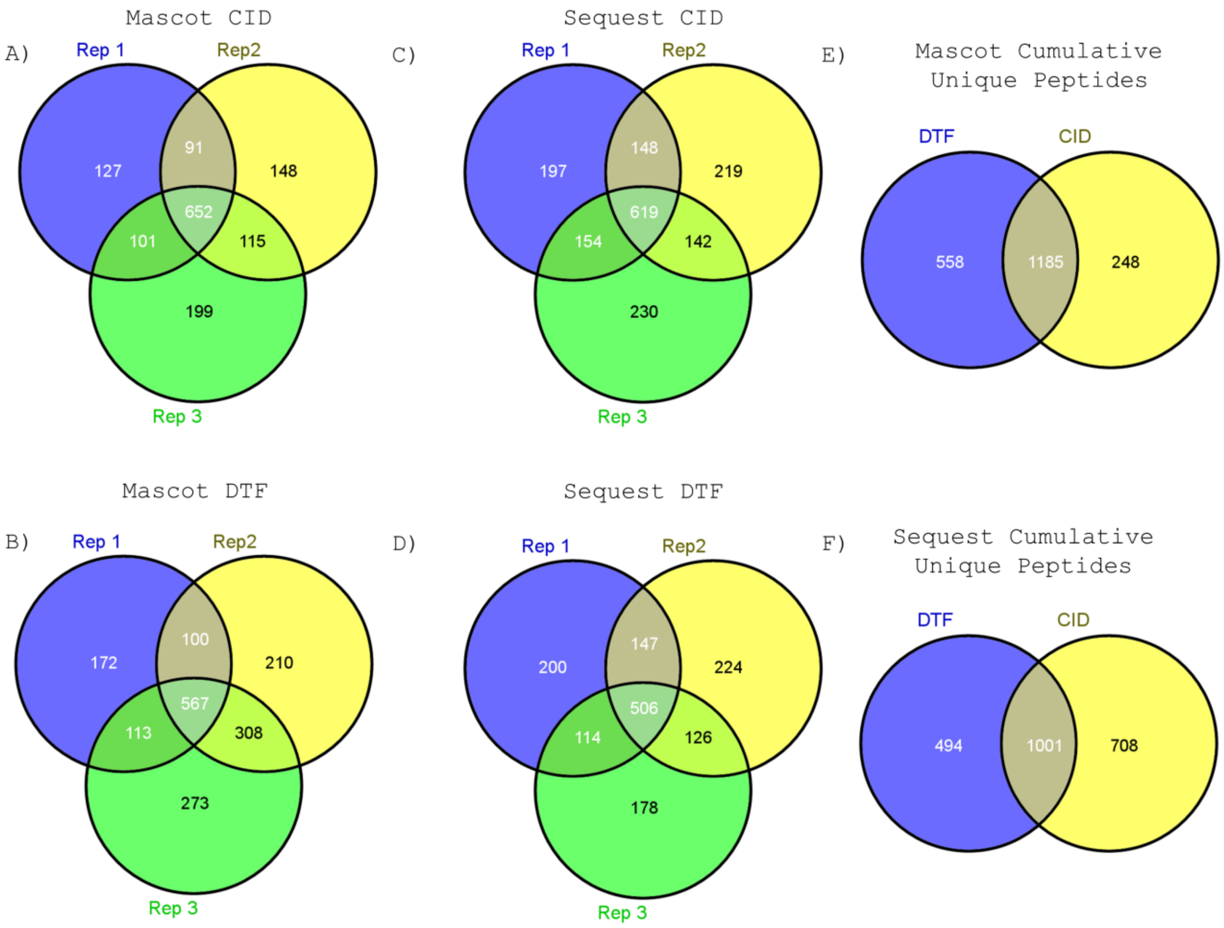

Figure 1.9 A+B) Venn diagram of technical triplicate LC-MS/MS Mascot uniquely identified peptides for CID and DTF respectively (>=5% FDR). C+D) Venn diagram of technical triplicate LC-MS/MS Sequest uniquely identified peptides for CID and DTF respectively (>=5 % FDR). E) Venn diagram of total unique peptides identified in CID and DTF using Mascot. F) Venn diagram of total unique peptides identified in CID and DTF using Sequest.

Student's t-test. These results indicate that the reproducibility of peptide identifications using both CID and DCF are not statistically different, even when processed through two separate database searching algorithms. However, after a significant number of technical replicates unique peptides are found with both DCF and CID, indicating that this technique may provide complementary peptide identifications not accessible to CID methods alone (Figure 1.9).

Conclusions:

Here we described a dual cell linear ion trap Fourier transform ion cyclotron resonance mass spectrometer, which we call the Velos-FT. This instrument is a viable upgrade option for those labs with LTQ-FT instruments.

Performance improvement from the LTQ-FT Ultra to the Velos-FT are comparable to the improvements observed between the LTQ-Orbitrap and the Velos-Orbitrap. The key technological advancements which increase performance are the radio frequency stacked ring ion guide and the high pressure dual cell linear ion trap. The stacked ring ion guide provides a 5-10 fold increase in ion transmission efficiency in the source, the HPC provides more efficient ion accumulation and fragmentation, and the LPC allows for faster scan rates. The overall data dependent repetition rate increases from about 4 Hz for the LTQ-FT Ultra to 10 Hz for the Velos-FT. The increased scan speed and accumulation efficiency directly result in an increased number of identifications. The observed increase in identifications achieved using the Velos-FT over the LTQ-FT Ultra is ~100% when considering unique peptide sequences. When protein group identifications are considered ~50% more increase in identifications was observed. This instrument is well suited to bottom-up proteomics; however, we show that accumulation and fragmentation of intact proteins with the Velos-FT is highly efficient and should enable acquisition of higher quality on-line top-down proteomic measurements. This instrument configuration allows the execution of DCF experiments, providing a significantly reduced low m/z cut-off. Also, a unique subset of identified peptides are obtained using DCF when compared directly to CID.

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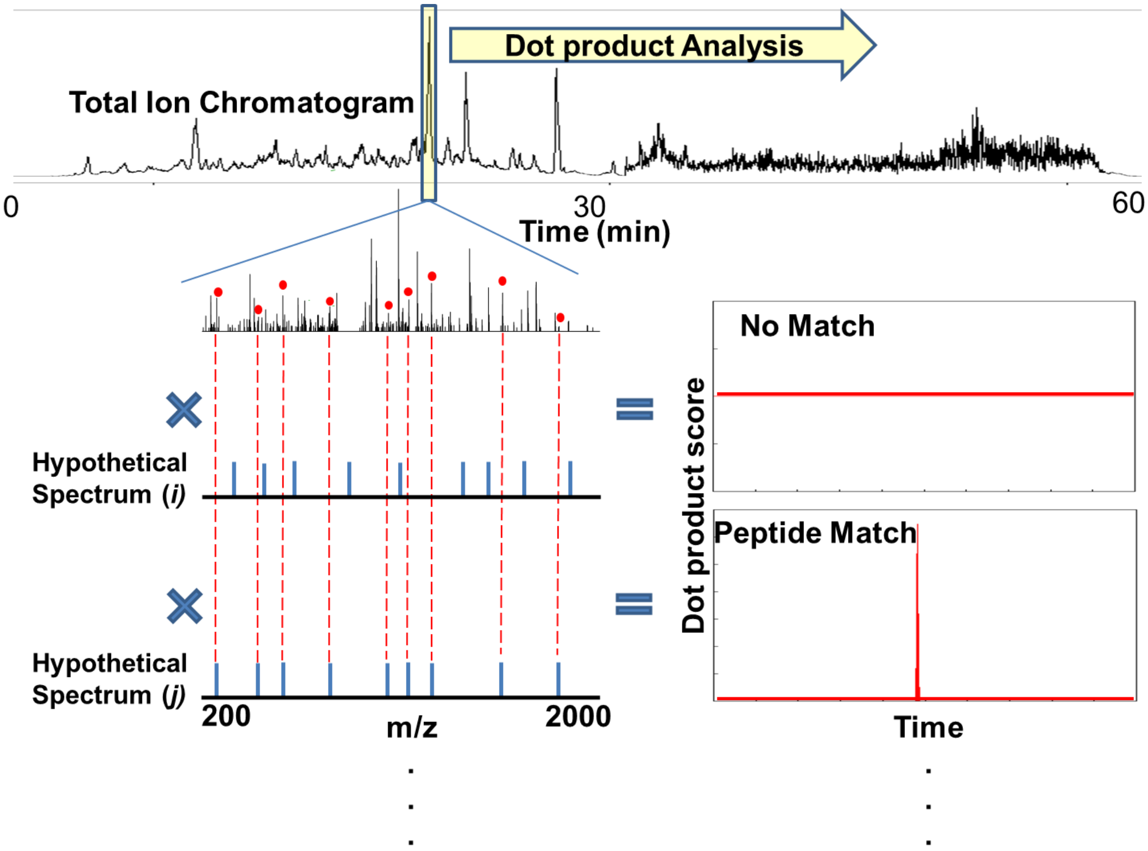
Dot product Analysis
Total Ion Chromatogram
0
30
60
Time (min)
Hypothetical Spectrum (i)
Hypothetical Spectrum (j)
200
m/z
2000
No Match
Peptide Match
Dot product score
Time

Introduction:

To date, the most popular method for peptide and protein identification using mass spectrometry is bottom-up or shotgun proteomics.(1) Shotgun proteomics technology is comprised of the following basic steps: enzymatic digestion of the sample, separation of the resultant peptides (liquid chromatography, capillary electrophoresis, etc.), and MS/MS peptide sequencing. MS/MS analysis of peptides is commonly achieved with an approach called data-dependent acquisition (DDA). DDA works by identifying the most abundant peptides present in a precursor scan. In a serial fashion, the top *n* precursors identified in the precursor scan are subject to a product ion scan to obtain fragmentation patterns (MS/MS) for the peptides. Narrow-band isolation of each peptide is performed to enable the highest quality MS/MS spectrum acquisition to aid in the identification process. The data generated from a shotgun proteomics experiment is then analyzed by database searching algorithms.(2, 3) (4-6) Database searching algorithms are designed to provide the most probable peptide match based upon the theoretical information derived from known or predicted protein polypeptide sequences. In practice, proteome measurements using DDA mass spectrometry have yielded up to 60% observation of the proteins predicted from the genome.(7) However, 60% proteome coverage is not routinely achievable. Many reasons have been suggested for the low proteome coverage including poor quality MS/MS spectra(8, 9) and incorrect genome annotation.(10, 11) There is also strong evidence that the primary reason for the low coverage is the DDA paradigm.(12, 13) DDA methods have been shown to limit the dynamic range of the analysis(14) leading to inadequate sampling of the proteome, even for relatively simple organisms. For example, in yeast nearly the entire proteome (98%) was quantified with tandem affinity purification-tag (TAP-tag) Western-blotting(15), yet such coverage has not been achieved by DDA methods with yeast whole cell lysate protein digests. Nonetheless, the TAP-tag work of Ghaemmaghami *et al.* serves as a “roadmap” for mass spectrometry based proteomics as suggested by the authors. Picotti *et al.*(16) used this roadmap to demonstrate that detection of proteins across the entire dynamic range of the yeast proteome is possible with targeted mass spectrometry. Both of these publications(15, 16) suggest that DDA methods can be complemented by parallel measurement strategies and new technology.

Multiplexed fragmentation, or simultaneous isolation and fragmentation of multiple peptides, has been developed to increase peptide identification rates in many laboratories. Recent multiplexed approaches include MS^E (17-19) and others.(20-24) During the course of our preparation of this manuscript, All Ion Fragmentation (AIF) was reported by Geiger *et al.*(25) AIF was designed specifically for use with the Orbitrap Exactive. In this technique and MS^E, MS scans are alternated with fragmentation scans where a large mass range is subject to fragmentation and the subsequent product ions are measured. Formation of the parent-product ion relationships must be established for subsequent database search identification. These relationships are reformed through chromatographic elution profile correlation. The pseudo MS/MS patterns generated from co-eluting fragments are extracted and submitted for database searching as though the data had been acquired with traditional DDA mass spectrometry. Both techniques, AIF and MS^E, have shown that parallel peptide fragmentation has benefits over serial peptide fragmentation measurements. In the case of AIF, the instrument utilized is a single stage mass spectrometer so typical DDA mass spectrometry or product ion scanning is not possible with this instrument, which prevents a direct comparison. Geiger *et al.* indicate that DDA mass spectrometry on a two-stage mass spectrometer still outperforms AIF.

Here we present a novel approach toward peptide identification and quantification in complex mixtures using a combination of high mass accuracy data-independent acquisition (DIA) and spectral correlation analysis. We call this technique FT-All Reaction Monitoring (FT-ARM). In short, a relatively wide *m/z* range is accumulated and all ions within this mass range are subject to activation (collision-induced dissociation(CID), infrared multiphoton dissociation(IRMPD), etc.). Mass analysis of the fragment ions is performed with high mass accuracy (<5 ppm) such as is afforded by Fourier Transform Ion Cyclotron Resonance(FTICR), Orbitrap, or modern quadrupole time-of-flight(qTOF) instruments. A database of theoretical or empirical peptide fragmentation patterns are used to calculate the dot-product score for each peptide against each DIA scan event of a DIA-LC-MS experiment. The result of this analysis is a score chromatogram for each peptide contained in the database. A reverse sequence decoy database is searched to estimate false discovery rate (FDR). The FT-ARM process is fundamentally different than other DIA approaches, including MS^E and all ion fragmentation(AIF), in that chromatographic elution profile characteristics are not used to cluster precursor peptide signals to their respective fragment ions. Instead FT-ARM relies upon the specificity in peptide fragmentation and high mass accuracy measurement and is therefore, independent of precursor mass. Simulations indicate that sufficient mass accuracy and number of matching fragment ions permits low false discovery rates (FDR), even when considering large databases. The area calculated from the score chromatogram for each peptide is shown to scale linearly as a function of concentration. Using this technology we are able to identify and quantify peptides present within a complex mixture in an unbiased way. Preliminary experiments using FT-ARM indicate that phosphorylated peptides can be detected when searching with unmodified peptide sequences. To illustrate quantification using FT-ARM within a complex background matrix, a Bovine serum albumin (BSA) digest was spiked into whole yeast cell lysate digest, and the BSA peptides were quantified using the FT-ARM process. This technique presents an attractive alternative to quantification using selected reaction monitoring (SRM) since

FT-ARM simplifies proteotypic peptide(26) selection and transition selection(27) from the SRM assay development process. This strategy has already been adopted by others as an approach toward quantification using DIA data as demonstrated by incorporation of an FT-ARM like processing option in the popular MRM software Skyline(27, 28).

Experimental:

BSA Sample

Bovine serum albumin was used as received (Sigma Aldrich, St Louis, MO). A total of 8.0 mg BSA was suspended in 1.00 mL of 100 mM ammonium bicarbonate (pH 7.8) to generate a BSA stock solution that was diluted to obtain a 1.0 mg/mL BSA working solution. The BSA sample was reduced using 5mM dithiothreitol (DTT) for 30 minutes at room temperature. Cysteine residues were blocked using 15mM iodoacetamide (IAA) for 30 minutes in the dark at room temperature. The remaining IAA was quenched using 5 mM DTT for 15 minutes in the dark at room temperature. Protein digestion was achieved with 10 ug of sequencing grade trypsin (Pierce, Rockford, IL) with cleavage specificity to arginine and lysine amino acid residues. This reaction was performed at 37°C for 12 hours under constant agitation. The reaction was quenched by acidification (pH 2.0) and desalted using C18 Sepak (Waters Corporation, Milford, MA). The peptides were lyophilized and redissolved using 1.00 mL mobile phase A (99.9% ultrapure water, 0.1% formic acid).

Yeast Sample

Saccharomyces cerevisiae strain S288C (Baker’s yeast) was grown in glucose rich media to mid-log phase. Cells were collected by centrifugation and resuspended in 100 mM ammonium bicarbonate buffer at a concentration of 400 mg/ml. The cells were lysed using a bead-beater. The lysate was centrifuged at 1,000 g for five minutes to remove cell wall particles and unbroken cells. The lysate was centrifuged again for 30 minutes at 15,000g to separate the soluble and membrane protein fractions. The soluble fraction was assayed for protein concentration using Coomassie Plus Protein assay (Pierce, Location) and found to be ~5.0 mg/mL. The sample was reduced with 5 mM dithiothreitol (Sigma-Aldrich, St. Louis, MO) at room temperature for the duration of 30 minutes. The cysteine residues were blocked using iodoacetamide (Sigma-Aldrich, St. Louis, MO) 15 mM at room temperature for the duration of 30 minutes. The lysate was digested using 1:250 ratio of sequencing grade trypsin (Promega, Madison, WI). The reaction was allowed to proceed for 2 hours at 37°C while under constant agitation via orbital shaking. The digest was quenched and frozen at -20°C. This sample was desalted using C18 Sepak (Waters Corporation, Milford, MA). The peptides were lyophilized and redissolved in mobile phase A (99.9% ultrapure water, 0.1% formic acid).

E. coli Sample

Escherichia Coli strain K12 was grown in LB to mid-log phase. Cells were collected by centrifugation and resuspended in 100 mM ammonium bicarbonate buffer at a concentration of 400 mg/ml. The cells were lysed using a ultra-sonication. The lysate was centrifuged at 1,000 g for five minutes to remove cell wall particles and unbroken cells. The lysate was centrifuged again for 30 minutes at 15,000g to separate the soluble and membrane protein fractions. The soluble fraction was assayed for protein concentration using Coomassie Plus Protein assay (Pierce, Location) and found to be ~6.2 mg/mL. 1.0 mg from the stock solution was reduced with 5 mM dithiothreitol (Sigma-Aldrich, St. Louis, MO) at room temperature for the duration of 30 minutes. The cysteine residues were blocked using iodoacetamide (Sigma-Aldrich, St. Louis, MO) 15 mM at room temperature for the duration of 30 minutes. The lysate was digested using 1:250 ratio of sequencing grade trypsin (Promega, Madison, WI). The reaction was allowed to proceed for 2 hours at 37°C while under constant agitation via orbital shaking. The digest was quenched and frozen at -20°C. This sample was desalted using C18 Sepak (Waters Corporation, Milford, MA). The peptides were lyophilized and redissolved in mobile phase A (99.9% ultrapure water, 0.1% formic acid).

Quantification Samples

A set of dilutions were made to test the sensitivity of FT-ARM. The BSA digest stock solution was diluted 1:100, 1:1000, 1:10000, 1:100000, and 1:1000000. The amount of sample loaded onto the column using the starting amount of protein in the digest corresponds to 1.5, 0.15, 0.015, 0.0015, and 0.00015 pmol. This same set of dilutions was made into a yeast lysate background to test robustness of FT-ARM.

Large-scale quantification using FT-ARM was performed by diluting *E. coli* digest into a yeast digest background. These samples were prepared through the addition of 50 µg of yeast digest to 5, 10, 25, and 50 µg(10:1, 5:1, 2:1, and 1:1) of *E. coli*. Each sample composed of 50 µL of 1.0 mg/mL yeast lysate digest, the remainder of the composition is solvent A and E. coli digest 1.0 mg/mL depending on the dilution(ex. 50 µL yeast lysate, 25 µL ecoli lysate, and 25 µL solvent A = 2:1 dilution).

Liquid Chromatography

Liquid chromatography was performed using a Waters NanoAcquity UPLC (Waters Corporation, Milford, MA). Pulled tip columns were constructed in-house using a laser-pulling device (Sutter Instrument Company, Novato, CA) from 75 um ID x 360 um OD fused silica capillary. The packing material used for peptide separation was 100 Å C18 magic beads (Microm Bioresources Inc., Auburn, CA). A fused silica trap column was constructed from 100 um ID x 360 um OD fused silica capillary. A frit was made on one end of the trap with Kasil (PQ Corporation, Valley Forge, PA) to contain C18 packing material. The packing material used in the trap was 200 Å C18 magic beads (Microm Bioresources Inc., Auburn, CA). A binary solvent gradient was used for peptide separation. The mobile phase A consisted of 99.9% water with 0.1%

formic acid. Mobile phase B consisted of 95.0% acetonitrile, 4.9% 18 MΩ water, and 0.1% formic acid. The gradient was setup as follows 5%-35% B in 30 minutes. Column washing was done by transitioning from 35% B to 80% B in 0.1 minutes and holding for 20 minutes. This was followed by re-equilibration for 30 minutes using 5% B. Large-scale identification experiments with yeast lysate digest and large-scale quantification experiments with E. coli lysate digest within a yeast background were conducted with a 2 hr. separation. The solvent compositions for each step was the same as with the 30 min. gradient, however, the analytical portion of the gradient was changed to 5-35% over 120 min.

Mass Spectrometry

All data were acquired on the LTQ-FT or the LTQ-Orbitrap mass spectrometers (Thermo Electron, San Jose, CA.). DDA experiments for identification comparison were conducted using a "top 5" approach in which a high resolution FTMS acquisition (30,000 resolution at 400 *m/z*) was followed by 5 ion trap MS/MS acquisitions. The AGC target value for the precursor scan was set to $1x10^6$ counts (FTMS 30,000 RP) and for ion trap MS/MS scans to $3x10^4$ counts. All MS/MS targets were chosen from the high resolution FTMS scan. Charge state screening was applied with consideration of only 2 and 3 plus isotope distributions. Dynamic exclusion was used with the following parameters: one repeat count, 15 second repeat duration, 500 exclusion list size, and 90 second exclusion duration.

All FT-ARM data were acquired using data-independent acquisition using 100 Da isolation windows unless otherwise specified. FT-ARM sensitivity characterization was performed by fragmenting all ions within a 100 Da window in the range 700-800 *m/z*. The resolution of the instrument was set to 25,000(at 400 *m/z*) for the LTQ-FT or 30,000(at 400 *m/z*) for the LTQ-Orbitrap. The automated gain control (AGC) settings utilized for this experiment were $1x6^6$ ions with a maximum ion injection time of 1 second. For validation of

FT-ARM targets from BSA, a DDA experiment was incorporated parallel to the DIA acquisition event. In this acquisition scheme, a precursor scan was performed over the *m/z* range 700-800 in the FT analyzer ($1x10^6$ ions, 1.0 s max ion injection time). Three of the most abundant ions were selected from this precursor scan for MS/MS sequencing in the linear RF ion trap (30,000 ions, 100 ms max ion injection time). Dynamic exclusion was used with 1 repeat count, a list of up to 500 entries, and exclusion duration set to 90 seconds. This was followed by a data-independent acquisition over the same *m/z* range 700-800 as described above. Experiments which utilized 12 Da DIA scan widths were setup the same as in the 100 Da window experiments described above, with the exception of dynamic exclusion. Dynamic exclusion was not enabled during these experiments since doubly or triply protonated peptide isotope distributions typically occupy spectral regions of 2.0-3.0 Da. Enabling dynamic exclusion on this mass range would impair the performance of DDA. Activation energy used was 60% relative energy with an activation time of 50 ms. The collision energy was optimized through obtaining the number of peptides identified at a fixed fragment ion mass tolerance, matchcount, and FDR.

To compare FT-ARM peptide identification capability versus DDA, spectra were acquired in two LC-DIA-MS/MS acquisitions using 5 x 100 Da windows spanning 500-1500 *m/z*(i.e. 2 DIA-LC-MS/MS and 2 DDA-LC-MS/MS). The first acquisition consisted of 100 Da windows from 500-1000 *m/z*, while the second set of acquisitions spanned 1000-1500 *m/z*. The resolution for these experiments was set to 30,000 at 400 *m/z*. An ACG target value of $1x10^6$ ion counts was used. Peaklist generating software for this data was ReAdW (version 4.2.1), followed by MzXML2Search (version 4.4) both of which are packaged tools included in the Trans-Proteome Pipeline(29). Mascot (version 2.3.01) was used to search the DDA data. Carbamidomethyl cysteine was the only static modification considered in all database searches. No variable modifications were searched. No missed cleavages were allowed. The precursor mass tolerance utilized in all Mascot searches was 5 ppm. Both forward and reverse sequence databases were searched and FDR estimated using these data. The quotient of reverse database hits over target hits was used to estimate FDR.

SRM data were acquired using a TSQ Vantage triple quadrupole mass spectrometer. A direct infusion experiment of BSA digest was used to confirm the most intense transitions for the BSA peptides(DAFLGSFLYEYSR:y6,y7,y8 and VPQVSTPTLVEVSR:y8,y9,y10). The ENO2_YEAST normalization peptide(AVDDFLISLDGTANK:y6,y7,y9) transitions were determined directly from previously acquired data-dependent acquisisions and used to normalize for comparison between FT-ARM and SRM. The mass spectrometer was set to monitor three transitions per peptide. The scan width for the experiment was set to 30 mDa. Dwell time for each transition was set to 100 ms per transition to provide high sensitivity. Optimized collision energies were provided from the linear calibration in the Skyline(27) software package.

FT-ARM program

The FT-ARM program was written in the C++ programming language using Microsoft Visual Studio Developers Suite (Microsoft Corporation, Redmond, WA). This program was designed to accept two input data streams: theoretical or empirical reference spectra (.FASTA or .TXT peptide list format) and DIA multiplexed fragmentation target data acquired on the sample of interest. When operated using .FASTA or .TXT peptide lists, only 2 and 3 plus precursor m/z’s are calculated for peptide targets and determined to be within the defined DIA isolation window. The program first populates an array of masses and intensities for each target spectrum. Each spectrum in the target data is treated as a vector with *n* intensity values where *n* is the number of *m/z* values for which an ion signal exceeding an intensity threshold was observed. The reference spectra, derived from theoretical calculations or empirical data, are converted to vectors with the same properties. Theoretical reference spectra are generated directly from predicted monoisotopic *b* and *y* ions from the peptide sequences obtained from *in silico* database digestion. The program performs a dot-product calculation (Equation 1) between vectors from each reference spectrum and vectors from each measured target spectrum acquired during chromatographic separation.

Equation (1): $$\text{dot-product} = \sum_{i=1}^{n} R_i \cdot T_i$$

Where R is the reference spectrum vector, T is the target spectrum vector, R_i is the intensity of the i^{th} m/z value of the reference spectrum, T_i is the i^{th} m/z value of the target spectrum, and n is the number of peaks in the spectrum. Large positive dot-product scores are obtained at spectra/times when the peaks in the reference spectrum align with peaks in the target spectrum within the user specified mass tolerance. Peaks must be within a user specified mass tolerance (5 ppm for data presented here) in order to contribute to the dot product score. A match threshold for the number of *b* and *y* fragment ions matching a given reference spectrum is applied as a filter for each dot-product calculation. It was found in our analyses that match threshold values between 8 and 12 achieved(values used for data presented) the desired specificity without diminishing analysis sensitivity. If more than one peak exists within the user specified window the first peak in m/z space, most intense, or closest in ppm error to the target spectrum can be utilized. In this manuscript, we utilized the first peak in m/z space. However, it is possible for a fragment ion to contribute to more than one peptide score since peaks are not removed or subtracted from the analysis. Peptide targets and decoys are only considered if their hydrophobicity is within a user specified tolerance (± 10 hydrophobicity units) of a linear regression between retention time and hydrophobicity

(SSRCalc)(30). The current implementation forms the retention time and hydrophobicity regression based on the high confidence identifications from the CID acquisition; a future revision will calculate this regression solely from the FT-ARM analysis using a two-pass approach. The output from the program is an array containing the scan number, dot-product score, and match count (number of matching peaks within ppm tolerance of reference spectrum), retention time, and theoretical m/z for each query peptide. The dot product score is then weighted by the number of observed fragment ions generated for each time point in the data to increase the signal-to-noise ratio. It was determined that the algorithm is the most sensitive when the data is post-processed as little as possible (i.e. centroided, no peak smoothing, no deconvolution, no charge state determination). More importantly, the signal from score chromatograms can be integrated to obtain total area under the curve which is treated in much the same way as SRM acquired data. To achieve this, the areas obtained from quantified peptides were first normalized to reference peptide areas from the same analysis (or a stable heavy isotope standard). In the rare case that two different peptides presented to the mass spectrometer at the same time dissociate to yield fragment ions within 5 to 10 ppm of one another, the contribution to overall error in quantitation of either peptide is small due to the fact that the match count parameter typically requires 8 or more ions. The ratio of the area between these two peaks was normalized and used for comparison across samples. Identification using FT-ARM is performed by recording the maximum dot-product score for each peptide in both the target and decoy databases. FDR estimation is performed on the basis of maximum dot-product score for targets and decoys which reside within the DIA mass range acquired. A graphical user interface has been developed for use with this software to perform FT-ARM analysis, FDR estimation, and data comparison operations. The database used for all searches, both FT-ARM and DDA-Mascot, was NCBI *Saccharomyces cerevisiae* downloaded September 9, 2009. See Supporting Information for FT-ARM simulation and other data handling details.

Results and Discussion:

FT-ARM analysis begins with selection of *m/z* range for the DIA scan event. Here we are using 12 or 100 Da isolation windows. Narrow isolation windows can increase the dynamic range of the peptides observed in the analysis since the fixed charge capacity of the linear ion trap in conjunction with AGC fundamentally limits the dynamic range of the measurement.(31, 32) Ions present in the *m/z* range of interest are fragmented in the linear ion trap and transferred to the FT analyzer for high resolution measurement. This process is repeated during the entire LC separation. Precursor mass measurement is not necessary for FT-ARM. However, a precursor scan can be used to validate FT-ARM results using accurate precursor mass if desired. FT-ARM is analogous to SRM analysis on a triple quadrupole instrument. For example, in SRM analysis, low resolution precursor mass selection combined with two or more fragment ion masses also recorded with low mass accuracy provide specificity for identification and quantitation of peptides from complex samples. In FT-ARM, we have replaced the need for precursor mass selection with high resolution mass measurement on all fragment ions. Here ions are not physically filtered during the analysis as in the SRM assay. Highly accurate fragment mass measurements provide the selectivity required for identification and quantitation from complex samples, in the absence of peptide precursor mass determination. FT-ARM assays are conducted in a parallel as opposed to the serial transition measurements made in SRM assays. Prior identification of the most sensitive transitions is not required for FT-ARM, since “all transitions” are used in the FT-ARM scoring process. This can significantly reduce the time required to develop sensitive quantitative assays for targeted proteome quantification.

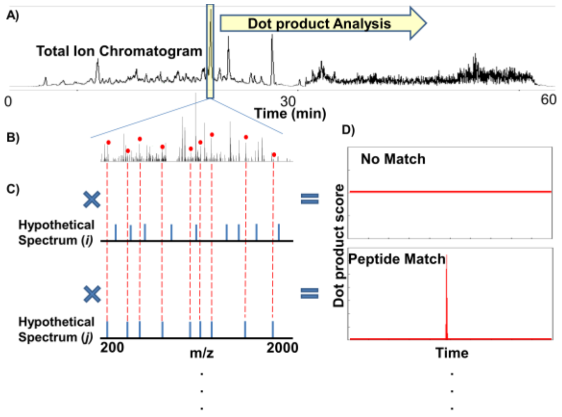

Figure 2.1: Diagram illustrating FT-ARM strategy based on accurate peptide fragment mass measurements. All ions are fragmented in every scan during LC separation to produce the total ion chromatogram in **A)**. **B)** Complex fragmentation spectrum of all ions. **C)** Hypothetical peptide fragmentation spectra. **D**) Dot product analysis result called a *Score Chromatogram*.

The FT-ARM process is shown in Figure 2.1. Here a DIA LC-MS total ion chromatogram (TIC) is shown for yeast whole cell lysate digest spiked with BSA digest at a 1:100 ratio. The reference window in the center of the chromatogram in Fig. 2.1A is placed to simulate the position of a single FT-ARM calculation. A DIA spectrum acquired within this reference window is shown in Fig. 2.1B along with two theoretical reference spectra (Fig. 2.1C and Fig. 2.1D). The hypothetical spectrum *i* in this example contains no matching peaks in the target spectrum at this time point in the chromatogram, while *j* has many matching peaks as depicted with the red dots above the correctly matching peaks. The score chromatograms (Fig. 2.1D) show a matching peptide eluting (bottom inset) and no signal (top inset). Score chromatograms are integrated to obtain a score area which is proportional to the amount of analyte present in the mixture. Global FT-ARM datasets can be re-analyzed with a specific subset of hypothetical spectra computed for only the peptides of particular interest. Alternatively, for greater dynamic range targeted analyses, FT-ARM can also be operated such that only those *m/z* values of targeted peptides are accumulated and fragmented. Generally, FT-ARM data are acquired with an unbiased mass spectrometry approach and as such, these datasets can be re-mined with different hypothetical spectra or empirical peptide spectral databases. Global quantification of the peptides can be accomplished by generating hypothetical spectra for every peptide candidate in an entire organism.

The FT-ARM analysis scores all possible tryptic peptides in a given database against every acquired spectrum. This approach differs from DDA and conventional database searching algorithms, where the massive search space of entire databases containing all possible peptides is made efficient using precursor mass measurements to significantly reduce the pool of possible peptides which match an MS/MS spectrum. In contrast, FT-ARM analysis includes a single pass dot product calculation for each target spectrum against every peptide in the database. Despite the large search space, optimized design of the algorithm produces a modest runtime of ~5 minutes on a modern desktop computer for FT-ARM analysis when applied to whole yeast lysate digest over a 100 Da window (700-800 *m/z*). This search time was obtained when considering only the 2+ and 3+ peptides residing in this window. Thus, even though FT-ARM imposes greater computational demands, the overall analysis need not present a time bottle-neck in proteomics pipelines.

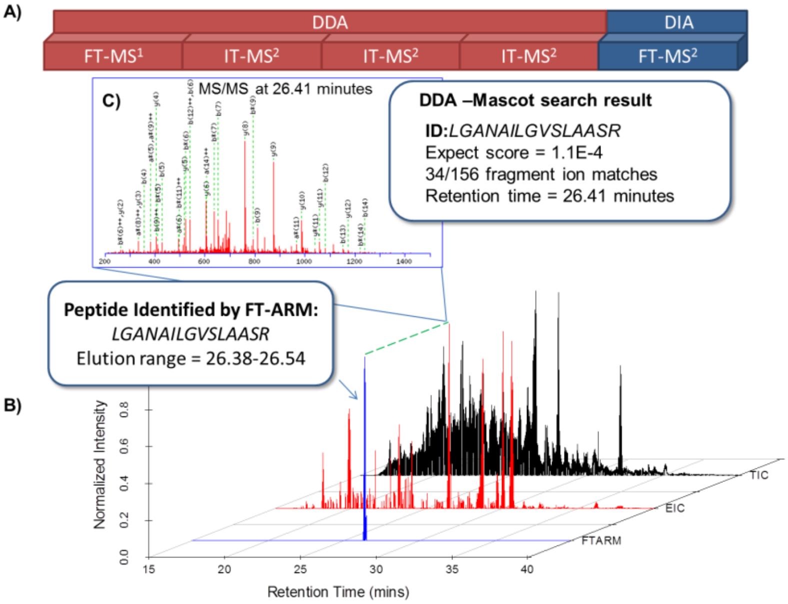

Figure 2.2: **A)** Experimental scan sequence. **B)** Correlation between data-dependent acquisition (DDA) identification of a yeast tryptic peptide (*LGANAILGVSLAASR*) from a whole cell lysate digest. Extracted ion chromatogram (EIC) for the *m/z* of this peptide shown in red (20 mDa window). The FT-ARM score chromatogram of the same sequence is shown in blue. **C)** Mascot annotated spectrum for the identification of the peptide.

Peptide identification within a complex mixture, without narrow band isolation and without precursor mass confirmation, has not been demonstrated previously. FT-ARM peptide identification is demonstrated through its application to yeast whole cell lysate digest samples (Fig. 2.2). In this case, the experiment was designed to allow both

DDA and DIA scan types so that identified peptides from each approach could be compared. FT-ARM does not require precursor masses or use the results from the DDA scans. The hybridized DDA-FT-ARM experiment was done by programming the mass spectrometer to first acquire a precursor spectrum over the range of 700-800 *m/z*, followed by three data-dependent scans (referencing the precursor scan), and finally, the data-independent scan window (700-800 *m/z*) for FT-ARM analysis (Fig. 2.2A). The total cycle time for this sequence of scans at maximum ion injection is 3s. Fig. 2.2B includes three traces: the total ion chromatogram (TIC) (Black), the extracted ion chromatogram (EIC) for the peptide of interest within 20 mDa (Red), and the FT-ARM score chromatogram (Blue) where all data have been normalized so they can be presented on the same plot. A peptide identified in this acquisition from the yeast protein enolase II was used in this example. The noise level found in the EIC for the peptide results from many confounding ions that appear with *m/z* similar to the identified peptide during the entire experiment. However, when the DIA scans are subject to FT-ARM analysis using the hypothetical b and y ions for this peptide, the score chromatogram generated is nearly noise free. This is important since quantification based upon FT-ARM relies on the score chromatogram area; it must be free from spurious or interfering peaks not directly resultant from the analyte of interest. Also, from this analysis we found that the retention time of the DDA MS/MS spectrum for which this same peptide was identified coincides with the signal acquired from the FT-ARM analysis, as one would expect. This example provides proof of concept for FT-ARM, i.e., identification of the tryptic peptide LGANAILGVSLAASR in the yeast digest was achieved by FT-ARM using only the accurate fragment masses, independent of precursor mass.

Low noise score chromatograms generated from FT-ARM result from high mass accuracy fragment ion measurement and match count(Supporting Information Figures 1). Highly accurate mass measurements have been used for increased specificity and simplification of complex mixture analysis.(33) The effect of mass accuracy and match count on the FT-ARM analysis is shown using the same dataset as Fig. 2.2. As the mass tolerance is varied from 1000 ppm to 1 ppm, specificity in detection is gained.(34) The other contributing factor in the specificity of FT-ARM is the match count parameter. In database searching algorithms, an analogous type of discrimination is utilized when attempting to make MS/MS identifications. An MS/MS pattern with few matching peaks receives a poor score and is not the most probable peptide match for the MS/MS pattern. Similarly, match count allows the user to specify a minimum number of *m/z* values to match the reference for a dot-product score to be recorded. The effect of varying the match count threshold when the ppm tolerance is fixed to 20 ppm is shown in Supporting Information Figure 2. As match count threshold is increased, the overall noise level decreases. This effect supplements accurate mass measurement by eliminating spurious peptide identification events in which only a small number of matching, high intensity peaks generate strong signal. Currently both parameters are implemented statically throughout the analysis, although they could be treated dynamically to best fit the data presented to the FT-ARM program. Additionally, relative ion intensities could be utilized, in an analogous way in MRM relative transition signal is used to limit false quantification(35).

In an effort to understand the performance of this technique when applied to large-scale databases, a simulation was performed to ascertain the number of theoretical possible false matches for the FT-ARM process under defined circumstances. False matches occur when another peptide in the database or a higher order combination fragments from multiple peptides produce similar fragmentation patterns to the target peptide (i.e. b and y ions overlap at the specified mass tolerance). In the absence of precursor m/z information, peptides which fall within the same m/z window and have similar hydrophobicity could contribute to a peptide identity falsely and also invalid signal quantification. This simulation reveals how often this chimeric or multiplexed fragmentation patterns amongst peptides could align and generate a false positive match. In fact, predicted false positive matches are well below 1% when applying FT-ARM to the entire *Saccharomyces cerevisiae* database with at least 6 ppm fragment mass tolerance and match count of 5 or higher. It was assumed for this simulation that all peptide fragment ions in the m/z window of interest were detectable. This represents a worst case scenario, since all peptides in a FASTA database are not detectable with current mass spectrometry technologies for various reasons(36). In Figure 2.3, the results from a simulation performed on the yeast database are presented as a function of m/z fragment ion tolerance (ppm) versus match count. This simulation was performed over the window of 700-800 m/z, in which, all 2-3+ tryptic peptides are considered. It reveals that given the appropriate m/z fragment ion tolerance and match count, FT-ARM is capable of providing highly specific identities. Modified peptides, missed cleavage sequences and other factors will further complicate databases and may yield higher false discovery rates. However, the simulations, like the results above demonstrate, suggest that the precursor-mass independent approach described in FT-ARM is feasible and will offer advantages for proteome analyses.

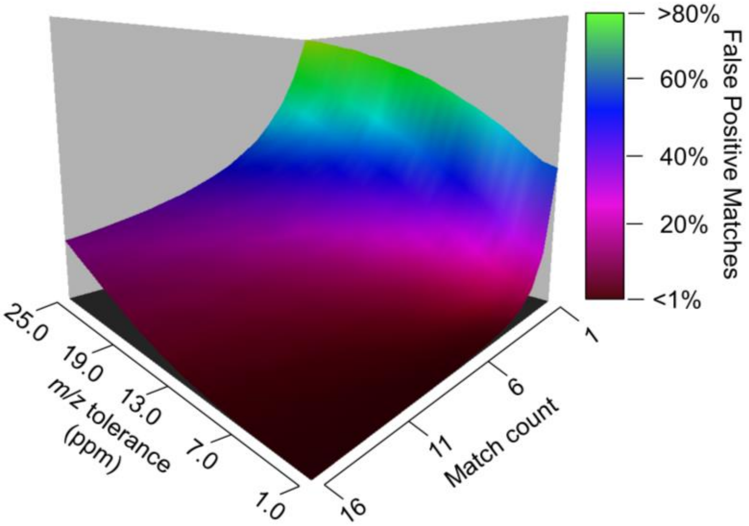

Figure 2.3: A three dimensional plot presenting data from an FT-ARM simulation which allows for estimation of the number of potential false peptide matches in a fasta database. Empirical data presented in this manuscript has been collected in the regime in where this data suggests false matches are below 1%.

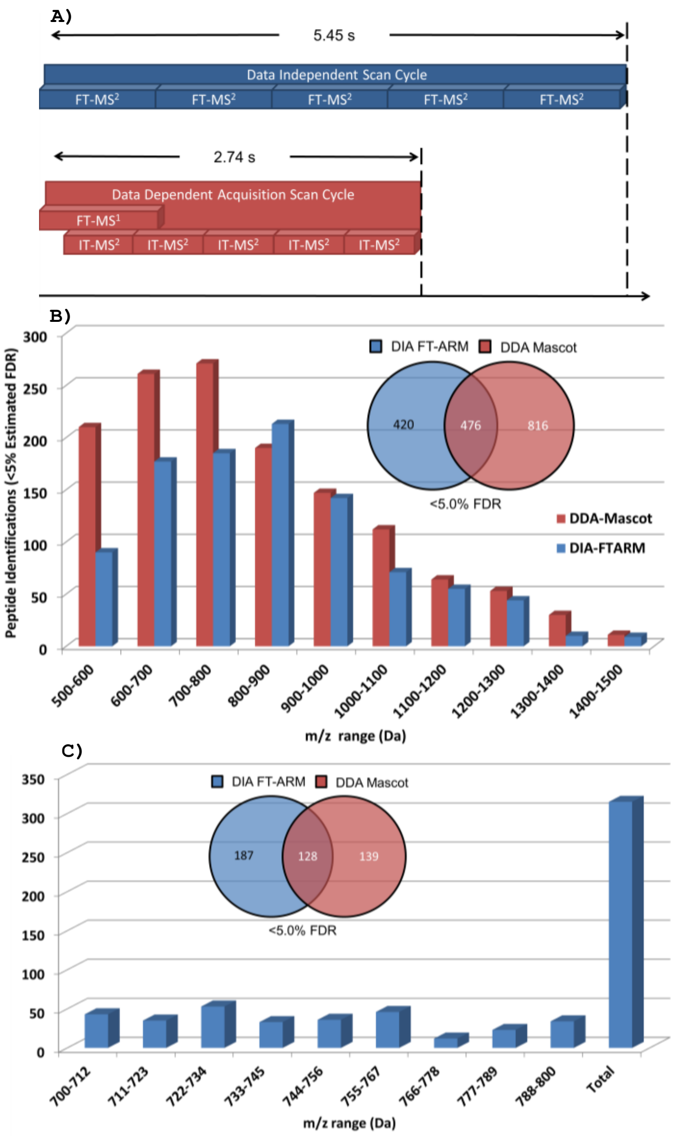

Figure 2.4: A) Experimental scan cycle for both DIA and DDA acquisitions **B)** Histogram of the identifications made using DDA mass spectrometry with Mascot versus DIA mass spectrometry with FT-ARM during equivalent acquisition periods. Inset shows identifications made when DIA acquisition window is reduced from 100 Da to 12 Da. Venn diagram inset showing the overlap between the identifications made with each approach at <5% estimated FDR. **C)** Histogram shows identifications made when DIA acquisition window is reduced from 100 Da to 12 Da. Venn diagram inset showing the overlap between the identifications made with each approach at <5% estimated FDR.

Identification of peptides from complex matrices is perhaps the best metric for the effectiveness of FT-ARM. In order to demonstrate the identification capability of FT-ARM, DIA LC-MS was acquired on yeast whole cell lysate digest. Separate experiments were used for both DDA Mascot(1292 unique peptides) and DIA FT-ARM(896 unique peptides), with data acquired using the scan cycle shown in Figure 2.4A. Both DDA and DIA data were obtained over the same mass range, overall acquisition time, and peptide charge state considered (2+ and 3+ only). The results from the analyses are summarized in Figure 2.4B. Identifications have been broken down into individual mass ranges. FDR was estimated using a decoy database strategy(37) both in FT-ARM and Mascot analyses (see Supporting Information). Unlike the DDA analysis, the FT-ARM identifications were made without the need for narrow *m/z* isolation of each peptide or accurate precursor ion. Data acquired with 12 Da DIA scan widths over the range 700-800 m/z are shown in the inset. These data show that identifications increase as the DIA window size is decreased. The Venn diagram inset within Figure 2.4B shows the overlap between FT-ARM and Mascot peptide sequence identifications on the peptide level. About 40% of the peptides identified(476 unique peptides) with DDA methods were also identified by FT-ARM. This level of overlap indicates that the FT-ARM technique provides a significant complementarity in number of additional peptide identities which were not identified by DDA and *vice versa*. In many cases, FT-ARM identifications were achieved where DDA failed due to overlapping isotope distributions that were isolated, as shown in Figure 2.5A. Manual inspection of random peptides uniquely identified by FT-ARM yielded the following reasons for missed peptide identifications in the DDA experiment: overlapping isotope distributions(34.9%), MS/MS acquisition but no identification(8.4%), and no MS/MS acquisition(56.7%). Of the reasons, the first two are unlikely to be alleviated by mass lists or technical replicates using DDA. On the other hand, peptides uniquely identified by DDA were in some instances found to be the most abundant peptide in the precursor spectrum. Upon inspection of the flanking DIA scan events, fragment ions from the putative precursors are not present. Direct infusion experiments were performed to investigate this problem. Results from these efforts suggest that broadband isolation (100 Da) and CID activation in the ion trap is not occurring with the same efficiency as in narrow band isolation/activation and thus, product ions observed from narrow band isolation of the precursor are not present in the DIA scan (data not shown). These represent technical details that can be optimized to further improve the FT-ARM approach. Figure 2.5B illustrates the effect of reducing the DIA window size on the number of identifications/amu. In the case of FT-ARM, the IDs/amu grows exponentially with decreasing window size, whereas, DDA appears constant. In the case of DDA, the result is that identificaitons/amu effectively scales with the MS1 window size so the peptides identified per amu remains approximately constant.

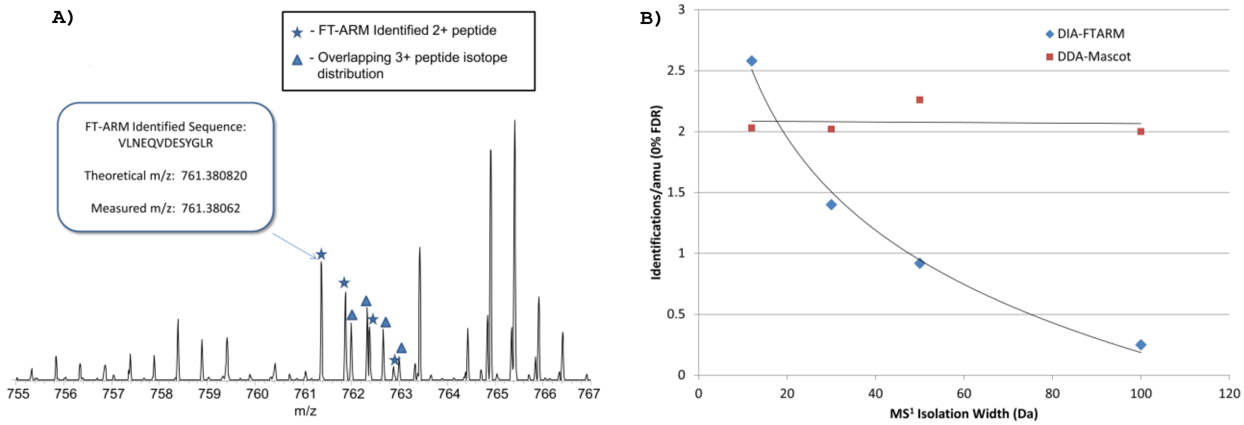

Figure 2.5 A) An example of co-eluting peptides which FT-ARM was capable of identifying. B) The effect of narrowing the tandem MS isolation width on DIA-FTARM and DDA-Mascot identification strategies.

The ability to quantify peptides and proteins, in complex samples is of great importance in systems biology. SRM quantification is gaining traction in the field of proteomics due to its many desirable qualities such as high reproducibility, sensitivity, selectivity, and large linear dynamic range of five orders of magnitude or greater.(16) This is very important in development of high throughput proteomics assays where minimal sample preparation is required. FT-ARM analysis shares these same properties; however, it also improves upon SRM analysis in two aspects. The first improvement is simplification of method development. SRM assays are time consuming to develop and often require empirical data for optimum sensitivity. It has been shown that tuning the instrument with synthetic peptides derived from a list of target peptides increases the sensitivity of this technique tremendously.(16) This is primarily due to the inability for *in silico* prediction of the most sensitive transitions, or highest yielding CID products, to focus on for a given target peptide. FT-ARM analysis can make use of the entire hypothetical or empirical spectrum, and thus, all transitions are considered. The second improvement is multiplexed analysis. The mass analyzer used for SRM analysis is a triple quadrupole. The triple quadrupole has many benefits; however, it is by nature a spatially resolving mass analyzer, requiring physical separation of the ions. Physical ion separation limits SRM assays to a single analyte detected at any given instant. Efforts to increase the quadrupole scan speed and the ability to schedule SRM assays have increased the number of analytes quantifiable in a single acquisition. FT-ARM, in contrast, allows simultaneous detection of many fragments from all precursors within the selected *m/z* range and relies on accurate fragment mass to achieve specificity. Here a direct comparison of SRM vs. FT-ARM (100 Da DIA window) has been made to illustrate these methods can provide similar quantification information. For this comparison, a sample of BSA digest spiked into a yeast whole cell lysate digest (0.150-1500 fmol) was used. The yeast lysate digest provides a highly complex background matrix. In fact, careful measurements of the yeast proteome indicate that the dynamic range of SRM is likely greater than six orders of magnitude.(15, 16) In Figure 2.6A and 2.6B, the two BSA peptides are quantified in the complex yeast background using FT-ARM and SRM with a TSQ Vantage. The peptides are quantified over four orders of magnitude. Linear regression data show that the relationship between FT-ARM signal and amount of analyte is linear in this complex background. The achieved FT-ARM dynamic range was observed to be nearly the same as that achieved using SRM by limiting the *m/z* range of the DIA to a smaller value such as 10 *m/z*. Detection of the lowest dilution level became possible using the narrower DIA window. This corresponds to 150 attomoles of BSA protein loaded on the column.

In order to illustrate the reproducibility, linearity, and robustness in quantification of large-scale measurements with FT-ARM, E. Coli lysate was diluted into a yeast lysate background. This sample set presents a significant challenge to the technique in terms of potential spurious quantitative signal. A summary of the ratios obtained for each *E. coli* peptide identified and quantified (<5% FDR; see Supporting Information) is presented in Figure 2.6C. Each dilution level was measured in triplicate to provide statistics. The median ratio for each dilution level is highly reproducible between replicates, as indicated by the notches in the box plot. These notches indicate at 95% confidence whether a median is statistically different. The box encompasses 50% of the measurements. Dotted blue lines indicate the expected ratio for each dilution level and "whiskers" represent

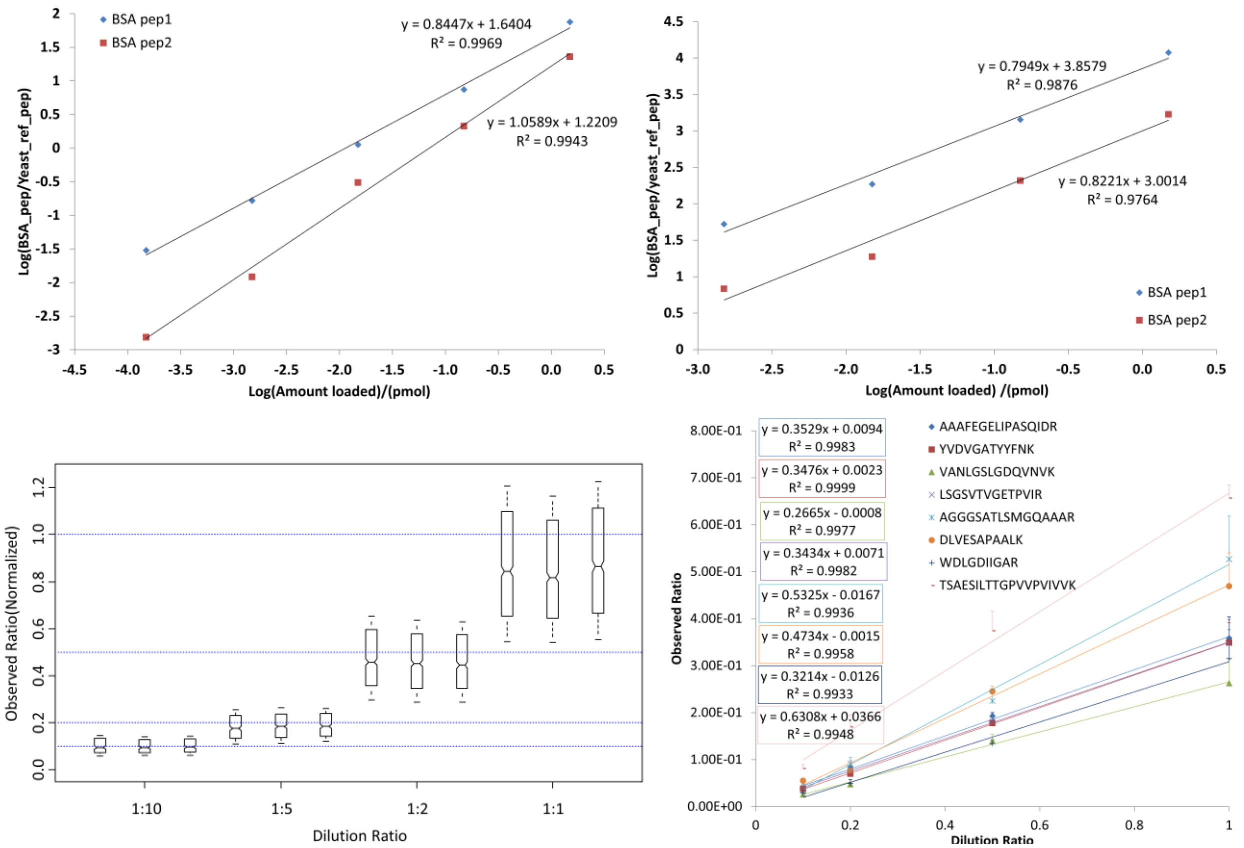

Figure 2.6. SRM and FT-ARM quantification of BSA digest spiked into yeast whole cell lysate digest(DAFLGSFLYEYSR and VPQVSTPTLVEVSR). **A)** Integrated area as function of concentration of BSA peptides using SRM. **B)** Integrated score area as function of concentration of BSA peptides using FT-ARM. **C)** Box and whisker plot for all peptides quantified from *E. coli* at <5% FDR normalized to 1. **D)** Random selection of peptides from the *E. coli* dataset in linear regression format of the average +/- σ at each dilution.

+/- σ for the dataset. Although some variation in peptide response can be observed from this plot, most of the data(i.e. the box) corresponds very closely to the expected ratio. This response is comparable to other label free techniques including SRM, however, in this case no assay development was required to quantify hundreds of E. coli peptides within a very complex matrix. The measured ratios +/- σ for a random subset peptides has been shown in Figure 2.6D to illustrate linearity in peptide response in addition to reproducibility of measurements on the individual peptide level. As indicated by the peptides shown individual peptide quantification error is much lower. Average relative standard deviations for peptide level measurements are 11.3%. Precursor based label-free quantification studies report similar relative standard deviations (10-20%)(28, 36, 38). Quantitative reproducibility and linearity are perturbed by overlapping fragment ions from contaminating ion signal. Since yeast peptides have an equal probability of yielding isobaric fragment ions (within the applied mass tolerance) as E coli peptides, linearity of quantification signals would not be possible due to the constant concentration of yeast peptides if fragment overlap contributed in any significant way to the FT-ARM score chromatograms. However, as predicted by simulation this phenomenon is not prevalent in our data.

Conclusions:

FT-ARM is a novel mass spectrometry method and algorithm designed to combine peptide identification and quantification using multiplexed high mass accuracy fragment measurement. This approach presents an attractive complement to DDA mass spectrometry and SRM analysis. Dot-product score calculation allows signals specific to individual peptides to be observed even from highly complex mixtures. In addition, FT-ARM enables unique identification of a significant number of peptides that are missed by traditional DDA methods. This observation suggests that adding a DIA scan in conjunction with conventional DDA analysis will enhance the overall number of identifications in an analysis. Further refinement of the FT-ARM scoring algorithm will result in even greater numbers of identifications. Quantification is linear, highly sensitive, and measurable for every peptide using FT-ARM. Targeted quantification with FT-ARM can be performed without the need for FT-ARM identifications, if peptides were identified by another technique. Peptides from BSA were quantified within a yeast whole cell lysate background over the range of 1.5-1500 fmoles total BSA protein loaded. The dynamic range and sensitivity of FT-ARM appears to be limited by that of the linear ion trap and AGC. When the DIA window was limited to 10 Da, peptides from 150 attomoles of BSA total protein were detected. Robust, linear, and reproducible quantification was demonstrated on a large-scale with no assay development. FT-ARM methodology has been presented here as a proof of principal, and as such, underlying software will continue to be developed and optimized. FT-ARM is freely available and open source at http://brucelab.gs.washington.edu/.

Acknowledgments:

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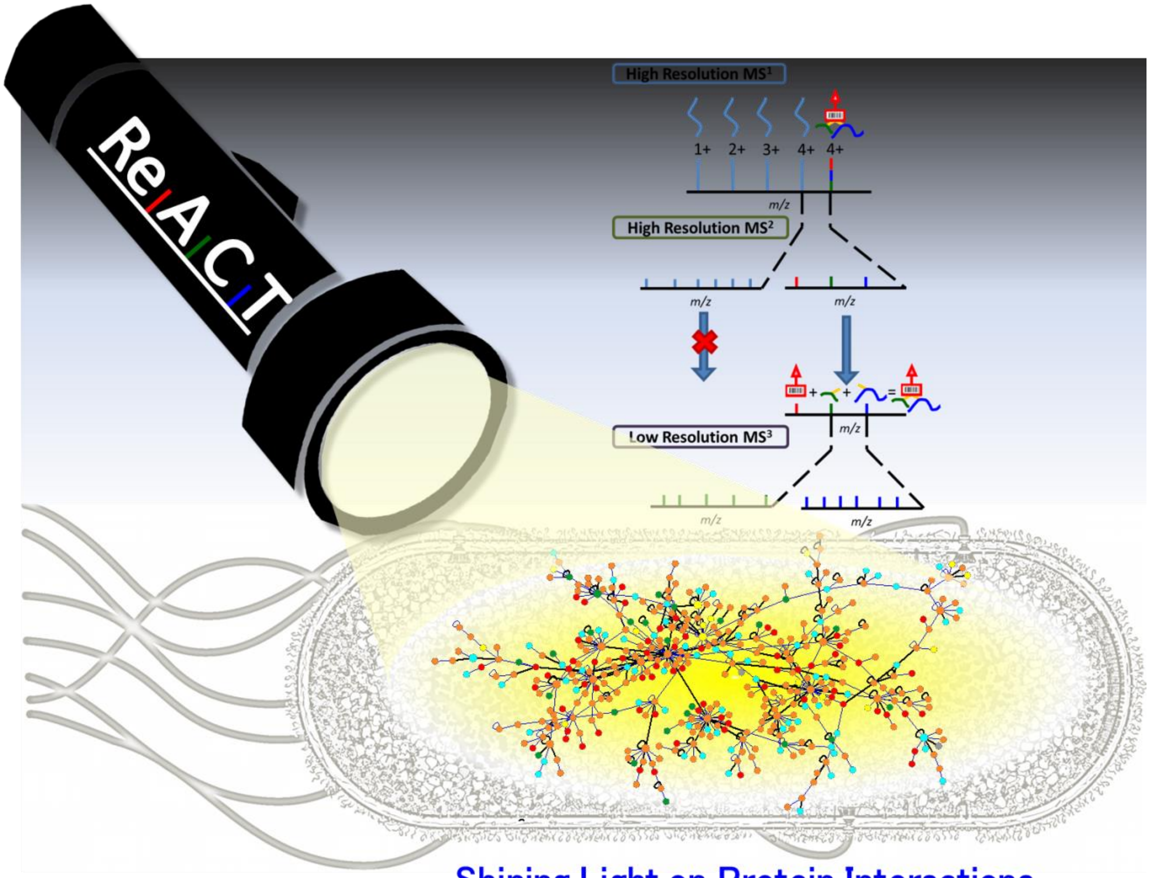
Chapter III: Real-time Analysis for Cross-linked peptides Technology



Shining Light on Protein Interactions

Introduction:

Proteins are the most abundant functional molecules inside cells and perform a bewildering array of biological processes required to support life. The versatility of protein function has its origins in topological shapes and features that these polymeric macromolecules can adopt. Moreover, the crowded intracellular environment profoundly influences their shape such that proteins that appear unstructured *in vitro*, can adopt a more defined conformation inside cells(1)′(2). These induced topological features occur as a consequence of interaction within cellular compartments that may not be replicated in cell lysates or purified components(3-6). Thus, methods that can reveal information about global protein topology under physiologically-relevant conditions, within native interactions with intended partners inside cells could greatly advance understanding of protein function.

Recently, methods based on cross-linking-mass spectrometry (XL-MS), have emerged as viable techniques to investigate protein-protein interactions (PPIs(7-14). These methods involve "fixing" the biological system through covalent chemical modification of amino acid residues and investigating the cross-linked sites using mass spectrometry methods. An attractive aspect of this technology is the potential to identify PPIs and unique topological features and yield large-scale data. Recent efforts have shown feasibility for measurements of PPIs in bacterial cells(15-17). An advantage of cross-linking is the potential to study protein topologies that are resistant to other techniques, such as disordered protein domains and membrane proteins. Unlike X-ray crystallography or NMR structure determination, cross-linking data can provide unique structural insight on many proteins as they exist in their natural cellular environment in a single experiment. XL-MS technologies have the capacity to produce large-scale datasets; although technical limitations have constrained the scope of current methods to the identification of a few (< 100) cross-linked peptides *in vivo*(10, 15-17).

Real-time Analysis for Cross-linked peptide Technology or ReACT, was developed to enable large-scale application of cross-linking technology. ReACT analysis of cross-linked peptides from cross-linked *E. coli* cells yielded datasets approximately ten-fold larger than previously reported. The increased capacity for cross-linked peptide identification achieved with ReACT enabled creation of the first PPI network derived solely from covalent chemical cross-linking on cells. These data provide *in vivo* topological information on many known interactions, including ribosomal proteins, elongation factor TU, 60 kDa chaperonin, and more. Excitingly, many of the cross-linked sites can be mapped onto existing co-crystal structure data and support the existence of these complex structures inside cells. Furthermore, many cross-linked sites were identified among proteins known to participate in complexes, but not known to interact directly. Finally, although the results acquired with ReACT represent only a very small fraction of those possible in cells, the new capabilities presented by ReACT suggest that cross-linking technologies will grow to provide large-scale topological data on protein interactions in cells.

Methods:

ReACT Algorithm

The ReACT algorithm was written in ion trap control language, a native language used with Thermo Electron mass spectrometers. The flow chart in Figure 1 outlines how the algorithm operates. Charge state exclusion alternates between two parameter sets depending on the order, *n* of each stage of MS^n analysis. The set of parameters allows ions with charge state ≥ 4+ to be selected from high resolution mass spectral acquisition. This is done to focus instrument capabilities on cross-linked species for subsequent tandem mass spectrometry analyses. All ions generated during high resolution MS^2 acquisition for which charge states are assigned are considered during the mass relationship discovery phase of the experiment. By identifying these relationships as the analytes elute from the LC column, ReACT effectively achieves real-time application of previously described analysis strategies for PIR cleavable cross-linkers(18, 19). Any two released and observed peptide masses added to the reporter mass must equal the observed precursor mass within a user definable mass tolerance (Equation 1).

$$PRECURSOR = REPORTER + PEPTIDE_1 + PEPTIDE_2 \qquad \text{Equation 1}$$

Where *PRECURSOR* is the mass of any selected precursor ion, *REPORTER* is the mass of the reporter ion(14) and $PEPTIDE_n$ is the mass of the released peptide *n*. This equation is applied during real-time data acquisition and requires checking N MS^2 high resolution product ions with each other. This amounts to $N^2/2$ calculations where N is equal to the number of detected isotopic distributions in the MS^2 pattern. In an effort to make this process more efficient, masses observed in the MS^2 spectra are only considered if they satisfy the following statement:

$$PEPTIDE_{1\,or\,2} < PRECURSOR - REPORTER - STUMP \qquad \text{Equation 2}$$

where *STUMP* is the residual mass modification which remains on lysine residues after CID cleavage. This limits the computational space of the calculation by only considering ions lower in mass than PIR partial cleavage products. Partial cleavage products result from incomplete cleavage of the PIR cross-linked products and are observed when the reporter ion remains covalently linked to one of two peptides involved in the cross-link. These products are not used to determine whether equation 1 has been satisfied, but can be used to add further confidence to putative relationships. In the event that two ion masses from the MS^2 spectrum satisfy equations 1 and 2, they are stored for targeted MS^3 analysis in the next scan cycle. In this way, no loss of instrument duty cycle occurs during the relationship calculation. Up to two ^{13}C offsets are considered to allow for possible incorrect monoisotopic peak assignment for cross-linked precursors or product ions. A ^{13}C offset is defined as the mass difference in Daltons (Da) between ^{12}C and ^{13}C.

Liquid Chromatography-Mass Spectrometry

All samples were analyzed on a custom dual linear RF ion trap Fourier transform ion cyclotron resonance mass spectrometer, hereafter referred to as the Velos-FT. However, it should be noted that in principle, ReACT-based experiments are possible on any mass spectrometry platform that is capable of high resolution MS^2 and low resolution MS^3. The mass spectrometer is directly coupled with a Waters NanoAcquity UPLC system. Cross-linked peptide samples were loaded onto a trap column (3 cm x 100 μm i.d.) packed with 200 Å Magic-C4AQ (Michrom) using a flow rate of 2 μl/min of 99% solvent A (H_2O containing 0.1% formic acid) and 1% solvent B (acetonitrile containing 0.1% formic acid) where they were washed for a total of 10 minutes. Peptides were then eluted from the trap column and separated by reversed-phase chromatography over an analytical column (30 cm x 75 μm i.d.) packed with 100 Å Magic- C4AQ at a flow rate of 200 nL/min using a linear gradient from 90% solvent A/ 10% solvent B to 60% solvent A/40 % solvent B over 120 min for a 2 hr data acquisition or 240 min for a 4 hr data acquisition. The structure of a ReACT method consists of the following mass spectrometry data acquisition parameters. The first acquisition is a high-resolution precursor acquisition (50,000 resolving power (RP) @ 400 *m/z*). The second is a high resolution MS^2 acquisition on ≥4+ charge state isotope distributions. This requires the use of charge state exclusion. Dynamic exclusion is utilized with the following parameters: repeat count = 2, repeat duration = 15 s, dynamic exclusion list size = 500, dynamic exclusion duration = 30 s. FT preview mode and predictive automated gain control (pAGC) were not utilized. Monoisotopic precursor selection was used. A series of four RF ion trap MS^3 acquisitions were used to acquire fragmentation spectra of peptides observed in cross-linked relationships. These MS^3 events include acquisition on the 1+ and 2+

charge states of the peptides found in PIR relationships. Acquisition of MS^3 spectra on two charge states better allows one to address unequal charge state distribution that may result from cleavage of the cross-linked complex.

PIR Cross-linker Synthesis

PIR synthesis was performed using solid phase peptide synthesis (SPPS) methods(20). The Endeavor 90 (Apptec, Louisville, KY) SPPS unit was used for all PIR synthesis steps with the single exception of the final N-hydroxy ester (NHX, where X = succinimide or phthalimide) ester formation step. Biotin Rink-PIR (BRink) (14) and Rink-PIR (2Rink) synthesis has been previously described(12). Briefly, the super acid sensitive resin (SASRIN) with a glycine residue pre-coupled was utilized (Bachem, Munich, Germany). Synthesis of the cross-linker proceeds through fluorenylmethyloxycarbonyl (Fmoc) N-terminally protected SPPS methods(21). Additions to the resin occur in order and are the following, Fmoc-Lys (biotin), Fmoc-Lys (Fmoc), Fmoc-Rink(All amino acids obtained from Bachem), and succinic anhydride (Sigma-Aldrich, St. Louis, MO). 2Rink is synthesized through the same series of steps with the exception of the addition of Fmoc-Lys (biotin). The activated NHS-ester form of the cross-linker is created in a final esterification step immediately prior to use with TFA-NHS(22). Overall yield for this synthesis is ~90%. Purity was confirmed by direct infusion ESI-MS analysis. Cross-linker is cleaved from the resin using 1% trifluoroacetic acid (TFA) in methylene chloride and purified using a semi-preparative partisil C18 column (Whatmann, United Kingdom) at low pH to prevent hydrolysis of the NHS ester. BRink and 2Rink was dissolved in dimethylsulfoxide to a concentration of 100 mM.

Biotin Aspartate Proline-PIR (BDP) synthesis is also accomplished using Fmoc chemistry. SASRIN-glycine resin was used for the solid support. Amino acid additions to the resin occur in order and are the following, FMOC-Lys (Biotin), FMOC-Lys (FMOC), FMOC-Pro, FMOC-Asp (otBu), and succinic anhydride.

The activated NHX form of the cross-linker is created in a final esterification step immediately prior to use with TFA-NHX(22)(X = phthalamide or succinimide). Cleavage from the solid support and deprotection of Asp (otBu) was performed simultaneously using 95% TFA 5% methylene chloride. Purification was performed immediately subsequent to Asp deprotection and cleavage via diethyl ether precipitation using 1:15 (cleavage mixture: diethyl ether). Diethyl ether solution was centrifuged at 3400 g to pellet precipitate. Diethyl ether was decanted and pellet was dried to yield ~90-95% pure BDP-ester. Purity was assayed via direct infusion ESI-MS analysis. BDP was dissolved in dimethylsulfoxide to a concentration of 500 mM to form the stock solution.

Purified Protein Sample Preparation

Alcohol dehydrogenase (S. *cerevisiae*), α-lactalbumin (*Bos taurus*), carbonic anhydrase (*Bos taurus*), cytochrome C (*Equus caballus*), hemoglobin (*Homo sapiens*), ribonuclease A (*Bos taurus*), and myoglobin (*Equus caballus*) were all obtained from Sigma Aldrich (St. Louis, MO) and used as received. Each protein was dissolved at a concentration of 1 mg/mL in phosphate buffered saline (PBS) buffer, pH 7.4. The cross-linking reaction was performed by adding BDP-NHS at a final concentration of 1 mM and incubating the reaction solution at room temperature for 1 hour with constant mixing. A second sample of ribonuclease A was labeled using 2Rink at the same concentration at the same concentration as the BDP RNase A sample analog. After cross-linking, disulfide bonds were reduced using 5 mM tris (2-carboxyethyl) phosphine (TCEP) and the resulting free thiols were alkylated using 10 mM iodoacetamide (IAA). Digestion was carried out using a 1:200 w/w ratio of sequencing grade modified trypsin (Promega, Madison, WI) to protein and incubating at 37°C overnight with constant mixing. The samples were desalted using C18 Sep-Pak (Waters Corporation, United Kingdom) and dried in a centrifugal concentrator (Genevac, Gardiner, NY). The cross-linked, digested samples were redissolved in solvent A then stored at -80°C until LC-MS analysis.

E. coli sample preparation

In vivo cross-linking of *E. coli* was performed as described previously(16). Briefly, *E. coli* K12 cell suspensions were harvested at O.D. 0.6-0.8. The cells were pelleted and washed 5 times with 1 mL PBS before cross-linking. A 150 µL cell pellet was resuspended in 150 mL PBS and BDP-NHP was added to the suspension with a final concentration of 10 mM. The reaction was carried out at 4°C for 1 hr. The cells were pelleted, washed, and then lysed by heating to 95°C in 4% sodium dodecylsulfate (SDS) 1x Tris buffer at pH 8.5. The sample was ultra sonicated to shear DNA, centrifuged at 16 kg for 10 min to remove insoluble material, and then added to a 30 kDa molecular weight cut-off (MWCO) filter (Millipore, Billerica, MA) and concentrated by centrifugation at 7.5 kg for 30 min. A protein extract yield of 2.0 mg/mL was determined using a Coomassie Plus assay (Pierce, Rockford, IL). The sample was reduced, alkylated and digested as described above for the purified protein samples. Strong cation exchange (SCX) fractionation of the sample was performed using Macro SCX Spin Columns (Nest Group Inc., Southborough, MA) and ammonium acetate in 25% acetonitrile 75% water for elution. Fractions were collected at 0, 50, 80, 300, 500, and 1000 mM ammonium acetate. Prior to affinity enrichment each fraction was de-salted using C18 Sep-Pak 50cc (Waters Corporation, United Kingdom). The fractions were biotin affinity enriched for BDP cross-linked peptide products using Ultralink Monomeric Avidin (Pierce, Rockford, IL). To each fraction 300 µL of settled avidin resin was added in 500 µL of 100 mM ammonium bicarbonate. Enriched cross-linked peptide samples were stored at -80°C until LC-MS analysis.

In addition to two biological replicates using the above protocol, a third sample was prepared with 10x greater number of cells by volume (1.5 mL cell pellet) to ascertain whether cross-linking reaction product concentration serves to limit detection by ReACT. This sample was prepared with the same protocol as above with a few minor exceptions. The first exception is SCX separation was done online using a 4.6 mmD x 100 mmL SCX column packed in-house with polysulfoethyl aspartamide media, identical to that which is used in the spin columns, (Nest Group Inc., Southborough, MA) on a stand-alone liquid chromatograph (Agilent Technologies, Santa Clara, CA). The separation was achieved using an isocratic step gradient at a flow rate of 1.5 mL/min and steps at 0, 50, 100, …, 300 mM with 5 min. per step. Solvent A consisted of 25% acetonitrile and 75% water, while solvent B consisted of 25% acetonitrile, 75% water, and 1M ammonium acetate.

Data Interpretation and Sequence Identifications

ReACT provides a list of cross-linked relationships observed during an entire data acquisition. Raw mass spectrometry data is converted to mzXML format using ReAdW (version 4.3.1). MS^2 accurate precursor mass and MS^3 fragmentation patterns are extracted from the mzXML files and converted to Mascot Generic Format (mgf) for Mascot (version 2.3.1) sequence database searches using MzXML2Search (version 4.4) or mzXML was searched directly using SEQUEST (version UWPR2011.01.1). Mascot searches were conducted with a 10 ppm precursor mass tolerance and 0.8 Da fragment ion tolerance. SEQUEST searches were conducted with 10 ppm precursor mass tolerance and 0.36 da fragment tolerance (0.11 Da fragment offset). The most probable match for each query was accepted (with an expectation value threshold <0.05) and mapped back to the cross-linked relationship for *in vitro* experiments with purified proteins. Sequence databases utilized here include those of all proteins (21 sequences including isoforms) and SwissProt *E. coli* (4178 sequences) (http://www.uniprot.org). False discovery (peptide level) during sequence identification for cross-linking experiments with *E. coli* cells was estimated using well-described reverse sequence decoy database search methods(23). Relationship discovery in real-time was performed with 20 ppm tolerance between the putative cross-linked precursor and released peptide product and reporter masses. 20 ppm tolerance was chosen for relationship discovery as an effective compromise between method sensitivity and false relationship discovery. False relationship discovery was estimated by performing ReACT analysis on a *E. coli* lysate digest without cross-linker added and fewer than <5% of all acquired MS^2 spectra result in false mass relationships with 20 ppm relationship tolerance. For example, in a series of three technical replicate ReACT experiments of all MS^2 spectra (10451) acquired, 31 yielded false mass relationships containing the expected PIR reporter ion (+/- 20 ppm) within non-cross-linked *E. coli* digest. After performing database searches on all falsely discovered mass relationships, none resulted in fully identified cross-linked products, illustrating the stringency of filtering results using 20 ppm on the mass relationship stage and <5% FDR on the peptide identification. At the mass tolerance utilized in ReACT experiments, it is concluded there is negligible contribution of the real-time PIR mass relationship FDR on the overall FDR for reported cross-linked identifications. For comparison, the *E. coli* cell results presented here are comprised of 84154 MS^2 spectra searched by ReACT from both biological and technical replicates. ReACT identified 3960 cross-linked mass relationships containing reporter ion from these spectra. 2934 fully identified cross-linked relationships were made where both released peptides were identified with <5% sequence assignment FDR. From these results after reducing for redundancy, 708 unique cross-linked sites were identified with <5% false discovery. All discovered relationships were filtered for mass redundancy on the precursor, MS^2, and peptide sequence level to curate only the highest confidence set of results. The results are presented in tabular format within the Supplemental Materials.

Structural Modeling

All models were created and rendered using Pymol (Delano Scientific). *E. coli* tryptophanase and 30s ribosome structural models were created using coordinates from PDB identifiers 2OQX and 3FIH, respectively.

Results and Discussion:

ReACT is an integrated mass spectrometry analysis platform for real-time identification of cross-linked peptides. This approach relies on measurement and validation of mass relationships that arise from CID cleavable cross-linkers illustrated above in Equation 1 (see methods). The general ReACT strategy is outlined in Figure 3.1. High resolution MS^1 spectra are acquired and deconvoluted to obtain the neutral mass and charge states of all species detected. For any species with charge state 4+ or greater, a high resolution MS^2 is acquired in a data-dependent fashion (e.g. selection of the top N most abundant 4+ ionic species). Next the MS^2 is deconvolved to obtain the neutral mass and charge state of all species detected. ReACT analysis automatically identifies spectral features that satisfy the mass relationship defined in Equation 1 as expected for MS-cleavable cross-linkers. Released peptide ions found to fulfill these relationships are then automatically selected for MS^3 analysis and peptide fragmentation spectra are acquired. Simple real-time informatics strategies for mass spectrometry have recently been explored by others(24) successfully increasing specificity and sensitivity of the overall analysis, while minimizing the need for repeated sample analyses or lengthy post-analysis data processing. With ReACT, the final step is to extract the MS^3 information and perform a database search with conventional proteome database search tools such as SEQUEST, Mascot, or others. Since ReACT uses mass relationships to direct MS^3 events, the number of spectra to be searched scales with the number of relationships found. The selectivity of ReACT decreases demand on instrument duty cycle and yet, enables specific targeting of cross-linked peptides which are often observed with lower abundance. These species may be missed by intensity-based data-

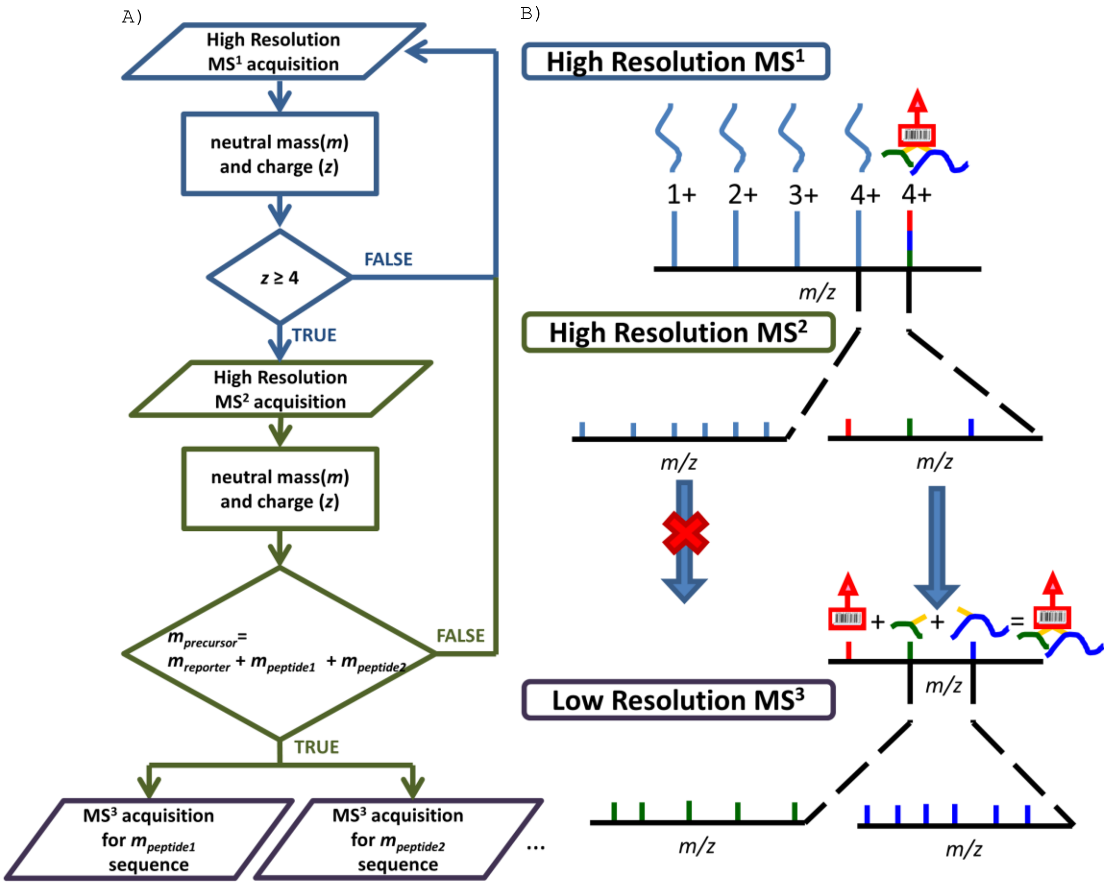


Figure 3.1. A) A flow chart which describes how the REACT algorithm functions during LC-MS^n experiments. B) An idealized practical diagram of how the algorithm would operate on real data directly corresponding to the flow charge in A).

dependent analyses. The loss of analysis time spent on species that do not meet these criteria is eliminated using ReACT, allowing for improved detection of many more cross-linked peptide species than possible previously. ReACT is a relatively simple algorithm which could be implemented on any mass spectrometer with high mass measurement accuracy capabilities and the capacity to make experiment decisions on-the-fly. Hopefully, these capabilities will be incorporated on future MS operating systems to allow ReACT to be implemented in many labs.

Chemical cross-linkers compatible with ReACT must possess a low energy CID cleavage site to facilitate cross-linked peptide relationship recognition and subsequent MS^3 peptide fragmentation pattern acquisition. A series of CID cleavable cross-linkers developed in-house, named Protein Interaction Reporter (PIR) cross-linkers, were utilized in this work (Supplemental Figure 1). Although these compounds have a variety of structural and chemical properties, each contains the basic features of a mass encoded reporter ion and two low energy CID cleavable bonds. In addition, the BDP and BRink cross-linkers include a biotin moiety, useful for affinity purification of the conjugated reaction products. Among the benefits of using PIR cross-linkers are the engineered fragmentation patterns and the use of a reporter ion as an indicator of labeled species.(13) For further information regarding PIR molecules used in this study see Supplemental Materials.

ReACT has been developed to provide selectivity in LC-MS^n analyses to focus on only those ions which are likely cross-linked peptides. This selectivity is illustrated with an example of a cross-linked site identified from *E. coli* cells (Figure 3.2). ReACT selectivity for cross-linked species is achieved first on the MS^2 precursor stage through exclusion of ions with charge less than 4$^+$, since two tryptic peptides covalently linked will possess on average 4$^+$ charge state or greater(10, 25). Many potential analytes are present within the spectrum in Figure 3.2A; however, the ReACT algorithm selects only those ions with 4$^+$ charge state or higher for MS^2 analysis. In fact, the analyte of interest, 718.174 *m/z*, is the 576th most abundant peak within the spectrum and would likely never have been sampled by conventional intensity-driven data dependent analyses. Requirement of the CID cleavable linker mass relationships to be observed with narrow mass tolerance (+/- 20 ppm) imparts additional specificity in the analysis of the selected high charge state ions. In the example shown, the measurement error between the observed precursor and sum of masses of the relationship (Equation 1) is less than 1.5 ppm (Figure 3.2B). Typically, mass measurement error for observed cross-linked relationships is less than or equal to 5.0 ppm which significantly reduces false relationship discovery (see Supplementary

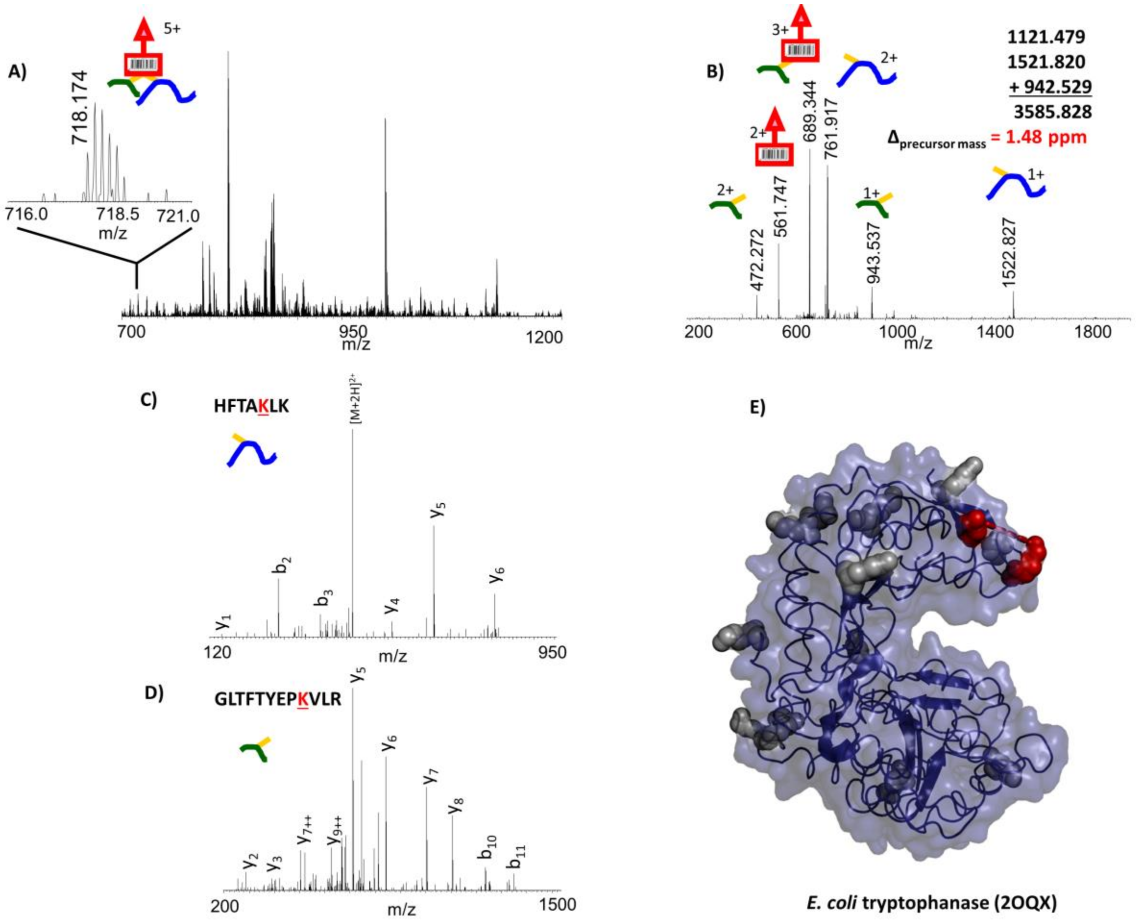


Figure 3.2. An example of ReACT data acquired from PIR labeled *E. coli* cells. A) High resolution MS^1 acquisition for precursor information; inset is an expanded view of the spectrum surrounding the cross-linked peptide precursor, 718.174 *m/z*. B) High resolution MS^2 acquisition for cross-linked peptide relationship information C) and D) Low resolution MS^3 acquisition for peptide sequence information. E) Tryptophanase crystal structure (*E. coli*, PDB 2OQX) with all observed cross-linked sites marked in gray; the cross-link observed in this data is marked in red, while other sites observed in additional cross-linked sites are in gray.
To view an animated illustration of cross-linked sites on the molecular structure see: http://brucelab.gs.washington.edu/ReACT_movies.php

Information). Upon successful relationship detection, ReACT directs MS^3 events to automatically acquire fragment ion spectra for sequence identification of the released peptides (1+ and 2+ charge states for each). Both peptides identified in this example belong to tryptophanase (TNAA_ECOLI). The cross-linked sites were mapped onto the existing crystal structure for *E. coli* tryptophanase (PDB 2OQX), where the red highlighted lysine residues represent the cross-linked sites in this example (gray residues indicate other cross-linking sites found; Figure 3.2E).

ReACT was initially applied to a set of commercially available purified proteins. The data resultant from this set of experiments is presented in Supplemental Table S1. An unambiguous α-β hemoglobin cross-link was observed as well as unambiguous homodimeric cross-links supporting protein dimerization of ribonuclease A and carbonic anhydrase. Several cross-linked peptide products were successfully identified in these samples even with a signal-to-noise ratio of ~2, suggesting the ability to discriminate against lower charge state ions improves the dynamic range over which cross-linked species can be interrogated. The ability of ReACT to extract useful information, even from ions with low signal intensity is most beneficial for complex samples, as illustrated with *in vivo* cross-linking samples below. ReACT is customizable for use with any cross-linker that can be cleaved within the mass spectrometer including linkers with mono, bi, or higher order CID cleavage sites. To demonstrate this flexibility, Ribonuclease A (RNase A) was cross-linked with two different PIR molecules, 2Rink and BDP (14, 16) and the ReACT approach was applied. For this sample, the respective reporter masses were entered into ReACT so that ions matching either the mass relationship for 2Rink or for BDP would be identified as cross-linked peptide pairs. In either case, ReACT selected the released peptide ions that fulfilled the relationships in Eqn. 1 for MS^3 analysis. BDP and 2Rink labeled RNase A digests were mixed in equimolar ratios and four fully identified cross-linked products are discussed next. Of the four, two are obtained from BDP and two are obtained from 2Rink. All four share a single peptide with a unique second peptide. One pair overlaps between the two linkers (ETAAAKFER-NLTKDR). In Figure 3.3, this cross-linked site has been identified with both linkers within a single ReACT experiment. These two PIR cross-linkers differ in their engineered cleavage site. In BDP, the proline-aspartate amide bond acts as the low energy cleavage site, whereas, in 2Rink it is the tertiary amine within the Rink core structure. The permanent lysine modification or

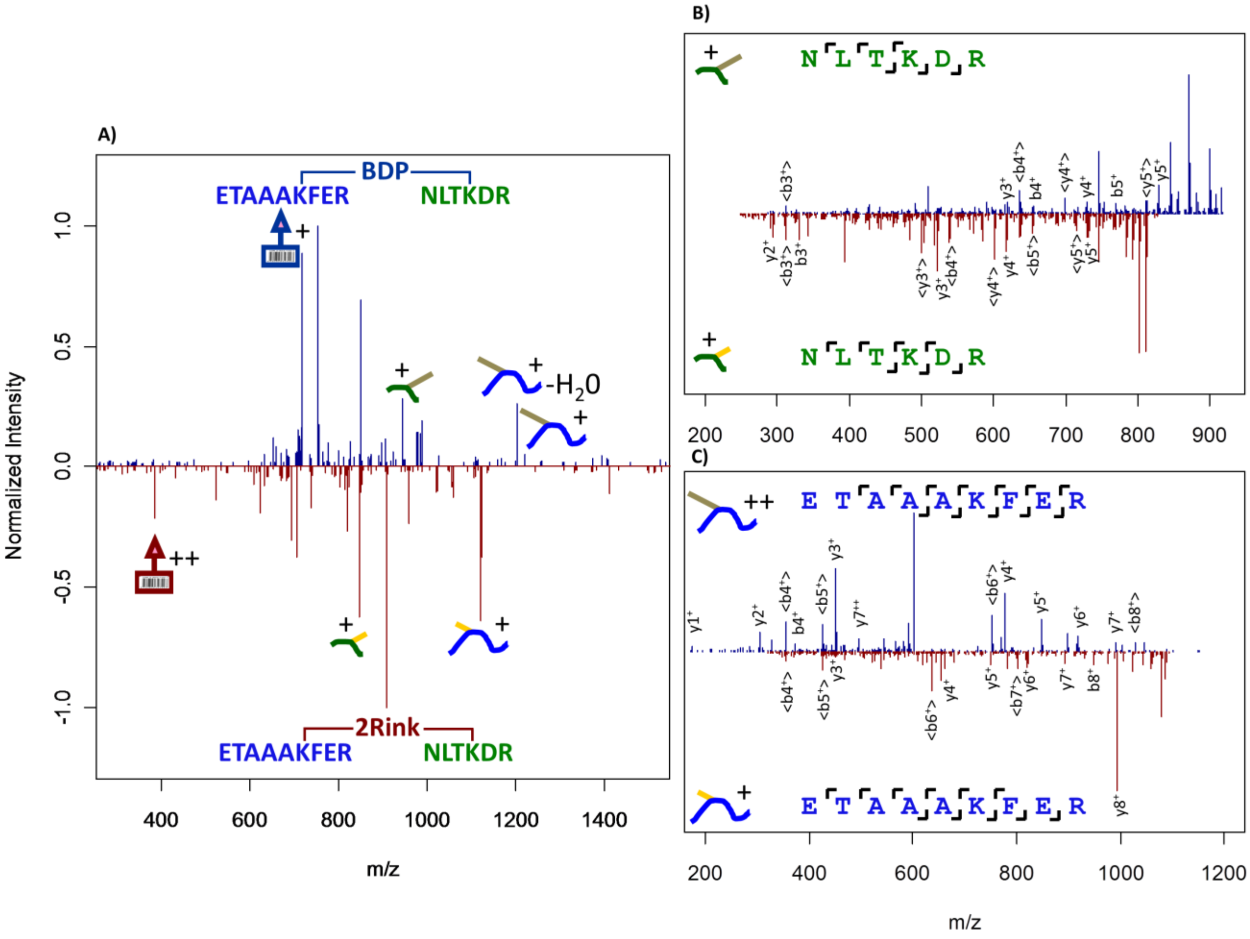


Figure 3.3. A) High resolution MS^2 spectra acquired on a cross-linked species with two different cross-linkers within the same LC-ReACT experiment. The cross-linked site identified involves the same two peptides from RNase A (ETAAAKFER and NLTKDR). The top contains this site identified with BDP cross-linker (blue) and the bottom contains this site identified with 2Rink cross-linker (red). Low resolution MS^3 was utilized for peptide sequence identification of NLTKDR (B) and ETAAAKFER (C) for both linkers.

"stump" mass of these linkers differs (99.032 Da for 2Rink or 197.032 Da for BDP). Therefore, peptides identified with this site have *b* and *y* fragment ions with different mass shifts due to the modification (Figure 3.3A-B). Although this effort is focused on the initial description and application of ReACT, these results demonstrate the capacity of multiple simultaneous cross-linker analyses with ReACT. This feature of ReACT will benefit sample analyses with multiple cross-linker molecules, e.g., with variable structure lengths, reactivity or physiochemical properties, and may further increase the number of observed cross-linked sites from cells.

PIR technology was used previously to study PPIs and topologies *in vivo* within *E. coli*(16) . In that study, a total of 65 cross-linked peptide pairs were identified using previously published mass spectrometry analysis methods and informatics tools(18, 19). Conclusive identification of these 65 cross-linked pairs was a labor intensive process, requiring multiple LC-MS runs, multiple sample preparations, and significant efforts in data processing and analysis. Since ReACT achieves both PIR relationship and identification of both released peptides within a single run, this approach is at least twice as efficient as previous methods, from sample consumption and instrument time considerations. With cross-linking conditions similar to those of Zhang *et al.*(16), ReACT analysis of three bioreplicates (one of which was the preparation was scaled up by 10x) resulted in 708 fully identified cross-linked peptide pairs, where both released peptides were identified using SEQUEST with false discovery rate (FDR) below 5% (Supplemental Table S3). Technical reproducibility of the ReACT method determined from replicate analysis of the same sample twice showed ~70% reproducibility on the basis of uniquely identified linkages (40% reproducibility among bioreplicates). Tabb *et al.*(26) suggest that 35-60% repeatability/reproducibility for technical replicates as an upper limit within standard discovery based proteomics experiments. Both technical and biological reproducibility observed with ReACT is well within this range. For further discussion see Supplemental Materials. Cross-linked sites where both peptide identities occurred at <5% FDR are referred to as high confidence sites. Because identification of each linked peptide proceeds via independent MS^3, it is possible that only a single peptide is identified by MS^3 while the other linked peptide fragmentation pattern fails to yield a conclusive assignment at the 5% FDR cutoff. Within *E. coli*, an additional 657 cross-linked relationships were observed in this category (referred to as low confidence sites). In these cases, accurate released peptide masses and the number of observed matching fragment ions were used to make putative sequence assignments to the peptides above the 5% FDR threshold. Even though the observed SEQUEST score for these ions did not fall within the 5% FDR cutoff, in all cases the accurate peptide mass and the largest number of matching fragment ions search yielded the top scoring SEQUEST candidate. Inclusion of these assignments increased the total number of cross-linked pairs to 1318 cross-linked peptides from *E. coli*. For the full list of 1318 cross-linked pairs including relationship mass accuracy and peptide sequence FDR (q-values) see Supplemental Materials. Parallel to ReACT development, a database for storage, visualization, and interpretation of large-scale cross-linking results has been developed (CrossLink-DB, http://brucelab.gs.washington.edu/CrossLinkDB)(27).

Cross-linked sites from *in vivo* experiments with *E. coli* cells were assembled into a protein interaction network (Figure 3.4A). High confidence cross-linked sites are indicated by a solid black edge and low confidence cross-linked sites are represented with light blue edges. Major "hubs" for cross-linking have been labeled with their UniProt identifier. Omitted from this network are nodes/proteins which are only represented by a single edge or only contain intramolecular cross-linked sites. Although far from comprehensive, these exciting maps are the first such direct interaction networks derived solely from *in vivo* cross-linking data acquired from *E. coli* cells. Figure 3.4B provides sub-cellular localization for all proteins identified within cross-linked sites as predicted with PSORTb(28). Approximately 25 % of the proteins found within cross-linked sites were found within cell envelope proteins (membrane, cytoplasmic membrane, periplasm). This suggests that cellular cross-linking may be viable for isolating and studying cell envelope proteins and their interactions, which is currently an area not well served by other techniques.

ReACT is a shotgun proteomics approach that advances peptide sequence identification for peptides in cross-linked relationships. Identified

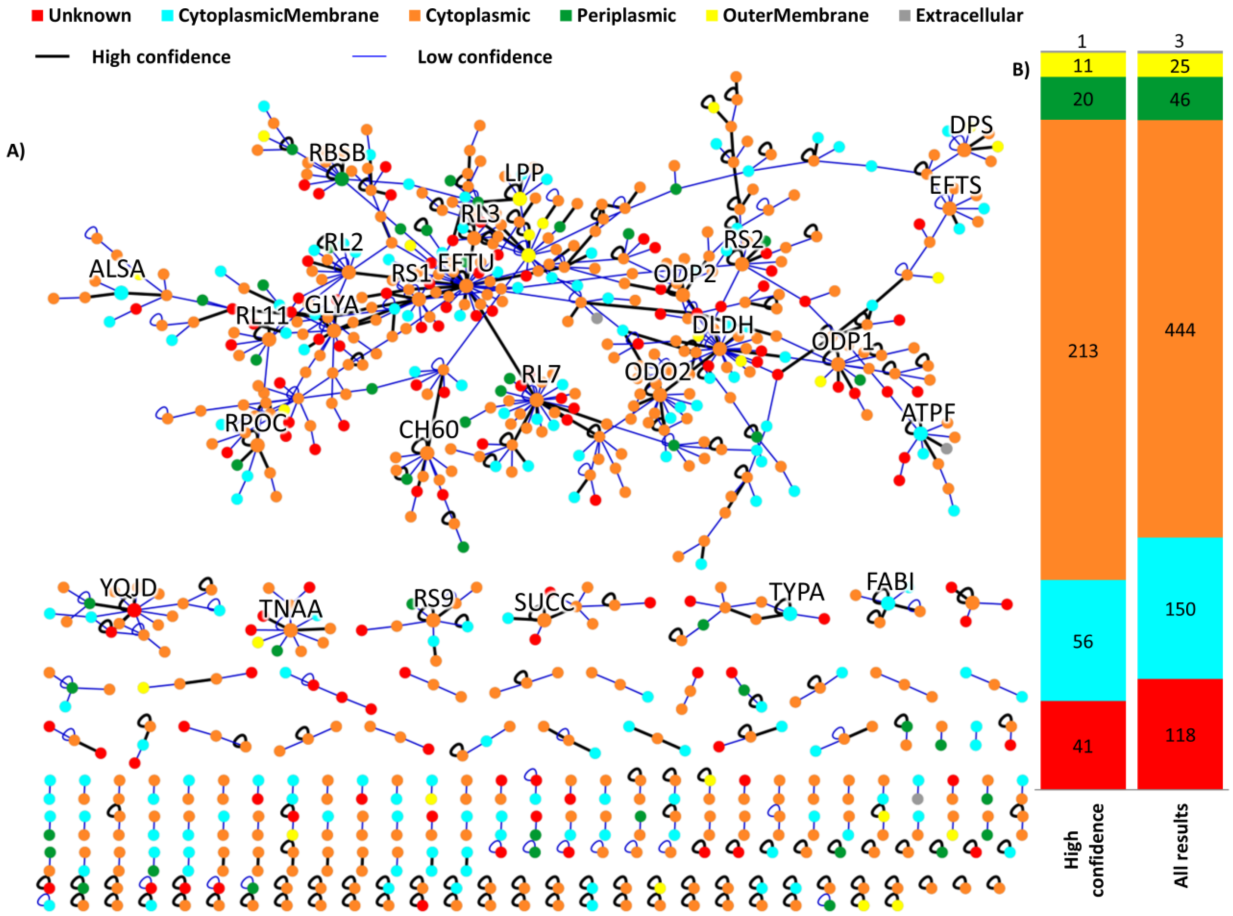


Figure 3.4. A) Interaction network comprised of cross-linked information obtained using ReACT on *E. coli* cells. Node colors represent the sub-cellular localization for the proteins identified in cross-linked sites. Large nodes represent "hubs" for which many cross-links between proteins were detected. B) Sub-cellular localization of cross-linked proteins.

peptides are used to infer protein identity. However, in contrast to typical shotgun proteomics experiments where identification of many peptides from a single protein supports that protein or protein family's presence within the sample, a single cross-linked peptide may be the only reactive site identified from an entire protein sequence. It should be noted that this same issue exists for all large-scale cross-linking and post-translational modification studies. To date, this remains a difficult problem to adequately address in large-scale proteomics datasets where modifications are considered. ReACT analysis results in identification of two peptides cross-linked to each other that may or may not belong to the same protein/family. Within the high confidence *E. coli* cell data presented here, 81% of the cross-linked sites reported have both peptides are non-redundant (described by a single protein) within the database. Additionally, 12.4% (88 of 708 identified) of the time one of the peptides associated with a cross-linked site is redundant (peptide sequence shared by multiple proteins). Finally, in only 1.5% (11 of 708 identified) of the cases are both peptides redundant in the database. Redundancy values are included for each of the peptides identified in Supplemental Table 3.

For peptides that are redundant among two or more proteins sequences, putative protein identities were inferred through a set of logical criteria derived to address this issue and described here. First, a peptide is preferentially assigned to a single protein from the list if that peptide can be mapped to the same protein as the other peptide in the cross-linked site. This logical assumption is derived from the fact that lysine residues nearby any reacted lysine site will predominantly be within the same protein sequence. Thus, if one of the redundant proteins is the same as the protein that yielded the other non-redundant cross-linked peptide, this entity is chosen. If this step cannot be satisfied, the redundant peptide is preferentially assigned to a protein from the pool of proteins resultant from all non-redundant peptides identified within ReACT datasets. This logical assumption arises from the fact that, because the protein was identified as cross-linked on other sites, cross-linker accessibility and reactivity with this protein is demonstrated. If one or more proteins in this pool contain the redundant peptide sequence, the proteins are assigned based upon their order of appearance within the database. Finally, if neither of the associations above can be made, a putative protein ID is assigned based upon the order of appearance within the entire protein database. With acquisition of larger cross-linking datasets where the number of redundant peptides is likely to become larger, advanced protein assignment methodologies will be implemented. These efforts will rank such assignments based on the frequency of representation of the protein family within the database, relative genomic distance between the two cross-linked proteins (e.g., are the genes for the two proteins within the same operon or under control of a single promoter), established protein interaction databases, or based on proteins uniquely identified in other cross-linked sites (or e-values)(29, 30).

The primary utility of cross-linking data from cells includes the identification of PPIs and topologies directly from their native physiological environment. These capabilities were specifically illustrated with intact virion capsid proteins in the *Potato Leafroll Virus*(31) and with discovery of OmpA multimer interactions and others in *E. coli* cells(16, 17). Here we focus on the ReACT method and its advanced capacity for identification of structurally-informative cross-linked peptides from cells. The size of resultant ReACT datasets presents a significant wealth of structural information derived from cells and precludes full discussion within a single publication. However, key macromolecular interactions within *E. coli* include the ribosome for which structural data are available and ReACT data on these complexes is discussed below. Nonetheless, the entire datasets of cross-linked peptides from *E. coli* cells are presented in Supplemental Information.

In *E. coli*, ribosomes have two subunits and are comprised of RNA and protein molecules with 56 different protein sequences. Figure 3.5 illustrates the *E. coli* ribosome structure (PDB 3FIH) with 3 of 4 inter-protein cross-linked pairs identified from cells in this study using ReACT. Visualization of macromolecular complexes such as the ribosome has led to a better understanding of how these complexes function within the cell(32). Here we present measurements from ReACT which for the first time, confirm the protein-protein proximity within cells. In this figure, all inter-protein cross-linked sites indicating PPI’s are presented where linkage between two different ribosomal protein sequences was observed. For clarity, other ribosomal intra-protein cross-linked pairs (200 cross-linked pairs) that were identified are omitted; however, these cross-links still provide unique topological information such as proximity and solvent accessibility of lysine residues as they exist in cells. Also omitted are inter-protein cross-linked pairs between ribosomal and non-ribosomal proteins e.g. elongation factor TU. Three of four inter-protein cross-linked sites within the ribosome assembly were mapped directly to crystallographic data (all cross-link sites are < 25 Å). One observed cross-linked pair was not mapped since the available ribosomal crystal structure does not contain these proteins (RL7_ECOLI and RL10_ECOLI). The peptides identified with this cross-linked site are shown to be non-redundant or unique to the protein which they are associated (Appendix C). RL10 and RL7 have been co-crystalized with the ribosome in *T. thermophilus*(33) but never resolved. This cross-link between RL7-RL10 illustrates how ReACT can provide new and complementary information on complexes as they exist in cells that have been heavily studied using *in vitro* techniques. ReACT enables confirmation of many crystallographic measurements of the ribosomal structures with data obtained directly from cells. Many (194 <5% FDR) other non-ribosomal inter-protein linkages are

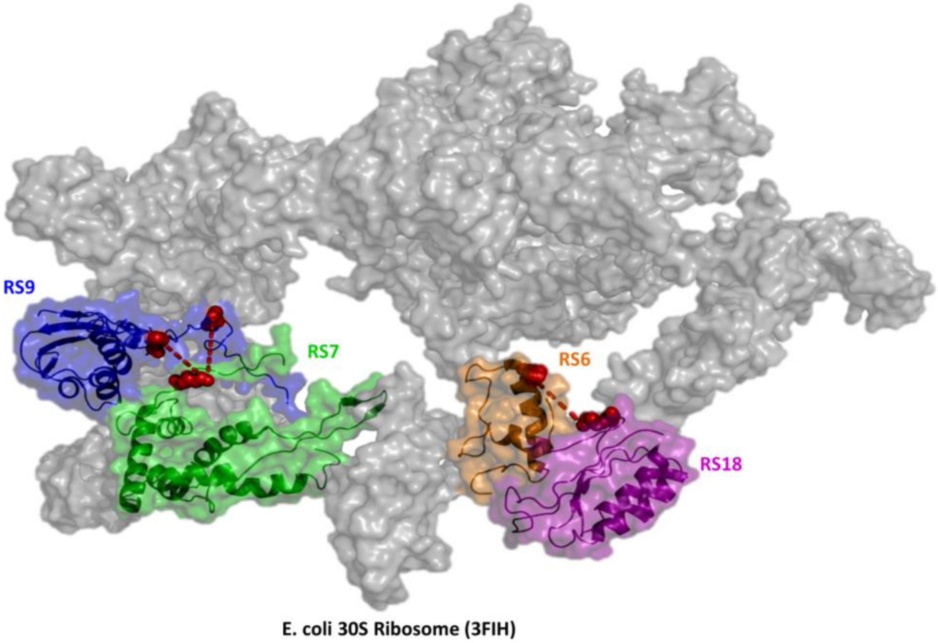


Figure 3.5. *E. coli* 30s ribosome (PDB 3FIH) with 3 of 4 observed inter-protein ribosomal cross-links mapped (RNA has been omitted). To view an animated illustration of cross-linked sites on the molecular structure see: http://brucelab.gs.washington.edu/ReACT_movies.php

present within these data which provides new knowledge beyond previously characterized PPIs and topologies. For a summary number of inter- and intra-protein cross-links see Appendix C.

Inter-protein cross-links discovered with ReACT provide new information about protein interactions directly from E. *coli* cells. These data can be broken down into three separate categories: previously observed, likely, and uncharacterized. To do this, the inter-protein cross-link results presented in Figure 3.4 were compared to available protein interaction data from Ecocyc.org (EciD – protein interaction database). From this comparison, 39% of the PPI’s presented here have been observed previously through alternative experimental techniques (yeast two hybrid, coIP, etc.). However, even for these known interactions, the data acquired with ReACT provide new topological information on these and help visualize how these proteins interact as they exist inside cells. Moreover, 50% of the PPI’s discovered using ReACT were found within one node of a known interacting pair discovered using other experimental techniques. That is, 50% of the PPI discovered in cells with ReACT include proteins that are known to participate in the same complexes, but not previously known to interact directly. For example, protein A interacts with protein B and protein B interacts with protein C, but protein A is not known to interact directly with protein C based on empirical data. Here, these PPI’s are classified as secondary interactors and include for example, N-acetylmuramoyl-L-alanine amidase (AmiA) that has been shown to interact directly with proteins in the 30s (rpsA and rpsO) and the 50s (rplD) ribosome. Although direct cross-linked sites between AmiA and rplD, rpsA, or rpsO were not observed, AmiA was identified as a cross-linked product with rplB (a known direct interaction partner of rplD) of the 50s ribosome with two unique sites. Although this and other interactions appear in existing databases as secondary interactions, *in vivo* cross-linking results made possible with ReACT illustrate they are present in cells close to one another and can be linked directly together. If these proteins are not directly interacting, the cross-linking data suggests they are at least participating in the same complexes at the same time with non-random relative orientation. In summary, 89% of the interactions identified with ReACT are previously known as direct or secondary interactors. Excitingly, ReACT yields new topological data on all these interactions as they exist in cells. This new topological data is really just the tip of the iceberg. Although ReACT represents a significant breakthrough in terms of number of cross-linked species identified in a single biological system, there is still much improvement to be made for a more comprehensive interactome "view" can be achieved in a single experiment. Two major areas exist where significant technological advancement could improve interactome coverage through cross-linking studies. The first area is with the database search strategies. Post-search rescoring approaches as described(34) are really only applicable to large datasets with the appropriate statistics. A rescoring approach which operates under new models that account for XL-MS specific assumptions, akin to that which was described for non-cleavable linkers(29, 30) would make further advancement on ReACT data analysis. In addition, application of a so-called stage 1 database restriction as described by Anderson *et al.*(18) also appears to yield a 30% improvement in the number of identified cross-linked species. The second area for improvement is cross-linked sample preparation and purification of cross-linked peptides from complex mixtures. Although significant headway is being made(35), many unidentified and unlabeled tryptic peptide species are observed in the final purified samples. This added complexity hinders ReACT and limits the dynamic range of cross-linked species that can be observed. A multi-faceted approach, including orthogonal separation techniques, will be required on the protein and peptide levels to truly achieve samples comprised primary of cross-linked species from cellular, tissue, or otherwise complex cross-linked samples.

Conclusions:

ReACT is a new method for identifying cross-linked peptide pairs using mass spectrometry cleavable cross-linkers that is directly integrated into the mass spectral acquisition. ReACT extends current detection and identification limits of cross-linked peptide pairs by focusing the analysis time and instrument duty cycle on those ions which specifically meet the mass relationships engineered in PIR chemical cross-linkers or similar molecules. Operational time is reduced by not having to perform post-acquisition data analysis beyond that of a conventional proteome database search. The ReACT algorithm is compatible for use with any flexible high resolution mass spectrometry platform with up to MS^3 capability as well as a wide range of cross-linker chemistries for PPI and topology studies within complex biological systems. ReACT enables the first large-scale identification of cross-linked species from cells, on the order of 1000's of cross-linked sites, which represents a 10-fold improvement over any previous report. With further improvements in cross-linked sample preparation methods, cross-linker molecular design and advanced database search strategies optimized for released peptide identification, proteome-wide PPI and topological analyses are a realistic goal.

Acknowledgements:

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Chapter IV: Directed Interrogation from Feature Ratios

Introduction:

A primary objective of quantitative proteomics research includes identification of differences in abundance levels of proteins, posttranslational modifications and interactions, often to enable functional inferences. The observation that several proteins change in abundance levels in a related way can sometimes help establish functional connection between proteins of unknown function(1). Proteome-wide quantification with mass spectrometry based proteomics is achievable through many independent strategies(2). These include MS(3) and MS/MS(4, 5) mass tagging methods whereby ions in either the mass or tandem mass spectra are used for peptide quantitation to estimate protein levels in original proteome samples. With samples from systems amenable to cell culture, Stable Isotope Labeling of Amino acids in Cell culture (SILAC) is a commonly used method(3) where Arginine and Lysine amino acid labeling is commonly employed, allowing all tryptic peptides to be observed as a heavy and light pair for relative quantitation (refs). In general however, any tag that adds observable mass to peptides (peptide fragments or reporter ions) but otherwise does not alter chromatographic or mass spectral properties imparts the ability to yield relative proteome quantitation within a single LC/MS/MS acquisition.

A key challenge in proteome quantitation revolves around the dynamic range over which proteins can be effectively quantified(6). Achievable dynamic range is normally a product of MS/MS acquisition speed since most commonly, data-dependent acquisition (DDA) is achieved by ion intensity-based automated decisions. Ions that appear most intense in spectra are first to be isolated and analyzed by tandem MS methods. For proteome mining efforts, DDA methods present a useful approach since replicate analyses can be performed to dig ever deeper into lower level peptide signals by placing identified peptides on exclusion lists to make more time available for lower abundance peptides. However for quantitative proteomics efforts with goals focused as described above, DDA methods are less desirable since proteins with altered abundance levels may not produce peptides that appear in the top tier of observed intensities, meaning these species are never isolated/identified/quantified. In quantitative proteomics experiments, it is often more useful to focus tandem mass spectral capabilities on only those peptides that appear with altered intensities. To effectively achieve this in multiple, replicate LC/MS/MS experiments, we previously developed and presented a post-acquisition software tool called SILACtor(7) that can yield target masses and retention times for ions with SILAC peptide pair ratios that appear significantly different from the measured distribution of ratios. Ideally, this could be accomplished within a single LC/MS/MS acquisition so that sample fractionation steps such as strong cation exchange, gas phase fractionation do not yield prohibitively large numbers of repeat analyses that must be acquired on SILACtor-targeted masses. Here, we describe a new real-time acquisition strategy called Directed Interrogation from Feature Ratios (DIFR) that uses accurate mass differences from SILAC or other samples with expected mass relationships to pinpoint differentially-labeled mass pairs. The intensity ratios of all assigned mass pairs in every spectrum are automatically determined with DIFR to define real-time sample ratio distributions on-the-fly during LC/MS/MS acquisition. Ions with observed intensity ratios outside the inter-quartile range (or user-defined limits) are then immediately selected with DIFR to enable real-time MS/MS analyses on peptides that appear with altered levels. DIFR makes more efficient use of MS/MS time during LC separation of peptides by targeting only those peptides with ratios that differ from most of the population. DIFR is advantageous since replicate runs need not be performed and ions with altered ratios are isolated and fragmented when first observed. Another DIFR advantage is that, since the distribution of ratios is defined in real time, shifts in the median of the ratio distribution do not prevent MS/MS targeting of outliers with DIFR. For instance, unintended shifts in the ratio distribution median that might occur from sample mixing errors or even larger shifts from time-course samples where the median ratio can change dramatically do not deter effective DIFR analysis. The distribution of ratios measured in real time is used within DIFR to define dynamic limits for ions to be targeted for MS/MS analysis. DIFR is demonstrated with SILAC samples from sensitive and drug resistant HeLa cells, although DIFR is compatible with virtually any mass tagging strategy to enable more efficient identification of proteome differences.

Methods:

DIFR Algorithm

The DIFR algorithm was written in ion trap control language, a native language used with Thermo Electron mass spectrometers. The flow chart in **Figure 1** outlines the basic steps achieved automatically during LC separation of analytes with DIFR. First, a high resolution mass spectrum is acquired and mined for SILAC pairs. Pairs are automatically identified as m/z values whose delta m/z are within +/- 1 ppm of the expected mass difference defined by the user. These pairs must have the same charge state to be considered. All pairs regardless of their observed relative isotope abundance (RIA) are added to a cache for statistical distribution analysis. Once this cache reaches capacity, distribution statistics are automatically calculated in DIFR (inter-quartile range, mean, 10% trimmed-mean, and standard deviations). Successive MS1 acquisitions are used to replace pair ratios with the longest residence time within the cache so that newly eluting peptide pair ratios continually displace previously measured ratios. Therefore, these statistical parameters are monitored in real-time DIFR through-out the acquisition. With this information, DIFR then targets MS/MS sampling to only identified SILAC peptide pairs which exceed user-defined ratio criteria. For

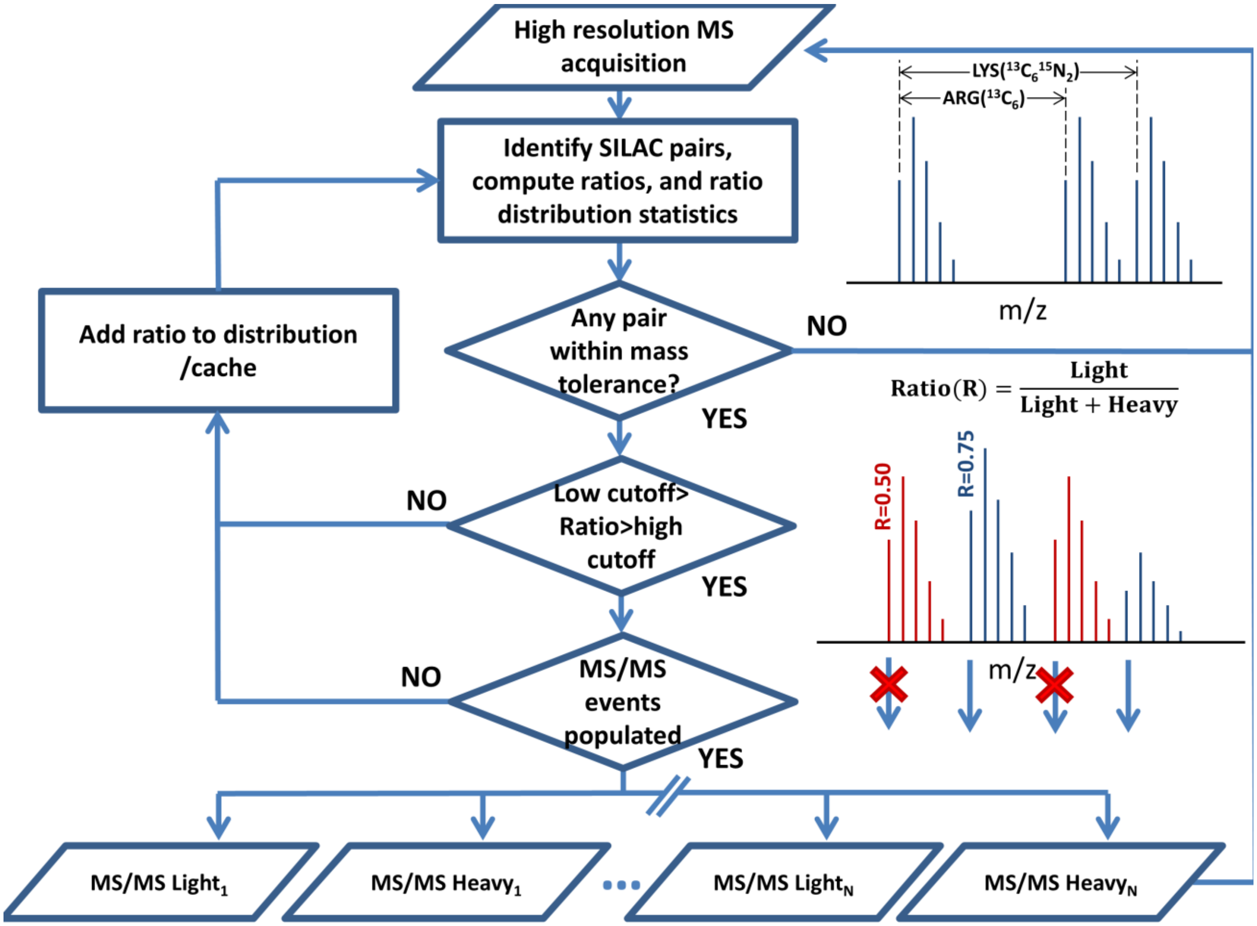

Figure 4.1: A diagram of the DIFR algorithm. This process directs sampling in real-time during data acquisition.

data presented here, we required our ratios be outside the inter-quartile range. This effectively removes the middle 50% of the observed ratios from the available precursors for MS/MS sampling, making instrument MS/MS time available for those species which have shown altered ratios. A histogram is plotted and displayed on the DIFR user GUI in real-time during acquisition to assess sample quality and track the acquisition progress. Finally, DIFR is also compatible with the dynamic exclusion process so once peptides with altered ratios are investigated with MS/MS, they need not be isolated and fragmented again, leaving greater mass spectrometry acquisition time available for other species.

Cell Culture

HeLa cells were cultured in DMEM supplemented with 10% FBS and 100 units/mL penicillin-streptomycin, in a humidified atmosphere containing 5% CO_2 at 37°C with media renewal every 2-3 days. The cisplatin-resistant derivative line, HeLa/CDDP (8), was maintained in identical conditions and media with 1μM cisplatin. Additional samples of HeLa/CDDP were grown in the absence of cisplatin for a period of 48 hours prior to harvesting to allow observation of the effects of the presence of cisplatin on the proteome of these cells. For SILAC experiments, cells were cultured in heavy DMEM containing L-arginine-$^{13}C_6$ and L-lysine-$^{13}C_6{}^{15}N_2$ for at least five cell doublings. Cells were harvested using 0.05% trypsin with EDTA (Thermo, San Jose, CA), followed by washing with ice cold PBS and stored at -80°C.

Liquid Chromatography-Mass Spectrometry

All samples were analyzed on a custom dual linear RF ion trap Fourier transform ion cyclotron resonance mass spectrometer, hereafter referred to as the Velos-FT. The mass spectrometer is directly coupled with a Waters NanoAcquity UPLC system. Peptides were then eluted from the trap column and separated by reversed-phase chromatography over an analytical column (55 cm x 75 μm i.d.) packed with 100 Å Magic- C4AQ at a flow rate of 200 nL/min using a linear gradient from 90% solvent A/ 10% solvent B to 60% solvent A/40 % solvent B over 120 min for a 2 hr data acquisition. The structure of DIFR consists of the following mass spectrometry data acquisition parameters. The first acquisition is a high-resolution precursor acquisition (50,000 resolving power (RP) @ 400 *m/z* over the range 400-2000 *m/z*). Dynamic exclusion is utilized with the following parameters: repeat count = 2, repeat duration = 15 s, dynamic exclusion list size = 500, dynamic exclusion duration = 30 s. FT preview mode and predictive automated gain control (pAGC) were not utilized. A series of 20 RF ion trap MS^2 acquisitions were used to acquire fragmentation spectra of peptides with identified SILAC pairs targeted by DIFR. The overall acquisition cycle is ~5.2 sec. in length when ion injection times are at their maximum values (0.5 for FTMS, 0.1 for ITMS).

HeLa Cell Sample Preparation

The cells were lysed by heating to 95°C in 4% sodium dodecylsulfate (SDS) 1x Tris buffer at pH 8.5. The sample was ultrasonicated to shear DNA and was centrifuged at 16 kg for 10 min. to remove insoluble material. The sample was then added to a 30 kDa molecular weight cut-off (MWCO) filter (Millipore, Location) and concentrated by centrifugation at 7.5 kg for 30 min. A protein extract yield of 3.0-8.0 mg/mL was determined using a Coomassie Plus assay (Pierce, Rockford, IL). Prior to digestion heavy/light cultured samples were mixed at 1:1 (protein concentration) based upon protein assay results. The disulfide bonds were reduced using 5 mM tris (2-carboxyethyl) phosphine (TCEP) and the resulting free thiols were alkylated using 10 mM iodoacetamide (IAA). Digestion was carried out using a 1:200 w/w ratio of sequencing grade modified trypsin (Promega, Madison, WI) to protein and incubating at 37°C overnight with constant mixing. The samples were desalted using C18 Sep-Pak (Waters Corporation, United Kingdom) and dried in a centrifugal concentrator (Genevac, Location). The resulting samples were stored at -80°C until LC-MS analysis.

Results and Discussion:

The DIFR algorithm is designed to identify spectral features with static mass differences at high mass measurement accuracy (MMA). Therefore, it is universally applicable to any form of stable isotope labeling mass spectrometry experiment. Figure 1 provides a conceptual diagram of the logic carried out within the DIFR algorithm. First, charge states for all isotopic distributions observed in the present spectrum are calculated. The charge state is used to calculate monoisotopic mass. These masses are sorted and then sequentially mined in pairs to ascertain delta masses which correspond to the expected stable isotope label. The intensity ratio, expressed as the relative isotope abundance (RIA) for convenience, is then calculated:

$$RIA=\frac{I_{light}}{I_{light}+I_{heavy}} \qquad \text{(Eqn. 1)}$$

Where I_{light} is the intensity of the identified light mass and I_{heavy} is the intensity of the identified heavy mass. RIA is a continuous numerical ratio which always exists between zero and unity with 0.5 representing equivalent amounts of heavy:light (1:1). The RIA is then utilized to build up a statistical distribution of observed ratios. The RIA can now act as the final trigger for tandem MS interrogation of ions. Only, ion pairs which exhibit the user defined RIA thresholds for sampling undergo tandem MS. This allows for allocation of mass spectrometry resources to only ion pairs which are observed to be differentially expressed. The DIFR algorithm on average adds a minimal overhead to each scan cycle (36.1 +/-1.0 ms in HeLa digest; however, it remains dependent upon spectral complexity). With consideration of present state-of-the-art tandem MS acquisition rate ~10 Hz or 0.1 sec per spectrum this calculation adds minimal overhead to the overall experimental scan cycle.

DIFR has been directly incorporated into the instrument control software on a custom dual RF ion trap-FTICR mass spectrometer. This enables real-time output viewing of the statistical distribution through a graphical user interface (GUI). In addition, all identified isotope pairs are reported in real-time in tabular format. This list includes the m/z values for the ions in the pair, MMA for the pair, charge states, and precursor scan for the identification. This information could presumably be utilized in post-acquisition sequence identification to help limit search space (eg. SILAC ion pairs indicate tryptic cleavage residue (K/R) and number of missed cleavages). If tandem MS are acquired on both the light and heavy ions the spectral data taken together could aid in *de novo* peptide sequence identification.

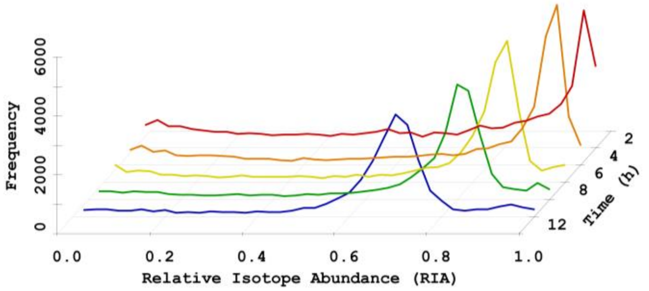

Figure 4.2: Heavy isotope incorporation of HeLa cells monitored using DIFR. Each histogram represents a separate experiment performed at each harvested time point. DIFR is capable of obtaining an accurate survey of heavy:light RIA ratios on-the-fly.

As a proof of principal, DIFR was utilized to monitor heavy isotope incorporation of HeLa cells after switching to heavy cell culture media (LYS-$^{13}C_6{}^{15}N_2$ and ARG-$^{13}C_6$). Cells were harvested at regular intervals and the lysate digest was analyzed via LC-DIFR (Figure 4.2). The initial addition of heavy media is defined as t=0. In this experiment, drug sensitive (wild-type) HeLa cells were allowed to incorporate heavy isotopes from the media. As a function of time all light protein in the cells was replaced with heavy isotope labeled counterparts. The RIA in this experiment represents the percent completion of isotope incorporation. Typically, the SILAC process involves growth of one conditional cell sample upon heavy media. Here we are simply utilizing the incorporation process as a de facto proof of principle measurement for DIFR. DIFR has been developed to adapt to any distribution of RIA ratios and adjust tandem MS sampling accordingly. This uniquely demonstrates that DIFR is able to track the incorporation of heavy isotope in this series of samples and perform as requested. Figure 4.2 illustrates that DIFR is capable of identifying isotope pairs from stable isotope labeling in cell culture (SILAC) experiments. More importantly , this experiment demonstrates that determination of the RIA ratios on-the-fly follows the expected incorporation rate of HeLa cells after switching to heavy media. The RIA ratios determined by DIFR are “instantaneous” in that they are not area under the curve measurements from liquid chromatography elution profiles. These instantaneous measurements are made from a single spectrum, however, the quantitative information obtained via DIFR is often in good agreement with post-processing techniques based on area under the curve.

Through the focusing of mass spectrometry resources only on isotope pairs observed to change, in principal, tandem MS sampling should occur deeper into the dynamic range on a per spectrum basis. This hypothesis has not yet been proven in our studies with DIFR, presumably due to inherent limitations with the data acquisition computer. On a per spectrum basis, a peak list of 500 is supplied to downstream data dependent logic. This peak list was originally optimized by the instrument vendor for simple DDA tasks and therefore is limited in size. We have observed a limitation in DIFR due to the small size of accessible peaks for on-the-fly processing. In practice, most top N DDA experiments include 10-20 tandem MS events. This requires intensity dependent selection

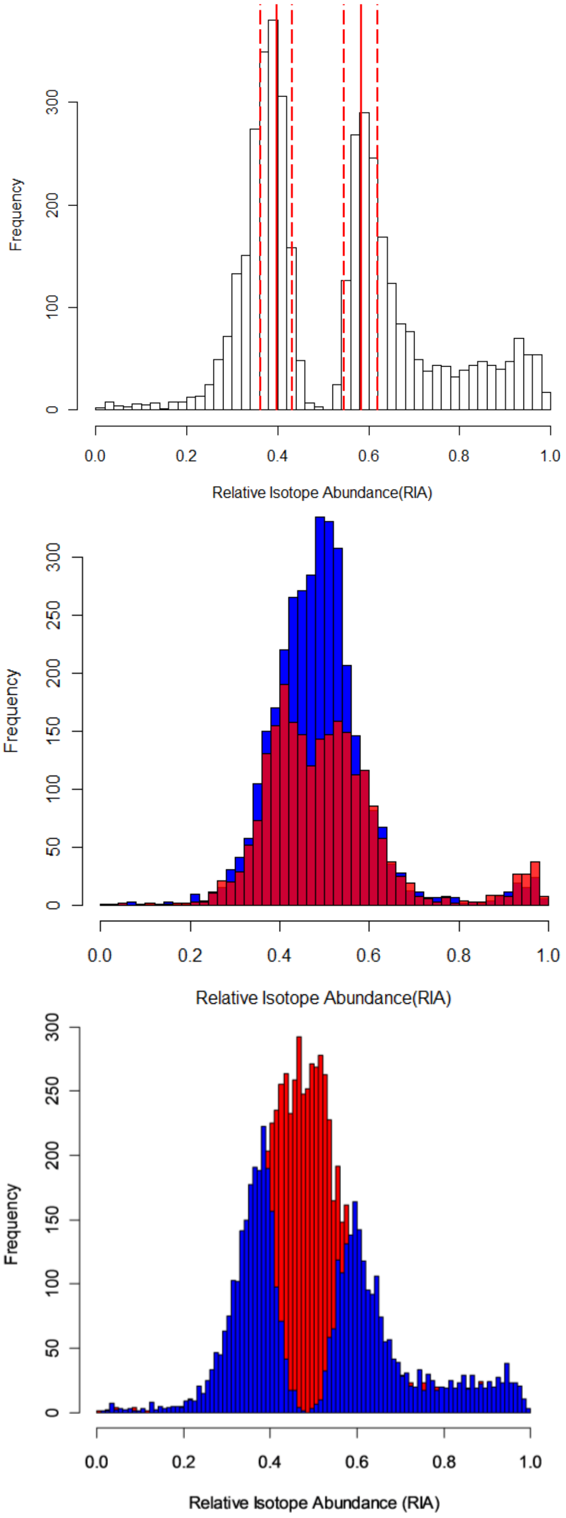

Figure 4.3: A) Raw distribution of RIA ratios determined on-the-fly by DIFR. Solid red vertical line represents average lower and upper IQR; Dashed red line represents +/- σ. B) RIA rations from both DIFR(red) and DDA(blue) post-processed. C) DIFR comparison with(blue) and without(red) IQR sampling thresholds.

of 10-20 precursors from the high resolution MS^1 acquisition. Therefore, the list of 500 peaks from the spectrum never imposes limitation in the DDA logic/sampling. However, with DIFR, selection of targets for tandem MS has been brought out of intensity space and is based on RIA of peak pairs. The mere fact that the experiment has been performed on stable isotope labeled samples decreases the effective peak list by ½ by virtue of heavy:light pairing. In addition, this list contains all peaks, not just monoisotopic peaks. This translates to fewer targets for DIFR to mine because the algorithm requires monoisotopic peaks. The overarching notion that hundreds of thousands or millions of peptides, and isotope pairs, are evidenced from post-processing MS^1 data, provides potential for DIFR to make tremendous impact on identification of differentially observed species. In a comparison between DDA and various operating parameters using DIFR (Figure 4.3), it is shown that DIFR is capable of sampling approximately the same number of low and high RIA species DDA, but doesn't appear to increase sampling at the lower and upper quartile range of RIA as intended. This observation supports the notion that DIFR is limited by the peaks the algorithm is supplied by the onboard acquisition computer.

This limitation can be overcome. The raw acquisition data could be intercepted and processed in parallel by another pipeline and reintroduced with all peaks from the spectrum. While this could present overhead to scan cycles, in principal the impact DIFR could still be evaluated without limitations on the peak list. An alternative approach of using logic to attempt to work around the peak list limitation may also represent a viable opportunity. A definitive study to determine the impact of utilizing DIFR will require this obstacle surmounted before proceeding.

Conclusions:

DIFR has been used to analyze HeLa cell samples cultured with SILAC. DIFR utilized RIA distribution in real-time to exclude SILAC peptide pairs which exhibit little relative change (interquartile range (IQR)) from selection for MS^2 analysis. We compared DIFR to a typical data-dependent acquisition (DDA) SILAC approach and show increased MS/MS acquisition of peptides with significantly altered SILAC ratios in HeLa cells. DIFR is used to demonstrate how real-time informatics can provide focus to SILAC mass spectrometry experiments, to potentially identify more peptides with altered SILAC ratios, and increase useful content of each experiment. Further progress will be required for an unbiased comparison with DDA, such increasing the peak list depth available to DIFR on a per precursor acquisition basis.

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Conclusions

With mass spectrometry technology advancing, especially in the realm of mass analyzers, it is expected that MMA will only improve and become a less cost prohibitive merit when purchasing new equipment. A large install base of mass spectrometers capable of high MMA will likely drive further innovation in terms of applications and methodologies which rely heavily this discriminating quantity. The preceding research demonstrates novel applications for MMA within proteomics to enable new capabilities. The Velos-FT instrument design provides a unique test-bed for development of mass spectrometry techniques due to its unique dual RF ion trap FTICR-MS hardware configuration. Increased peptide (50%) and protein (30%) identification was observed over the most immediately comparable predecessor (LTQ-FT). On average, the Velos-FT was capable of identifying more low copy-number proteins than the LTQ-FT from yeast lysate digest. The high MMA of this instrument enabled development of a novel DIA strategy/approach called, FT-ARM. This approach leverages high resolution MS^2 fragmentation patterns and number of matching fragment ions to identify and quantify peptides within complex mixtures. Quantification is linear over nearly the same range as widely used MRM methods. Atto-mole level detection was observed using this technique, which proves that broadband DIA is capable of similar sensitivity levels as DDA. While it was observed that the peptide identifications/amu improves with narrower band isolations for the multiplexed MS^2 acquisition, it was shown that with 100 amu isolation width the FT-ARM algorithm was capable of identifying nearly all that a DDA-SEQUEST pipeline could. Finally, this approach alleviates the need to develop labor intensive MRM assays.

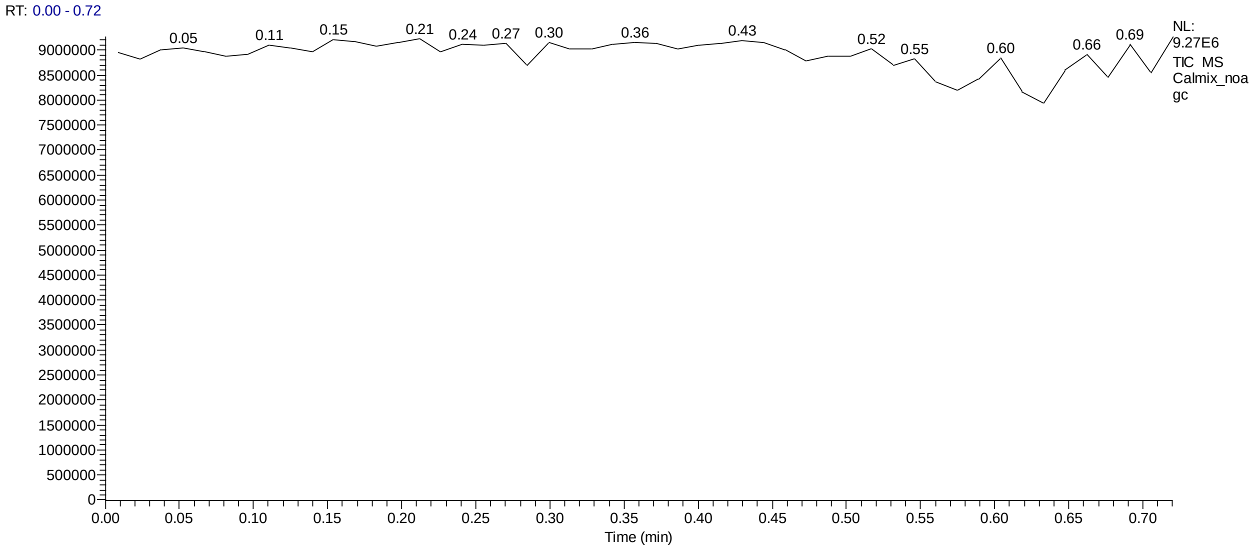
Real-time informatics will likely become common-place in mass spectrometry acquisitions in the near future. This is because of the performance improvement real-time or on-the-fly informatics promises. Mass spectrometry acquisitions are made more effective by incorporation of real-time informatics in that species of greatest importance are assigned and interrogated on the fly. This effectively bridges the gap between purely targeted and discovery experiments. MMA is a characteristic which permits rapid assignment of mass differences and other spectral features for further informatics processing. Here, I have shown how real-time informatics can be utilized to greatly influence the number identifiable cross-linked species from XL-MS studies of *in vivo* cross-linked cells. This method was applied to CID cleavable cross-linkers, chemically engineered to dissociate from intact precursor to individual peptides plus a reporter ion. The mass relationship which arises between the precursor and the sum of its parts (peptide A, peptide B, and reporter ion) are exploited in real-time to directly target both peptides for MS3 analysis aimed at identification of their primary amino acid sequence. This method produced the largest and most comprehensive cross-linked protein measurements directly from cells (708 unique cross-linked peptide pairs). Cellular systems which have been successfully probed with this technique since its inception include *E. coli, A. baumannii*, HeLa, *P. aeruginosa*, and *S. cerevisiae* resulting in identification of thousands of cross-linked sites. Development of sample preparation methodologies, refinement of the ReACT algorithm, and new cross-linker chemistries will further advance cross-linking technologies for global interactome analyses.

New capabilities that target mass spectral features based on mass differences has been the focus of the final chapter presented here. In DIFR, the expected mass difference between a peptide containing the natural abundance of organic elements from which it is comprised and that of a stable isotope labeled version of the same peptide is identified on-the-fly. The intensity ratio between these light:heavy pairs is used to identify peptides which are altered in abundance. This provides the opportunity to focus tandem MS duty cycle on the most important species within the sample; those which are changing under a test condition.

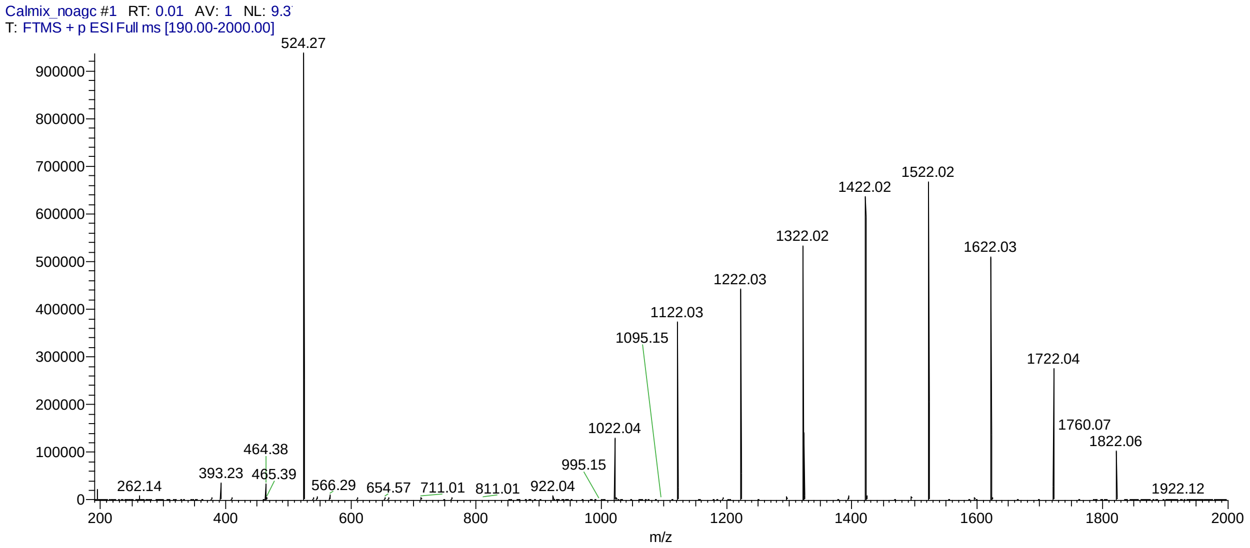
Appendix A: Supporting information for the Velos-FT

Appendix Figures 1-4 are the TIC’s and spectra for an Ultramark standard direct infusion experiment to discern whether major differences in ion transfer efficiency exist between the two systems. These data indicate that only major distinguishing factor between the two instruments are the performance enhancements of the dual linear RF ion trap mass spectrometer. For instance, when AGC is turned off and the ion accumulation time is held constant at (25 ms) for each system, there is roughly a factor of 10 higher observed signal intensity in the case of the custom FT-ICR MS. This can be rationalized in that this instrument has the capability to transfer and accumulate ions in the HPT with a factor of 10 greater efficiency. When the dynamic range of the spectra collected in the case of the custom FT-ICR MS and LTQ-FT where evaluated from these data it was found that the dynamic range observed was identical within error of the instruments (~30,000). This also can be rationalized because no modification was made to either ICR cell, both of which are Thermo Ultra cells. Appendix Figure 6A-6B shows a comparison of normalized spectra collected from a QqQ instrument (Peptide Atlas) against CID data acquired on the custom FT-ICR MS (6A) and the same QqQ spectrum compared to a DCF spectrum acquired on the custom FT-ICR MS (6B). The peptide identified as belonging to these spectra is TNNPETLVALR from the yeast protein YAL038W. Here it is visually apparent that the DCF fragmentation pattern is much closer to the QqQ acquired spectrum in both fragments observed and their relative intensities than the CID spectrum.

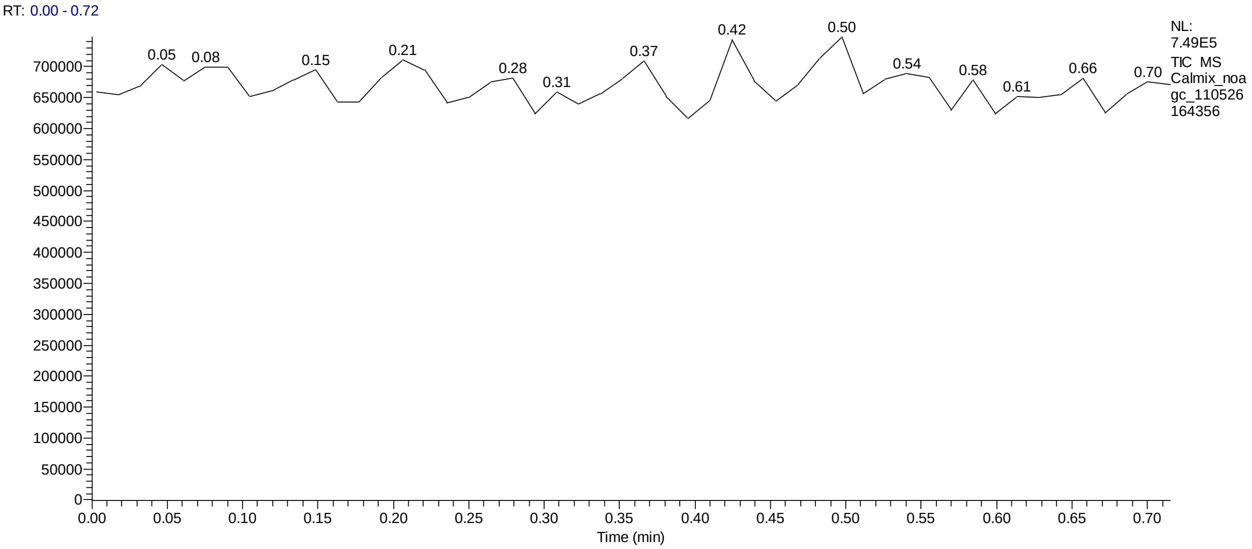
Appendix Figure A.1A: Custom FT-ICR MS Ultra TIC w/o AGC



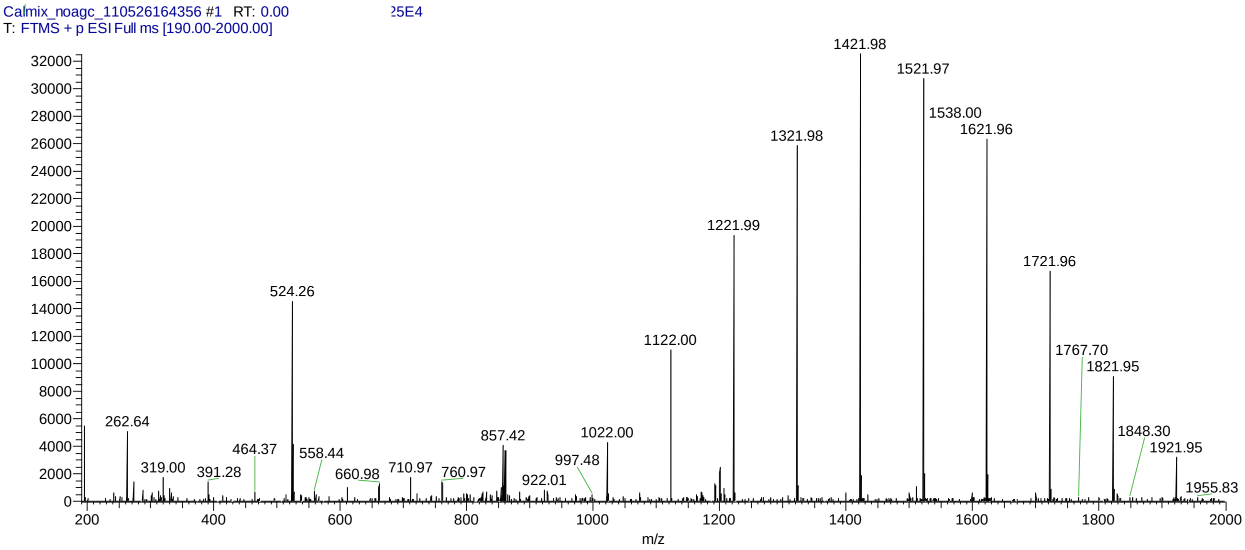
Appendix Figure A.1B: Custom FT-ICR MS Ultra spectrum w/o AGC



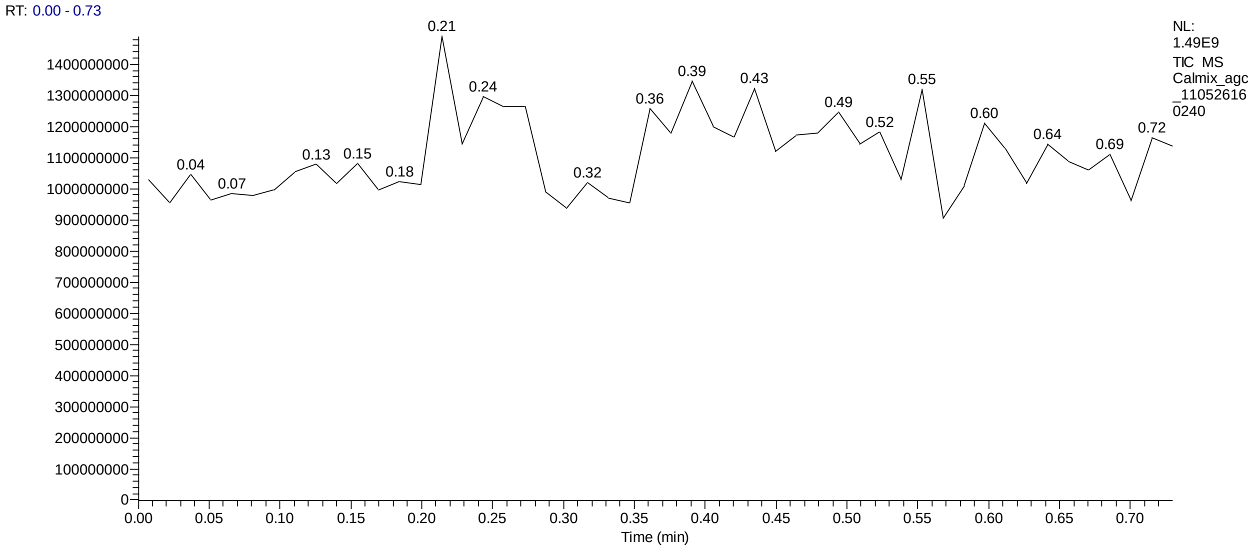
Appendix Figure A.2A: LTQ-FT Ultra TIC w/o AGC



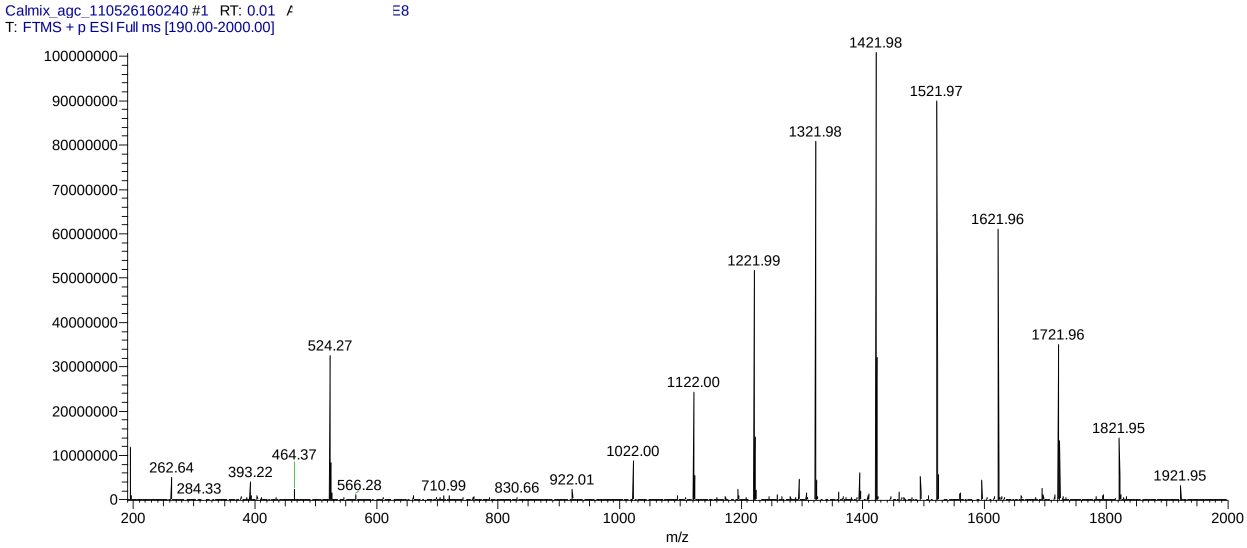
Appendix Figure A.2B: LTQ-FT Ultra spectrum w/o AGC



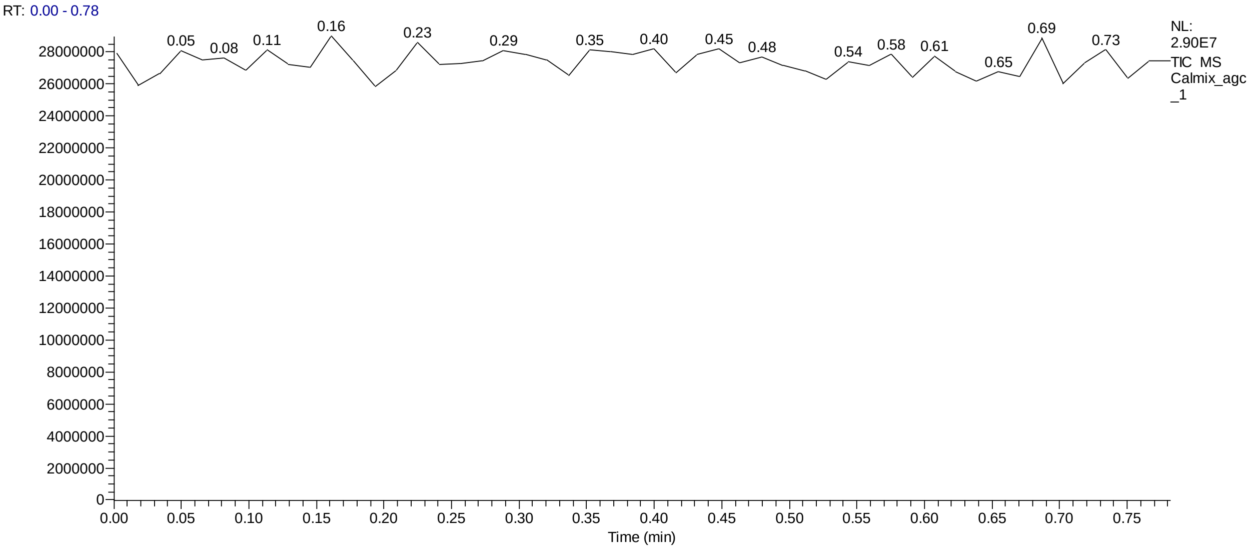
Appendix Figure A.3A: Custom FT-ICR MS Ultra TIC with AGC



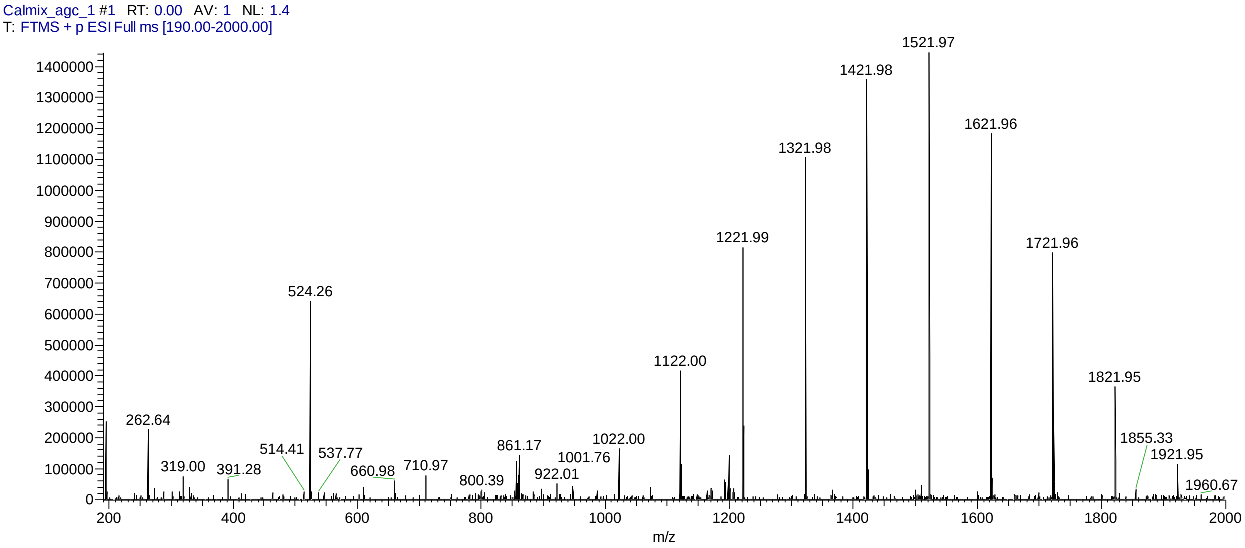
Appendix Figure A.3B: Custom FT-ICR MS Ultra spectrum with AGC



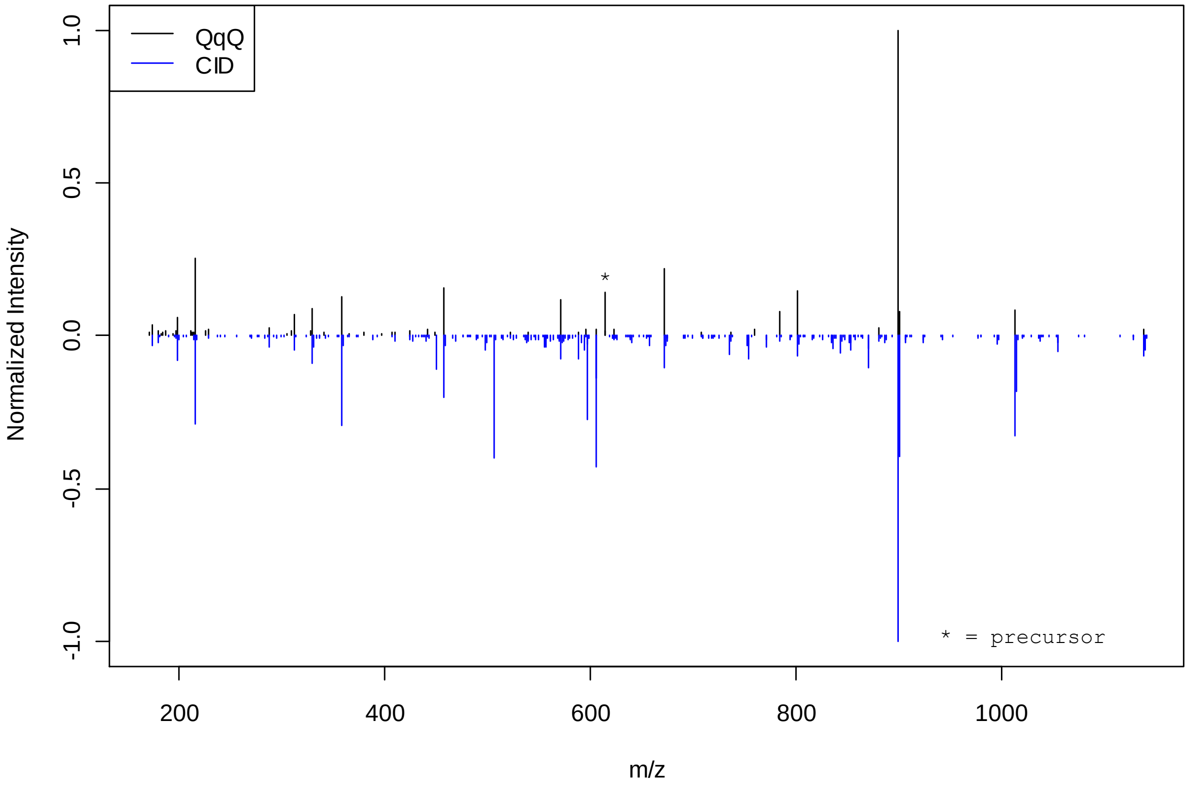
Appendix Figure A.4A: LTQ-FT Ultra TIC with AGC



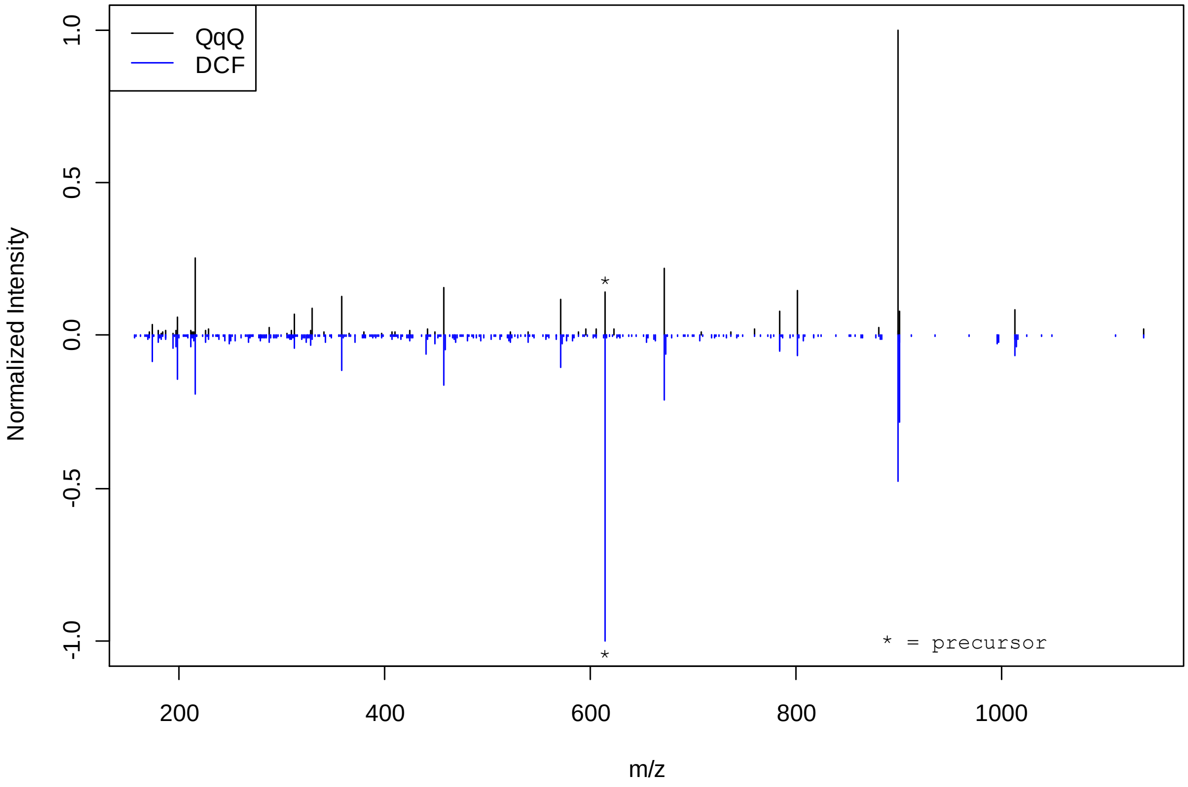
Appendix Figure A.4B: LTQ-FT Ultra spectrum with AGC



Appendix Figure A.5A



Appendix Figure A.5B



Appendix B: Supporting information for FT-ARM

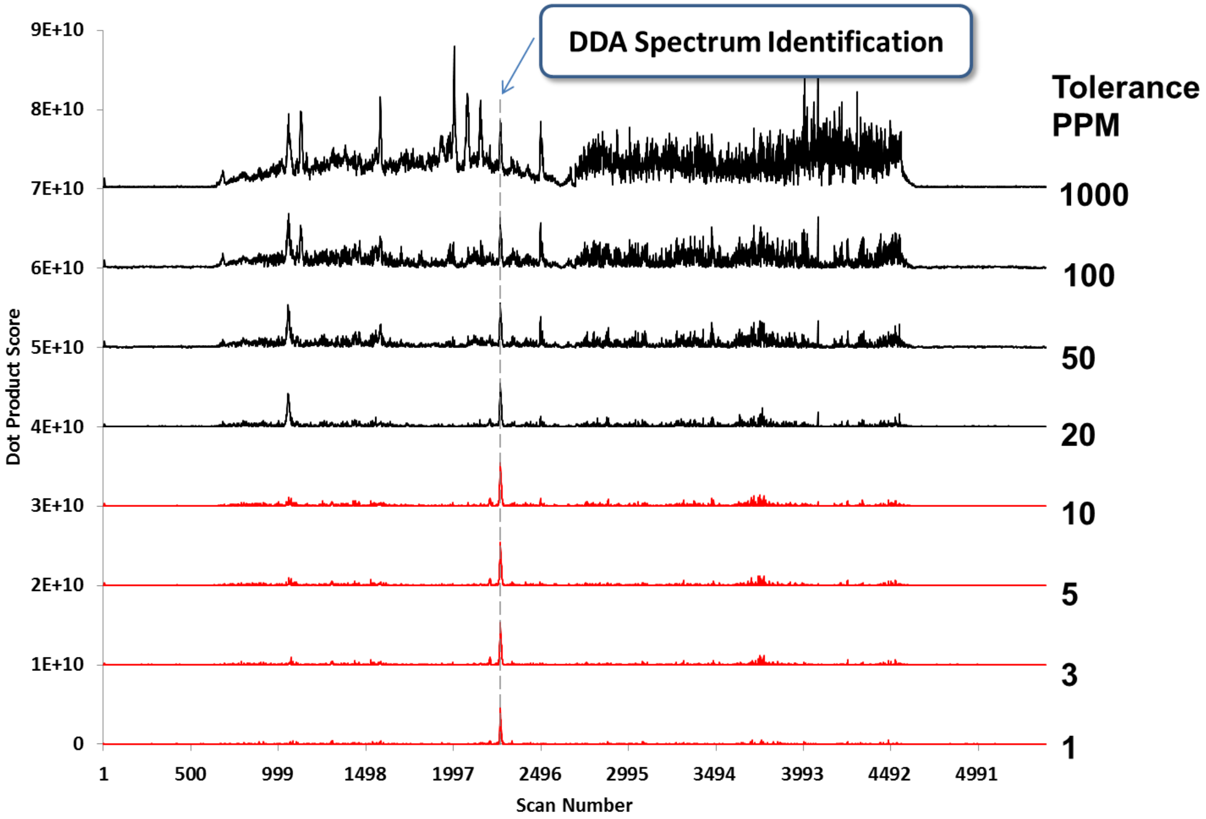
FT-ARM Theoretical False Peptide Match Simulation

The program was developed in-house using the C++ programming language. This program is a branch from the FT-ARM code which allows the user to input a FASTA database, a center mass, an isolation width, a number of replicates, and a match count threshold. The following parameters were used to generate simulation data: 750 m/z center, 100 m/z width, 5 replicates, and 1-16 match count threshold. Given the input parameters the program calculates tryptic peptides whose m/z value lie within the isolation window of interest. For each peptide in the database, a random subset of b and y fragment ions are sampled without replacement from that target peptide. This data stream is designed to simulate the hypothetical or spectral library data within the dot product calculation of FT-ARM. This set of fragment ions is utilized for an FT-ARM calculation against all other queried peptides in the database which fall in the isolation window and have a predicted hydrophobicity(1) within ±0.5 (SSRCalc)(1). The data stream of peptides calculated from the FASTA database within a set hydrophobicity window are designed to simulate the multiplexed data acquired by the mass spectrometer. All predicted b and y fragment ions are considered from the queried peptides in this calculation. In this way, any peptide which has met the latter criteria can contribute to the false identification of the target peptide. Target peptides are not scored against themselves during this simulation. If the number of matching b and y ions exceeds the match count for a given query this is termed a false positive match from the database. The percentage of false positive matches has been calculated by taking the average of 5 replicate simulations and dividing by the total number of queries in the FT-ARM search (# of peptides residing in the m/z window of interest).

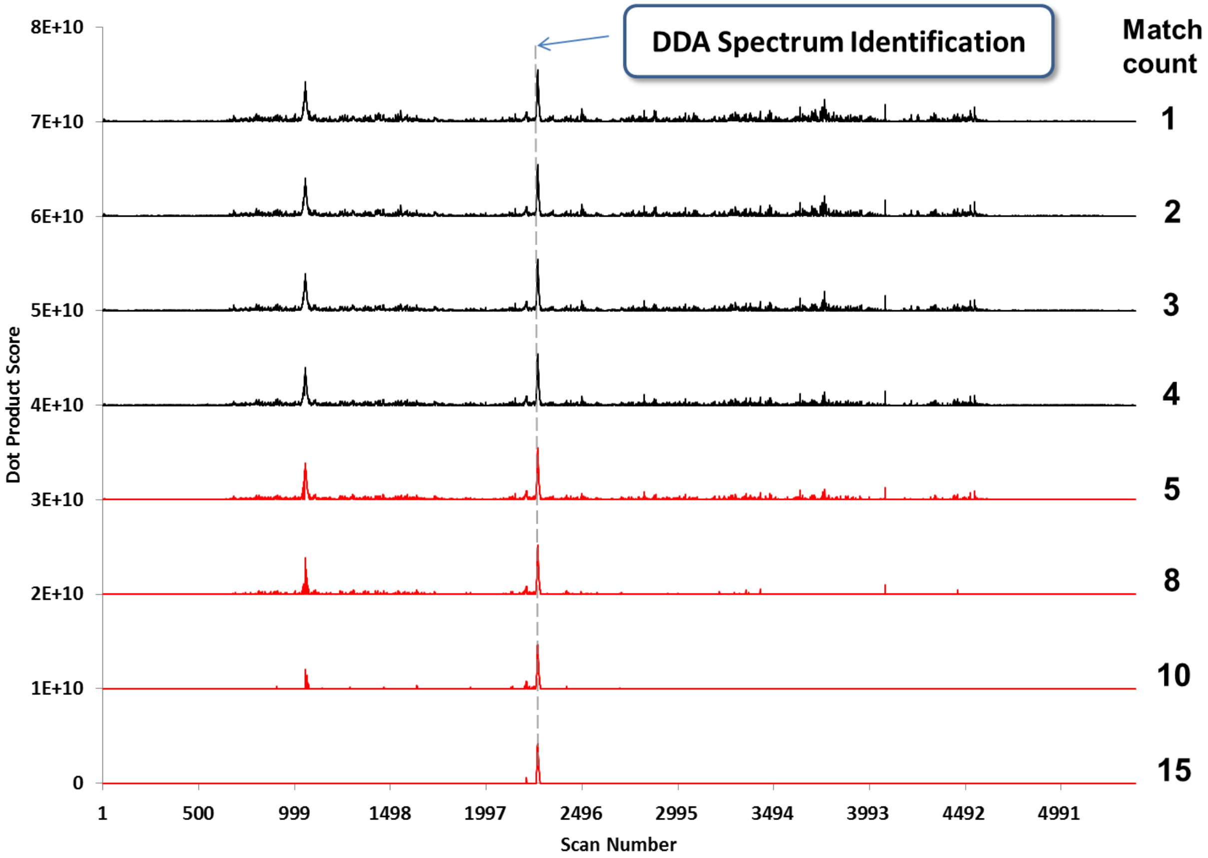
Post FT-ARM Data Processing

FT-ARM output includes peak areas for identified peptides integrated directly from score chromatograms, however, normalization and other post processing was performed using Excel (Microsoft, Redmond,WA)or R: A Language and Environment for Statistical Computing(R Group, Vienna, Austria). Specifically, quantification data presented in the BSA dilution series(DAFLGSFLYEYSR and VPQVSTPTLVEVSR) here has been normalized to a reference analyte yeast enolase 2(AVDDFLISLDGTANK). Peptide areas were extracted from SRM data using Xcalibur(Thermo Scientific, Bremen, Germany).

All peptides above 5% FDR were quantified in the *E. coli* dilution series. Peptides identified were normalized to a separate FT-ARM acquisition on *E. coli* lysate without the yeast lysate background. Each peptide sequence detected was normalized to the same sequence identified in the reference acquisition. Each dilution was analyzed in triplicate to provide statistics. Observed ratios (normalized to the reference acquisition) were plotted against the dilution ratio. In bar plots shown, “whiskers” represent one standard deviation, boxes represent 25th and 75th quantile, notches represent 95% confidence interval for determining difference between two medians, and the solid line represents the median of the data.



Appendix Figure B.1



Appendix Figure B.2

Appendix Figures B.1-2. **A)** Effect of fragment mass tolerance on FT-ARM identification of a single tryptic peptide *(LGANAILGVSLAASR)* in a yeast whole cell lysate digest spiked with digested BSA. Tolerance of 10 ppm smaller yields highly specific detection. **B)** Effect of match count on FT-ARM identification of the same tryptic peptide with the ppm tolerance set to 20 ppm.

Lists of peptide identifications for both DIA-FT-ARM and DDA-Mascot have been provided in **Appendix Figures B.1-2.**

Appendix Table B.1: DIA-FTARM Peptide Identifications (<5% FDR)

peptide	q-value	FT-ARM	m/z 2+	m/z 3+	scan #	RT	protein	match count
AAAPTVVFLDELDSIAK	0.006	1.55E+05	880.477	587.321	5504	89.7	YDL126C	10
AAEAATTDLTYR	0.007	1.84E+05	641.817	428.214	1387	28.8	YOR230W	9
AAEEADADAELADEEDAIHDEL	0.000	4.21E+04	1171.49	781.331	2827	72.8	YCL043C	10
AAEPHAVSLAWSADGQTLFAGYTDNVIR	0.007	4.90E+04	1480.73	987.489	3910	65.4	YMR116C	11
AAGANVDNVWADVYAK	0.000	3.98E+05	832.407	555.274	3624	61.4	YDL130W	12
AAGLVDIATVLSTSAYLIESK	0.032	2.60E+04	1061.59	708.06	6733	116.1	YER055C	10
AAPIVDDEETEFDIYNSK	0.028	1.94E+04	1028.47	685.985	2441	62.9	YER070W	8
ADDDSVTIISAGNDK	0.010	6.61E+05	760.857	507.574	1833	35.5	YMR116C	15
ADLMLYVSK	0.000	8.69E+05	520.278	347.188	3071	53.6	YDR385W	8
ADTGIAVEGATDAAR	0.032	1.02E+05	709.35	473.235	1453	29.9	YGL008C	10
ADYANGVLTLTVPK	0.010	5.10E+05	731.401	487.936	3613	61.3	YBR072W	10
AEAESLVAEAQLSNITR	0.000	1.83E+05	901.468	601.315	3680	62.3	YGR086C	15
AEAPKPEVPEDEPEGEPDVK	0.021	1.46E+05	1081.51	721.343	1463	30	YCR088W	10
AEELNISGEFFR	0.010	6.66E+05	706.346	471.233	4103	67.9	YIL133C	13
AEEWLYDEGFDSIK	0.000	1.06E+06	851.386	567.926	4359	71.5	YPL106C	16
AELDPLDIDAVLLTGGVSFTPK	0.032	4.91E+04	1136.11	757.742	6298	105.7	YHR064C	10
AELINNLGTIAK	0.000	1.52E+06	628.864	419.578	2987	52.4	YMR186W	11
AEPIDEEVSLAIENGIINPR	0.010	3.65E+05	1090.07	727.046	4813	78.1	YDR385W	14
AEQLYEGPADDANCIAIK	0.000	3.42E+05	960.954	640.972	2835	50.1	YDR385W	11
AEQVFQNVK	0.026	4.04E+05	531.783	354.857	1256	26.8	YIL051C	8
AEVSDVGNAILDGADCVMLSGETAK	0.000	2.94E+06	1233.08	822.389	5284	85.7	YAL038W	18
AEVSDVGNAVLDGADCVMLSGETAK	0.000	2.31E+06	1226.07	817.717	5284	85.7	YOR347C	12
AFEHTADYDAAISDFFR	0.000	7.65E+05	988.445	659.299	4727	76.8	YLR028C	12
AFIDEQFPQGISEPIPLGFTFSFPASQNK	0.000	1.68E+05	1606.8	1071.54	4011	102.2	YGL253W	10
AFPLADAALTQQILDVVQQAANLR	0.006	1.43E+05	1283.7	856.138	7144	126.6	YEL026W	19
AGAGHSNTLQVSTV	0.000	1.89E+06	671.341	447.897	1427	29.5	YAL038W	9
AGANSMIQNVVDSDTISETAAR	0.000	3.75E+04	1125.54	750.694	2542	65.5	YLL026W	8
AGAPVDALINQIVPLLEK	0.000	2.32E+05	931.043	621.031	6440	109	YHR183W	17
AGAVAPEDIWVR	0.000	1.40E+06	642.341	428.563	3212	55.7	YLR340W	10
AGELTQEELER	0.000	1.93E+06	637.815	425.546	1442	29.7	YDR450W	11
AHPDVLTVMLQMLDDGR	0.025	1.04E+05	955.977	637.654	6292	105.6	YLL026W	12
AHSSMVGFDLPQR	0.016	1.91E+05	722.854	482.238	2428	44.1	YCR012W	10
AIEMEGLTWGAHQFIPIGFGIK	0.006	2.17E+05	1208.13	805.756	5649	92.5	YAL003W	15
AIEQLNYTPIK	0.007	3.21E+05	645.359	430.575	2577	46.3	YER165W	11
AIFEELSDIPVSVELASDFLDR	0.020	4.73E+04	1233.13	822.42	6739	116.2	YKL104C	10
AIGYNPTNQLVQDIINADSSLR	0.006	1.52E+05	1201.62	801.415	5924	97.9	YGL106W	13
AIMPIIEGHDVLAQAQSGTGK	0.010	5.54E+05	1068.56	712.709	3623	61.4	YJL138C	15
AIPGEYITYALSGYVR	0.006	1.69E+05	886.965	591.645	5004	81	YJL136C	10
AIPSALSYVGEDEYHGGQALQQLIR	0.000	9.54E+04	1358.19	905.796	4845	78.5	YHR064C	12
AIQVEGQPIILTGAPAINK	0.000	1.16E+05	967.059	645.042	3780	63.7	YNR016C	14
ALDDFGVDYIELTSPVASEQSR	0.000	9.33E+04	1206.58	804.724	3313	84.9	YDL131W	10
ALDTVTNVLNFIK	0.032	8.26E+04	724.411	483.277	5363	87.2	YKL182W	10
ALELASAEQR	0.026	3.19E+05	544.291	363.196	1401	29.1	YJL167W	8
ALENPTRPFLAILGGAK	0.006	1.03E+05	884.509	590.009	4699	76.4	YCR012W	10
ALENTNYAVDLGR	0.021	1.57E+05	718.362	479.244	2473	44.8	YDR129C	10
ALGGAPKPDYPIATQDTLTEYDAFLFGIPTR	0.000	4.64E+04	1669.85	1113.57	3662	93.6	YDR032C	9
ALGIMALLDEGETDWK	0.006	2.70E+05	881.44	587.962	5679	93.1	YBR011C	12
ALLPHLTNAIVETNK	0.026	3.48E+05	817.467	545.314	3141	54.6	YLR249W	8

ALNGVSTDVQGTDFSEVSYDSVLER	0.000	2.68E+04	1344.64	896.759	2824	72.7	YLL050C	8
ALPDAVTIIEPK	0.000	9.87E+05	633.869	422.915	3512	59.9	YNL178W	11
ALTEQAQTLTLSSR	0.032	5.91E+04	759.91	506.942	2223	41.1	YLR438W	10
ALYELLSAADQK	0.025	1.09E+05	661.354	441.238	3677	62.2	YER110C	9
AMYTLSAQDEVFSLAFSPNR	0.000	4.04E+04	1124.04	749.697	3457	88.5	YMR116C	8
ANELLINVK	0.000	7.31E+06	507.303	338.538	2521	45.5	YOL086C	11
ANFEIDLPDAK	0.000	4.37E+05	616.812	411.543	3342	57.6	YGL245W	9
APEAEQVLSAAATFPIAQPATDVEAR	0.006	2.06E+05	1327.18	885.12	2784	49.4	YDL082W	10
APEALFHPSVLGLESAGIDQTTYNSIMK	0.000	6.62E+04	1495.25	997.171	3235	56	YFL039C	10
APEGELGDSLQTAFDEGK	0.007	3.12E+04	932.434	621.958	3685	62.3	YEL034W	11
APFDLFESK	0.000	9.51E+05	527.266	351.847	3791	63.8	YMR186W	8
APIVAYAELIAAR	0.030	7.55E+04	679.396	453.266	4632	75.4	YGL245W	10
APLEEIVISNDYLNK	0.006	1.04E+05	859.454	573.305	4244	69.9	YOR332W	10
APYNISSLASEYALK	0.020	4.16E+04	813.922	542.951	4259	70.1	YIL116W	10
AQFETLTAPLVK	0.000	5.13E+05	659.374	439.919	3372	58	YJR045C	11
AQLTSSSGGNIIVVSNR	0.020	6.35E+04	851.958	568.308	2059	38.8	YBR126C	13
AQPTEVSSILEER	0.010	3.22E+05	729.875	486.919	2898	51	YBL099W	12
AQYNEIQGWDHLSLLPTFGAK	0.000	4.60E+04	1194.6	796.738	3732	95.3	YLR044C	8
ASAPGSVILLENLR	0.010	4.29E+05	720.414	480.612	4223	69.6	YCR012W	10
ASGEIVSINQINEAHPTK	0.000	1.43E+05	954.495	636.666	2125	39.7	YMR242C	11
ASGTVVVADTGDFGSIAK	0.000	5.28E+05	847.933	565.625	2969	52.1	YLR354C	20
ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR	0.000	2.42E+05	1524.3	1016.54	2956	76.1	YFR031C-A	15
ASLVPGTVLILLAGR	0.010	4.52E+05	740.467	493.98	5888	97.2	YLR448W	11
ATAGDTHLGGEDFDNR	0.000	5.18E+05	838.369	559.248	1224	26.3	YAL005C	16
ATDGGAHGVINVSVSEAAIEASTR	0.000	1.77E+06	1156.58	771.387	3303	57	YOL086C	18
ATGQEMDVVSEEPLIEWLAANYK	0.024	3.40E+04	1297.13	865.088	6189	103.3	YBR143C	10
ATNGGAHGIINVSVSEAAIEASTR	0.000	1.22E+06	1163.09	775.731	3298	57	YMR303C	10
ATNGGSHGVINVSVSEAAIEASTR	0.000	1.47E+06	1164.08	776.391	3303	57	YBR145W	12
ATVDEFPLCVHLVSNELEQLSSEALEAAR	0.000	5.05E+05	1585.79	1057.53	4501	114.6	YLR075W	9
ATVPVLEQQGTVITR	0.006	1.55E+05	806.457	537.974	2754	48.9	YGR234W	13
AVASSGQELSVEER	0.010	6.73E+05	731.363	487.911	1288	27.3	YDR099W	10
AVDDFLISLDGTANK	0.000	6.07E+06	789.904	526.939	4778	77.5	YGR254W	18
AVDDFLLSLDGTANK	0.000	6.07E+06	789.904	526.939	4778	77.5	YHR174W	18
AVEALNDSELNGEK	0.032	4.94E+04	744.862	496.911	1693	33.5	YER165W	11
AVEESAEPAQVILGEDGKPLSK	0.032	1.04E+05	1134.09	756.397	2883	50.8	YLL018C	10
AVGDNDPIDVLEIGETIAYTGQVK	0.000	6.52E+05	1259.14	839.762	5884	97.1	YBR011C	13
AVGGEVGASAALAPK	0.000	1.45E+06	649.359	433.242	1637	32.7	YDR418W	16
AVGSLTFDENYNLLDTSGVAK	0.000	1.63E+05	1107.55	738.702	2912	75	YNR034W-A	11
AVLEFTPETPSPLIGILENK	0.032	8.25E+04	1084.6	723.4	5728	94	YGR240C	12
AVNELPTKPSTDELLELYALYK	0.000	6.08E+05	1254.17	836.448	5149	83.4	YGR037C	14
AVTASQTTIAEVISNLYDDSK	0.018	2.10E+04	1113.56	742.709	3857	98.4	YCR009C	7
AVVAGAGTGGTISGISK	0.016	1.97E+05	723.402	482.603	1638	32.7	YGR155W	15
AVVESVGAEVDEAR	0.010	2.48E+05	715.86	477.576	1988	37.7	YDR382W	14
AWNLNQFQIEADFIGHNSNINTLTASPDGTLIASAGK	0.000	1.59E+05	1964.98	1310.32	3639	93.1	YMR116C	13
CAADDLDATVVQLTVLTEK	0.016	4.34E+04	1003.01	669.01	4101	104.4	YNL134C	8
CLVNDPNIEIVADLSSDILSR	0.018	1.65E+04	1143.59	762.726	4857	123.7	YOR184W	7
DAGLSTSDISEVLLVGGMSR	0.028	1.89E+04	1004.01	669.674	3456	88.5	YJR045C	10
DAGTIAGLNVLR	0.007	2.42E+05	600.341	400.563	3537	60.2	YAL005C	10
DAQIVVGTPGR	0.034	2.80E+05	556.807	371.54	1391	28.9	YJL138C	9
DASLVDYVQVR	0.000	5.63E+05	632.83	422.223	3377	58.1	YJR123W	10
DASSLTLDQITGLIEVNEK	0.028	1.72E+04	1023.53	682.692	3601	92.1	YGL106W	8
DAVVTVPAYFNDSQR	0.006	2.24E+05	841.413	561.278	3184	55.3	YER103W	10
DESSPYAAMLAAQDVAAK	0.007	4.33E+04	919.435	613.293	3890	65.1	YCR031C	12
DETLDDWFDNDLSLFPSGFGFPR	0.000	3.57E+05	1345.61	897.406	4609	117.3	YBR072W	12
DFDGTGALEFPSEEILVEALER	0.000	3.46E+04	1219.09	813.064	4278	108.9	YDR432W	6
DGEIMLWNLAAK	0.007	4.26E+05	680.85	454.236	4857	78.7	YMR116C	10
DGKPYVFFTIPDGK	0.034	3.10E+05	792.409	528.608	4066	67.4	YGL245W	8

DIEVVAVNDPFISNDYAAYMVK	0.020	5.56E+04	1237.1	825.07	5459	88.9	YJL052W	10
DIFSNDELLSDAYDAK	0.000	4.56E+05	908.418	605.948	4535	74	YKL056C	19
DIGGSSSTTDFTNEIINK	0.007	3.52E+04	949.953	633.637	3315	57.2	YNL037C	12
DINSYTNSTSVINELR	0.007	3.33E+04	913.45	609.302	3685	62.3	YGR061C	10
DIYGWTQTSLDDYPIK	0.000	3.84E+05	957.96	638.976	4160	68.7	YGL253W	11
DLAAATAESAPNAAILVISNPVNSTVPIVAQVLK	0.000	6.21E+04	1679.44	1119.96	4267	108.6	YKL085W	9
DLNKPFLMPVEDIFSISGR	0.032	5.67E+04	1089.57	726.714	5853	96.5	YOR187W	10
DLSEASVYPEYALPK	0.006	3.41E+05	841.42	561.282	3659	61.9	YER131W	13
DLTNLLFETALLTSGFSLEEPTSFASR	0.000	2.81E+04	1480.25	987.169	4500	114.5	YMR186W	6
DNAEGQGESLADQAR	0.026	6.88E+05	780.848	520.901	856	19.8	YFL014W	8
DPANLPWASLNIDIAIDSTGVFK	0.000	5.87E+05	1229.14	819.76	5399	87.8	YJR009C	11
DPANLPWGSSNVDIAIDSTGVFK	0.000	6.70E+05	1202.09	801.732	5399	87.8	YGR192C	17
DPITIVPAEDGSGAGAAVIAALSEK	0.000	2.74E+05	1176.62	784.748	3682	94.1	YFR053C	11
DPMGNNITFSGLANATDSAPTSK	0.000	3.91E+04	1155.04	770.362	3367	86.3	YGR240C	9
DQVVLIQVSSPTANR	0.006	1.31E+05	813.944	542.965	2914	51.3	YDR074W	13
DQYVPEVSALDLSR	0.000	1.73E+06	796.402	531.27	3096	53.9	YDR447C	11
DTLPLGFTFSYPASQNK	0.000	1.83E+05	943.47	629.316	4850	78.6	YFR053C	10
DVAAQDFINAYASFLQR	0.000	1.12E+05	964.979	643.655	5690	93.3	YNL302C	11
DVNNVWIQSVK	0.000	4.47E+05	651.346	434.566	3187	55.3	YAR042W	9
DVPEPITEFTSPPLDGLLLENIK	0.024	3.19E+04	1269.17	846.451	6214	103.8	YOR204W	10
DVQEAGSTEPIVK	0.007	2.87E+05	686.851	458.237	1207	26	YBR121C	10
DVQQIDYK	0.034	2.70E+05	504.753	336.838	1081	23.9	YNL096C	8
DVTFLNDCVGPEVEAAVK	0.000	7.07E+05	953.467	635.98	4500	73.6	YCR012W	11
DYGVLIEEEGVALR	0.000	1.09E+06	781.907	521.607	3653	61.8	YML028W	10
DYRPAEETEAQAEPVEA	0.000	1.75E+06	952.929	635.622	1755	34.4	YNL178W	17
EAQADAAAEIAEDAAEAEDAGKPK	0.021	1.42E+05	1186.05	791.035	3793	63.8	YLR150W	11
EASYVNIPVIALTDLDSPSEFVDVAIPCNNR	0.000	1.24E+05	1681.33	1121.23	4187	106.6	YGR214W	8
EAVESADLILSVGALLSDFNTGSFSYSYK	0.000	1.92E+05	1542.26	1028.51	5861	149.5	YLR044C	16
EELFTSLGGEVFIDFTK	0.000	7.15E+05	966.485	644.659	4107	68	YMR303C	9
EEVTEEQAEATEWAEENADNVEW	0.000	6.80E+04	1354.56	903.375	4399	112	YGR214W	8
EEVTEGQAEATEWAEENADNVEW	0.000	6.80E+04	1318.55	879.368	4399	112	YLR048W	8
EFEEGGGLPEQPLNPDFSK	0.000	8.84E+04	1045.49	697.329	2336	60.2	YER025W	8
EFGTTPEKPEETPLEELAETFQDTFSGALGK	0.000	4.42E+04	1699.81	1133.54	4737	120.6	YPL231W	8
EFQIIDTLLPGLQDEVMNIKPVQK	0.000	4.41E+05	1384.75	923.502	6025	99.8	YGL123W	11
EGGLGPINIPLLADTNHSLSR	0.010	3.17E+05	1087.58	725.39	4208	69.4	YML028W	10
EGIPAGWQGLDNGPESR	0.020	3.85E+04	891.924	594.952	2689	47.9	YCR012W	10
EIGDFEDLSTENEK	0.006	1.07E+05	813.362	542.577	2799	49.6	YLL018C	10
EIHAVLSADANITSNEK	0.040	5.78E+04	906.46	604.643	3297	56.9	YPR033C	9
EKPETLVLFDVDGTLTPAR	0.021	1.62E+05	1051.06	701.044	4438	72.7	YFL045C	10
ELAEEGYSGVEVR	0.010	2.52E+05	719.346	479.9	1963	37.4	YNL178W	11
ELDEIAASLENL	0.007	2.48E+05	658.833	439.558	5477	89.2	YNL079C	13
ELGLTVVTDEAIEQMR	0.000	9.28E+04	902.461	601.977	4960	80.2	YLR359W	10
ELMDEIHQLEDMFTVDSETLR	0.018	6.62E+04	1276.09	851.061	6554	111.7	YFR053C	10
ELMQQIENFEK	0.021	1.47E+05	704.842	470.231	3633	61.5	YGL253W	10
ELPGVAFLSEK	0.000	1.23E+06	595.327	397.22	3541	60.3	YCR012W	8
ELPIEIVALINDTVGTLIASYYTDPETK	0.016	5.83E+04	1539.81	1026.88	5081	129.4	YFR053C	8
ELQFSEIDTVK	0.007	1.73E+05	654.838	436.894	3092	53.9	YPL160W	9
ELSWIDVENWHNLGGSEIGTNR	0.020	5.88E+04	1263.6	842.738	4839	78.5	YGR240C	10
ELYGNIVMSGGTTMFPGIAER	0.000	5.92E+04	1122.05	748.366	3207	82.3	YFL039C	8
EMAFNLLGLLTPEVVELCQK	0.000	5.36E+04	1124.09	749.73	4667	118.8	YPL231W	7
EMIQEVIVEEDLEPFEASK	0.018	3.11E+04	1118.04	745.696	3452	88.4	YPL231W	10
ENDILVLMESER	0.010	6.59E+05	724.358	483.241	4568	74.5	YLR264W	14
ENILIGDSNIIESYQK	0.020	1.24E+05	918.473	612.651	3962	66.1	YDR166C	9
ENSLETTFSSVNTR	0.016	1.82E+05	792.879	528.922	2433	44.2	YDR432W	10
ENTLLGEFDLK	0.000	9.22E+05	639.832	426.891	4437	72.7	YDL229W	10
EQAANLIAAGADGLR	0.010	3.35E+05	735.389	490.595	3098	54	YHR216W	13
EQIYQIFTLLPPTTQVVLLSATMPNDVLEVTTK	0.000	2.85E+04	1852	1235	5868	149.6	YJL138C	6

EQPTCSLITGENWTK	0.020	4.36E+04	853.906	569.607	1484	30.4	YJR073C	10
EQQDNFAIESYQK	0.006	8.43E+04	800.368	533.914	2094	39.3	YPL028W	10
ESGNYLAIDLGGTNLR	0.000	3.98E+05	846.931	564.957	3904	65.3	YFR053C	11
ETAENYLGTTVNDAVVTVPAYFNDSQR	0.000	2.66E+06	1487.71	992.14	3465	59.3	YBL075C	10
ETAPVIDTLAAGYGK	0.000	1.24E+06	753.396	502.6	3368	57.9	YGL103W	13
ETELSLLQSLR	0.007	3.31E+05	644.859	430.242	4317	70.9	YCL040W	10
ETFLAGLIDSDGYVTDEHGIK	0.032	1.14E+05	1140.56	760.706	4923	79.7	YDL185W	10
ETGELEELLEPILAN	0.000	5.18E+05	835.43	557.289	6239	104.4	YCL035C	12
ETITEALNLPEANLSEIPSLQDAIQR	0.000	2.51E+05	1433.25	955.833	5725	93.9	YGR061C	15
ETNPGTDVTVSSVESVLAHL	0.020	1.19E+05	1028.02	685.68	6162	102.7	YLR109W	13
ETSTDPSYDAFLEK	0.006	2.09E+05	801.862	534.911	2929	51.5	YLL050C	10
ETVESESSQTALSK	0.010	5.25E+05	748.36	499.242	913	20.8	YDR385W	15
EVASAALSELALGTK	0.016	1.82E+05	730.404	487.272	3843	64.5	YER110C	13
EVDQVIVVTVDNPFANQAWAK	0.000	5.75E+04	1172.1	781.737	3362	86.2	YLR109W	8
EVIDTILALVK	0.007	1.99E+05	607.374	405.252	5792	95.3	YLR044C	10
EVQGSTLAQLTSK	0.007	1.98E+05	681.367	454.581	2142	40	YLR441C	10
EVQNSTLAQLTSK	0.000	1.07E+06	709.878	473.588	2213	40.9	YML063W	12
EYLNLPEHIVPGTYIQER	0.000	1.25E+06	1086.06	724.376	3923	65.6	YMR230W	11
FADGFLIHSGQPVNDFIDTATR	0.000	1.62E+06	1211.1	807.733	4704	76.4	YNL178W	16
FAIPAINVTSSSTAVAALEAAR	0.010	4.94E+05	1080.59	720.727	5263	85.3	YKL060C	13
FDDMELDENLLR	0.010	5.20E+05	755.348	503.901	4153	68.6	YJL138C	15
FDGILGLGYDTISVDK	0.006	2.34E+05	856.941	571.63	5059	81.9	YPL154C	10
FDVGALMALHGEGSGEEK	0.007	2.80E+05	923.936	616.293	2297	42.2	YLR441C	10
FEDLNAALFK	0.000	3.17E+06	584.306	389.873	3761	63.4	YDL229W	10
FEQASESEPTTVSYEIAGNSPNAER	0.000	6.67E+05	1357.11	905.079	2640	47.2	YJR104C	18
FGDPETQAVLSLLDDQTDLAQVFLAAAEHR	0.016	2.87E+04	1635.82	1090.88	4876	124.2	YGL234W	8
FGSGIELESLPITPGQYITVNTHPIR	0.000	1.41E+05	1420.25	947.171	4975	80.5	YGR234W	16
FINFINNANQSASNK	0.020	3.88E+04	841.418	561.281	2159	40.2	YDL073W	10
FISEVENTDPTQER	0.006	2.78E+05	832.892	555.597	1749	34.3	YKL085W	13
FISTSQSVVEPK	0.007	3.46E+05	661.354	441.238	3517	60	YDR463W	9
FLFENTGLDLYSNLVNMIFPVDSVK	0.000	4.82E+04	1438.23	959.158	5870	149.7	YNL041C	5
FNYVAVGDVSNLPYLDEL	0.000	7.90E+04	1014.5	676.67	3981	101.5	YPR191W	11
FPELGAELAR	0.026	4.16E+05	551.798	368.201	3246	56.2	YPR074C	9
FPGWDFETEEIDPELLR	0.000	6.69E+05	1047	698.334	3641	93.1	YPL131W	14
FQPQDSTTNPSLILAAAK	0.000	1.52E+05	951.502	634.67	3495	59.7	YLR354C	12
FSADIVTLFDLIEK	0.006	9.61E+04	805.937	537.627	6454	109.4	YLR354C	11
FTLEVVDAVVDAIGPEK	0.000	3.42E+05	901.483	601.324	6040	100.1	YHR179W	20
FTNAAFPFHDPEAR	0.020	4.61E+04	810.384	540.592	2504	45.3	YHL030W	10
FTVSAIYSDLPQQER	0.006	3.33E+05	877.441	585.297	2499	45.2	YJL138C	11
FVIGGPQGDAGLTGR	0.010	2.92E+05	722.881	482.256	2748	48.8	YDR502C	10
FVPSKPMCVEAFSEYPPLGR	0.000	1.97E+06	1127.56	752.039	3498	59.7	YBR118W	10
FVQGLLQNAAANAEAK	0.000	1.33E+06	822.939	548.962	3134	54.5	YJL177W	24
FYSTQIEELPSDIATLLN	0.000	3.72E+05	1027.52	685.349	4251	108.2	YJL138C	11
GAAEALENANDISEGLVSESLK	0.018	2.39E+04	1109.05	739.701	3047	78.3	YLR197W	8
GAARPTGGAGTVAMWIGPDAPIVFDSVR	0.000	8.78E+04	1385.21	923.81	5170	83.7	YML126C	10
GAAYVLGAGQVVYFGSVGK	0.007	4.09E+04	921.991	614.996	4390	72	YJR105W	12
GADTNTPLEYLSK	0.010	3.24E+05	704.851	470.237	3178	55.2	YLL026W	12
GAIVGPDLAVLALVIVK	0.000	4.39E+05	824.524	550.018	6509	110.7	YBR181C	20
GASDGGLYVPHSENR	0.000	1.17E+06	779.866	520.246	1176	25.5	YPL131W	8
GATTEEDDALADQLR	0.020	6.15E+04	802.874	535.585	2304	42.3	YER090W	10
GATYGKPTNQGVNELK	0.006	9.79E+04	838.934	559.625	959	21.7	YLR029C	11
GAVEFDPWLKPFADVLSER	0.032	4.92E+04	1088.56	726.041	5733	94.1	YEL011W	11
GDIPGVVAFFGGLVAQEVLK	0.040	5.72E+04	1008.56	672.71	7177	127.4	YKL210W	10
GDIVGVEGYVGR	0.007	3.39E+05	610.817	407.547	2577	46.3	YDR037W	13
GDLGIEIPAPEVLAVQK	0.000	1.21E+07	874.993	583.665	4689	76.2	YAL038W	20
GDLLQEAIDFAQK	0.021	1.37E+05	724.375	483.252	5383	87.5	YOR362C	12
GDTYVSIQGFK	0.000	2.74E+06	607.806	405.54	2777	49.3	YAL038W	13

GDVDLVINYLK	0.007	2.91E+05	624.845	416.899	4497	73.5	YOR374W	10
GDVEEYQYLR	0.007	2.02E+05	636.299	424.535	2227	41.2	YBR126C	10
GEALLVVLVSSVTEANIIK	0.000	1.02E+05	978.075	652.386	6840	118.8	YOR369C	15
GEFHPVLLAETSFPVQK	0.007	3.70E+05	950.004	633.672	3937	65.8	YHR064C	9
GEQELEGLTDTTVPK	0.026	6.28E+05	808.904	539.605	2196	40.7	YBR181C	11
GEYETAISTLNDAVEQGR	0.000	1.28E+05	976.963	651.645	4095	67.8	YOR027W	11
GFALANPSITLVPEEK	0.006	2.70E+05	843.459	562.642	4244	69.9	YML070W	10
GFDEAVADPTFWEDFK	0.000	1.79E+05	937.418	625.281	5295	85.9	YGL026C	14
GFDIPNVEGHDVVPLLQNEISK	0.000	8.05E+05	1210.63	807.42	4854	78.7	YFR053C	12
GFDQSLAQSLDTITSK	0.006	9.09E+04	855.931	570.956	4519	73.8	YKL157W	11
GFDQTLAQALDTIR	0.032	8.02E+04	774.904	516.939	5303	86	YHR047C	11
GFEIGSGFQGVSVPGSK	0.006	1.54E+05	826.918	551.614	3829	64.3	YGL148W	10
GFLSDLPDFEK	0.000	2.51E+06	634.314	423.212	4677	76.1	YLR340W	12
GGGQIIPTMR	0.000	1.08E+06	515.279	343.855	2026	38.3	YDR385W	8
GGIGAVFAELNQGENITK	0.000	1.59E+05	909.473	606.651	4665	75.9	YNL138W	14
GGIPLVFPVFGK	0.007	2.57E+05	615.866	410.913	5392	87.7	YMR099C	12
GGLTYNDFLVLPGLVDFPSSEVSLQTK	0.000	9.96E+04	1448.75	966.171	6320	106.2	YLR432W	10
GGLTYNDFLVLPGLVNFPSSAVSLQTK	0.000	5.79E+04	1419.26	946.508	6305	105.9	YML056C	10
GGTLISYDGQVR	0.000	9.16E+05	633.328	422.554	2137	39.9	YKL035W	11
GHYTEGAELVDSVMDVIR	0.030	7.12E+04	995.981	664.323	5287	85.7	YFL037W	10
GIDIVVNEVSNR	0.000	6.86E+05	657.854	438.905	2917	51.3	YPL106C	11
GIDLTNVTLPDTPTYSK	0.000	1.52E+06	917.975	612.319	3870	64.9	YBR011C	17
GIDVQQVSLVINYDLPANK	0.016	6.90E+04	1043.56	696.044	3076	79.1	YJL138C	9
GIEAAGGSADIYQVEETLSPEVVK	0.000	2.54E+04	1231.62	821.415	3008	77.3	YDR032C	8
GIEQLESAIEK	0.007	1.67E+05	608.825	406.219	3282	56.7	YJR007W	9
GINSSYAVWNDVTGK	0.006	2.57E+05	805.894	537.598	3564	60.6	YLR355C	17
GISNEGQNASIK	0.000	3.52E+06	609.31	406.542	717	17.1	YKL060C	15
GISSSAIPYSR	0.026	5.52E+05	569.299	379.868	1716	33.8	YDR064W	8
GIVPDSSPLNVSSAR	0.016	1.95E+05	749.897	500.267	2873	50.7	YEL020C	10
GIVVEAYSPFGSANAPLLK	0.000	1.16E+05	967.025	645.019	4725	76.7	YDR368W	16
GLGSSGAAVVAGVILGNEVAQLGFSK	0.020	6.22E+04	1201.16	801.108	6319	106.2	YHR025W	15
GLILVGGYGTR	0.000	1.93E+06	553.322	369.217	3056	53.4	YDL055C	9
GLLSATQFTQPALTLMEK	0.000	6.54E+04	975.024	650.352	5270	85.4	YKL182W	12
GLNTGGMGAYAPAPVATPSLLK	0.000	8.63E+04	1043.55	696.038	2596	66.9	YGL234W	8
GLQTVVVEEDA	0.000	9.72E+05	580.296	387.2	2616	46.9	YDL075W	11
GLSVVDTYAILSNK	0.010	2.45E+05	740.406	493.94	4218	69.5	YJL167W	11
GLTPSQIGVLLR	0.000	8.37E+05	627.382	418.591	4132	68.3	YDR064W	11
GLVWEGSVLDPEEGIR	0.006	3.20E+05	878.449	585.969	4594	74.9	YNR001C	11
GMGLLTAIVIDPSK	0.032	3.54E+04	707.902	472.271	5008	81	YLR438W	10
GNEEVEQDEPLSLQTK	0.000	1.11E+05	908.434	605.958	2085	39.2	YGL137W	13
GNPTVEVELTTEK	0.000	1.04E+07	708.864	472.912	2128	39.8	YGR254W	17
GNVGFVFTNEPLTEIK	0.000	3.77E+06	882.962	588.977	4564	74.5	YLR340W	16
GNYPINAVTTMAETAVIAEQAIAYLPNYDDMR	0.000	3.16E+05	1758.34	1172.57	4987	127	YAL038W	12
GNYTDFENTFQK	0.010	3.37E+05	732.326	488.553	2753	48.9	YKL182W	14
GPLVLEYETYR	0.007	2.92E+05	670.348	447.235	3302	57	YER178W	10
GPLVVYAEDNGIVK	0.010	4.39E+05	737.401	491.936	3193	55.4	YBR031W	13
GQCLATLLGHNDWVSQVR	0.000	8.13E+05	999.005	666.339	4207	69.4	YMR116C	12
GQDFAPAFDVAPDWESYEYTK	0.006	1.66E+05	1218.54	812.694	4969	80.4	YKL081W	18
GQDYVPAFDVAPDWESYDYAK	0.000	5.53E+04	1218.54	812.694	3183	81.7	YPL048W	11
GQTPEGEDPLGKPEEELTVIPEFGGADNK	0.000	2.17E+05	1527.23	1018.49	2776	71.5	YCL050C	11
GQTYSPAQIGGFVLNK	0.000	5.15E+05	840.441	560.63	3859	64.7	YJR045C	16
GQVVGSIIALDR	0.007	1.97E+05	614.356	409.907	3242	56.1	YML106W	10
GQVVSEEQRPGTPLFTVK	0.000	2.11E+05	986.529	658.021	3535	60.2	YDR385W	10
GSDPDTTWLIISPNAK	0.006	2.02E+05	857.936	572.293	4119	68.1	YCR088W	15
GSIDEQHPR	0.026	3.87E+05	519.752	346.837	491	12.6	YGR087C	9
GSLEEIIAEGQK	0.000	6.41E+05	637.335	425.226	3157	54.9	YDR382W	12
GSPFQCNIGVGQVIK	0.016	1.96E+05	773.906	516.273	3208	55.6	YNL135C	12

GSSSLYTLVINDAGK	0.000	1.40E+06	762.899	508.935	3928	65.7	YLR325C	13
GTDYDFYEAWGPVFEAEAR	0.000	9.23E+04	1111.99	741.66	3642	93.1	YGR285C	8
GTGLMSANNIIAEGIEK	0.006	1.67E+05	859.443	573.298	3894	65.2	YPL231W	11
GTIADGAPIVPISAQLK	0.006	3.61E+05	825.975	550.986	3639	61.6	YER025W	10
GTIEIVSDVK	0.000	2.62E+06	530.798	354.201	2141	40	YLR340W	12
GTITWIAPAGEYTLDEK	0.000	9.10E+05	932.97	622.316	4150	68.6	YDL185W	15
GTLEGHNGWVTSLATSAGQPNLLLSASR	0.000	7.08E+05	1419.23	946.49	4860	78.8	YMR116C	14
GTQAPNLQER	0.044	2.31E+05	557.286	371.86	766	18.1	YDR226W	9
GVAINFVTNEDVGAMR	0.006	1.24E+05	846.922	564.951	3674	62.2	YJL138C	13
GVETLAEAVAATLGPK	0.010	5.28E+05	763.925	509.619	5558	90.8	YLR259C	18
GVFQGVHDSAEK	0.000	4.40E+05	637.312	425.211	962	21.8	YFL014W	11
GVGVFGNNAQDSGISPSVWR	0.016	3.40E+04	1024	683.005	2646	68.2	YGR264C	8
GVLGYTEDAVVSSDFLGDSHSSIFDASAGIQLSPK	0.018	3.51E+04	1785.37	1190.58	5972	151.8	YGR192C	11
GVLGYTEDAVVSSDFLGDSNSSIFDAAAGIQLSPK	0.018	2.80E+04	1765.86	1177.58	4642	118.2	YJR009C	7
GVLGYTEDAVVSSDFLGDTHASIFDASAGIQLSPK	0.018	3.51E+04	1784.38	1189.92	5972	151.8	YJL052W	11
GVLLAADLGGTHFR	0.016	2.09E+05	713.894	476.265	3888	65.1	YDR516C	10
GVLLAADLGGTNFR	0.010	5.16E+05	702.386	468.593	3883	65.1	YCL040W	16
GVMNAVNNVNNVIAAAFVK	0.000	1.41E+06	973.02	649.016	5515	89.9	YHR174W	21
GVNLPGTDVDLPALSEK	0.000	3.58E+06	862.957	575.64	4184	69.1	YAL038W	22
GVPQIEVTFDVDSNGILNVSAVEK	0.000	3.89E+04	1265.66	844.106	5863	149.5	YAL005C	6
GVVDSEDLPLNLSR	0.000	2.78E+06	757.396	505.267	3513	59.9	YMR186W	16
GVVIEGYPTIVLYPGGK	0.006	2.28E+05	881.493	587.998	4529	74	YCL043C	13
GWLSEGGTLIGTAR	0.010	7.00E+05	709.375	473.253	3848	64.6	YGR240C	16
GYDAGENTYQAPPADR	0.006	1.22E+05	862.879	575.589	1159	25.2	YLR304C	11
GYKPVAVPAR	0.022	7.48E+05	529.311	353.21	861	19.9	YLR044C	8
GYLADDIDADSLEDIYTSAHEAIR	0.000	1.24E+06	1327.12	885.08	5094	82.4	YPL131W	19
GYLVAMTGDGVNDAPSLK	0.007	3.18E+04	904.448	603.301	3425	58.7	YGL008C	11
GYPIQFLTIGAGVPSLEVASEYIETLGLK	0.028	2.55E+04	1533.33	1022.55	4916	125.2	YKL182W	10
GYQFAAALEGALK	0.030	6.61E+04	669.856	446.907	4607	75.1	YKL104C	9
GYWGTNLGQPHSLATK	0.034	2.64E+05	865.436	577.293	2481	44.9	YGL123W	8
HCGWLALMAGIATGADYIFIPER	0.006	1.62E+05	1253.12	835.752	4149	68.6	YGR240C	11
HELSSLADVYINDAFGTAHR	0.000	1.46E+06	1108.54	739.363	4318	70.9	YCR012W	19
HGIPLISIEELAQYLK	0.045	3.25E+04	912.517	608.68	5927	98	YDR487C	9
HGYIGEFEYIDDHR	0.022	7.05E+05	875.895	584.266	2666	47.5	YJL190C	11
HIDASGSINR	0.000	9.24E+05	535.273	357.184	571	14.2	YNL302C	9
HITINDLPVGR	0.000	8.76E+05	617.849	412.235	2272	41.8	YML028W	9
HLEDNTLLISGPFK	0.026	5.84E+05	792.425	528.619	3536	60.2	YML073C	10
HLEDNTLLVTGPFK	0.026	5.98E+05	792.425	528.619	3306	57.1	YLR448W	8
HLEGISDADIAK	0.000	3.74E+06	634.828	423.554	1492	30.5	YKL152C	15
HLGSLFSDAVQTASVQWFER	0.032	1.25E+05	1139.57	760.047	5483	89.3	YLR359W	12
HLNICGTVGSIDNDMSTTDATIGAYSALDR	0.016	5.27E+04	1556.22	1037.82	3026	77.8	YMR205C	8
HNLEFINILTDDGLLNEECGPEWQGMK	0.016	2.92E+04	1558.23	1039.15	3746	95.7	YGR094W	9
HQEELWSFIADSLK	0.020	4.00E+04	851.925	568.286	5474	89.2	YFR053C	12
HSEFVAYPIQLLVTK	0.006	9.58E+04	872.985	582.326	4704	76.4	YMR186W	10
HSEFVAYPIQLVVTK	0.000	9.71E+05	865.977	577.654	4701	76.4	YPL240C	8
HSGNIQLDEIIEIAR	0.006	8.18E+04	854.455	569.972	4259	70.1	YDR418W	12
HSTTAIQGSISDSATTTPR	0.014	1.51E+05	965.977	644.32	2672	47.6	YBL101C	9
HTLDIINVLTDQNPIQVVVDAITNTGPR	0.000	1.61E+05	1528.82	1019.55	4996	127.2	YJR123W	16
HVEITDDEIAK	0.007	2.45E+05	635.32	423.882	1187	25.7	YLR359W	11
HVLTILTDMSSYADALR	0.020	1.42E+05	953.491	635.996	5227	84.7	YBR127C	12
HVSPAGAAVGIPLSDVEK	0.026	5.99E+05	873.973	582.984	2661	47.5	YMR120C	12
HVVFGEVVDGYDIVK	0.000	1.05E+06	838.438	559.295	3609	61.2	YDR155C	20
IAAQTLEEDE	0.000	8.14E+05	559.764	373.512	1701	33.6	YNL302C	10
IADQATENVADISNLK	0.020	6.10E+04	851.436	567.96	2694	48	YER070W	11
IAEFPEEGIDPSTYLNN	0.000	1.92E+05	954.947	636.967	4650	75.7	YDL084W	13
IAEGSDPSLLLDQR	0.010	4.51E+05	757.396	505.267	2873	50.7	YHR019C	12
IAILAAISAMVDAAK	0.032	9.73E+04	729.423	486.618	6553	111.7	YLR249W	19

IALSRPNVEVVALNDPFITNDYAAYMFK	0.000	1.75E+05	1586.31	1057.88	3491	89.4	YGR192C	9
IASTWEGIQAAK	0.007	1.80E+05	637.841	425.563	2282	42	YLR354C	9
IDGALILAYAELNK	0.032	9.11E+04	752.424	501.952	5108	82.7	YGL206C	11
IDGYSGPELGELMEK	0.006	1.65E+05	819.39	546.596	3914	65.5	YBR121C	11
IDIDVLAPLSSFAATAHK	0.007	1.67E+05	935.009	623.675	5327	86.5	YLR359W	13
IDNLAAVFDAR	0.000	8.52E+05	602.82	402.216	3887	65.1	YKL081W	9
IDTVVLDALQLLK	0.032	9.47E+04	720.937	480.961	6088	101.1	YNL138W	13
IDVAVDSTGVFK	0.000	3.51E+06	625.835	417.559	2972	52.1	YJL052W	13
IEAALSDALAALQIEDPSADELR	0.000	9.49E+05	1206.12	804.415	5839	96.2	YDL229W	14
IEALEFADDAAK	0.000	5.00E+05	646.822	431.55	3027	52.9	YPL160W	9
IEDDPFENLEDTDDIFQK	0.021	1.47E+05	1091.99	728.327	5038	81.5	YFR053C	14
IEDVIDELIPK	0.030	6.80E+04	642.358	428.575	4952	80.1	YER007C-A	9
IEDVTPVPSDSTR	0.000	2.08E+06	708.354	472.572	1378	28.7	YCR031C	15
IEEDPFENLEDTDDLFQNEFGINTTVQER	0.000	1.74E+05	1729.28	1153.19	3882	99	YGL253W	14
IEEVIDLILR	0.007	3.08E+05	606.864	404.911	5287	85.7	YHR087W	12
IEGVATPQDAQFYLGK	0.000	1.70E+06	868.946	579.633	3434	58.8	YPL143W	17
IEGVATPQEAQFYLGK	0.000	5.31E+05	875.954	584.305	3504	59.8	YOR234C	11
IEIDSFVDGIDLSETLTR	0.016	3.67E+04	1012.02	675.013	3631	92.9	YJL034W	8
IENQQGVNNFDEILK	0.000	3.94E+06	880.944	587.632	3394	58.3	YAL038W	16
IEQELGTEIAAIPATIDK	0.000	9.08E+04	956.517	638.014	4345	71.3	YDL160C	10
IETGNFSWASEGISK	0.000	1.70E+06	813.394	542.598	3324	57.3	YBL072C	20
IEVLEQELVR	0.007	2.41E+05	614.351	409.903	3162	54.9	YGR086C	9
IEVSSQESWGN	0.000	4.66E+05	618.281	412.523	2147	40.1	YBR072W	11
IFVLAEENLPSLGYK	0.006	1.33E+05	846.964	564.978	4764	77.3	YGR185C	13
IGAHDDIINGDSTFK	0.006	8.93E+04	801.892	534.93	2004	38	YCR092C	10
IGDIIQFER	0.026	4.17E+05	545.798	364.201	3111	54.2	YGL245W	8
IGGIGTVPVGR	0.000	1.87E+07	513.309	342.542	1951	37.2	YBR118W	12
IGGLLKPSELDD	0.020	1.13E+05	628.84	419.563	2812	49.8	YGR218W	11
IGPDVVIGPNVTIGDGVR	0.006	1.33E+05	889.494	593.332	3884	65.1	YDL055C	10
IGSEVYHNLK	0.022	7.41E+05	580.309	387.208	1056	23.4	YGR254W	8
IGTINEEDILANQPLLLQSIQDR	0.000	4.52E+04	1297.2	865.133	3223	82.7	YKR048C	8
IGTQEDIFPFLGGAGPYFSFPGDYGISR	0.016	5.94E+04	1504.73	1003.49	4251	108.2	YBR092C	8
IGVADAINELLEPIR	0.047	2.26E+04	811.959	541.642	6109	101.5	YGR185C	11
IHLEGSEAPQEPK	0.032	7.30E+04	717.865	478.912	1018	22.7	YGL245W	10
IHQYLFQEGVVVAK	0.020	4.96E+04	815.951	544.303	2874	50.7	YMR230W	10
IIAAIPNPEDVVAISSR	0.000	1.50E+06	882.996	589	4034	67	YGR214W	14
IIDDDVPTILQGAK	0.010	7.30E+05	749.412	499.943	3563	60.6	YLL026W	12
IIDFGLSNIYDSR	0.021	1.67E+05	756.888	504.928	4588	74.8	YDR122W	10
IIEILQGLNETSTNAYR	0.000	7.18E+04	968.013	645.678	4395	72	YKL080W	16
IIFGTQSDAFQEDR	0.006	7.79E+04	813.892	542.93	3049	53.2	YLR027C	10
IIGIATTFDLDFLK	0.016	2.17E+05	783.943	522.964	5468	89.1	YER062C	10
IINEPTAAAIAYGLDK	0.000	1.28E+06	830.451	553.97	3809	64.1	YAL005C	16
IINEPTAAAIAYGLGAGK	0.000	2.35E+06	865.478	577.321	4129	68.3	YDL229W	21
IINSSEIQSAIRPAGQATQK	0.016	2.12E+05	1056.57	704.718	2423	44.1	YBR031W	18
IIVDAYGGASSVGGGAFSGK	0.000	2.30E+05	906.96	604.976	3035	53	YDR502C	23
IIVHTDTEPLINAAFLK	0.007	3.22E+05	948.035	632.359	4152	68.6	YGR234W	10
IIYVDDGVLSFQVLEVVDDK	0.000	3.15E+05	1133.6	756.067	5857	149.4	YAL038W	15
ILATLQGLEAVNAVLESTPDTPSPLIAVNENK	0.000	8.18E+04	1659.4	1106.6	4102	104.5	YMR205C	14
ILDSALVTAAQLAK	0.010	4.99E+05	707.419	471.949	4043	67.1	YLL026W	16
ILEDLVFPTEIVGK	0.000	9.83E+05	786.948	524.968	5128	83	YOR096W	11
ILEQFEYVLYPSK	0.006	1.58E+05	814.932	543.624	4709	76.5	YPL231W	12
ILGYDPLASPALLQVQIPATPTSLETAK	0.000	1.53E+05	1454.31	969.874	5695	93.4	YBR249C	13
ILLPFLEQSLSQGIQDQAVYNALAK	0.007	4.25E+04	1380.25	920.504	6300	105.8	YGL206C	10
ILNHMIETGAEYIMELTDK	0.016	2.01E+05	1111.05	741.034	5838	96.2	YKL035W	17
ILPEPTEGFAADDEPTTPAELVGK	0.006	9.33E+04	1249.12	833.083	4109	68	YKL182W	10
ILSQAPSELELQVAK	0.000	8.15E+05	813.459	542.642	3174	55.1	YNL096C	18
ILSQAPTELELQVAQAFVELENSSPELK	0.000	4.57E+05	1542.31	1028.54	4546	115.7	YOR096W	15

ILYEALDANSDFYNVPVDPK	0.018	1.90E+04	1142.06	761.711	2877	74.1	YOR184W	9
INAGLYILNPEVIDLIEMKPTSIEK	0.000	8.56E+04	1407.27	938.517	6075	100.8	YDL055C	12
INEIEESIASGDLSLVQEK	0.000	9.29E+04	1037.53	692.023	2921	75.2	YOR198C	9
INELLSSLEGK	0.007	3.12E+05	601.835	401.559	3527	60.1	YDR382W	9
INELTLLVQK	0.000	2.27E+06	585.858	390.908	3576	60.8	YNL178W	12
IPDDLLDDENVTSDDLFGFLAR	0.020	5.40E+04	1240.6	827.399	6219	103.9	YCL040W	10
IPEIPLVVSTDLESIQK	0.000	1.47E+06	941.033	627.691	5420	88.2	YBR031W	20
IPNFESGLLHLIFEAGLLYQSLGYK	0.000	1.19E+05	1411.76	941.509	3470	59.3	YNL126W	10
IQEPVFLVEIQCPEQAVGGIYSVLNK	0.000	7.18E+05	1437.26	958.509	6300	105.8	YDR385W	18
IQIVGADPFGSILAQPENLNK	0.000	4.86E+04	1112.6	742.071	3302	84.7	YGR155W	10
ISDDILSVLDSHLIPSATTGESK	0.000	1.18E+06	1199.62	800.083	5419	88.2	YDR099W	18
ISGVEVESPTSFPVQSLIPKPLESVK	0.000	8.33E+04	1384.26	923.176	5090	82.4	YJR139C	10
ISHVSTGGGASLELLEGK	0.006	8.50E+04	877.968	585.648	2719	48.4	YCR012W	11
ITDEEASYK	0.000	1.18E+06	528.248	352.501	701	16.8	YHR203C	8
ITEKPELINDILLECGFPNTSGQKPNEYNY	0.018	2.59E+04	1720.34	1147.23	3262	83.7	YCL050C	9
ITTIEEIFLHSLPVK	0.006	1.60E+05	870.501	580.67	5449	88.7	YGL123W	11
IVAVTGTEAFEAQR	0.032	7.97E+04	746.394	497.932	2428	44.1	YOR335C	10
IVDLEQSSEFASLFPLK	0.000	4.75E+05	962.009	641.675	5615	91.8	YKL081W	19
IVDMVSYGIWEPEVIK	0.007	3.94E+04	939.49	626.662	5125	83	YJL014W	10
IVDTNGAGDAFAGGFMAGLTK	0.000	8.10E+04	1006.99	671.663	3111	79.9	YJR105W	11
IVEQLADYLIGVQY	0.000	2.13E+06	812.435	541.959	5839	96.2	YOR122C	18
IVFELYNDIVPK	0.032	9.86E+04	725.403	483.938	4878	79	YLR216C	10
IVGIATTFDLDFLK	0.016	2.03E+05	776.935	518.292	5463	89	YIL053W	11
IVGIVSGELNNAAAK	0.016	2.04E+05	728.412	485.944	2588	46.4	YDR023W	11
IVNDVTAAGVSYGIFK	0.043	2.58E+04	827.446	551.966	4159	68.7	YPL106C	10
IVNEEFDQLEEDTPVYK	0.016	3.66E+04	1034.49	689.997	2541	65.5	YLR200W	10
IVNEPTAAAIAYGLDK	0.000	1.22E+06	823.443	549.298	3809	64.1	YJL034W	13
IVPAEDGSGAGAAVIAALAQK	0.000	3.67E+05	955.023	637.018	4430	72.5	YGL253W	24
IVSTEGNVPQTLAPVPYETFI	0.021	1.57E+05	1138.1	759.067	5533	90.3	YBR191W	11
IVTEAVEIEQR	0.007	4.20E+05	643.851	429.57	1852	35.8	YJL026W	9
IVVEYIAAIGADLIDER	0.000	8.25E+04	930.509	620.675	6275	105.2	YLR249W	14
IWCFGPDGNGPNLVIDQTK	0.016	5.58E+04	1037.51	692.007	2936	75.6	YDR385W	9
IYASFNDTFVHVTDLSGK	0.007	2.18E+05	1007.5	672.002	3757	63.3	YCR031C	9
IYPTYDFCVPIVDAIEGVTHALR	0.020	5.75E+04	1296.66	864.777	6669	114.5	YGL245W	10
IYTISETPEALPILLEDASR	0.021	1.39E+05	1116.09	744.398	5683	93.1	YLL018C	11
LAFYQVTPEEDEEEDEE	0.000	1.24E+06	1036.43	691.288	2506	64.6	YLR061W	15
LALTTAEYLAYQTER	0.006	2.28E+05	871.952	581.637	2964	52	YBR127C	11
LATGANIVGNALIDPTAK	0.006	2.85E+05	869.989	580.328	3604	61.2	YDL055C	12
LDDATEDVFNK	0.007	2.49E+05	633.796	422.866	2007	38	YGL245W	10
LDEVVVITK	0.026	3.63E+05	508.305	339.206	2146	40	YER091C	8
LDGLSVQELMDSK	0.016	1.98E+05	717.861	478.91	4093	67.8	YLR432W	10
LDLFPEDLNILGK	0.010	2.93E+05	743.911	496.277	5528	90.2	YNL220W	13
LDPNISNNLGIFYTGK	0.020	3.90E+04	883.46	589.309	5914	97.7	YLR260W	10
LDQLIYVPLPDENAR	0.006	3.71E+05	878.467	585.981	4434	72.6	YDL126C	12
LDQVWGSETVASSK	0.000	1.89E+06	753.875	502.919	2243	41.4	YBR031W	15
LDVDEVSDVAQK	0.007	2.79E+05	659.33	439.889	2137	39.9	YGR209C	11
LEAEEIPSEDQNEFLLER	0.016	4.05E+04	1081.02	721.015	4291	109.2	YPL231W	8
LEDLSPSTHNMEVPVVK	0.007	1.68E+05	947.983	632.324	2422	44.1	YEL034W	9
LEDPSGQQPIWGR	0.032	1.21E+05	741.87	494.916	2478	44.9	YAL035W	11
LESYVASIEQTVTDPVLSSK	0.000	2.31E+05	1083.56	722.711	3216	82.5	YDL229W	11
LEVGTETLIDK	0.007	2.88E+05	609.335	406.559	2542	45.8	YML126C	9
LEVPGYVDIVK	0.000	1.87E+06	616.35	411.236	3707	62.6	YNL302C	11
LFPTGGPFGGNDVTTIFGK	0.007	4.04E+04	962.994	642.332	3975	66.3	YGR270W	10
LGDTLYEEFGISK	0.021	1.73E+05	736.369	491.249	4088	67.7	YGL202W	10
LGEMPADQGFPAYLGAK	0.006	1.54E+05	882.935	588.959	3849	64.6	YDL185W	11
LGFTFSYPVDQTSLNSGTLIR	0.018	3.08E+04	1158.6	772.734	3287	84.3	YCL040W	7
LGGEVFIDFTK	0.000	3.42E+06	613.327	409.22	4062	67.4	YMR083W	12

LGGIPLGVIGVETR	0.007	2.11E+05	690.914	460.945	3692	62.4	YNR016C	9
LGSADLVEEIDSDGSK	0.006	9.62E+04	817.891	545.597	3389	58.2	YDL143W	10
LGSLVGQDSGYVGGLPK	0.006	9.17E+04	823.941	549.63	3124	54.4	YKR048C	13
LGYSVYEDAQYIGHAFK	0.007	1.74E+05	980.976	654.32	4382	71.8	YNR034W-A	11
LHDIPDEFLTDAMPIAK	0.007	1.79E+05	963.488	642.661	4552	74.3	YDL125C	10
LIDLTQFPAFVTPMGK	0.000	1.20E+07	889.481	593.323	5234	84.8	YLR044C	12
LIEAFNEIAEDSEQFEK	0.000	2.47E+05	1006.48	671.321	3126	80.3	YPL240C	13
LIEFGFTDEMIAMPISALSGGWK	0.006	9.45E+04	1257.13	838.42	6679	114.7	YLR249W	11
LIEPYVAYGYPSYSTIR	0.000	1.64E+06	996.509	664.675	3605	61.2	YGL076C	10
LIESSNLEMEIIPNQK	0.000	1.92E+05	929.485	619.992	3730	63	YKL035W	12
LISDYDADELAEALQPVIVNTPHLK	0.000	2.12E+05	1382.72	922.152	5525	90.1	YHR064C	16
LLDAVDEYIPTPER	0.006	2.26E+05	815.92	544.282	3994	66.5	YOR187W	11
LLEPAYDGASVEQQ	0.016	1.82E+05	760.367	507.247	2588	46.4	YHR025W	11
LLGAQHLIEAGVDALIVCGGDGSLTGADLFR	0.016	3.98E+04	1541.31	1027.87	4171	106.2	YMR205C	9
LLPWFDGMLEADEAYFK	0.016	4.43E+04	1022.99	682.329	4361	111	YKL060C	9
LLQENDTTLVK	0.007	1.90E+05	637.354	425.238	1812	35.2	YKL182W	10
LLQLAGVEDVYTQSNGK	0.000	9.80E+04	917.981	612.323	3790	63.8	YGL123W	10
LLTLTNAANVPVENIWADIFAK	0.006	3.40E+05	1207.16	805.109	6539	111.3	YDL081C	16
LLYETALLTSGFSLDEPTSFASR	0.000	4.58E+04	1259.64	840.095	3673	93.9	YPL240C	9
LNDAVEYVSGR	0.000	2.10E+06	611.807	408.207	1857	35.9	YFL014W	11
LNDIEDVEK	0.026	3.41E+05	537.769	358.849	1321	27.8	YBR011C	8
LNIGIVHVGAPSAALNAATR	0.007	2.13E+05	973.053	649.037	3732	63	YGR240C	10
LNILTQEDNTVMVSQIAENNTTK	0.006	1.81E+05	1288.65	859.434	3804	64	YDR484W	10
LNNVFVIGEQGKPYISLPK	0.010	3.05E+05	1058.59	706.065	4213	69.5	YHR203C	14
LNNVSLSSDAFFPFPDNVYR	0.000	7.94E+04	1151.56	768.043	3492	89.4	YLR028C	7
LNPEYTISAYSDNAAVLDSENDAFFFAPNSTTK	0.000	1.99E+04	1806.84	1204.89	3543	90.7	YGR061C	7
LNYNTVSGVNGPLVILEK	0.007	5.11E+04	965.536	644.026	4535	74	YBR127C	11
LPLSVINVSAQR	0.000	1.47E+06	648.885	432.926	3197	55.5	YDR447C	11
LPLVGGHEGAGVVVGMGENVK	0.000	1.80E+06	1010.04	673.695	3152	54.8	YMR303C	14
LPTESVPEPK	0.026	6.80E+05	548.798	366.201	1386	28.8	YMR242C	10
LQDVLDGFINK	0.007	1.78E+05	631.343	421.231	4047	67.2	YPR041W	9
LSAEEVDFVEIIGGTTR	0.000	2.97E+05	918.473	612.651	5260	85.3	YPL106C	17
LSEVVELFEVFTPQDGR	0.000	6.96E+04	983.002	655.67	6095	101.2	YHR087W	11
LSNASNSPGMLANSSTATSASANER	0.020	5.36E+04	1219.56	813.379	1499	30.6	YDR472W	10
LSQSLETLDSQLNLR	0.006	3.72E+05	858.96	572.976	3409	58.5	YGL245W	13
LSQVNCNTVFGLPGDFNLSLLDK	0.000	4.23E+06	1247.64	832.093	5784	95.1	YLR134W	11
LSQYVQEMALGGPITK	0.006	1.58E+05	867.958	578.975	2979	52.2	YPL231W	12
LSSESVIEQIVK	0.000	1.62E+06	666.374	444.585	3967	66.2	YDR064W	13
LSVDSMTTLLEVENDPTQLR	0.018	3.25E+04	1131.07	754.383	3277	84	YNR016C	7
LTADYDALDIANR	0.000	8.67E+05	725.862	484.244	3113	54.2	YOL127W	13
LTDDSSPIPYPEQPPIK	0.000	9.66E+04	948.983	632.991	3055	53.3	YER090W	10
LTNVSLSSDAFFPFPDNVYR	0.000	8.70E+04	1145.06	763.711	3492	89.4	YMR120C	8
LTSLNVVAGSDLR	0.000	2.51E+06	672.878	448.921	2217	41	YAL038W	10
LTTNLEYTLPESVEILGPQNK	0.000	1.00E+05	1180.12	787.085	3107	79.8	YHR064C	8
LVADGVFYAELNEFFTR	0.030	7.76E+04	995.999	664.335	6292	105.6	YNL178W	13
LVEDPQVIAPFLGK	0.000	2.28E+06	763.435	509.292	4453	72.9	YLR249W	16
LVTDLSVQQPEVLGEGVDVNEDLIK	0.000	6.61E+04	1355.21	903.811	4750	77.1	YKL210W	14
LWDVATGETYQR	0.000	1.98E+06	719.852	480.237	2678	47.7	YMR116C	14
LWTEFNEDAEPVTTDAIILATGASAK	0.000	1.69E+05	1382.19	921.796	5605	91.6	YDR353W	13
LYGTDDNTQEVEAVTNK	0.007	2.73E+04	948.945	632.966	2020	38.2	YJR014W	10
LYQAGGAPGGAAGGAPGGFPGGAPPAPEAEGPTVEEVD	0.000	2.51E+05	1688.29	1125.86	2457	63.4	YAL005C	14
MAEGVFQGAIGIDLGTTYSCVATYESSVEIIANEQGNR	0.000	4.82E+04	1997.45	1331.97	5099	129.9	YDL229W	8
MATLEELDAQTLPGDDELDQEILNLSTQELQTR	0.000	4.28E+04	1865.4	1243.94	4388	111.7	YOR117W	7
MFILDEADEMLSSGFK	0.000	1.30E+05	916.926	611.62	6075	100.8	YJL138C	15
MGTTGVQSSVASDLDELISR	0.016	6.10E+04	1033.51	689.341	3341	85.6	YGL026C	8
MIEIMLPVFDAPQNLVEQAK	0.000	2.34E+06	1143.6	762.734	5163	83.6	YLR044C	10
MIPGAKPLQVGDVVSTTAVIESVVNQPTGK	0.028	2.79E+04	1518.33	1012.55	3316	85	YKL182W	8

MPELIPVLSESMWDTK	0.030	7.42E+04	938.465	625.979	5872	96.9	YNL014W	9
MPELIPVLSETMWDTK	0.025	9.84E+04	945.473	630.651	5872	96.9	YLR249W	13
MSANISETTAMITDIANAPAEIDR	0.000	8.86E+05	1268.11	845.74	5589	91.3	YLR134W	12
MSANISETTAMITDIATAPAEIDR	0.000	1.80E+06	1261.61	841.409	4649	75.7	YLR044C	10
MSLPATFDLTPEDAQLLLAANTHLGAR	0.000	5.92E+05	1433.74	956.164	6035	100	YGR214W	11
MSNPFDLLGNDVEDADVVVLPPK	0.000	2.07E+04	1242.62	828.749	4078	103.9	YLR150W	6
MSPEQALLSLHADYIGGDTANYK	0.000	3.66E+04	1247.6	832.069	3413	87.4	YGR032W	6
MSQVYFDVEADGQPIGR	0.000	2.13E+06	956.449	637.968	4215	69.5	YDR155C	11
MSTATTTVTTSDQASHPTK	0.000	1.03E+05	982.965	655.646	815	19	YLR244C	11
MSTFNAETADNLEDIEK	0.000	9.32E+04	964.433	643.291	3805	64	YPL225W	10
NAAWLVFANK	0.026	5.93E+05	567.309	378.542	3956	66	YDL192W	11
NAESLSVLDIENEIVR	0.000	1.13E+05	900.971	600.983	5050	81.7	YDR148C	15
NAFEGVLDWLK	0.007	2.11E+05	646.338	431.228	5747	94.4	YPL160W	12
NAPAIIFIDEIDSIAPK	0.000	1.82E+05	913.999	609.668	6190	103.3	YDL126C	14
NASNNPNELAASGAALQAR	0.000	2.77E+05	934.964	623.645	2000	37.9	YHR064C	16
NATFPGVQMK	0.000	3.00E+06	546.779	364.855	2141	40	YLR044C	9
NAVVTVPAYFNDSQR	0.006	2.39E+05	840.921	560.95	3184	55.3	YJR045C	11
NCTPKPTSTTETVAASAVAAVFEQK	0.000	2.21E+06	1276.14	851.095	4514	73.8	YAL038W	11
NDAIINQSTFK	0.007	3.80E+05	625.822	417.551	2027	38.3	YLR028C	10
NDLAITGAPDNAYAK	0.032	4.56E+04	767.381	511.923	1348	28.2	YDR301W	11
NDPTLYESIISLLK	0.020	4.31E+04	803.44	535.963	6354	107	YNL287W	11
NDPTWQGPILAPGLINR	0.000	2.79E+05	931.5	621.335	4470	73.1	YNL117W	10
NDVDVIANPDGER	0.010	3.51E+05	707.334	471.892	1608	32.2	YHR064C	13
NEFSGALSGLTR	0.000	6.12E+05	626.32	417.882	3257	56.3	YIL078W	9
NEGVTVPIILMGYYNPILNYGEER	0.007	2.89E+04	1377.69	918.798	6285	105.4	YGL026C	10
NFEVLFLTDPIDEYAFTQLK	0.006	2.34E+05	1202.11	801.742	6419	108.6	YMR186W	16
NFGIGQAVQPK	0.000	1.93E+06	579.817	386.88	1996	37.9	YHL033C	10
NFLETVELQVGLK	0.010	5.99E+05	745.417	497.28	5433	88.4	YGL135W	15
NFNDPEVQADMK	0.000	1.44E+06	704.314	469.878	1798	35	YAL005C	12
NFTPEQISSMVLGK	0.000	2.89E+06	775.898	517.601	4783	77.6	YAL005C	15
NGFILDGFPR	0.000	9.21E+05	568.298	379.201	4816	78.1	YDR226W	8
NILAESNSSLDNIVK	0.000	6.17E+05	808.928	539.621	3479	59.5	YIL051C	18
NINSETTDEQFQELFAK	0.000	1.19E+05	1007.47	671.985	2786	71.8	YER165W	10
NIPIEVVALINDTTGTLVASYYTDPETK	0.000	3.42E+05	1519.28	1013.19	4746	120.9	YGL253W	16
NISGASDETLHELGVPITPIAFDYPTVVK	0.016	6.53E+04	1542.3	1028.54	3426	87.8	YOR184W	8
NIYYITGESLK	0.000	3.16E+06	650.843	434.231	2947	51.8	YMR186W	11
NLAGVDYLTISPALLDK	0.000	6.99E+05	901.999	601.668	5105	82.6	YLR354C	20
NLATLLLTDYIQK	0.010	2.35E+05	753.432	502.624	5643	92.4	YDR071C	16
NLEILDLQDNTFTK	0.006	1.64E+05	832.431	555.289	4524	73.9	YMR235C	13
NLFTGWVDVK	0.000	9.10E+06	589.814	393.545	4631	75.4	YKL152C	11
NLFTVEDAIK	0.026	4.40E+05	575.311	383.877	3606	61.2	YLR355C	8
NLIAATAIAIVGFVQAVIGVYGEGQFI	0.000	1.91E+05	1367.76	912.177	4015	66.7	YLR356W	10
NLPDMIEELDLHED	0.006	1.78E+05	841.883	561.591	5039	81.5	YDL022W	14
NLQYYDISAK	0.007	4.07E+05	607.806	405.54	2247	41.5	YLR293C	9
NLSIVGLVGSIDNDMSGTDSTIGAYSALER	0.016	4.07E+04	1528.25	1019.17	3391	86.9	YGR240C	9
NLTEQAIIDLTVATIAIK	0.000	1.13E+05	964.059	643.042	6415	108.5	YMR120C	13
NLVNDEIIAALIELAK	0.020	6.00E+04	870.001	580.336	6849	119	YBR196C	12
NMITGTSQADCAILIIAGGVGEFEAGISK	0.000	4.25E+05	1433.72	956.149	6700	115.2	YBR118W	18
NNLNTENPLWDAIVGLGFLK	0.032	4.70E+04	1114.59	743.395	6973	122.2	YDL185W	11
NNLWDDDVLAR	0.000	4.28E+05	665.823	444.218	3647	61.8	YGR155W	9
NNYDGDTVTFSPTGR	0.020	5.93E+04	822.368	548.581	2124	39.7	YMR314W	10
NPEEVEQVAEEAAAAEEGEEEEVK	0.000	8.31E+04	1308.08	872.387	4399	112	YLR048W	9
NPHDIIEGINAGEIEIPEN	0.016	7.22E+04	1037.51	692.008	2791	71.9	YDR418W	10
NPLFSYVEPVLVASAK	0.006	2.41E+05	867.477	578.654	5269	85.4	YDL075W	11
NPSDITQEEYNAFYK	0.000	1.26E+06	909.913	606.944	3125	54.4	YMR186W	16
NQAAMNPSNTVFDAK	0.000	1.85E+06	804.378	536.588	2084	39.2	YAL005C	17
NQDLEQQLEDSEAK	0.020	3.70E+04	823.879	549.588	2359	43.1	YIL138C	10

NQEIFDANVQR	0.000	3.15E+06	667.328	445.221	1862	35.9	YDL082W	12
NQILVSGEIPSTLNEESK	0.000	1.26E+05	979.507	653.341	3210	55.6	YBR072W	14
NQLESIAYSLK	0.000	3.97E+06	633.34	422.563	3437	58.9	YAL005C	12
NQQIVAGKPLYVAIAQR	0.007	2.08E+05	935.039	623.695	2802	49.6	YER165W	10
NQQLEEDLEESDTK	0.006	1.13E+05	839.376	559.92	1889	36.3	YNL079C	10
NSNPENTVGLISGAGANPR	0.007	5.01E+04	934.466	623.313	2425	44.1	YHR200W	10
NSSCYFLGDATNDSLQR	0.000	1.54E+05	945.918	630.948	3000	52.5	YIL078W	10
NTAAWHPVIENLVGTVDDDSLVSIYKPYTEESE	0.000	2.41E+05	1846.39	1231.26	3663	93.6	YOR230W	9
NTTRPDFIFYSDR	0.034	2.73E+05	816.394	544.599	2941	51.7	YHR128W	8
NTWGSQLVDQIMDQVVTK	0.028	2.33E+04	1031.52	688.014	3996	101.9	YGL037C	8
NVAAIILEPIQGEAGIVVPPADYFPK	0.000	1.91E+05	1361.25	907.834	5915	97.7	YLR438W	13
NVAFLYDMVDAEGFK	0.020	4.24E+04	859.908	573.608	5384	87.6	YBL064C	10
NVEVVALNDPFISNDYSAYMFK	0.000	3.51E+04	1268.61	846.074	3543	90.7	YJR009C	7
NVLEASNSSLDR	0.007	2.78E+05	652.826	435.553	1472	30.2	YER057C	9
NVNDVIAPAFVK	0.000	4.77E+06	643.859	429.575	3177	55.2	YGR254W	14
NVPGVETANVASLNLLQLAPGAHLGR	0.000	1.58E+06	1306.22	871.149	5079	82.2	YBR031W	17
NVPLYQHLADLSK	0.000	2.09E+06	749.407	499.94	3228	55.9	YHR174W	14
NVQVLESVENK	0.007	2.05E+05	629.836	420.226	4587	74.8	YGR130C	9
NVVALGCGFVEGLGWGNNASAAIQR	0.020	6.45E+04	1252.13	835.089	5284	85.7	YDL022W	10
NWGAETDELSMIMEHFSQQ	0.032	7.18E+04	1126.98	751.658	5978	98.9	YOR369C	14
NYASEALISYFK	0.021	1.58E+05	703.354	469.238	4633	75.5	YKL081W	10
QAEITQGLESIDTVK	0.024	3.16E+04	816.428	544.621	3174	55.1	YDR044W	10
QAFDDAIAELDTLSEESYK	0.032	1.31E+05	1073	715.667	5508	89.8	YDR099W	13
QAINLGQVVLTPLTFALPR	0.007	2.85E+05	1026.1	684.405	6242	104.4	YHL001W	15
QAVESADLILSVGALLSDFNTGSFSYSYK	0.000	1.28E+05	1541.77	1028.18	5861	149.5	YGR087C	9
QDGVLLVALSNEPAAR	0.000	3.81E+05	826.952	551.637	3889	65.1	YPL231W	15
QDLPEAMSAAEITEK	0.006	3.59E+05	816.893	544.931	2944	51.7	YDL137W	14
QDVEALIEFIYDTEK	0.000	9.62E+04	906.949	604.968	6085	101	YPL231W	11
QFGYVILTTSAGIMDHEEAR	0.000	5.14E+04	1119.55	746.7	3917	99.9	YJL190C	7
QIAPAELEGLLDLER	0.006	1.71E+05	833.954	556.305	5304	86	YPL231W	10
QIIENAGEEGSVIIGK	0.020	6.29E+04	828.944	552.965	2709	48.2	YLR259C	10
QITVVGATSGDTGSAAIYGLR	0.028	1.33E+04	1019.03	679.692	2921	75.2	YCR053W	8
QLDNLYSSSNHSK	0.032	6.02E+04	746.855	498.239	1723	33.9	YOR093C	10
QLEDLNLFDNLR	0.010	3.28E+05	745.386	497.26	4818	78.1	YGR155W	11
QLENVSSNIVK	0.000	1.10E+06	615.838	410.894	1647	32.8	YHL015W	11
QLEQLGPNVLDEFDYSFSENGLTAYR	0.016	3.34E+04	1503.21	1002.48	3856	98.4	YFL045C	8
QLGEWAGLGK	0.000	1.04E+06	529.785	353.526	2851	50.3	YOR369C	8
QNPQAIGQDLFTDPR	0.006	7.17E+04	850.424	567.285	3259	56.4	YOR027W	10
QPASFLFLGLSGSGK	0.032	1.10E+05	754.909	503.608	4943	80	YLL026W	11
QSISEAFGKPLSTTLNQDEAIAK	0.006	1.87E+05	1224.63	816.759	3624	61.4	YPL106C	11
QTSFASTASTASVVSSTSGR	0.000	1.87E+05	966.469	644.648	3470	59.3	YER132C	10
QVLVASSEVLYAEAADEK	0.007	2.56E+04	961.491	641.33	5255	85.2	YLR216C	10
QVNVNTIFGLPGDFNLSLLDK	0.021	1.47E+05	1152.62	768.746	6013	99.6	YGR087C	10
QVNVNTVFGLPGDFNLSLLDK	0.010	3.33E+05	1145.61	764.074	6023	99.8	YLR044C	11
QVYFVADIENLSPLACAYAR	0.021	1.57E+05	1122.06	748.377	5698	93.4	YMR120C	10
RPGADSDIGGFGGLFDLAQAGFR	0.016	1.88E+05	1162.57	775.385	5608	91.7	YGL234W	15
SAAIVNESLGGLDPK	0.028	1.33E+05	735.894	490.931	2888	50.9	YPL262W	11
SANLMAGHWVAISGAAGGLGSLAVQYAK	0.000	2.90E+05	1350.7	900.802	8470	149.8	YOL086C	12
SASEVASDLAQLTDFPVIR	0.016	5.72E+04	1010.02	673.685	3641	93.1	YGR279C	9
SASEYDSALASGDK	0.010	2.30E+05	700.812	467.544	1243	26.6	YGR209C	11
SAYLAAVPIAAILIK	0.032	6.78E+04	757.471	505.317	5878	97	YDR516C	10
SAYLAAVPLAAILIK	0.032	6.78E+04	757.471	505.317	5878	97	YCL040W	10
SAYVTTEEFIDAVESR	0.007	4.10E+04	908.934	606.292	4960	80.2	YLR174W	10
SDEEIIDIISK	0.000	9.50E+05	631.33	421.222	3967	66.2	YLR180W	14
SDLVDLLNIYK	0.007	1.61E+05	646.858	431.575	5322	86.4	YDL131W	10
SEAEAEAAGLPVVNLDTR	0.000	3.39E+05	921.466	614.646	3425	58.7	YLL018C	19
SEELYPGRPLAIALDTK	0.000	5.76E+05	937.007	625.007	3002	52.6	YAL038W	11

SEGIEFFASPVTLGPDGIEK	0.000	2.48E+05	1047.03	698.353	3271	83.9	YKL085W	14
SEGNPVIGVFQK	0.007	2.93E+05	637.841	425.563	2942	51.7	YPL231W	12
SEIFSTYADNQPGVLIQVFEGER	0.000	4.73E+05	1300.14	867.094	5699	93.4	YAL005C	13
SEIPEHVIQLLDSLPK	0.007	2.27E+05	909.504	606.672	5522	90.1	YNR001C	16
SELEYYAMLSK	0.000	1.16E+06	667.321	445.216	3567	60.6	YGL030W	13
SEPHITELDNQVGDGDCGYTLVAGVK	0.007	4.31E+04	1359.14	906.429	3425	58.7	YML070W	11
SEVFSTYADNQPGVLIQVFEGER	0.000	4.00E+05	1293.13	862.422	5699	93.4	YER103W	11
SEWPSLIEELLK	0.010	4.48E+05	722.39	481.929	6208	103.7	YMR205C	11
SEYTDMLATGIIDPFK	0.000	3.37E+05	900.94	600.962	5420	88.2	YLR259C	18
SFDELGLAPELLK	0.021	1.66E+05	716.39	477.929	4873	79	YOR046C	10
SFDVPPPPIDASSPFSQK	0.000	1.80E+06	958.475	639.319	3960	66.1	YKL152C	21
SGAATLLVATAVAAR	0.025	8.93E+04	686.401	457.937	3767	63.5	YOR204W	9
SGETEDPFIADLVVGLR	0.000	4.59E+06	909.468	606.648	5955	98.5	YMR323W	11
SGETEDTFIADLVVGLR	0.000	6.28E+06	911.465	607.979	5950	98.4	YGR254W	22
SGNNLVDLSDADTLQR	0.006	7.61E+04	859.421	573.283	3009	52.7	YBR079C	10
SGVAVADESLTAFNDLK	0.000	7.64E+05	868.939	579.628	4174	68.9	YLL050C	18
SGVVNSAFPADESLK	0.010	2.38E+05	760.883	507.591	2543	45.8	YMR105C	11
SHDVVIIGGGPAGYVAAIK	0.025	8.71E+04	912.504	608.672	3552	60.4	YFL018C	10
SHPDAFALDPLEFEK	0.026	3.58E+05	858.417	572.614	4166	68.8	YOR285W	10
SIDDVDELIWTIGR	0.006	1.37E+05	816.417	544.614	5724	93.9	YPL091W	14
SIGGEVFIDFTK	0.000	3.15E+06	656.843	438.231	4417	72.4	YOL086C	12
SIIGATSIEDFISK	0.010	6.23E+05	740.898	494.268	4833	78.4	YHR183W	16
SINPDEAVAYGAAVQAAILTGDESSK	0.000	1.44E+06	1289.14	859.761	5499	89.6	YAL005C	19
SINPDEAVAYGAAVQAAILTGDQSTK	0.006	2.29E+05	1295.65	864.105	5499	89.6	YBL075C	10
SINPDEAVAYGAAVQGAILTGQSTSDETK	0.000	2.71E+04	1447.21	965.14	5890	149.9	YDL229W	5
SIQTLEMELAQIMK	0.020	5.59E+04	817.928	545.621	6109	101.5	YKL104C	11
SISIVGSYVGNR	0.000	1.02E+06	626.338	417.895	2702	48.1	YMR303C	12
SITGFTDVGETILGVDSILK	0.016	3.50E+04	1033.06	689.04	3971	101.2	YDR533C	8
SIVPSGASTGVHEALEMR	0.000	4.98E+05	920.965	614.312	2930	51.5	YGR254W	18
SIVTLDVKPWDDETNLEEMVANVK	0.000	4.87E+05	1373.19	915.793	5410	88	YAL003W	18
SIYLLAGNDPEGR	0.021	1.57E+05	702.86	468.909	2993	52.4	YOR335C	12
SLANTFLSLDTEGR	0.021	1.59E+05	762.389	508.595	4353	71.4	YGL202W	10
SLFQGYFTDSAENVNMYLTQPNFVEQTLK	0.000	5.98E+04	1692.81	1128.87	3967	101.1	YKL210W	7
SLFVVGVDNVSSQQMHEVR	0.010	2.22E+05	1066.03	711.025	3318	57.3	YLR340W	11
SLGNVIDPLDVITGIK	0.000	3.88E+05	827.475	551.986	5709	93.6	YGR094W	12
SLTTVWAEHLSDEVK	0.006	2.52E+05	857.936	572.293	3764	63.4	YOR063W	10
SLVALGIDPQDLK	0.007	3.65E+05	684.89	456.929	3032	53	YDL132W	10
SLVDNMITGVTK	0.000	1.04E+06	639.342	426.564	3637	61.6	YGL147C	13
SMTVFDPEPVQLADLSTQFFLTEK	0.007	4.28E+04	1372.18	915.123	6420	108.6	YKL210W	10
SNAIDLFVTGQIPTEEPELSEYQSK	0.000	1.50E+05	1398.18	932.459	5090	82.4	YMR120C	12
SNDSEQELLEAFK	0.021	1.51E+05	755.357	503.907	3978	66.3	YBR109C	11
SNFATIADPEAR	0.000	1.92E+06	646.317	431.214	2237	41.3	YLR249W	14
SNGVLNVDNQTSDLVK	0.000	4.58E+05	851.934	568.292	2789	49.4	YDR447C	10
SNYDTDVFTPLFER	0.006	2.88E+05	852.399	568.602	4759	77.3	YOR335C	14
SNYGMIAINPGR	0.007	1.95E+05	646.824	431.552	2622	46.9	YKL182W	9
SPQLSAAAASAASAASPDR	0.024	3.04E+04	864.929	576.955	2439	44.3	YLR219W	10
SPSALELQVHEIQGK	0.024	3.18E+04	818.439	545.962	2474	44.8	YDR032C	10
SQAANSVDEALAAVK	0.021	1.43E+05	737.381	491.923	3058	53.4	YJL130C	10
SQIDEIVLVGGSTR	0.000	2.03E+06	737.399	491.935	2858	50.4	YBL075C	12
SQIDEVVLVGGSTR	0.000	3.06E+06	730.391	487.263	2863	50.5	YDL229W	16
SQVDEIVLVGGSTR	0.000	3.51E+06	730.391	487.263	2863	50.5	YAL005C	17
SSNITISNAVGR	0.000	5.24E+05	609.825	406.886	1557	31.5	YDL229W	10
SSPDENSTLLSNDSISLK	0.000	2.45E+05	953.966	636.313	3065	53.5	YMR205C	16
SSQSPETVYFASELK	0.006	2.01E+05	836.907	558.274	3259	56.4	YGR124W	10
SSVLADALNAINNAEK	0.000	3.04E+06	815.426	543.953	5289	85.8	YJL190C	23
STLEPVEQVLK	0.000	4.48E+06	621.851	414.903	2922	51.4	YDL229W	9
STLIEPTSGNTGIGLALIGAIK	0.016	4.07E+04	1063.61	709.407	3431	87.9	YGR155W	8

STSGNTHLGGQDFDTNLLEHFK	0.000	4.62E+05	1209.57	806.716	3624	61.4	YDL229W	14
SVAVDSSESNLK	0.007	2.19E+05	618.309	412.542	897	20.6	YPL061W	9
SVAVPVDILDHDNNYELK	0.007	2.82E+05	1021.02	681.013	3797	63.9	YBR072W	9
SVDELITEGNEK	0.000	1.27E+06	667.328	445.221	1972	37.5	YOL039W	12
SVDELLTFIEGDSSNSK	0.000	8.07E+04	920.944	614.299	5380	87.5	YMR012W	10
SVDSIYQVVR	0.044	2.42E+05	583.314	389.212	2691	47.9	YBR025C	8
SVEMHHEQLEQGVPGDNVGFNVK	0.000	1.99E+06	1275.61	850.74	2344	42.9	YBR118W	18
SVGETVDYIASNPDAN	0.006	2.19E+05	826.376	551.253	2749	48.8	YKL192C	12
SVGFGLVYNSVAEAK	0.000	1.14E+06	770.904	514.272	3928	65.7	YER074W	10
SVLYNPPIEEFAVLETTFDEK	0.020	5.25E+04	1221.11	814.409	6194	103.4	YER003C	13
SVQYVLEDPIAGPLVK	0.000	4.12E+05	864.483	576.657	4439	72.7	YHR019C	15
SYIEGTAVSQADVTVFK	0.000	2.71E+05	907.962	605.644	3495	59.7	YAL003W	17
TAEEYLKPIINSVIK	0.034	2.66E+05	859.49	573.329	4436	72.6	YMR105C	9
TAELQAEIDDTVGIMR	0.026	5.50E+05	881.438	587.961	2141	40	YAL030W	8
TAEQLENLNIQDDQK	0.006	1.50E+05	879.929	586.955	4109	68	YER165W	10
TAGIQIVADDLTVTNPAR	0.000	1.70E+07	928	619.002	4000	66.6	YHR174W	22
TAGIQIVADDLTVTNPK	0.000	4.03E+06	878.478	585.988	3794	63.9	YGR254W	21
TAQLSLQDYLNQQANNQFNK	0.018	1.81E+04	1169.57	780.052	2692	69.4	YLR150W	7
TASEIATTELPPTHPIR	0.020	1.37E+05	917.489	611.995	2067	38.9	YDR099W	9
TASGNIIPSSTGAAK	0.000	2.05E+07	687.865	458.912	1232	26.4	YGR192C	11
TAVALDTILNQK	0.020	1.39E+05	643.869	429.582	3447	59	YBL099W	10
TAVELGAVALK	0.034	2.89E+05	536.324	357.885	2701	48.1	YPL028W	8
TAVFYGGTPISK	0.007	3.18E+05	620.832	414.224	2277	41.9	YDL084W	10
TDLFADLDPSQYFETR	0.000	1.54E+05	959.447	639.967	5570	91	YDR037W	12
TDTTYPAGFMDVITLDATNENFR	0.006	1.99E+05	1296.6	864.736	5624	92	YHR203C	14
TELDGILPLVAR	0.007	3.84E+05	648.88	432.922	4687	76.2	YAR015W	9
TELIHDGAYWVSDPFNAQFTAAK	0.006	1.37E+05	1291.12	861.083	4609	75.1	YFR044C	10
TEWIADYGAAASGR	0.016	1.90E+05	734.347	489.9	2893	51	YLR060W	12
TFIDLESSSPELK	0.010	4.21E+05	733.375	489.252	3428	58.8	YNL096C	13
TFSPQEISAMVLTK	0.010	6.71E+05	776.408	517.941	4748	77.1	YDL229W	12
TFTTCADNQTTVQFPVYQGER	0.000	2.14E+05	1203.56	802.706	2398	61.8	YDL229W	6
TFTTVSDNQTTVQFPVYQGER	0.006	3.40E+05	1209.58	806.724	3544	60.3	YNL209W	14
TFTVDVSSPTENGVFDPASYAK	0.000	3.60E+05	1166.55	778.038	2942	75.7	YLR061W	8
TGDLAGTATTSSFTEAVIK	0.000	8.01E+04	935.476	623.986	3390	58.2	YOR136W	13
TGGFLFPVLSESFK	0.010	2.96E+05	764.906	510.273	5623	92	YOR204W	12
TGIWAGVDASQPPATVWADILNK	0.006	2.87E+05	1205.62	804.085	5784	95.1	YDR226W	12
TGLDISDDAR	0.000	1.63E+06	531.757	354.84	1511	30.8	YDL229W	11
TGLVSVDDDIYQK	0.010	2.58E+05	726.864	484.912	2683	47.8	YNR016C	11
TGTLTTSETAHNMK	0.032	1.21E+05	746.359	497.908	658	16	YDR385W	10
TGTTTNDVDYPIPPNHEMIFTTDDK	0.007	3.81E+04	1411.64	941.432	3355	57.7	YAL038W	12
TGVIVGEDVHNLFTYAK	0.000	3.23E+05	931.986	621.66	4015	66.7	YKL060C	12
TGWLVEIVNYNVENQQYVAAGDLR	0.007	4.19E+04	1376.19	917.796	5695	93.4	YKL182W	10
THSTYAFESNTNSVAASQMR	0.010	2.38E+05	1101.5	734.668	1863	35.9	YKL035W	12
TIAETLAEELINAAK	0.010	5.37E+05	793.935	529.626	5933	98.1	YJR123W	13
TILEDGPESELLEPLYER	0.000	8.34E+04	1052.03	701.688	3256	83.5	YER036C	10
TIVWNGPPGVFEFEK	0.000	2.39E+06	860.441	573.963	4904	79.4	YCR012W	15
TLEDELEVTEGMR	0.021	1.57E+05	761.359	507.908	3513	59.9	YLR259C	10
TLEEGVEMANSSEFGLGSGIETESLSTGLK	0.000	8.61E+04	1536.73	1024.82	2626	67.7	YPL061W	9
TLELDEYQFNFDGDAEDLAAFADSANEEELQNK	0.000	2.40E+04	1876.32	1251.22	3893	99.3	YER110C	8
TLLEAIDAIEQPSRPTDKPLR	0.000	2.39E+06	1182.15	788.436	3928	65.7	YBR118W	10
TLSSSAQTSIEIDSLFEGIDFYTSITR	0.000	2.45E+04	1491.23	994.492	4500	114.5	YER103W	5
TLSSSAQTSVEIDSLFEGIDFYTSITR	0.000	2.45E+04	1484.23	989.821	4500	114.5	YAL005C	5
TLSSVTQTTVEVDSLFDGEDFESSLTR	0.000	5.14E+04	1482.2	988.472	3855	98.4	YDL229W	6
TMVGGNDYEIFVDER	0.006	1.51E+05	872.896	582.266	3774	63.6	YFL045C	11
TMYAADGDYLETYK	0.006	1.01E+05	820.861	547.576	2899	51	YBR149W	11
TNEAAGDGTTSATVLGR	0.006	2.52E+05	810.895	540.932	1294	27.4	YLR259C	14
TNEIILVDEVLTPDSSR	0.000	1.84E+05	950.997	634.334	4910	79.5	YAR015W	10

TNNPETLVALR	0.000	5.01E+06	614.338	409.895	2542	45.8	YAL038W	14
TNQLVPEVLEYNVR	0.000	5.72E+05	837.446	558.633	4054	67.3	YGL234W	10
TPANAAVPASTPLK	0.000	9.45E+05	669.375	446.586	1422	29.4	YLR044C	10
TPGPGGQAALR	0.026	3.66E+05	512.78	342.189	796	18.7	YCR031C	10
TPTAAAWDSPESHIGVAK	0.007	4.83E+04	919.458	613.307	2295	42.2	YGR155W	10
TQDLLLLDVAPLSLGIETAGGIMTK	0.006	1.41E+05	1285.21	857.143	6439	109	YBL075C	10
TQDLLLLDVAPLSLGIETAGGVMTK	0.006	3.77E+05	1278.2	852.472	6449	109.2	YAL005C	14
TQELPSLAQSTQR	0.032	1.21E+05	729.881	486.923	1903	36.5	YIL041W	10
TQFENSNEIGVFSK	0.020	4.63E+04	800.386	533.926	2764	49.1	YPR016C	11
TQFSWQYYYYTLTEEGVEYLR	0.007	3.48E+04	1370.13	913.759	6320	106.2	YMR230W	10
TSAVAALTEVR	0.000	1.56E+06	559.314	373.212	2436	44.3	YHL033C	10
TSEIMHLVNPIIENVR	0.007	1.98E+05	933.001	622.336	4447	72.8	YCL030C	9
TSFFQALGVPTK	0.000	8.54E+05	648.353	432.571	4397	72.1	YLR340W	11
TSLFLNLANDPTIER	0.006	1.85E+05	852.452	568.637	4419	72.4	YBR127C	11
TSPTGVSNDVMGSVPR	0.047	2.29E+04	802.391	535.263	2904	51.1	YBR161W	10
TSPYVLPVPFLNVLNGGSHAGGALALQEFMIAPTGAK	0.000	2.44E+05	1869.49	1246.66	4338	110.4	YGR254W	13
TTANLPANSSTSPAPSIPSTGFK	0.032	2.84E+04	1123.57	749.381	5288	85.8	YLR335W	10
TTPSFVAFTDTER	0.010	4.54E+05	736.357	491.24	3283	56.7	YAL005C	12
TTPSFVGFTDTER	0.000	1.64E+06	729.349	486.568	3048	53.2	YLL024C	13
TTQNPDELWEFIADSLK	0.007	2.11E+05	1003.99	669.662	6417	108.5	YGL253W	12
TTYTTQRPVYLGLPANLVDLNVPAK	0.000	5.88E+06	1372.75	915.504	4880	79	YLR134W	11
TTYVTQRPVYLGLPANLVDLNVPAK	0.000	8.09E+06	1371.76	914.844	4880	79	YLR044C	20
TVAGGAYTVSTAAAATVR	0.000	8.63E+05	833.942	556.297	2444	44.4	YJR094W-A	25
TVASSGQELSVEER	0.010	7.08E+05	746.368	497.914	1288	27.3	YER177W	16
TVAVDSVFEQNEMIDAIAVTK	0.032	7.20E+04	1140.58	760.719	5063	81.9	YOR063W	11
TVEQLGQEEYEK	0.010	2.47E+05	726.846	484.9	1443	29.7	YJL167W	10
TVESVNVIVSTYADEVLGDVQVYPAR	0.000	6.10E+05	1412.22	941.819	6415	108.5	YDR385W	15
TVFESLDQAWSLLR	0.006	1.20E+05	832.936	555.626	6009	99.5	YBR127C	10
TVFIQELINNIAK	0.032	7.96E+04	751.932	501.624	5913	97.7	YJR121W	11
TVIFTHGVEPTVVVSSK	0.007	4.16E+04	900.499	600.668	2775	49.2	YJR105W	12
TVLVYGHYDVQPAQLEDGWDTEPFK	0.000	8.72E+04	1454.2	969.799	4595	74.9	YFR044C	10
TVPFVPISGWNGDNMIEATTNAPWYK	0.000	2.21E+06	1454.7	970.137	5875	96.9	YBR118W	15
TVPGSSLTSVPGFFAAGDVQDSK	0.000	8.06E+04	1134.06	756.378	2877	74.1	YDR353W	7
TVSQADFPGLEGVAK	0.010	2.42E+05	759.894	506.931	3113	54.2	YIL078W	13
TVVVVGTVTDDAR	0.000	2.45E+06	666.362	444.577	1937	37	YNL301C	16
TYIGNLLALSISSDNLVNK	0.000	9.66E+04	1018.06	679.041	3701	94.5	YGR180C	8
TYPVEDPSTENTVCEVSSATTEDVEYAIECADR	0.000	8.24E+04	1812.28	1208.52	3928	100.2	YPL061W	7
VAASFSQEALQYVVER	0.020	3.77E+04	898.963	599.644	4339	71.2	YKL182W	10
VAAVETLYQDMAAR	0.010	5.56E+05	769.388	513.261	3998	66.5	YMR242C	15
VAPEEHPVLLTEAPMNPK	0.000	1.07E+06	986.514	658.012	2562	46.1	YFL039C	11
VASANATAAESDVAK	0.010	2.38E+05	702.852	468.904	848	19.7	YIL133C	11
VAVDDPSVLAEVEAVLAGVEAEK	0.032	6.88E+04	1155.61	770.741	6733	116.1	YDR342C	10
VDALEQETVYR	0.030	7.59E+04	661.833	441.558	2017	38.2	YDL110C	9
VDDELLVAR	0.000	9.47E+05	515.282	343.857	2226	41.1	YDR226W	10
VDFNVPLDGK	0.000	8.12E+05	552.29	368.529	2896	51	YCR012W	10
VDIIANDQGNR	0.000	4.33E+05	607.81	405.542	1157	25.2	YAL005C	9
VDPLVIELVTGAK	0.045	5.09E+04	677.403	451.938	5207	84.4	YGL195W	13
VEEQEQQQQQIIK	0.006	1.72E+05	814.418	543.281	999	22.4	YHL015W	18
VEFLEDTSR	0.000	2.91E+06	548.269	365.849	2051	38.7	YLR264W	11
VEGIGYDFVPQVLDR	0.006	2.63E+05	853.941	569.63	5059	81.9	YGR155W	10
VELDALFNIAELK	0.032	1.07E+05	737.911	492.277	5703	93.5	YPL218W	15
VENIISWGYGTPGAGAYDYIK	0.000	1.11E+05	1137.56	758.707	3127	80.3	YLR179C	12
VENPFDFMENISLAGK	0.000	1.08E+05	905.938	604.294	5775	94.9	YJL026W	12
VESIVAEASDFVTEVLK	0.014	2.39E+04	918.485	612.659	6740	116.2	YJL080C	10
VESLGSPSGATK	0.026	4.09E+05	566.796	378.2	751	17.8	YDR155C	8
VETGVIKPGMVVTFAPAGVTTEVK	0.000	1.24E+07	1215.67	810.782	3959	66.1	YBR118W	19
VFAEDYLDINGSPINPYAR	0.016	3.32E+04	1077.53	718.688	3011	77.4	YBR127C	10

VFDALNDLEQLK	0.010	2.86E+05	702.872	468.917	4593	74.9	YBR218C	12
VFEEEGAFIEALER	0.006	2.53E+05	819.904	546.939	5089	82.4	YJR016C	13
VFITDEAEDLIPEWLSFVK	0.000	3.30E+05	1126.08	751.056	4682	119.2	YMR186W	12
VFNLPLFPTTTIGSFPQTK	0.000	9.72E+04	1054.57	703.386	3676	94	YER091C	9
VFNTVVSTDSTPVTNQK	0.007	3.50E+04	918.971	612.983	2145	40	YNL239W	10
VFQVGNIVHPSVVVSNDEENNELVR	0.000	6.60E+04	1397.21	931.81	3805	64	YDR023W	16
VFSLDPQYLVDDLRPEFAGYSK	0.006	2.81E+05	1280.14	853.764	5689	93.2	YMR116C	13
VGDPFDESTFQGAQTSQMQLNK	0.020	5.32E+04	1214.56	810.041	3499	59.7	YOR374W	14
VGEYNAETDEVELIFDDYLYAK	0.006	6.93E+04	1298.6	866.071	6184	103.1	YIL053W	11
VGIPAGVVNIVPGPGR	0.000	1.94E+06	751.446	501.3	3858	64.7	YPL061W	17
VGIVGLGGIGSMGTLISK	0.018	6.77E+04	829.979	553.655	5049	81.7	YMR318C	10
VGLIGSCTNSSYEDMSR	0.000	7.58E+04	909.903	606.938	2565	46.1	YLR304C	10
VGVVSILEAGDSDILTTLA	0.000	7.87E+05	937.012	625.01	6510	110.7	YGL030W	21
VGYTLPSHIISTSDVTR	0.000	3.50E+05	923.489	615.995	3000	52.5	YBR031W	16
VIDVDGNPVIEVQYLEETK	0.010	7.37E+05	1080.56	720.707	4808	78	YDL229W	18
VIEQPITSETAMK	0.000	9.54E+05	723.879	482.922	1798	35	YOL127W	12
VILFIGDGSLQLTVQEISTMIR	0.020	5.49E+04	1217.17	811.786	8444	149.5	YGR087C	11
VINDAFGIEEGLMTTVHSLTATQK	0.000	3.07E+06	1288.16	859.107	5884	97.1	YGR192C	21
VINDAFGIEEGLMTTVHSMTATQK	0.000	8.18E+05	1297.14	865.093	5884	97.1	YJL052W	12
VITLPDYPGVDADNIK	0.000	2.00E+06	865.454	577.305	3764	63.4	YBR072W	14
VLDEVVVDNFDQK	0.010	7.00E+05	760.386	507.259	3183	55.3	YLR259C	16
VLENTEIGDSIFDK	0.000	2.95E+06	790.396	527.267	3538	60.2	YCR012W	17
VLEQLSGQTPVQSK	0.000	2.75E+06	757.415	505.279	1668	33.1	YGR085C	18
VLNEQVDESYGLR	0.010	2.32E+05	761.381	507.923	2283	42	YER110C	12
VLVLDGGQGTELENR	0.006	7.84E+04	800.42	533.949	2599	46.6	YPL273W	10
VNDAVVTVPAYFNDSQR	0.000	3.07E+06	947.968	632.315	3465	59.3	YAL005C	19
VNGSPITLVEPEILR	0.000	2.24E+06	818.967	546.314	4809	78	YDL083C	10
VNLAVITVPAYFNDSQR	0.000	9.86E+05	954.005	636.339	3480	59.5	YLR369W	10
VNLDTDCQYAYLTGIR	0.000	4.18E+06	922.946	615.633	3830	64.4	YKL060C	11
VNLENPIPIAVLDSYTPSTNEPYAR	0.000	3.70E+05	1387.21	925.14	5340	86.7	YKL182W	17
VNNLIFLSGQIPVTPDNK	0.000	1.09E+05	985.041	657.03	4580	74.7	YER057C	10
VNNPNVSLIK	0.000	9.06E+05	549.319	366.549	1686	33.4	YOR234C	9
VNPETGIIDYDTLEK	0.000	1.73E+06	853.928	569.621	3344	57.6	YLR058C	19
VNQAIALLTIGAR	0.000	5.16E+05	670.406	447.273	4207	69.4	YJR123W	14
VNQIGTLSESIK	0.000	1.71E+07	644.859	430.242	2322	42.6	YGR254W	17
VPAINVNDSVTK	0.000	5.61E+05	628.846	419.566	1752	34.4	YER043C	9
VPIPAYLIGIASGDLSSAPIGPR	0.032	8.59E+04	1132.64	755.426	6123	101.8	YNL045W	10
VPLSDNAIIEANLGK	0.010	6.73E+05	777.43	518.623	3368	57.9	YGL076C	16
VPPTIAQFQYTLDR	0.006	2.03E+05	824.938	550.295	4059	67.3	YHL033C	10
VPTVDVSVVDLTVK	0.000	6.85E+06	735.924	490.952	4053	67.2	YGR192C	18
VQGGEEVNAEELK	0.010	2.31E+05	701.346	467.9	1303	27.5	YJR045C	10
VQPVQPSQTSTYPGQGMPTPK	0.032	6.06E+04	1114.55	743.372	1998	37.9	YNL007C	10
VQQLQQQQAQQELFQQQLQK	0.043	2.65E+04	1235.15	823.766	2809	49.7	YNL243W	10
VQSEYLGIPEEGPFK	0.000	4.75E+05	846.928	564.954	3809	64.1	YER043C	13
VSQFQSVVIPVGITK	0.006	1.34E+05	801.467	534.647	3869	64.9	YHR020W	14
VSVEGVNVEK	0.000	1.16E+06	530.288	353.861	1496	30.6	YLR448W	8
VTDGALVVVDTIEGVCVQTETVLR	0.006	1.25E+05	1258.67	839.447	6309	106	YDR385W	14
VTELLGFDK	0.026	4.63E+05	511.282	341.19	2956	51.9	YLR359W	10
VTPEEADLGMIAYYFQK	0.040	5.45E+04	987.98	658.989	5747	94.4	YMR205C	9
VTVIGSGNWGTTIAK	0.016	2.03E+05	752.412	501.944	2703	48.1	YDL022W	10
VTYDITSKPPATVEWE	0.000	9.36E+04	918.457	612.64	3435	58.9	YMR217W	14
VVADDLVLVTPK	0.007	2.77E+05	634.877	423.587	3297	56.9	YOR198C	11
VVDLIEYVAK	0.000	5.64E+06	574.832	383.557	4011	66.7	YJL052W	11
VVDLVEHVAK	0.000	2.88E+06	554.822	370.217	1521	30.9	YGR192C	10
VVEIGPSPTLAGMAQR	0.006	1.86E+05	813.438	542.628	3174	55.1	YPL231W	16
VVGLSTLPEIYEK	0.000	1.01E+07	724.406	483.273	3883	65.1	YOL086C	18
VVITAPSSSAPMFVVGVNHTK	0.010	3.09E+05	1071.07	714.386	3428	58.8	YJL052W	10

VVITAPSSTAPMFVMGVNEEK	0.000	1.70E+06	1104.06	736.374	4303	70.7	YGR192C	17
VVNEPTAAALAYGLDK	0.000	1.22E+06	816.436	544.626	3809	64.1	YEL030W	12
VVNEPTAAALAYGLEK	0.000	7.70E+05	823.443	549.298	3549	60.4	YJR045C	21
VVNGNSADAAYAQVEIQPR	0.000	8.09E+04	1001.5	668.004	1831	47.2	YPL231W	8
VVNQLLTEMDGMNAK	0.006	1.10E+05	831.913	554.945	3739	63.1	YDL126C	11
VVSVGKPIEELLANPANEEWTK	0.006	1.55E+05	1212.14	808.432	4709	76.5	YOR335C	10
VVVFEDAPAGIAAGK	0.000	1.14E+06	722.396	481.933	3023	52.9	YER062C	17
VWLDPNETSEIAQANSR	0.000	4.86E+05	965.469	643.982	3200	55.5	YBL027W	18
VYEPLLLVGLDK	0.000	1.89E+06	679.9	453.603	5042	81.6	YDL083C	15
VYYFQGGNNELGTAVGK	0.000	2.95E+05	908.947	606.3	2975	52.2	YGL030W	19
WAGNANELNAAYAADGYAR	0.000	1.65E+06	999.459	666.642	2270	41.8	YGR087C	13
WGLKPYIFVLNNNGYTIEK	0.010	6.24E+05	1135.1	757.072	5158	83.5	YLR134W	10
WGLKPYLFVLNNDGYTIEK	0.000	2.50E+06	1135.6	757.4	5148	83.4	YGR087C	14
WSFEEVEVK	0.000	9.03E+05	576.782	384.857	3521	60	YJR123W	8
WTANLLPAR	0.026	5.75E+05	521.296	347.866	2901	51.1	YJL190C	9
YAAAAPAATSAASGDAAPAEEAAAEEEEESDDDMGFGLFD	0.000	6.80E+04	1960.81	1307.54	3074	79	YLR340W	8
YAQDGAGIER	0.026	5.07E+05	540.259	360.509	731	17.4	YOR063W	9
YATASAIAATAVASLVLAR	0.007	3.62E+04	910.517	607.347	5990	99.2	YBR031W	11
YDIGNPVTGETLESPR	0.006	3.13E+05	874.428	583.288	3004	52.6	YBR121C	12
YDLEAWFPYQK	0.010	3.76E+05	730.348	487.235	4858	78.7	YDR023W	12
YDLLCIEGISQSLNEYLER	0.000	3.82E+04	1129.55	753.372	4077	103.8	YLR060W	7
YDNQIAVFGLDFQK	0.018	6.62E+04	829.415	553.279	4744	77	YKL210W	10
YDTATAADLR	0.034	2.62E+05	548.767	366.18	1256	26.8	YLL026W	8
YEIISQQPENVSNLSK	0.000	2.88E+05	924.971	616.983	2555	46	YKL035W	16
YESATASALVN	0.026	4.62E+05	563.275	375.852	1821	35.4	YDR064W	9
YFEVILVDPQHK	0.010	3.03E+05	744.398	496.601	3498	59.7	YLR029C	10
YGASAGNVGDEGGVAPNIQTAEEALDLIVDAIK	0.000	4.87E+06	1629.31	1086.54	4961	126.4	YGR254W	16
YGGVYVGTLSKPEVK	0.021	1.41E+05	798.935	532.959	1663	33	YLR044C	10
YGHAEDFVPILESPEGK	0.007	2.63E+05	944.46	629.976	3557	60.5	YLR438W	9
YGVIVHDIATPNLIDR	0.006	1.03E+05	898.489	599.328	3699	62.5	YDL055C	10
YGYQLYTSNPSGNYTGWK	0.028	2.07E+04	1049.98	700.322	2386	61.5	YGR135W	8
YIEDFVGVPVEWVGTGPAR	0.000	5.24E+05	1046.03	697.69	3396	87	YNL220W	12
YIETQALLLAPIAPHFAEYIYR	0.020	5.99E+04	1296.7	864.8	5674	93	YPL160W	10
YIQTEQQIEIPEGVTVSIK	0.010	2.20E+05	1088.08	725.723	3643	61.7	YNL067W	10
YIQTEQQIEVPEGVTVSIK	0.016	2.13E+05	1081.07	721.051	3638	61.6	YGL147C	11
YLAAYLLLVQGGNAAPSAADIK	0.032	5.67E+04	1110.11	740.407	5318	86.3	YDR382W	10
YLAEFSSGDAR	0.000	8.04E+05	608.286	405.86	1852	35.8	YDR099W	9
YLGLKPGSIDAISQVINIAK	0.010	3.17E+05	1050.61	700.74	5103	82.6	YKL182W	13
YLIENFSAQLQNPEGK	0.000	3.21E+05	925.968	617.648	3925	65.6	YGR180C	14
YNEIVNLTLPDGTVR	0.000	7.59E+05	852.452	568.637	4009	66.7	YBR127C	14
YNPDDTIAPPQDATEESQTK	0.000	2.65E+05	1110.5	740.669	1392	35.9	YOR230W	7
YNVIVTFPSTPDDELVSFVGLR	0.024	3.13E+04	1234.64	823.428	5954	98.5	YJL080C	10
YPIEHGIVTNWDDMEK	0.000	6.18E+05	973.951	649.637	3332	57.4	YFL039C	13
YSSSGTPENITGEADDEDEDIIR	0.000	2.51E+04	1257.04	838.365	2008	51.8	YLR257W	7
YTNPVVIQGAGAGAAVTAAGVLGDVIK	0.006	1.80E+05	1256.69	838.131	5549	90.6	YJR139C	18
YTQVLKPIAFPGGLLEDNVK	0.032	9.38E+04	1101.61	734.744	4583	74.7	YJL130C	10
YTVSFIEGDGIGPEISK	0.000	2.00E+05	906.457	604.64	4075	67.5	YOR136W	14
YVDPNVLPETESLALVIDR	0.000	8.92E+05	1072.07	715.048	5348	86.9	YKL152C	17
YVHVSEVGNCSGSGMGGVSALR	0.032	1.09E+05	1083.51	722.674	2303	42.3	YPL231W	12
YVYAHFPINVNIVEK	0.007	2.48E+05	903.483	602.658	3957	66	YGL147C	10

Appendix Table B.2: DDA-Mascot Peptide Identifications (<5% FDR)

peptide	**Mascot score**	**m/z 2+**	**m/z 3+**	**scan #**	**RT**	**protein**
AAADALSDLEIK	47.66	608.825	406.219	8079	57	YJL026W
AADETAAAFYPSK	57.59	671.32	447.882	4976	37.9	YER023W
AAEAATTDLTYR	26.27	641.817	428.214	3697	30	YOR230W

AAEEADADAELADEEDAIHDEL	90.4	1171.49	781.331	8468	70.6	YCL043C
AAEPHAVSLAWSADGQTLFAGYTDNVIR	78.63	1480.73	987.489	11866	80.8	YMR116C
AAGANVDNVWADVYAK	86.44	832.407	555.274	9078	63.2	YDL130W
AAGSYYVEAQHK	30.59	662.32	441.882	1918	19.2	YGL076C
AASDAIPPASPK	14.86	562.801	375.536	2236	21.1	YBR011C
ADDDSVTIISAGNDK	36.93	760.857	507.574	4781	36.7	YMR116C
ADEINQIFDAISYSK	29.39	857.42	571.949	12380	84.1	YKL157W
ADHLVEEVLEAR	18.98	690.859	460.909	8070	56.9	YBR121C
ADILLLDEPTNHLDVSNVK	17.89	1053.56	702.707	9415	65.3	YPL226W
ADIMELLNHSDSR	27.97	750.859	500.909	8904	62.1	YPR036W
ADPAFKPTEK	17.21	552.29	368.529	1463	16.4	YPL131W
ADQEYEIEK	42.98	562.759	375.508	2591	23.3	YOR332W
ADQILQFSTNPQSK	64	788.902	526.27	6796	49	YGR218W
ADTGIAVEGATDAAR	24.85	709.349	473.235	3847	31	YGL008C
ADVLTAFLNK	42.84	546.308	364.541	10451	71.8	YJL167W
ADVQVALPEGLDAK	44.93	713.383	475.924	7693	54.6	YMR027W
ADWGCAEDPSGR	46.93	660.767	440.847	3605	29.5	YGR124W
ADWGDDIPTTK	19.76	609.785	406.859	5887	43.4	YGR124W
AEALNISGEFFR	53.18	677.343	451.898	9969	68.8	YNL069C
AEELNISGEFFR	54.84	706.346	471.233	10023	69.1	YIL133C
AEPIDEEVSLAIENGIINPR	31.28	1090.07	727.046	9644	78.8	YOR133W
AEQGEHDENISPAQAAELVGEDLSR	16.98	1333.12	889.083	8602	71.6	YAR015W
AEQLYEGPADDANCIAIK	55.19	989.465	659.979	7231	51.7	YOR133W
AEQVFQNVK	53.45	531.783	354.857	3309	27.7	YIL051C
AEQVLQNAEK	36.4	565.296	377.2	1872	18.9	YDR129C
AESITAVLYPNDNFAQGK	27.18	969.484	646.658	9442	65.5	YPR160W
AETAAQDVQQK	20.57	594.796	396.867	992	13.5	YOL109W
AEVAALAAENK	71.79	543.793	362.864	3025	25.9	YGR240C
AEVSDVGNAILDGADCVMLSGETAK	78.35	1261.59	841.396	10818	87	YAL038W
AEVSSMPTLIFYK	39.71	743.386	495.927	10527	72.3	YGR209C
AFHDTEWATQDPR	47.71	787.355	525.239	4280	33.6	YPL061W
AFIDEQFPQGISEPIPLGFTFSFPASQNK	41.7	1606.8	1071.54	13254	103.8	YGL253W
AFPLADAALTQQILDVVQQAANLR	33.22	1283.7	856.138	16635	127.7	YEL026W
AGAGHSNTLQVSTV	32.89	671.341	447.897	3798	30.7	YAL038W
AGANSMIQNVVDSDTISETAAR	13.94	1125.54	750.694	9294	64.5	YLL026W
AGAPVDALINQIVPLLEK	32.27	931.043	621.031	15893	107.4	YHR183W
AGELTQEELER	17.69	637.815	425.546	3866	31.1	YML026C
AGGAAASLIMPFLDNQVNFK	31.3	1032.53	688.691	11993	95.1	YBL041W
AGGECITLDQLAVR	76.91	751.885	501.593	8292	58.3	YOL120C
AGHQTSAESWGTGR	50.4	722.832	482.224	1722	18	YDR012W
AGITWIGPPAEVIDSVGDK	14.32	963.004	642.339	11835	80.6	YBR218C
AGLLGVESIELTPHIISK	20.1	939.041	626.363	10565	72.5	YJL130C
AGSGTSQLDQLAALQALSSSLNK	42.26	1130.59	754.064	10428	84.3	YOL123W
AGTAAAAAAAALEDAK	81.83	686.857	458.24	7322	52.3	YHR020W
AHPDVLTVMLQMLDDGR	32.04	955.977	637.654	15462	104.5	YLL026W
AIDYVEATANSHSR	26.07	767.368	511.915	3303	27.6	YMR205C
AIEMEGLTWGAHQFIPIGFGIK	22.14	1208.13	805.756	13518	91.6	YAL003W
AIEQLNYTPIK	13.47	645.359	430.575	6619	47.9	YER165W
AIGSGSEGAQAELLNEWHSSLTLK	13.36	1249.63	833.422	10938	74.9	YGR253C
AIGYNPTNQLVQDIINADSSLR	55.59	1201.62	801.415	12674	99.8	YGL106W
AIIDCGFEHPSEVQQHTIPQSIHGTDVLCQAK	20.85	1808.37	1205.92	7624	54.1	YDL084W
AILANPSTYEILDPHDFGMK	13.71	1116.55	744.705	11296	77.2	YDL131W
AIMPIIEGHDVLAQAQSGTGK	33.25	1068.56	712.709	8891	62	YKR059W
AIVAELQETLKPDLALVEEK	38.64	1105.12	737.082	11778	80.2	YDR388W
AIYVDLEPNVIDEVR	63.58	872.959	582.309	10639	73	YML085C
ALELYGLDPAK	26.3	595.327	397.22	8665	60.6	YBR263W
ALENPTRPFLAILGGAK	37.57	884.509	590.009	11095	75.9	YCR012W
ALGIMALLDEGETDWK	68.63	881.44	587.962	14350	97	YBR011C
ALGLEYVDLLLQHWPLCFEK	31.57	1222.64	815.428	16858	114.1	YBR149W
ALLELQVSK	38.37	500.805	334.206	6976	50.1	YOR133W
ALLESDESLR	17.74	566.796	378.2	12345	83.9	YGR218W
ALLPHLTNAIVETNK	33.31	817.467	545.314	7856	55.6	YLR249W
ALTEQAQTLTLSSR	51.34	759.91	506.942	5715	42.4	YLR438W
ALYDTFSVFGDILSSK	51.27	881.948	588.301	14578	98.6	YER165W
ALYELLSAADQK	67.1	661.354	441.238	9117	63.4	YER110C
AMYTLSAQDEVFSLAFSPNR	31.48	1124.04	749.696	10926	87.7	YMR116C
ANADANEDNNVDEK	62.4	759.819	506.882	925	13.1	YGR124W
ANELLINVK	57.61	507.303	338.538	6428	46.7	YOL086C
ANELVESYR	40.65	540.77	360.849	3780	30.5	YDL185W
ANFEIDLPDAK	68.21	616.811	411.543	8382	58.9	YGL245W
ANITDVCIAVPPWYTEEQR	32.9	1131.55	754.7	9312	76.5	YPL106C
ANNFVYVSGQIPYTPDNKPVQGSISEK	53.71	1476.74	984.829	8074	56.9	YIL051C
ANVDTDAIIPK	24.07	578.814	386.212	5341	40.1	YGL009C
APEAEQVLSAAATFPIAQPATDVEAR	28.72	1327.18	885.12	9812	80	YDL082W
APEQFDEVVAAIGNK	52.17	794.404	529.939	9819	67.8	YER091C
APFAVVGHATAEQK	74.36	713.378	475.921	3505	28.9	YGR061C
APFDLFESK	49.58	527.266	351.847	9333	64.8	YMR186W
APIEIPLEK	30.63	505.3	337.202	6959	50	YJL080C
APIVAYAELIAAR	41.28	679.396	453.266	11058	75.7	YGL245W
APLEEIVISNDYLNK	62.82	859.454	573.305	10217	70.3	YOR332W
APLQTTDLMER	19.44	637.824	425.552	5740	42.5	YDR129C
APLVIADPTYFPEK	62.87	780.919	520.948	9191	63.9	YER136W
APQGPRPGNWDQED	16.71	783.85	522.903	3868	31.1	YJL008C
APTAAELQAPPPPPSSTK	14.41	880.465	587.312	4160	32.9	YPL004C
APTFFVSQDDNNFETEFFPR	19.96	1204.55	803.366	11031	88.4	YLR342W
APVYADAIDFIK	40.18	661.853	441.571	10613	72.8	YEL038W
AQFETLTAPLVK	24.69	659.374	439.919	8346	58.6	YJR045C
AQIPVTTTLQGLGSFDQEDPK	32.27	1123.07	749.05	8518	71	YMR108W
AQPTEVSSILEER	37.64	729.875	486.919	7374	52.6	YBL099W
AQYDSCDFVADVPPPK	27.22	904.912	603.61	7082	50.8	YGR285C
AQYNEIQGWDHLSLLPTFGAK	47.4	1194.6	796.738	10344	83.7	YLR044C
ASAPGSVILLENLR	55.05	720.414	480.612	10150	69.9	YCR012W
ASGEIVSINQINEAHPTK	46.01	954.495	636.666	5491	41	YMR242C
ASGTVVVADTGDFGSIAK	65.25	847.933	565.625	7461	53.1	YLR354C
ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR	38.18	1524.3	1016.54	9164	75.5	YIL018W

ASLVPGTVLILLAGR	18.41	740.466	493.98	14402	97.4	YLR448W
ASSEENISEAEK	52.14	647.294	431.865	1537	16.8	YGR162W
ASYVGDSSQVEDPGAVGLCEFLK	56.07	1214.57	810.049	9349	76.8	YML070W
ATAGDTHLGGEDFDNR	73.93	838.369	559.248	3286	27.5	YAL005C
ATDGGAHGVINVSVSEAAIEASTR	83.72	1156.58	771.387	6653	57.5	YOL086C
ATGQEMDVVSEEPLIEWLAANYK	18.95	1297.13	865.088	13392	104.7	YBR143C
ATHILDFGPGGASGLGVLTHR	26.64	1038.55	692.704	9226	64.1	YKL182W
ATNDVEPSTYDSK	56.55	713.82	476.216	2061	20.1	YPR145W
ATNSSLEAYK	33.06	542.269	361.849	2415	22.2	YDR099W
ATSPLLESDSIEK	44.85	695.359	463.908	5684	42.2	YGR253C
ATSSTDEESWFK	20.37	694.304	463.205	6632	48	YKL182W
ATVDEFPLCVHLVSNELEQLSSEALEAAR	59.55	1614.3	1076.53	15110	116.8	YLR075W
ATVPVLEQQGTVITR	27.83	806.457	537.974	6875	49.5	YGR234W
AVAPIDTDDVLLGQYGK	61.84	887.965	592.312	9535	66	YNL241C
AVASSGQELSVEER	70.64	731.363	487.911	3292	27.6	YDR099W
AVDDFLISLDGTANK	102.74	789.904	526.938	10995	75.3	YGR254W
AVDDFLLSLDGTANK	102.74	789.904	526.938	10995	75.3	YHR174W
AVDLLLPELER	34.82	634.366	423.247	10841	74.3	YGL195W
AVEESAEPAQVILGEDGKPLSK	15.58	1134.09	756.397	7226	51.7	YLL018C
AVEFAQQVQQSLPK	29.44	786.923	524.951	8102	57.1	YLR058C
AVEQGFNVKPR	29.94	622.841	415.563	2632	23.6	YBR127C
AVGDNDPIDVLEIGETIAYTGQVK	74.44	1259.14	839.762	14278	96.6	YBR011C
AVGGEVGASAALAPK	64.15	649.359	433.242	4283	33.6	YEL054C
AVGIDLGTTYSCVAHFANDR	36.19	1084.02	723.013	10341	71.1	YAL005C
AVGSLTFDENYNLLDTSGVAK	75.75	1107.55	738.702	9032	74.6	YNR034W-A
AVLEFTPETPSPLIGILENK	45.7	1084.6	723.4	13742	93	YGR240C
AVMDLLGSELQNK	16.7	709.371	473.25	9667	66.9	YBR263W
AVQNIILGIYYNSGEVCCAGSR	25.1	1222.59	815.395	12019	81.8	YOR374W
AVVAGAGTGGTISGISK	62.58	723.402	482.603	4264	33.5	YGR155W
AVVESVGAEVDEAR	48.62	715.86	477.576	5213	39.3	YDR382W
AWDLLQSGSQNISEFDSFTDILK	24.11	1307.64	872.094	13435	105	YFR052W
AWNLNQFQIEADFIGHNSNINTLTASPDGTLIASAGK	74.47	1964.98	1310.32	11772	93.6	YMR116C
AYEELSNTDLEFK	59.66	779.867	520.247	7848	55.5	YLR249W
AYPDLQIAYLDEEPPLTEGEEPR	43.75	1323.13	882.425	9560	78.3	YLR342W
CCIGFVGGSDLSK	50.11	700.321	467.216	6591	47.8	YFL045C
CCSDVFNQVVK	53.69	678.308	452.541	6147	45	YOL086C
CGDCGSALQGISTLRPR	20.57	924.446	616.633	6465	47	YIL052C
CPFTGLVSIR	50.06	575.308	383.874	8592	60.2	YDR025W
CPLGNPANYPFATIDPEEAR	92.3	1116.52	744.684	8306	69.5	YBR025C
DAGTIAGLNVLR	20.73	600.341	400.563	8762	61.2	YAL005C
DATPIEDVFSFNYPEGIEGPDIK	21.08	1277.11	851.739	11931	94.6	YGR162W
DAYEPLYPQQLEILR	13.63	924.48	616.656	15041	101.6	YIL065C
DETLDDWFDNDLSLFPSGFGFPR	31.89	1345.61	897.406	15452	119.2	YBR072W
DEYKPILQSLIVEALLK	21.31	986.572	658.05	15345	103.7	YOR332W
DFDGTGALEFPSEEILVEALER	23.52	1219.09	813.064	15921	107.6	YDR432W
DFKPQALGDTNLFKPIK	16.73	966.533	644.691	8828	61.6	YHR179W
DFLSGTVLYLNSLAK	44.22	820.948	547.635	15022	101.5	YDL055C
DGDDLIYTLPLSFK	26.56	798.911	532.943	13130	89	YNL007C
DGEIMLWNLAAK	60.6	680.85	454.236	11555	78.8	YMR116C
DGYLQNNATEGDAEHITPDNLR	26.39	1222.06	815.042	6555	47.5	YLR153C
DHGDVSNQLYAK	31.14	673.82	449.549	2300	21.5	YBR127C
DIEETIVFLQSDPSRPAYVEEIR	15.9	1353.68	902.792	10096	82	YDR127W
DIEFSVEELNAATGSK	33.66	855.415	570.612	10139	69.8	YFR044C
DIFPLQNIHVR	13.62	676.378	451.254	9155	63.7	YLR441C
DIFSNDELLSDAYDAK	95.73	908.418	605.948	10923	74.8	YKL056C
DIGGSSSTTDFTNEIINK	60.37	949.952	633.637	8351	58.7	YNL037C
DIICQIISSTITGDVVLAAAYSHELPR	44.44	1471.77	981.515	18231	123.9	YPL131W
DILDVLNLLK	16.34	578.353	385.904	15953	107.8	YIL002W-A
DIYGWTQTSLDDYPIK	32.74	957.96	638.975	11253	76.9	YGL253W
DLAAATAESAPNAAILVISNPVNSTVPIVAQVLK	46.67	1679.43	1119.96	14291	111	YKL085W
DLLATHGNDIQVPESQVK	14.42	982.508	655.341	6548	47.5	YDR214W
DLSSEVVGQMDAIK	41.25	746.372	497.917	10177	70	YLL026W
DNDLIGIAAK	13.57	515.282	343.857	5693	42.2	YNL128W
DPANLPWASLNIDIAIDSTGVFK	50.37	1229.14	819.76	16852	129.3	YJR009C
DPANLPWGSLK	26.73	599.317	399.88	8958	62.4	YJL052W
DPANLPWGSSNVDIAIDSTGVFK	96.48	1202.09	801.732	11201	89.6	YGR192C
DPITIVPAEDGSGAGAAVIAALSEK	28.41	1176.62	784.748	12890	87.4	YFR053C
DQYVPEVSALDLSR	38.57	796.402	531.27	9292	64.5	YML024W
DSSITVAGSSGLSENEIEQMVNDAEK	37.76	1355.62	904.083	10188	82.6	YJR045C
DSYVGDEAQSK	15.19	599.765	400.179	1634	17.4	YFL039C
DTDAEGKPLER	34.75	615.802	410.87	1124	14.3	YOR133W
DTPFTIYDGEAVAK	18.08	763.872	509.584	8435	59.2	YMR314W
DVLIPLGEYFQIQDDYLDCFGTPEQIGK	18.19	1637.29	1091.86	14489	112.4	YJL167W
DVSDGENYTILLNQLDPALCSK	31.21	1233.1	822.4	11543	92	YDR129C
DVTFLNDCVGPEVEAAVK	90.75	981.977	654.987	10845	74.3	YCR012W
DYRPAEETEAQAEPVEA	37.32	952.929	635.622	4637	35.8	YNL178W
EAAAEESEVDAAAR	43.59	709.823	473.551	2516	22.8	YER036C
EAAAEYAQLLAK	39.08	639.34	426.563	7604	54	YPL090C
EDGIIAQAVDDSR	33.63	694.836	463.56	6927	49.8	YBR088C
EDGTTPFVAIWK	23.13	682.348	455.235	10540	72.4	YKL056C
EDLYQTFAR	30.7	571.777	381.521	7381	52.6	YOR133W
EDTVSWFK	27.69	506.243	337.831	7676	54.5	YGR085C
EEAAPKPPSSAVFSMFGGK	18.59	968.977	646.321	9281	64.4	YDR002W
EEIAALIVNYFSSIVEK	19.24	963.017	642.347	18311	124.6	YOR007C
EEQNIADGVEQK	23.12	680.323	453.884	2444	22.4	YOL109W
EETLNPIIQDTK	30.15	700.867	467.58	6106	44.8	YBR011C
EETYYQESAGVADLITTCAGGR	88.21	1196.04	797.697	8855	73.4	YDL022W
EFDETIFNLPK	36	676.84	451.563	10637	73	YKL182W
EFLSNSFAEEPEAKPEVAEEEKPQTAISMNDEDDA	28.43	1948.86	1299.58	7089	60.7	YIL041W
EFQIIDTLLPGLQDEVMNIKPVQK	35.46	1384.75	923.502	14606	98.7	YGL123W
EGALLTDEVDLENVDASK	54.37	959.468	639.981	9061	63.1	YLR257W
EGFQIPTNLDAAAAGTSQAR	23	1009.5	673.336	7500	63.7	YHR143W-A
EGGLGPINIPLLADTNHSLSR	13.3	1087.58	725.39	11395	77.8	YML028W
EGIPAGWQGLDNGPESR	38.55	891.924	594.952	7878	55.7	YCR012W
EGPTIYYVDSDGTR	15.92	786.862	524.911	6064	44.5	YPR103W

EGTVPTDLDQETGLAR	23.12	851.418	567.948	6413	46.7	YGL187C
EHAPYTDELEEDVYLDPLAR	19.43	1188.06	792.373	10595	72.7	YPL231W
EHGEPLFSSHMLDLSEETDEENISTCVK	20.76	1617.22	1078.48	9639	66.7	YKL060C
EIADMGVECIVAGAGVGELALHYLNR	13.96	1379.19	919.795	14824	100.2	YJL008C
EIGDFEDLSTENEK	49.55	813.362	542.577	7180	51.4	YLL018C
EIGEDNVFLFGNLSENVEELR	27.07	1212.09	808.396	11791	93.7	YPR160W
EILENEYQELTSFDEYVAELDSK	33.79	1382.64	922.096	12980	101.9	YPR036W
EILGTAQSVGCR	45.69	645.827	430.887	4018	32	YEL054C
EISEDGADSLNVAMDCISEAFGFER	51.89	1381.6	921.402	14423	111.9	YOR007C
EITALAPSSMK	16.61	574.305	383.206	5111	38.7	YFL039C
EKPETLVLFDVDGTLTPAR	18.48	1051.06	701.044	10569	72.5	YFL045C
ELAEEGYSGVEVR	66.77	719.346	479.9	5154	38.9	YNL178W
ELASQSFINWLGEEK	34.98	875.936	584.293	12259	83.3	YFL045C
ELEDFAFPDTPTIVK	19	861.435	574.626	10793	74	YBR221C
ELGIHTRPVLLGPVSYLFLGK	13.94	1155.17	770.451	12928	87.7	YER091C
ELGLTVVTDEAIEQMR	75.64	902.461	601.977	11805	80.4	YLR359W
ELIHQNEVPLVLLSSGVGVTPLLAMLEEQVK	53.18	1678.43	1119.29	15723	121.1	YGR234W
ELISNASDALDK	53.1	638.325	425.886	5367	40.3	YMR186W
ELMQQIENFEK	39.88	704.842	470.231	9065	63.1	YGL253W
ELNPDITDETNEGK	15.72	787.863	525.578	4094	32.5	YGR162W
ELPGVAFLSEK	37.94	595.327	397.22	9963	68.7	YCR012W
ELPIEIVALINDTVGTLIASYYTDPETK	14.22	1539.81	1026.88	16877	129.5	YFR053C
ELQDIANPIMSK	24.8	679.853	453.571	6015	44.2	YAL005C
ELQEVANPIMSK	33.3	679.853	453.571	6015	44.2	YLL024C
ELSASLNLPAAASFK	69.12	759.912	506.944	9537	66.1	YMR120C
EMIQEVIVEEDLEPFEASK	95.36	1118.04	745.696	10899	87.5	YPL231W
ENTLLGEFDLK	30.96	639.832	426.891	10653	73.1	YNL209W
EQAANLIAAGADGLR	58.33	735.389	490.595	7825	55.4	YLR432W
EQDVPLIVPVVNPEHLDIVAQK	21.98	1226.68	818.12	9454	77.5	YDR158W
EQSAQAAQWESVLK	44.01	787.894	525.598	8240	58	YGL105W
ESGDFLAIDLGGTNLR	19.34	839.426	559.953	11005	75.3	YGL253W
ESGNYLAIDLGGTNLR	41.84	846.931	564.957	9549	66.1	YFR053C
ETAEAYLGKPVK	32.22	653.356	435.906	3408	28.3	YJR045C
ETELSLLQSLR	28.96	644.859	430.242	10386	71.4	YCL040W
ETFPILVEEK	15.02	602.827	402.22	8421	59.1	YDL055C
ETGELEELLEPILAN	14.66	835.43	557.289	15333	103.6	YCL035C
ETITEALNLPEANLSEIPSLQDAIQR	30.3	1433.25	955.833	13801	93.4	YGR061C
ETNPGTDVTVSSVESVLAHL	56.7	1028.02	685.68	13362	104.5	YLR109W
ETSTDPSYDAFLEK	56.09	801.862	534.91	7480	53.3	YLL050C
ETVESESSQTALSK	34.67	748.36	499.242	2315	21.6	YOR133W
EVARPNNYAGALYDPR	14.06	903.45	602.636	5221	39.4	YBR072W
EVQGSTLAQLTSK	68.35	681.367	454.581	5518	41.2	YLR441C
EVQNSTLAQLTSK	63.94	709.878	473.588	5722	42.4	YML063W
EVSDGSGEINIQQFAALLSK	52.98	1053.54	702.695	11863	94.2	YBR109C
EVVEAVTVVDTPPVVVVGVVGYVETPR	13.8	1404.77	936.851	18906	129.2	YOR063W
EVYEGEVTELTPEDAENPLGGYGK	55.13	1298.6	866.069	7857	66.3	YDR190C
EYIALVDQLIAK	38.44	688.395	459.266	11631	79.3	YGR037C
FADGFLIHSGQPVNDFIDTATR	72.11	1211.1	807.733	11152	76.2	YNL178W
FAEQYSDAAFYK	44.03	720.327	480.554	6835	49.3	YGR209C
FAGGDFTTTCEGYIPQTGR	67.34	1039.47	693.314	6158	53.7	YHR020W
FAIPAINVTSSSTAVAALEAAR	129.6	1080.59	720.727	11082	88.8	YKL060C
FASDPGCAFTK	50.62	600.771	400.85	4509	35	YLR109W
FCQEHDILVEAYSPLGPLQK	31.67	1172.59	782.06	10092	69.5	YDL124W
FDAKPAYPGHVQQGGLPSPIDR	17.75	1175.6	784.069	5908	43.6	YMR205C
FDATNTSVCK	22.59	571.761	381.51	2196	20.9	YGR054W
FDDGAGGDNEVQR	38.05	690.295	460.532	2031	19.9	YKL145W
FDDMELDENLLR	59.52	755.348	503.901	10078	69.4	YKR059W
FDDPPEWQEIIK	35.85	758.87	506.249	10349	71.1	YDR091C
FDGSLNVDLNEFQTNLVPYPR	57.93	1219.6	813.404	10836	87.1	YML124C
FDKPFVMDTSYPAR	24.41	837.403	558.605	7161	51.3	YGL253W
FDLALEYGNLDVALDEAK	46.78	998.499	666.002	12615	85.7	YDL145C
FDQYLDAENK	28.46	621.785	414.859	4355	34.1	YLR314C
FDVGALMALHGEGSGEEK	61.74	923.936	616.293	9375	65	YLR441C
FEASQVTEK	38.81	519.759	346.842	2327	21.7	YDL136W
FEDIHPYSVSYSWDK	39.54	936.926	624.953	8226	57.9	YPL106C
FEELCADLFR	67.93	650.306	433.873	10003	69	YAL005C
FEENVSVDDTTATPK	22.67	826.886	551.593	4440	34.6	YOL139C
FEEWIVPILDK	56.58	694.877	463.587	12668	86	YHR068W
FELSGIPPAPR	46.21	592.327	395.22	8166	57.5	YAL005C
FENELDSFFTLFR	18.97	832.901	555.603	15794	106.7	YKL035W
FEQASESEPTTVSYEIAGNSPNAER	27.48	1357.11	905.079	6757	48.8	YJR104C
FEQVPDSLDDQIFVCEK	34.26	1034.98	690.323	8116	68.1	YDL097C
FGDFGGQYVPEALHACLR	50.61	1018.99	679.66	9936	68.5	YGL026C
FGDPETQAVLSLLDDQTDLAQVFLAAAEHR	45.53	1635.82	1090.88	18237	124	YGL234W
FHAAQLPTETLEVETQPGVLCSR	36.48	1292.15	861.767	8870	61.9	YCL030C
FIETYVQQVNPSK	45	776.904	518.272	6622	47.9	YGL206C
FISEVENTDPTQER	54.89	832.892	555.597	4635	35.8	YKL085W
FNDTVNQLLEK	48.79	660.843	440.898	7777	55.1	YHR108W
FNNQFEPCAGNITNYLLEK	13.89	1136.54	758.028	9541	78.1	YMR109W
FNVEYFAK	24.68	509.256	339.84	7765	55	YLR448W
FPGWDFETEEIDPELLR	75.21	1047	698.334	11789	93.7	YPL131W
FPILTQEDLFSTIEK	14.6	890.972	594.317	12669	86	YDR129C
FQPGTSNETPEETYQR	40.85	942.424	628.618	3716	30.1	YOR027W
FQPQDSTTNPSLILAAAK	58.38	951.502	634.67	8634	60.4	YLR354C
FQYIAISQSDADSESCK	37.15	974.933	650.291	6716	48.5	YLR109W
FSAETLSELIR	43.32	633.34	422.563	11020	75.4	YKL182W
FSDALNDANECVK	74.64	741.83	494.889	4627	35.7	YOR027W
FSEAAFLGSTYGLGDDAVNDIVTK	34.7	1245.61	830.739	10886	87.4	YGL137W
FSEFLTTLLYDEIVSTK	16.11	1003.52	669.35	15908	107.5	YNL117W
FSSILDSIDVDQPEWSELTSVEEAK	38.23	1412.67	942.119	12127	96	YJR109C
FSVSPVVQVAVEVK	46.74	744.427	496.62	9907	68.4	YOR133W
FSYGQDLETYYQTGPGYDVVR	53.67	1229.56	820.045	8438	70.4	YAR071W
FTGCNVIGLNNNDYQIAK	51.39	1020.99	680.998	6636	57.3	YML008C
FTIEEVGAPTSSEEGDITMR	35.54	1085	723.672	7125	61	YJL080C
FTLEVVDAVVDAIGPEK	22.81	901.483	601.324	14673	99.2	YHR179W

FTVSAIYSDLPQQER	50.67	877.441	585.297	9389	65.1	YKR059W
FTYVTENTDPK	21.06	657.814	438.879	3926	31.4	YDR188W
FVEPIDDCPAGNIIGLVGIDQFLLK	32.63	1372.22	915.151	16505	111.6	YOR133W
FVQGLLQNAAANAEAK	84.84	822.939	548.962	7890	55.8	YJL177W
FYDILGVPVTATDVEIK	16.13	940.506	627.34	12541	85.2	YNL064C
GAAGIWTCSCCK	41.09	685.786	457.526	4644	35.8	YPR043W
GAAYVLGAGQVVYFGSVGK	21.17	921.991	614.996	10507	72.1	YJR105W
GAGSIFTSHTR	42.36	567.289	378.528	2905	25.2	YIL018W
GAIVGPDLAVLALVIVK	47.8	824.524	550.018	16273	110	YPL090C
GALATYGLTIDDLGVASFHGTSTK	33.92	1198.11	799.076	10987	75.2	YPL231W
GASDGGLYVPHSENR	46.4	779.866	520.246	3125	26.5	YPL131W
GATLVVGGDGR	41.03	501.272	334.517	2826	24.7	YMR105C
GATQNNLDDIER	40.48	673.321	449.216	3545	29.1	YJL008C
GATYGKPTNQGVNELK	24.16	838.934	559.625	2438	22.4	YLR029C
GCFDEEGYQK	25.66	616.748	411.501	3016	25.9	YHR068W
GDAIHATSSSSISK	15.5	680.839	454.228	1284	15.3	YDR238C
GDIPGVVAFFGGLVAQEVLK	30.29	1008.56	672.71	16804	129	YKL210W
GDLGIEIPAPEVLAVQK	31.5	874.993	583.665	11140	76.2	YAL038W
GDTYVSIQGFK	28.02	607.806	405.54	7107	51	YAL038W
GDVEEYQYLR	53.29	636.299	424.535	5837	43.1	YBR126C
GEALLVVLVSSVTEANIIK	67.14	978.075	652.386	17488	118.5	YOR369C
GEEILSGAQR	16.92	530.275	353.852	2926	25.3	YLL018C
GEELINPISDLMQDADR	39.41	958.457	639.307	12756	86.6	YGL037C
GEIGPFASPK	30.41	501.766	334.847	5419	40.6	YLR153C
GELTMNLPK	28.58	501.768	334.848	5419	40.6	YJR046W
GEQINIPLLPGEQTGPLAK	63.56	988.047	659.033	10510	72.2	YJR148W
GFDIPNVEGHDVVPLLQNEISK	48.69	1210.63	807.42	11518	78.6	YFR053C
GFDQSLAQSLDTITSK	46.75	855.931	570.956	10860	74.4	YKL157W
GFDQTLAQALDTIR	55.85	774.904	516.939	12652	85.9	YHR047C
GFEIGSGFQGVSVPGSK	36.1	826.918	551.614	9420	65.3	YGL148W
GFEVHWAEYNK	42.1	690.323	460.551	6974	50.1	YGR240C
GFFSFATQK	30.61	516.761	344.843	8995	62.7	YER091C
GFGFVCFSTPEEATK	53.67	838.885	559.592	10181	70.1	YER165W
GFLESLIQLHQQK	18.44	770.928	514.288	10554	72.4	YGR061C
GFLSDLPDFEK	38.68	634.314	423.212	11223	76.7	YLR340W
GFPGLIPPNSTLVFDVELLK	26.21	1078.6	719.405	13578	106	YNL135C
GGDEAAIAASNQDLK	29.28	730.355	487.239	3570	29.3	YMR012W
GGIPLVFPVFGK	17.1	615.866	410.913	12758	86.6	YMR099C
GGLTYNDFLVLPGLVDFPSSEVSLQTK	35.45	1448.75	966.171	13870	108.1	YLR432W
GGSLGDAGGASDR	29.44	560.255	373.839	1194	14.7	YDL126C
GGTLISYDGQVR	30.76	633.328	422.554	5558	41.4	YKL035W
GGVEAQQAENEEK	73.72	694.818	463.548	1131	14.4	YOR184W
GGYFDSIGIIR	38.06	599.317	399.88	9851	68	YNL241C
GGYPAPQGPYYCGVGAGK	40.19	899.914	600.279	5773	42.7	YPR035W
GIDVQQVSLVINYDLPANK	88.19	1043.56	696.044	9614	78.6	YKR059W
GIEAAGGSADIYQVEETLSPEVVK	15.97	1231.62	821.415	9243	76	YDR032C
GINSSYAVWNDVTGK	70.44	805.894	537.598	8887	62	YLR355C
GISELGIYPAVDPLDSK	38.72	887.467	591.98	10683	73.3	YJR121W
GISNEGQNASIK	61.52	609.31	406.542	1621	17.4	YKL060C
GLEVLQTIDR	18.5	572.322	381.884	8219	57.8	YIL137C
GLFGNTFVDLGDEFTVLDPTGEEPR	54.24	1363.15	909.105	13536	105.8	YKL210W
GLGGILLNPITGR	30.71	640.888	427.594	10623	72.9	YEL047C
GLGNPLLYDGVER	27.43	701.87	468.249	8384	58.9	YPR191W
GLIAGGGAPEIEISR	47.22	720.396	480.6	7705	54.6	YDL143W
GLILVGGYGTR	49.37	553.322	369.217	7648	54.3	YDL055C
GLINDPDVNNTFNINK	76.53	894.45	596.636	8455	59.3	YBR249C
GLLGLSLVEAK	49.13	550.34	367.229	10393	71.4	YGL068W
GLLVPTQTTDQELQHLR	14.22	975.026	650.353	8114	57.2	YPR016C
GLNINENADFIEK	44.78	738.87	492.916	7527	53.5	YNL189W
GLPESAVQAGQETR	26.95	721.865	481.579	3831	30.9	YBL076C
GLQTVVVEEDA	14.57	580.296	387.2	6713	48.5	YDL075W
GLSAVAQAESMK	68.51	596.306	397.873	5193	39.2	YNL178W
GLSVVDTYAILSNK	78.08	740.406	493.94	10182	70.1	YJL167W
GLTPSQIGVLLR	56.53	627.382	418.591	10000	68.9	YDR064W
GLVSDPAGSDALNVLK	41.09	778.42	519.282	8923	62.2	YML126C
GMDIAYEEAALGYK	62.69	765.861	510.91	9127	63.5	YPR062W
GMGLLTAIVIDPSK	55.57	707.902	472.271	11788	80.3	YLR438W
GNLAAFVEQKPEAK	38.14	751.404	501.272	5545	41.3	YPL226W
GNPTVEVELTTEK	83.97	708.864	472.912	5470	40.9	YGR254W
GNQLNANTELER	19.24	679.837	453.56	3305	27.6	YER125W
GNVGFVFTNEPLTEIK	29.78	882.962	588.977	10985	75.2	YLR340W
GNWGKPGDEINDLIDSGEIK	40.8	1079.03	719.687	10223	70.3	YLR327C
GNYPINAVTTMAETAVIAEQAIAYLPNYDDMR	45.94	1758.34	1172.57	16828	129.1	YAL038W
GPLVVYAEDNGIVK	66.49	737.401	491.936	8034	56.7	YDR012W
GQCLATLLGHNDWVSQVR	58.25	1027.52	685.346	8367	69.9	YMR116C
GQDYVPAFDVAPDWESYDYAK	14.24	1218.54	812.694	9886	80.5	YPL048W
GQHLADILNSASR	33.86	691.363	461.244	5961	43.9	YOR007C
GQNDDDLIR	28.98	523.249	349.168	2833	24.8	YGL206C
GQTYSPAQIGGFVLNK	50.78	840.441	560.63	9527	66	YJR045C
GQVVSEEQRPGTPLFTVK	60.46	986.528	658.021	6308	46	YOR133W
GRPYTGWVDSK	22.87	633.317	422.547	3828	30.8	YPL231W
GSGCVPINNLMEDAATAEVSR	23.93	1096.01	731.009	8528	71	YNL117W
GSIDEQHPR	58.58	519.752	346.837	864	12.7	YLR044C
GSIDITTTNSYEK	35.29	714.846	476.9	4447	34.6	YLR259C
GSKPGQQVDLEENEIR	19.58	899.95	600.302	3890	31.2	YER133W
GSPFQCNIGVGQVIK	75.29	802.417	535.28	8333	58.5	YNL135C
GSSSLYTLVINDAGK	56.61	762.899	508.935	9605	66.5	YLR325C
GSTLIVVPFNQGSK	19.36	723.901	482.937	8553	59.9	YPL231W
GTDYDFYEAWGPVFEAEAR	60.17	1111.99	741.66	11627	92.6	YGR285C
GTGLMSANNIIAEGIEK	63.21	859.443	573.298	9528	66	YPL231W
GTISAEEYEK	22.95	563.767	376.18	2797	24.6	YER091C
GTITWIAPAGEYTLDEK	62.17	932.97	622.316	10053	69.3	YDL185W
GTLEGHNGWVTSLATSAGQPNLLLSASR	36.42	1419.23	946.489	10980	75.2	YMR116C
GTVVDIPSLIQAVK	18.83	720.427	480.62	11785	80.3	YIL074C
GTYAAVSPEK	21.39	511.761	341.51	1844	18.7	YGL202W

GVAINFVTNEDVGAMR	48.61	846.922	564.951	9030	62.9	YKR059W
GVETLAEAVAATLGPK	49.73	763.925	509.619	13269	89.9	YLR259C
GVEVVLPVDFIIADAFSADANTK	99.27	1196.13	797.753	15385	118.7	YCR012W
GVFGYGFEEPSAIQQR	89.02	892.934	595.625	9364	65	YKR059W
GVIFYESHGK	35.61	568.79	379.529	3666	29.8	YOL086C
GVILYGPPGTGK	15.05	579.829	386.889	5732	42.5	YGL048C
GVLESISDSLSSKPHNFEDCIK	35.86	1231.6	821.4	9569	66.3	YKL210W
GVLGYTEDAVVSSDFLGDSHSSIFDASAGIQLSPK	66.13	1785.37	1190.58	15646	120.6	YGR192C
GVLGYTEDAVVSSDFLGDSNSSIFDAAAGIQLSPK	16.89	1765.86	1177.58	15973	122.9	YJR009C
GVLGYTEDAVVSSDFLGDTHASIFDASAGIQLSPK	23.86	1784.38	1189.92	19021	151.7	YJL052W
GVLLAADLGGTNFR	59.58	702.386	468.593	9465	65.6	YCL040W
GVLLYGPPGTGK	15.05	579.829	386.889	5732	42.5	YDR394W
GVLSCDLVGFHTYDYAR	23.69	986.965	658.312	9249	64.3	YBR126C
GVLVVPGSWFK	25.41	594.842	396.897	11260	76.9	YGL202W
GVMNAVNNVNNVIAAAFVK	94.92	973.02	649.016	13201	89.5	YHR174W
GVNLPGTDVDLPALSEK	65.62	862.957	575.64	10145	69.9	YAL038W
GVPYVVTHDGR	35.86	600.312	400.544	3179	26.9	YJR145C
GVTDDTGPLLSWINVVDAFK	59.76	1074.05	716.372	15403	118.8	YFR044C
GVVDSEDLPLNLSR	40.94	757.396	505.267	8688	60.8	YMR186W
GWGEAAHQPADFTWAPSLAVPK	30.1	1168.58	779.387	8595	71.5	YPL028W
GWTGQYTLDCNTR	14.61	786.349	524.568	6326	46.1	YPL154C
GYDSTGIAIDGDEADSTFIYK	46.54	1119.51	746.674	7694	65.1	YKL104C
GYLADDIDADSLEDIYTSAHEAIR	79.45	1327.12	885.08	10270	83.2	YPL131W
GYLRPETAQGQFLNFNK	27.89	992.008	661.674	7947	56.1	YBR121C
GYSDVCDIFTEDELVR	96.68	959.43	639.956	11053	75.6	YBR092C
GYSFSTTAER	20.41	559.759	373.509	3848	31	YFL039C
GYTCQFVDMVLPNTALK	22.66	978.981	652.99	11682	79.6	YKL182W
GYWGTNLGQPHSLATK	19.22	865.436	577.293	6417	46.7	YGL123W
HDLVDYLIDQIELR	19.16	871.46	581.309	15098	102	YOL090W
HDWIVLDVPLTR	19.85	732.404	488.605	14795	100	YHR035W
HELSSLADVYINDAFGTAHR	48.9	1108.54	739.363	10395	71.4	YCR012W
HFIDELNK	25.01	508.264	339.178	3757	30.4	YFR053C
HGENSLLSSGTSQDSLR	56.11	894.43	596.622	4202	33.1	YGR240C
HGIPLISIEELAQYLK	21.95	912.517	608.68	14346	97	YDR487C
HGIPVVVDNTFGAGGYFCQPIK	15.73	1188.59	792.732	10074	69.4	YLR303W
HGLVGLESLLK	24.12	583.351	389.236	9237	64.2	YCL030C
HIDASGSINR	21.87	535.273	357.184	1135	14.4	YOL121C
HIDDFYDSYNK	23.19	708.807	472.874	5160	39	YGR167W
HIDFAPTSPFGGARPGR	13.13	891.955	594.973	6385	46.5	YPL081W
HIDTGMGFER	18.32	581.769	388.182	3709	30.1	YOR335C
HIEPALAFQLELGR	22.57	797.441	531.963	9931	68.5	YNR016C
HIGGNDDLQELR	40.5	683.839	456.228	3872	31.1	YCL035C
HITINDLPVGR	42.47	617.849	412.235	5810	42.9	YML028W
HIYQSAAAGLK	21.45	579.817	386.88	2166	20.7	YOR374W
HLEDNTLLISGPFK	53.52	792.425	528.619	8708	60.9	YML073C
HLEDNTLLVTGPFK	48.61	792.425	528.619	8708	60.9	YLR448W
HLEGISDADIAK	19.63	634.828	423.554	4081	32.4	YKL152C
HLGSLFSDAVQTASVQWFER	26.98	1139.57	760.047	11361	90.7	YLR359W
HLGVVGECNIQYALNPVSK	19.53	1049.54	700.03	8119	57.2	YJL130C
HLTTPFQLSSEVLSHIEIDDSTGLR	35.38	1398.21	932.478	13400	90.8	YCL040W
HMVFYNSGPASGSSLDHK	40.68	967.447	645.3	4196	33.1	YCL050C
HNDPFYFEK	17.75	598.772	399.517	5516	41.2	YGL148W
HNLEFINILTDDGLLNEECGPEWQGMK	23.29	1586.74	1058.16	12126	96	YGR094W
HNVLLIVDEIQTGIGR	32.26	889.002	593.004	11548	78.8	YLR438W
HSEFVAYPIQLLVTK	36.42	872.985	582.326	11163	76.3	YMR186W
HSEFVAYPIQLVVTK	31.43	865.977	577.654	9792	67.6	YPL240C
HSGNIQLDEIIEIAR	72.88	854.455	569.972	10239	70.4	YEL054C
HTLDIINVLTDQNPIQVVVDAITNTGPR	74.48	1528.82	1019.55	18684	127.4	YJR123W
HVSPAGAAVGIPLSDVEK	72.05	873.973	582.984	6682	48.3	YMR120C
HVVFGEVVDGYDIVK	70.17	838.438	559.294	8900	62.1	YDR155C
HWGGGILGNK	29.77	519.778	346.854	4414	34.4	YHL033C
HWNAIDESTR	36.52	614.789	410.195	2834	24.8	YER110C
IADATEDLQNDSASR	26	803.371	535.917	3281	27.5	YDR091C
IADISLAAFGR	37.38	567.319	378.549	9503	65.8	YER043C
IAEFSAISFPYGAK	43.38	750.89	500.929	10315	70.9	YPL160W
IAFADAGDTVEDANFDESNANAAILR	53.39	1355.63	904.091	8384	70	YPL160W
IAGVVYHPSNNELVR	21.92	834.447	556.634	5073	38.5	YBL072C
IATSQEAIDQYNAQATGDR	15.08	1026.49	684.659	3906	37	YBR269C
ICDQVSDAILDACLAEDPHSK	28.66	1179.04	786.363	8978	62.6	YLR180W
ICLPTFDPEELITLIGK	22.26	980.029	653.688	16613	112.3	YJR148W
IDIDVLAPLSSFAATAHK	35.06	935.009	623.675	12590	85.5	YLR359W
IDQSFESLGENLSALSR	44.41	933.466	622.646	11052	75.6	YKL193C
IDVAVDSTGVFK	37.53	625.835	417.559	7579	53.9	YJL052W
IEAALSDALAALQIEDPSADELR	16.58	1206.12	804.415	11994	95.1	YDL229W
IEALEFADDAAK	55.8	646.822	431.55	7669	54.4	YPL160W
IEDDPFENLEDTDDIFQK	80.32	1091.99	728.327	10151	82.3	YFR053C
IEELQYDSTLSLPSSEFSK	50.26	1087.03	725.023	8210	68.8	YBR088C
IEEVIDLILR	69.96	606.864	404.911	12549	85.2	YHR087W
IEFGAASDGDGDR	57.68	655.286	437.193	3854	31	YMR105C
IEGVATPQDAQFYLGK	26.31	868.946	579.633	8526	59.8	YPL143W
IENQQGVNNFDEILK	47.25	880.944	587.632	8549	59.9	YAL038W
IEQELGTEIAAIPATIDK	40.18	956.517	638.014	10429	71.6	YDL160C
IEQLHPFPFAQLR	26.14	798.438	532.628	9619	66.6	YIL125W
IEQLYHEYEESIAK	30.15	876.428	584.621	6760	48.8	YJL167W
IEQNRPDDGVY	14.13	653.307	435.874	2757	24.3	YDR070C
IESSVESQFSAGR	64.97	698.839	466.228	4695	36.2	YBL072C
IFEGIPPPYDK	28.95	638.335	425.892	7357	52.5	YNL069C
IFESILNSPSSK	19.87	661.354	441.238	9118	63.4	YJL080C
IFVLDEADNMLDQQGLGDQCIR	20.34	1275.6	850.737	10573	85.3	YOR046C
IGCVLAQCLFDEDIVNEIAEHNAFFTK	24.45	1577.25	1051.84	13434	105	YPR041W
IGDENLTDIINTR	31.97	737.381	491.923	8909	62.1	YOL059W
IGEFESSFLSYLK	15.77	760.388	507.261	12837	87.1	YBL099W
IGGIGTVPVGR	43.72	513.309	342.542	4965	37.8	YPR080W
IGGLLKPSELDD	19.69	628.84	419.563	7131	51.1	YGR218W
IGICYEPPSVIPSSELANVDR	30.67	1158.58	772.723	8659	72	YML124C

IGLDCASSEFFK	64.05	687.324	458.552	9261	64.3	YGR254W
IGPDVVIGPNVTIGDGVR	53.27	889.494	593.332	9400	65.2	YDL055C
IGPQGALLGCDAAGQIVK	74.3	884.475	589.986	8289	58.3	YNL134C
IGQEVDGEAVGDEFK	57.76	796.876	531.586	6285	45.9	YPL090C
IGSEVYHNLK	38.09	580.309	387.208	2692	23.9	YGR254W
IGSLDTLIVESEELSK	15.69	866.964	578.312	12427	84.4	YKL080W
IHLEGSEAPQEPK	43.99	717.865	478.912	2618	23.5	YGL245W
IHPIGELSSEEEEMLQK	54.81	984.983	656.991	8067	56.9	YKL085W
IHQYLFQEGVVVAK	63.03	815.951	544.303	7288	52.1	YMR230W
IIAAIPNPEDVVAISSR	32.51	882.996	589	10704	73.4	YLR048W
IIDDDVPTILQGAK	46.48	749.412	499.943	8785	61.4	YLL026W
IIEEEQEDDALVQDLLK	56.88	1000.51	667.34	10092	81.9	YHR108W
IIEIDHDASLPSQYQK	23.12	928.973	619.651	6075	44.6	YGL206C
IIEILQGLNETSTNAYR	32.62	968.013	645.678	10530	72.3	YKL080W
IIEVTLDALENILK	31.08	792.466	528.647	15114	102.1	YNL189W
IIFGTQSDAFQEDR	57.09	813.892	542.93	7728	54.8	YLR027C
IINEPTAAAIAYGLDK	26.91	830.451	553.97	9351	64.9	YAL005C
IINEPTAAAIAYGLGAGK	83.49	865.478	577.321	9966	68.7	YNL209W
IINIEFVDDDWWLGELEK	30.57	1117.55	745.372	13706	106.9	YCR088W
IITEAVEIEK	17.9	572.827	382.22	5355	40.2	YGR180C
IIVDAYGGASSVGGGAFSGK	106.29	906.96	604.976	7646	54.3	YLR180W
IIVHTDTEPLINAAFLK	24.07	948.035	632.359	9993	68.9	YGR234W
IIYVDDGVLSFQVLEVVDDK	86.1	1133.6	756.067	17212	131.9	YAL038W
ILDSALVTAAQLAK	65.5	707.419	471.949	9777	67.6	YLL026W
ILEGIIGANFVGFQTK	30.35	853.977	569.654	12115	82.4	YMR261C
ILEQFEYVLYPSK	13.19	814.932	543.624	11191	76.5	YPL231W
ILNHMIETGAEYIMELTDK	44.13	1111.05	741.034	14132	95.6	YKL035W
ILPEPTEGFAADDEPTTPAELVGK	21.66	1249.12	833.083	8135	68.2	YKL182W
ILSQAPSELELQVAK	33.16	813.459	542.642	7974	56.3	YNL096C
ILTGTVVSTK	34.3	509.811	340.21	3478	28.7	YDR025W
ILVTPEYEK	23.53	546.303	364.538	4608	35.6	YPR041W
INAGLYILNPEVIDLIEMKPTSIEK	30.96	1407.27	938.517	14764	99.8	YDL055C
INELTLLVQK	63.79	585.858	390.908	8861	61.8	YNL178W
INHEDGFIETTELLNIYDSEDPQQVFDER	24.52	1733.8	1156.2	11315	90.4	YER021W
INLPCVNPTTGEVQTDFHTLR	23.84	1206.6	804.737	9240	64.2	YGL087C
INNALAQVLLAK	53.82	634.39	423.263	10054	69.3	YGL026C
INNPAIDTVTLNTVDTDIHSAK	20.9	1176.61	784.74	8843	61.7	YKL157W
IPALGLGTANPHEK	55.73	709.393	473.265	4894	37.4	YBR149W
IPAWFLNR	49.59	508.787	339.527	9600	66.4	YML026C
IPDDLLDDENVTSDDLFGFLAR	92.4	1240.59	827.399	13471	105.3	YCL040W
IPEIPLVVSTDLESIQK	40.44	941.033	627.691	12799	86.8	YDR012W
IPGGDVLDSR	15.32	514.772	343.517	4811	36.9	YJL014W
IPQQQPAPAEITPSYALGK	50.25	1005.04	670.362	5675	50	YLL026W
IPVGYSSNDDEDTR	27.78	784.347	523.234	3121	26.5	YMR307W
IPVLEQELVR	26.08	598.356	399.24	8468	59.4	YPL004C
IPVLGHADGICSIYLDEDADLIK	20.32	1264.14	843.096	11334	77.4	YOR323C
IPYPLENENTLSYR	26.93	854.931	570.29	8319	58.5	YER080W
IQDINANNVGALEELTLDILR	24.69	1162.63	775.42	14525	112.6	YDR238C
IQEPVFLVEIQCPEQAVGGIYSVLNK	73.1	1465.77	977.516	15511	104.8	YOR133W
IQGPNYVPGK	21.1	536.793	358.198	3273	27.4	YOR133W
IQNFGYNFDTNTADELIK	15.5	1052.01	701.672	8641	71.8	YDR293C
IQQDTLIQTK	44.72	594.335	396.559	3485	28.7	YIL041W
IQQGTDLAEVAPILCAGVTVYK	34.24	1173.62	782.751	11943	81.3	YMR083W
ISDDILSVLDSHLIPSATTGESK	29.24	1199.62	800.083	12852	87.2	YDR099W
ISGLESNTTLSEALK	41.01	781.917	521.614	7822	55.4	YDL195W
ISGVEVESPTSFPVQSLIPKPLESVK	36.04	1384.26	923.176	11985	81.6	YJR139C
ISHVSTGGGASLELLEGK	75.84	877.968	585.648	6866	49.5	YCR012W
ISIFEAVHGSAPDIAGQDK	24.78	977.997	652.334	8798	61.4	YOR136W
ISNEQYER	19.8	519.746	346.833	1242	15	YMR205C
ISSIQDILPALEISNQSR	15.78	992.539	662.028	12235	83.2	YLR259C
ISSTIVAQSAK	22.84	552.817	368.88	2582	23.2	YNR016C
ISVGIEDTDDLLEDIK	32.35	887.951	592.303	11733	80	YAL012W
ISYISDESK	22.33	521.259	347.841	2966	25.6	YLR354C
ITDEEASYK	31.36	528.248	352.501	1607	17.3	YJR145C
ITEKPELINDILLECGFPNTSGQKPNEYNY	37.16	1748.85	1166.24	10175	82.5	YCL050C
ITGMILDLPPQEVFPLLESDELFEQHYK	25.86	1651.34	1101.23	13926	108.5	YER165W
ITSTDPNADYGK	58.89	641.301	427.87	1735	18	YNR001C
ITTIEEIFLHSLPVK	62	870.501	580.67	13623	92.3	YGL123W
IVAGQVDTDEAGYIK	50.86	789.904	526.938	5642	41.9	YDR353W
IVAVTGTEAFEAQR	50.22	746.394	497.932	6208	45.4	YOR335C
IVDLEQSSEFASLFPLK	80.56	962.009	641.675	13488	91.4	YKL081W
IVDVVGTLSR	42.01	529.814	353.545	6868	49.5	YKL182W
IVELDHLTITGNVFLGK	29.59	935.028	623.687	11164	76.3	YKL035W
IVEQLADYLIGVQY	23.07	812.435	541.959	14137	95.6	YOR122C
IVNEEFDQLEEDTPVYK	51.69	1034.49	689.997	7506	63.7	YLR200W
IVPAEDGSGAGAAVIAALAQK	104.34	955.023	637.018	10582	72.6	YGL253W
IVQDISQLTLLETSSLINELK	14.02	1179.16	786.444	13939	108.6	YGL068W
IVSNASCTTNCLAPLAK	85.61	910.456	607.306	5587	41.6	YGR192C
IVTEAVEIEQR	47.51	643.851	429.57	4834	37	YJL026W
IVVEYIAAIGADLIDER	27.86	930.509	620.675	15612	105.5	YLR249W
IYPTYDFCVPIVDAIEGVTHALR	14.8	1325.17	883.784	17066	115.5	YGL245W
IYTISETPEALPILLEDASR	59.73	1116.09	744.398	11909	94.5	YLL018C
KPENAETPSQTSQEATQ	65.39	923.427	615.954	1095	14.1	YML008C
KPLLESGTLGTK	23.62	622.366	415.247	3663	29.8	YKL210W
KPLNPFLGELFVGK	19.14	779.953	520.305	11347	77.5	YPL145C
LAADVPLEPESK	21.71	634.84	423.563	5153	38.9	YDR233C
LADDIPSNSPMAINCEYGSFDNEHLVLPR	38.55	1637.76	1092.18	8779	72.8	YFR053C
LADELESQIDLVSSIEALDNGK	19.67	1180.1	787.067	12008	95.2	YPL061W
LADGLFVNVAK	67.1	573.829	382.889	8329	58.5	YOR136W
LAEELGLVSR	49.71	543.811	362.877	6476	47	YER063W
LAESSIGEAR	36.81	516.77	344.849	2274	21.4	YJR014W
LCDEIATIQSK	42.68	639.324	426.552	4911	37.5	YML024W
LDELTAYFIECMEK	63.55	881.407	587.941	13880	93.9	YDR516C
LDGLIILGGFEGFR	35.67	753.919	502.949	14206	96.1	YGR240C
LDGLSVQELMDSK	56.65	717.861	478.91	9934	68.5	YLR432W

LDIALSTSLPVALVFLPAADIPTFVGEGK	13.62	1477.83	985.554	17882	121.4	YER055C
LDLFPEDLNILGK	19.96	743.911	496.277	13189	89.4	YNL220W
LDNTVAEIEGLEATIENLK	42.35	1036.54	691.363	13442	105.1	YGR094W
LDQLIYVPLPDENAR	70.34	878.467	585.981	10575	72.6	YDL126C
LDQVWGSETVASSK	14.43	753.875	502.919	5861	43.3	YDR012W
LDVDELGDVAQK	70.07	651.333	434.558	7018	50.4	YLR043C
LEETCDDISASNDELFR	57.25	1007.44	671.962	6276	54.6	YJR064W
LESFQAVYNK	22.94	599.809	400.208	5638	41.9	YNL096C
LESYVASIEQTVTDPVLSSK	83.26	1083.56	722.711	10011	81.4	YDL229W
LEVGTETLIDK	25.1	609.335	406.559	6463	47	YML126C
LEVPGYVDIVK	20.82	616.35	411.236	9077	63.2	YOL121C
LFEQEGVSK	24.23	518.769	346.182	3079	26.3	YLR354C
LGANYAPCVLPQLQAASR	46.78	965.004	643.672	9238	64.2	YJR148W
LGECDVIEEIMLGEQPFLK	20.87	1110.55	740.702	13740	107.2	YIL142W
LGEGVNVEQVEGLMSLEQYEK	34.29	1176.08	784.386	10388	84	YAL044C
LGEHNIDVLEGNEQFINAAK	36.91	1106.06	737.706	8611	60.3	gi|136429
LGEMPADQGFPAYLGAK	53.57	882.935	588.959	9406	65.2	YDL185W
LGFTFSYPVDQTSLNSGTLIR	82.97	1158.6	772.734	10374	83.9	YCL040W
LGGEVFIDFTK	60.71	613.327	409.22	9981	68.8	YMR083W
LGGSSLLECVVFGR	23.1	747.393	498.598	12330	83.8	YEL047C
LGGTCLNVGCIPSK	28.73	738.371	492.583	6311	46	YFL018C
LGLEPDTEAR	38.09	550.783	367.524	3846	30.9	YOR335C
LGNPMPMEATQAAPTIK	31.14	885.45	590.636	6985	50.2	YLR179C
LGPEITVAALK	49.59	556.34	371.229	7996	56.4	YER110C
LGQEFADDDGELVSAADIVPIVQEK	50.15	1329.66	886.776	10149	82.3	YPR033C
LGSLVGQDSGYVGGLPK	37.26	823.941	549.63	7832	55.4	YKR048C
LGYSVYEDAQYIGHAFK	22.33	980.976	654.319	10572	72.6	YNR034W-A
LGYTEPDPR	28.01	524.259	349.842	3095	26.4	YJR139C
LHEEYFGEDK	19.19	633.785	422.859	3325	27.8	YNL247W
LIDEYGDDFAK	26.82	643.301	429.203	6379	46.4	YLR259C
LIDLTQFPAFVTPMGK	49.26	889.481	593.323	13341	90.4	YLR044C
LIDVDGKPQIQVEFK	18.05	864.98	576.989	7686	54.5	YAL005C
LIEAFNEIAEDSEQFDK	103.89	999.471	666.649	11439	78.1	YMR186W
LIEAFNEIAEDSEQFEK	53.53	1006.48	671.321	9656	78.9	YPL240C
LIEFGFTDEMIAMPISALSGGWK	39.36	1257.13	838.42	15037	116.3	YLR249W
LIEPYVAYGYPSYSTIR	51.68	996.509	664.675	9996	68.9	YGL076C
LIESSNLEMEIIPNQK	50.32	929.485	619.992	9142	63.6	YKL035W
LINQLAQELGIYSHELELYGHYK	36.95	1366.21	911.141	13284	90	YGR204W
LISDYDADELAEALQPVIVNTPHLK	26.66	1382.72	922.152	13158	89.2	YHR064C
LISETLNDPTEEYLLDMAK	51.7	1098.04	732.364	10047	81.6	YPR160W
LIYNLEDQGGELCSLR	70	940.465	627.312	9427	65.4	YPR033C
LLDTLSDESK	17.66	560.79	374.196	4338	34	YGL195W
LLEMSTEDFVK	51	656.329	437.888	8653	60.5	YOL040C
LLGAQHLIEAGVDALIVCGGDGSLTGADLFR	41.52	1569.82	1046.88	14082	109.6	YMR205C
LLNEATHETSGATEFFASEFNTK	31.34	1272.6	848.734	9955	68.7	YLR178C
LLPWFDGMLEADEAYFK	38.23	1022.99	682.329	14495	112.4	YKL060C
LLTLTNAANVPVENIWADIFAK	45.31	1207.16	805.109	14588	113.1	YDL081C
LLYETALLTSGFSLDEPTSFASR	68.04	1259.64	840.095	11849	94.1	YPL240C
LNDIEDVEK	46.08	537.769	358.849	3525	29	YBR011C
LNELLDAIR	22.16	528.806	352.873	8563	60	YCR084C
LNELTTDLQESQTK	58.92	810.41	540.609	5625	41.8	YBL047C
LNINVIDTPGFGDFIDNSK	14.4	1040.02	693.685	10543	85.1	YCR002C
LNNFNDVSSYNENK	46.36	829.376	553.253	4584	35.5	YGR155W
LNNVFVIGEQGKPYISLPK	26.37	1058.59	706.065	8373	69.9	YJR145C
LNNVSLSSDAFFPFPDNVYR	30.34	1151.56	768.043	10962	88	YLR028C
LNSHDQIIADEYQNTNVPNIYSLGDVVGK	18	1608.79	1072.87	9001	74.4	YPL091W
LNYNTVSGVNGPLVILEK	46.45	965.536	644.026	10757	73.7	YBR127C
LPAASLGDMVMATVK	28.1	752.399	501.935	11338	77.4	YBL087C
LPANLLQAQR	36.72	562.333	375.224	5895	43.5	YHR183W
LPELLQDAVLK	47.92	619.871	413.583	10372	71.3	YHR068W
LPENESLSTVMGILGSGVHR	16.09	1048.54	699.365	12153	82.7	YBR214W
LPETENLSTVIGILGSGVHR	26.3	1046.57	698.051	12457	84.6	YGL056C
LPGIIHIDAAEIYR	46.32	790.943	527.631	9574	66.3	YDL124W
LPIGDLATQFFADR	43.21	782.412	521.944	13190	89.4	YJL111W
LPLIPDQIGVENVDNADFLR	73.88	1119.59	746.73	10772	86.7	YDL190C
LPLTDEQTAEGR	55.29	665.336	443.893	3568	29.2	YHR146W
LPLVGGHEGAGVVVGMGENVK	92.34	1010.04	673.695	18790	149.8	YOL086C
LPTESVPEPK	47.29	548.798	366.201	3597	29.4	YMR242C
LPWSIVPSIK	32.73	570.345	380.566	10764	73.8	YML100W
LQDAPEESYTR	34.37	654.807	436.874	2815	24.7	YCL030C
LQETNPEEVPK	32.21	642.327	428.554	2612	23.4	YKL056C
LQLGQLYESGNPVNDANLLGAEVLIK	23.7	1384.75	923.499	11870	94.2	YBL045C
LQNTDLNELTDETQSILAQIK	62.44	1194.12	796.415	12650	99.6	YFL022C
LSAAQAELAYAETGAHDK	18.27	923.452	615.971	6410	46.6	YDR454C
LSAEEVDFVEIIGGTTR	42.49	918.473	612.651	12705	86.2	YPL106C
LSATSQTAASATPGVAQSR	20.3	902.463	601.978	2882	25.1	YDL226C
LSETVLEDVYNQLPELIGGSADLTPSNLTR	21.45	1622.83	1082.22	14351	111.4	YPR074C
LSEVVELFEVFTPQDGR	25.7	983.002	655.67	14830	100.2	YHR087W
LSFDTQATIEK	55	626.825	418.219	5974	44	YLR354C
LSSESVIEQIVK	68.33	666.374	444.585	9649	66.8	YDR064W
LTADYDALDIANR	96.52	725.862	484.244	7899	55.8	YOL127W
LTAPQDIQISEDGK	24.12	757.888	505.595	5608	41.7	YHL021C
LTIIPDGGVK	13.53	506.805	338.206	7270	52	YIR029W
LTTNLEYTLPESVEILGPQNK	62.29	1180.12	787.085	9739	79.5	YHR064C
LTYEPIDLSSILSDGEEK	42.32	1005	670.337	10881	87.4	YJL080C
LVADGVFYAELNEFFTR	18.77	995.999	664.335	15503	104.8	YNL178W
LVEGLANDPENK	52.45	649.833	433.558	3514	28.9	YOR369C
LVLIANDVDPIELVVFLPALCK	56.98	1226.2	817.803	15910	122.4	YHL033C
LVSWYDNEYGYSTR	52.63	876.897	584.934	8277	58.2	YGR192C
LVTDLSVQQPEVLGEGVDVNEDLIK	26.17	1355.21	903.811	11231	76.8	YKL210W
LWGDSFFNPK	28.65	605.798	404.201	10425	71.6	YOR133W
LWTEFNEDAEPVTTDAIILATGASAK	15.09	1382.19	921.796	13430	91	YDR353W
LYGTDDNTQEVEAVTNK	67.48	948.945	632.966	5323	40	YJR014W
LYQTEPSGIYSSWSAQTIGR	17.64	1122.55	748.703	7706	65.2	YOL038W
MEILCQQR	45.34	539.263	359.844	4133	32.7	YLR058C

MFILDEADEMLSSGFK	79.78	916.926	611.62	14818	100.2	YKR059W
MFTDLFDYFPITALVDNK	33.63	1075.53	717.355	15635	120.5	YDL134C
MFTDLFDYFPVTALVDNK	25.32	1068.52	712.683	14925	115.4	YDL188C
MGTTGVQSSVASDLDELISR	56.94	1033.51	689.34	10435	84.3	YGL026C
MGVPIYGIVAMAATATDK	18.78	904.968	603.648	13877	93.9	YPL231W
MIEIMLPVFDAPQNLVEQAK	76.64	1143.6	762.734	12834	100.9	YLR044C
MIPGAKPLQVGDVVSTTAVIESVVNQPTGK	23.14	1518.33	1012.55	10554	85.1	YKL182W
MPELIPVLSETMWDTK	53.32	945.473	630.651	14156	95.8	YLR249W
MPLVGLGCWK	21.63	580.801	387.537	9970	68.8	YHR104W
MPQTVEWSK	37.67	553.271	369.183	4791	36.7	YLR109W
MSAEGYIDYPTYEEALK	57.27	990.451	660.636	9408	65.2	YHR179W
MSANISETTAMITDIATAPAEIDR	83.82	1261.61	841.409	11616	92.5	YLR044C
MTAEKPDPTLAVICGAATK	15.33	987.505	658.673	6782	48.9	YNR016C
MYEEALWPGWKPFDITAK	31.2	1091.54	728.027	12286	83.5	YGR234W
NAAWLVFANK	63.74	567.309	378.542	9670	66.9	YDL192W
NADELSSYQK	26.39	577.77	385.516	2528	22.9	YMR314W
NAGLALTDTFGTDDFLK	29.39	899.946	600.3	11655	79.5	YOR209C
NAGQICSSGSR	53.43	568.759	379.509	941	13.2	YPL061W
NAGTAEFLVDNQNR	67.22	774.874	516.918	5696	42.3	YBR218C
NAIEEELAK	21.8	508.767	339.513	4928	37.6	YCR053W
NALKPVFQDLYESTK	45.55	876.962	584.977	8899	62.1	YLR355C
NAPAIIFIDEIDSIAPK	20.02	913.999	609.668	15081	101.9	YDL126C
NASNNPNELAASGAALQAR	79.3	934.964	623.645	5265	39.6	YHR064C
NATFPGVQMK	25.63	546.779	364.855	5477	40.9	YLR044C
NAVQNESVSSPIELNFDAVK	52.87	1081.04	721.031	8141	68.3	YPR191W
NAVSTKPTPPPAPEASAESGLSSK	24.41	1162.09	775.064	3735	30.3	YMR205C
NAVWFGGSLLAQTAEFK	38.49	919.975	613.653	12843	87.1	YJR065C
NAVWLVFANK	29.62	581.324	387.885	10680	73.2	YDL137W
NCTPKPTSTTETVAASAVAAVFEQK	37.07	1304.65	870.102	10794	74	YAL038W
NDELGTPFGVTIDFESAK	50.12	970.468	647.314	11847	80.7	YBR121C
NDPTWQGPILAPGLINR	57.78	931.5	621.335	10644	73	YNL117W
NDSLSGAVIAAIMQEAGLR	67.01	958.499	639.335	16132	109	YDR394W
NDVRPEWEDEANAK	16.13	836.882	558.257	3660	29.8	YOL139C
NEAVDATHLAEFHQVEGVLADYNITLGDLIK	15.17	1698.36	1132.58	14920	100.8	YFL022C
NEFSGALSGLTR	28.02	626.32	417.882	8245	58	YIL078W
NENEQVLIEPSVNSVR	22.08	913.966	609.646	6652	48.1	YKL013C
NEQASSVYSTQLLADIISEASK	54.04	1177.59	785.396	14618	98.8	YGR240C
NESMLTFETSQLQGAK	91.31	892.43	595.289	8694	60.8	YER009W
NETNNIDGNFK	53.26	633.291	422.53	3062	26.2	YOR332W
NEVQIPVTFYGYVDRPEGGK	17.73	1134.57	756.715	9607	66.5	YPR160W
NFAEFNSVYAK	42.8	645.312	430.544	7298	52.1	YIL051C
NFLETVELQVGLK	25.58	745.417	497.28	13434	91	YGL135W
NFNDPEVQGDMK	62.51	697.306	465.207	4193	33.1	YLL024C
NGFILDGFPR	52.54	568.298	379.201	10171	70	YDR226W
NGGLGWDLDAIIPFAAIPEQGIELEHIDSK	31.41	1609.82	1073.55	14202	110.4	YPL231W
NGMVVGLGAGQQSR	69.91	687.351	458.57	4605	35.6	YMR120C
NGPVYGVPPQGGFPR	18.99	771.397	514.6	6695	48.4	YER165W
NIAEAQGIVELLLSDYYSVEQK	25.98	1241.64	828.095	17237	116.7	YIL076W
NIDDLSVLMDHVK	51.81	749.882	500.257	10066	69.3	YGR234W
NIEPIDTPISFR	13.52	701.372	467.917	9089	63.3	YDR238C
NIFQSISAK	31.39	504.28	336.522	7120	51	YHR183W
NIGVSNFAVEDLQR	47.75	781.402	521.27	8773	61.3	YDL124W
NIIVATGSEVTPFPGIEIDEEK	27.66	1179.61	786.741	9522	78	YFL018C
NILAESNSSLDNIVK	88.52	808.928	539.621	8669	60.6	YIL051C
NINSETTDEQFQELFAK	56.7	1007.47	671.985	8318	69.6	YER165W
NIPIEVVALINDTTGTLVASYYTDPETK	40.49	1519.28	1013.19	15909	122.4	YGL253W
NIPSFLSTDNIGTR	27.79	767.897	512.267	9092	63.3	YDL185W
NISFTVWDVGGQDR	22.19	797.386	531.927	10482	72	YDL137W
NISSVPDELPDWLIPGSK	19.64	984.01	656.342	12622	85.7	YNL084C
NITLDVSER	19.57	523.777	349.521	5061	38.4	YJL130C
NITWIAECIAQNQR	41.94	858.928	572.954	10362	71.2	YLR447C
NIVEFHSDHMK	37.98	678.822	452.884	2916	25.3	YLR044C
NIYYITGESLK	49.99	650.843	434.231	7512	53.4	YMR186W
NKPDPAIVEK	18.93	555.811	370.877	1290	15.3	YJL026W
NLADNDEYPQLIELTQR	53.7	1016.5	678.004	8504	70.9	YMR250W
NLAGVDYLTISPALLDK	71.84	901.999	601.668	12059	82	YLR354C
NLATLLLTDYIQK	53.28	753.432	502.624	13577	91.9	YDR071C
NLFTGWVDVK	27.89	589.814	393.545	11681	79.6	YKL152C
NLPDMIEELDLHED	38.06	841.882	561.591	12035	81.9	YDL022W
NLQYYDISAK	34.11	607.806	405.54	5805	42.9	YOR185C
NLTEEVWAVK	15.19	594.817	396.88	8141	57.3	YLR249W
NLTEQAIIDLTVATIAIK	14.95	964.059	643.042	16060	108.6	YMR120C
NLVWEYESVVQYR	29.6	842.92	562.282	10915	74.7	YMR079W
NLYVGQEDNEMTIPTCSR	15.56	1063.98	709.654	5903	51.7	YGR094W
NMITGTSQADCAILIIAGGVGEFEAGISK	93.16	1462.23	975.156	17072	115.5	YPR080W
NNDDGELGFLILDAVLCK	90.55	1003.5	669.335	14960	115.7	YJL173C
NNDISFEIGK	15.77	568.783	379.524	6495	47.2	YMR012W
NNLNTENPLWDAIVGLGFLK	37.46	1114.59	743.395	17805	120.8	YDL185W
NNLWDDDVLAR	19.87	665.823	444.218	9043	63	YGR155W
NNQFLNPDNITYIFTSPR	33.32	1077.53	718.692	11149	89.2	YKR043C
NNSELLANLGNFVNR	71.98	837.932	558.957	11158	76.3	YGR264C
NNYDGDTVTFSPTGR	48.25	822.368	548.581	5591	41.6	YMR314W
NNYIGPGPPK	13.09	528.777	352.854	2811	24.6	YLR179C
NPHDIIEGINAGEIEIPEN	54.6	1037.51	692.008	8498	70.8	YEL054C
NPLFSYVEPVLVASAK	52.32	867.477	578.654	12688	86.1	YDL075W
NPSDITQEEYNAFYK	92.2	909.913	606.944	7950	56.2	YMR186W
NPVILADACCSR	71.86	688.326	459.22	4851	37.1	YLR044C
NPVTGAQGITLSEGNEILK	86.05	971.018	647.681	8659	60.6	YLR432W
NQAAMNPSNTVFDAK	92.94	804.378	536.588	5439	40.7	YAL005C
NQEIFDANVQR	14.04	667.328	445.221	4889	37.3	YDL082W
NQILVSGEIPSTLNEESK	88.26	979.507	653.341	8024	56.6	YBR072W
NQITETYPSGQITLSNAVTK	15.55	1083.06	722.374	6133	53.5	YOL057W
NRPAPSVEQVK	38.07	612.838	408.895	1277	15.2	YDR158W
NSFAVIEFTPEVLDR	14.87	868.946	579.633	12084	82.2	YDL051W
NSNPENTVGLISGAGANPR	47.45	934.466	623.313	6266	45.8	YHR200W

NSSAVITDGLKPIHIVTK	15.63	947.044	631.698	6832	49.3	YGR155W
NSSCYFLGDATNDSLQR	90	974.429	649.955	7659	54.3	YIL078W
NSYGSSNYGSSNNDDSYGSSNR	51.71	1166.45	777.971	1804	21.8	YMR173W
NTDDSVLVLVDLSAK	60.11	794.925	530.286	11603	79.1	YGR061C
NTENEQPASIFNK	49.83	746.357	497.907	5131	38.8	YOR198C
NTFAGGETSGLEVTDPSDPNSLLK	37.43	1225.09	817.062	7423	63.2	YBL058W
NTGIDSQTSDIFDPEAYTK	32.16	1051.48	701.323	7934	66.8	YIL137C
NTNIPLPALQK	43.45	604.853	403.571	7137	51.1	YPL160W
NTTRPDFIFYSDR	17.86	816.394	544.599	7498	53.4	YHR128W
NTWGSQLVDQIMDQVVTK	25.93	1031.52	688.014	14797	100	YGL037C
NTYEYECSFLLGENIGMK	46.87	1084.49	723.327	9300	76.4	YLR249W
NVIAETGAGQHGVATATACAK	23.75	1014	676.337	3519	28.9	YGL026C
NVLEASNSSLDR	77.6	652.826	435.553	3914	31.4	YER057C
NVLIVDEVDDTR	60.72	694.357	463.24	7508	53.4	YDR399W
NVNDVIAPAFVK	30.54	643.859	429.575	7898	55.8	YGR254W
NVPLYQHLADLSK	59.72	749.407	499.94	8184	57.6	YHR174W
NVPVHVSPAFR	29.23	611.838	408.228	4314	33.8	YDR025W
NVQEFTTAAR	53.5	568.788	379.528	3412	28.3	YKL080W
NVQVHQEPYVFNARPDGVHVINVGK	29.82	1408.73	939.491	7106	51	YLR048W
NVSGQDVAAALEANAK	25.12	779.397	519.934	7710	54.7	YER091C
NVVVQTDGQLR	41.73	614.836	410.226	3647	29.7	YDL171C
NWGAETDELSMIMEHFSQQ	61.71	1126.98	751.658	12852	101	YOR369C
NYASEALISYFK	46.46	703.354	469.238	11142	76.2	YKL081W
NYIIEELNVR	31.89	631.841	421.563	9042	63	YBL076C
PLFDLISPK	20.21	515.303	343.871	10288	70.8	YOR251C
QAAASVVPSASSLVITALK	21.09	907.025	605.019	11230	76.7	YEL054C
QAIECLEGMQLFAPEVK	47.13	981.987	654.994	11571	78.9	YPL160W
QAINLGQVVLTPLTFALPR	55.99	1026.1	684.405	13488	105.4	YHL001W
QATGGQAFPQMVFDHWSTLGSDPLDPTSK	53.8	1559.73	1040.16	11165	89.3	YOR133W
QAVVNPENTLFATK	29.6	766.409	511.275	7711	54.7	YJR045C
QDVEALIEFIYDTEK	34.01	906.949	604.968	14844	100.3	YPL231W
QDVSDLLDQDEYIDLVVPR	42.58	1116.56	744.706	11501	91.7	YOR323C
QEAGAFTFNEDF	32.63	688.294	459.198	11107	76	YJL026W
QEDSNLISSEYEVK	34.44	820.886	547.593	6088	44.7	YOR046C
QFGYVILTTSAGIMDHEEAR	22.96	1119.55	746.7	11051	75.6	YJL190C
QFYVNVEEEEYK	38.29	788.862	526.244	7304	52.2	YKR059W
QIAPAELEGLLDLER	63.07	833.954	556.305	12612	85.6	YPL231W
QIFDEELIK	18.98	567.806	378.873	11673	79.6	YCL025C
QIIENAGEEGSVIIGK	37.46	828.944	552.965	6881	49.6	YLR259C
QITVVGATSGDTGSAAIYGLR	75.36	1019.03	679.692	6994	60	YCR053W
QIVFEIPSETH	34.16	650.333	433.891	8821	61.6	YOR096W
QLAGIDDQGHLHTSGWSR	31.81	989.48	659.989	5406	40.5	YGR124W
QLGEWAGLGK	49.89	529.785	353.526	7273	52	YOR369C
QLLLLGNALPTVQSLSER	83.33	976.562	651.377	12739	86.5	YPR036W
QLSEDSHHLQSNNDNFSK	15.75	1050.47	700.651	2070	20.1	YNL079C
QLSIWGLENDDDVSDITDK	66.04	1082.01	721.674	9420	77.3	YGR086C
QLVDVYTTLPYDFILEK	18.61	1029.05	686.366	12223	96.7	YNL259C
QLYDYETEVSMR	32.58	767.348	511.901	7154	51.2	YMR205C
QLYSFDLEGFWMDVGQPK	84.06	1080.51	720.675	13068	102.5	YDL055C
QNEDTLLVGATDGVGTK	78.87	859.434	573.292	6849	49.4	YGL234W
QNPQAIGQDLFTDPR	35.1	850.424	567.285	8217	57.8	YOR027W
QNVETLDIVR	58.85	593.825	396.219	6140	45	YLR304C
QNWTMENFIDTEINR	49.93	955.939	637.628	12024	81.8	YMR217W
QPASFLFLGLSGSGK	26.87	754.909	503.608	11703	79.8	YLL026W
QPYIMDTSYPAR	26.5	721.343	481.231	6125	44.9	YFR053C
QQLSNPEFVFSDFAK	41.78	878.931	586.29	11076	75.8	YKL210W
QQQDLDPEDIAFK	22.07	773.873	516.251	7905	55.9	YLR262C-A
QQSLYLDPEPTFIEER	62.98	982.984	655.658	9941	68.6	YIL078W
QSQDSCYGVAFR	20.22	709.312	473.21	5147	38.9	YGR240C
QSSATSSFGGLGGGSVR	26.55	777.879	518.922	5140	38.9	gi|34783124
QSSPANPIGTYEYSR	49.32	835.394	557.265	5618	41.8	YAL012W
QVNLTPAPLPTSSPWK	65.89	868.472	579.317	8913	62.1	YCL037C
QVNVNTVFGLPGDFNLSLLDK	39.49	1145.61	764.074	14636	98.9	YLR044C
QVYFVADIENLSPLACAYAR	31.42	1150.57	767.384	13695	92.7	YMR120C
QWFEAHYGQTLGK	30.47	782.881	522.256	6812	49.1	YBL072C
QYSEGQAQITLR	47.28	697.357	465.241	4565	35.4	YMR120C
RPEYFITANDVK	33.84	726.878	484.921	5404	40.5	YIL053W
RPYIAGLGAEK	14.07	587.833	392.224	3739	30.3	YFL018C
SAADIVFLAPGLSAIIDALK	15.03	993.069	662.382	18172	123.5	YGL008C
SAFDVPEWVDPNVQNLVSK	47.86	1072.54	715.36	10482	84.6	YJL130C
SAGGNYVVFGEAK	44.2	649.822	433.551	5873	43.3	YHR193C
SANDLVETLSK	20.73	588.809	392.875	6639	48.1	YMR109W
SANLMAGHWVAISGAAGGLGSLAVQYAK	44.69	1350.7	900.802	12129	82.5	YOL086C
SANPSNDIPLSR	15.51	635.823	424.218	4043	32.2	YGL202W
SASEVASDLAQLTDFPVIR	82.37	1010.02	673.685	11741	93.3	YGR279C
SAVEVIEFVK	23.87	560.816	374.213	8784	61.3	YDL131W
SAVTVVVAAGGYPESYAK	22.54	884.959	590.309	7833	55.4	YGL234W
SCGVDAMSVDDLK	62.91	698.808	466.208	6335	46.2	YGL135W
SDAFAEFAEPLVNSAYEAIK	62.58	1086.53	724.688	12662	99.7	YER110C
SDFHVLFAVAQELR	18.7	816.431	544.623	12476	84.8	YJL130C
SDIVGSPVAELLK	24.18	664.377	443.254	10201	70.2	YGR204W
SDLFDLFGPIGK	43.61	654.845	436.899	13813	93.5	YCL011C
SDLTGANSIYSVEK	39.16	742.367	495.247	5884	43.4	YFR010W
SDLTLVQILK	23.27	565.345	377.232	10475	71.9	YGR218W
SDLVDLLNIYK	23.33	646.858	431.575	12670	86	YDL131W
SEAEAEAAGLPVVNLDTR	96.32	921.466	614.646	8491	59.5	YLL018C
SEELSEIDASTAK	60.11	690.33	460.556	4232	33.3	YPR036W
SEELYPGRPLAIALDTK	15.16	937.007	625.007	8879	61.9	YAL038W
SEGETEPPQPAESK	19.03	743.339	495.895	1255	15.1	YGL202W
SEGIEFFASPVTLGPDGIEK	72.69	1047.03	698.353	10362	83.8	YKL085W
SEIFSTYADNQPGVLIQVFEGER	79.65	1300.14	867.094	11969	94.9	YAL005C
SEIVGRPLAALLANDGATVYSVDVNNIQK	26.31	1514.31	1009.88	10093	81.9	YKR080W
SELEYYAMLSK	49.47	667.321	445.216	8975	62.5	YGL030W
SENPDITFGQVGK	45.32	696.344	464.565	5957	43.9	YPR052C
SENPDVTFGQVGR	49.03	703.339	469.228	5334	40.1	YBR089C-A

SEQHSVAVGK	16.76	521.27	347.849	10695	73.3	YIL009W
SESVVYQGSR	20.06	556.273	371.184	1830	18.6	YCL043C
SEVFSTYADNQPGVLIQVFEGER	58.28	1293.13	862.422	11597	92.3	YLL024C
SFANQPLEVVYSK	37.68	741.385	494.593	8004	56.5	YDR432W
SFDELGLAPELLK	28.3	716.39	477.929	11567	78.9	YOR046C
SFDPFADTGDDETATSNYIHIR	39.25	1236.55	824.703	8218	68.8	YNL244C
SFDVPPPPIDASSPFSQK	64.16	958.475	639.319	9784	67.6	YKL152C
SFEVTDPVNSSLK	49.52	711.859	474.909	7155	51.3	YML070W
SFLSPLETDEEIEVVIEQGK	20.62	1131.57	754.718	11873	94.2	YGL062W
SFLSYCGGLPAPEDSDNPLGYK	16.51	1194.05	796.367	8921	73.8	YNR050C
SFVVPQEVYDHYQK	34.36	869.925	580.286	7558	53.7	YPR074C
SFWDASDISDDVIELAGGMPNER	26.97	1262.57	842.048	13344	104.4	YHR137W
SGADDIVFATVQLK	30.32	732.391	488.596	10062	69.3	YMR315W
SGAHLLEFQPSGNVTELYGTAIGAR	33.08	1294.66	863.442	10631	72.9	YMR314W
SGETEDPFIADLVVGLR	24.75	909.468	606.647	14435	97.6	YPL281C
SGETEDTFIADLVVGLR	103.32	911.465	607.979	14625	98.9	YGR254W
SGQGAFGNMCR	36.86	592.75	395.503	3297	27.6	YDR012W
SGQIQPHLDQLNLVLR	28.71	916.013	611.011	9270	64.4	YGL105W
SGSAADTQAIADIVQYHLELYTSQYGTPSTETAASVFK	44.02	2010.97	1340.98	12858	101	YJL001W
SGSATQFDATDFATNEDLVELVK	81.56	1229.58	820.059	10063	81.7	YKL142W
SGTLTYEAVQQTTK	55	763.888	509.595	4552	35.3	YOR142W
SGVAVADESLTAFNDLK	82.18	868.939	579.628	10097	69.5	YLL050C
SGVVNSAFPADESLK	62.21	760.883	507.591	6524	47.3	YMR105C
SHINVVVIGHVDSGK	54.43	780.928	520.955	21004	150.2	YPR080W
SIACVLTVINEQQR	48.08	815.933	544.291	9736	67.3	YDL136W
SIAPAYGIPVVLHSDHCAK	68.51	1018.03	679.019	5644	49.8	YKL060C
SIGGEVFIDFTK	61.4	656.843	438.231	10578	72.6	YOL086C
SIIGATSIEDFISK	54.71	740.898	494.268	11495	78.4	YHR183W
SINPDEAVAYGAAVQAAILTGDESSK	78.7	1289.14	859.761	11339	90.6	YAL005C
SINPDEAVAYGAAVQGAILTGQSTSDETK	59.98	1447.21	965.14	9758	79.6	YDL229W
SINVDLEPGTIDAVR	51.94	799.923	533.618	8451	59.3	YFL037W
SIQGHVPGFAPNLAIIQVGNRPDSATYVR	44.62	1539.32	1026.55	9721	67.2	YGR204W
SISDVFGKPLSSTLNQDEAVAK	26.83	1153.6	769.401	9316	64.7	YBR169C
SISGPVITDVASLK	28.78	693.896	462.933	8603	60.2	YJL130C
SIVPSGASTGVHEALEMR	100.35	920.965	614.312	7444	53	YGR254W
SIVTLDVKPWDDETNLEEMVANVK	17.13	1373.19	915.793	11099	88.9	YAL003W
SIYLLAGNDPEGR	23.16	702.859	468.909	7562	53.8	YOR335C
SLANTFLSLDTEGR	111.23	762.389	508.595	10522	72.2	YGL202W
SLDEIIGSNK	46.08	538.285	359.192	5567	41.5	YDR381W
SLDFLNQSFIQQK	45.88	784.409	523.275	10512	72.2	YBL045C
SLDLDSIIAEVK	38.36	651.861	434.91	12349	83.9	gi|1346343
SLDYDQENTVR	21.67	670.31	447.209	3311	27.7	YIL074C
SLFEGLVADAPK	49.64	623.837	416.227	10002	69	YMR229C
SLGLVVSVNAEPAK	16.2	692.396	461.933	7306	52.2	YDL185W
SLIYSTHEVEDCTK	62.28	841.39	561.263	4249	33.4	YBR026C
SLLEVVQTGAK	61.41	572.832	382.224	7214	51.6	YOL038W
SLTVPELTQQMFDAK	21.06	854.435	569.959	11341	77.5	YFL037W
SLTYVLDESTAFSAER	14.57	894.936	596.96	10020	69.1	YNL287W
SMTVFDPEPVQLADLSTQFFLTEK	18.73	1372.18	915.123	15892	107.4	YKL210W
SMVEEAEASGR	54.45	583.261	389.177	2994	25.7	YGR155W
SMYQVQNDIGTGK	54.12	720.843	480.898	4769	36.6	YJR105W
SNAIDLFVTGQIPTEEPELSEYQSK	18.54	1398.18	932.459	10266	83.1	YMR120C
SNDSEQELLEAFK	57.45	755.357	503.907	9762	67.5	YBR109C
SNFATIADPEAR	42.5	646.317	431.214	5739	42.5	YLR249W
SNGVLNVDNQTSDLVK	16.56	851.934	568.292	6545	47.5	YML024W
SNLAGKPVICATQMLESMTYNPRPTR	46.58	1468.23	979.158	10821	74.1	YAL038W
SNYDTDVFTPLFER	69.93	852.399	568.602	11356	77.6	YOR335C
SNYGMIAINPGR	49.53	646.824	431.552	6676	48.3	YKL182W
SPALPQADDPIVETK	18.65	790.912	527.61	6190	45.3	YHR146W
SPDPFAVLTIDGYQTK	15.57	876.446	584.633	11389	77.8	YER125W
SPLNVGIVGTGIFAR	72.03	750.93	500.956	10931	74.9	YMR315W
SPNPMSLADGVSNDGPIQTNK	15.43	1071.51	714.676	6439	55.9	YNR067C
SPTESYSDIGGLESQIQEIK	70.35	1091.03	727.69	8372	69.9	YDL007W
SQAANSVDEALAAVK	83.24	737.381	491.923	7790	55.2	YJL130C
SQEVEYVDPTVNR	28.63	768.37	512.583	4571	35.4	YPR108W
SQFLSVFNNSPDETAFYR	25.99	1061.5	708.001	9492	77.8	YPR181C
SQIDEVVLVGGSTR	85.93	730.391	487.263	7118	51	YNL209W
SQIFSTAAAGQTSVEIR	32.19	883.458	589.307	7209	51.6	YJR045C
SQPTESQLILQSPTISSK	30.85	972.518	648.681	7329	52.3	YJL173C
SQVDEIVLVGGSTR	59.4	730.391	487.263	7118	51	YAL005C
SSAAGNTVIIGGGDTATVAK	67.71	895.468	597.314	4737	36.4	YCR012W
SSGLTPNAVVLVATVR	46.06	792.459	528.642	9787	67.6	YGR204W
SSHPIEVPVNNADEINQIFDAISYSK	36.88	1444.21	963.142	12817	87	YHR047C
SSLSEFTEGGFQWIIEDIEHGK	14.56	1255.1	837.068	15830	107	YIL125W
SSNITISNAVGR	59.94	609.825	406.886	4108	32.6	YNL209W
SSPDENSTLLSNDSISLK	59.65	953.966	636.313	7722	54.7	YMR205C
SSQSPETVYFASELK	59.11	836.907	558.274	8198	57.7	YGR124W
SSVLADALNAINNAEK	92.54	815.426	543.953	12726	86.4	YJL190C
SSYGSNNDDSYGSNNDDSYGSSNK	32.26	1267.48	845.32	1768	21.5	YMR173W
SSYGSSSNDDSYGSSNNDDSYGSSNK	16.68	1341	894.338	1740	21.3	YMR173W
STAISLYSEMSDEDVK	61.35	887.906	592.273	8567	60	YOR133W
STAQVASDLEQLTGFDNIR	53.65	1033.01	689.011	10766	86.6	YMR305C
STCACFEPSLDYCVVK	42.66	968.418	645.948	8558	59.9	YJL130C
STITYNLVLLAEAER	33.51	846.962	564.977	12171	82.8	YJR139C
STLEPVEQVLK	20.45	621.851	414.903	7320	52.3	YNL209W
STLIEPTSGNTGIGLALIGAIK	75.93	1063.61	709.407	11045	88.5	YGR155W
STLINVLTGELLPTSGEVYTHENCR	49.53	1402.2	935.136	11197	89.6	YLR249W
STQIPCVGISFGVER	35.47	825.419	550.615	9490	65.8	YPR033C
STSGNTHLGGQDFDTNLLEHFK	34.63	1209.57	806.715	9055	63	YNL209W
SVAAYPSDQDNDVFGEK	15.62	921.413	614.611	6127	44.9	YDL040C
SVAELVIGEIISLAR	29.11	785.464	523.979	18420	125.4	YIL074C
SVAVPVDILDHDNNYELK	37.43	1021.02	681.013	7552	64.1	YBR072W
SVDELITEGNEK	55.12	667.328	445.221	5211	39.3	YOL039W
SVDELTSLTDYVTR	53.94	799.899	533.602	10551	72.4	YMR186W
SVEMHHEQLEQGVPGDNVGFNVK	75.73	1275.61	850.74	6037	44.3	YPR080W

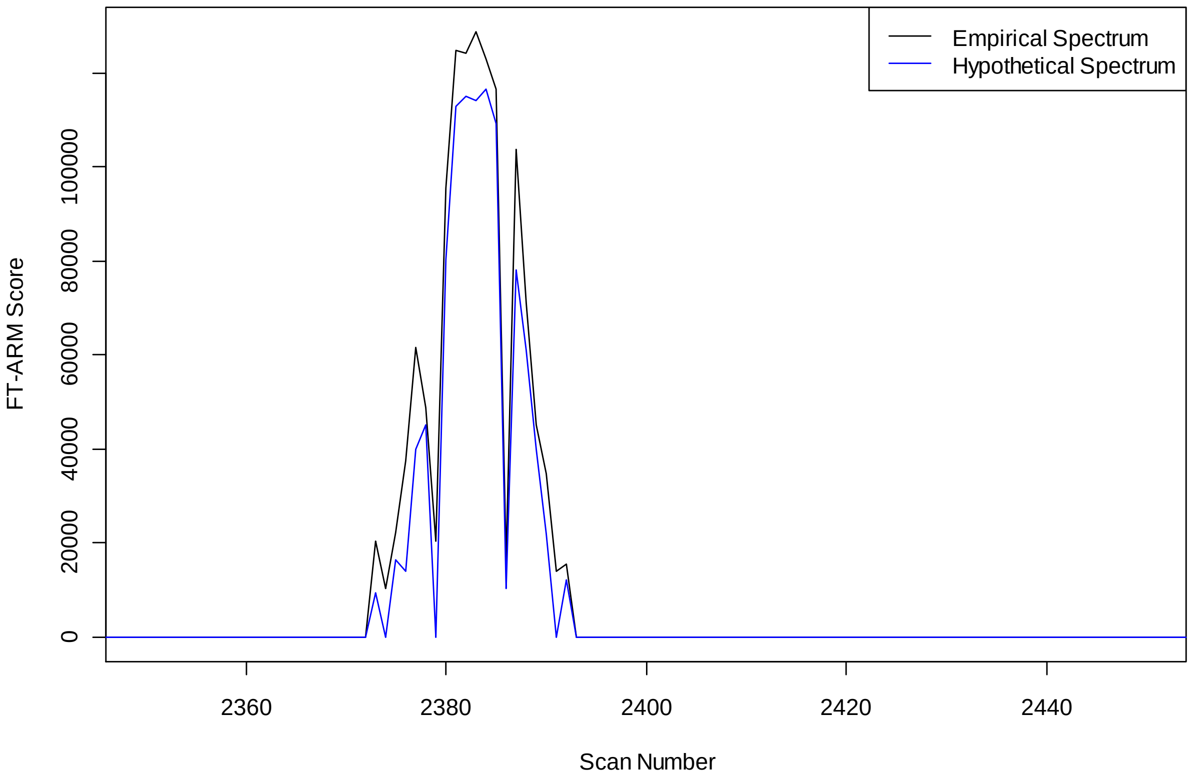
SVGCIVDGVPPGMSLTEADIQPQLTR	30.49	1370.69	914.126	9298	76.4	YGL148W
SVGETVDYIASNPDAN	41.36	826.376	551.253	7090	50.9	YKL192C
SVLDLLNAFTNAPGWPIADFEK	22.67	1209.62	806.749	16152	124.2	YML070W
SVQYVLEDPIAGPLVK	62.03	864.483	576.657	10588	72.7	YHR019C
SVVEDDAANNSLVK	46.01	730.865	487.579	4201	33.1	YHR063C
SVVLCNSTIK	25.93	560.805	374.206	3710	30.1	YDL055C
SYELPDGQVITIGNER	73.5	895.95	597.635	9598	66.4	YFL039C
SYIEGTAVSQADVTVFK	60.21	907.962	605.644	8667	60.6	YAL003W
TADLVLMVLDATK	31.3	695.386	463.927	14152	95.7	YGR173W
TAEEYLKPIINSVIK	23.68	859.49	573.329	10567	72.5	YMR105C
TAGGSSPATPATPATPATPTPSSGPK	20.38	1154.08	769.72	2791	29.1	YBR079C
TAGIQIVADDLTVTNPAR	91.57	928	619.002	9868	68.1	YHR174W
TANDVLTIR	49.42	501.783	334.857	4989	37.9	YAL038W
TAPLVVLGNPLLDFQADVTAEYLAK	17.55	1329.72	886.818	16365	110.6	YJR105W
TAQLSEFDEELYK	43.04	786.875	524.919	8459	59.3	YDR023W
TAQLTVEDGDNWEVVGK	68.88	930.952	620.971	8012	56.5	YPR163C
TASEFDSAIAQDK	69.93	691.825	461.553	4731	36.4	YLR043C
TASEIATTELPPTHPIR	34.92	917.489	611.995	5239	39.5	YDR099W
TASGNIIPSSTGAAK	39.76	687.865	458.912	3080	26.3	YGR192C
TATYDGEEGILAAK	57.69	719.857	480.24	5737	42.5	YGL148W
TAVDTVYEAVK	49.92	598.314	399.212	6163	45.1	YGL234W
TAVELGAVALK	40.68	536.324	357.885	6781	48.9	YPL028W
TAVVDGVFDEVSLDK	45.34	797.404	531.938	9804	67.7	YML028W
TCFYAEQGGQEYDTGK	72.71	927.386	618.593	4661	35.9	YOR335C
TCSDLLLVK	31.38	524.789	350.195	6423	46.7	YKL035W
TCSSCGYPAAK	22.2	601.252	401.171	1141	14.4	YLR185W
TDEEVAEVIGCER	27.92	753.841	502.896	6381	46.5	YMR300C
TDLGQSLVIGMGGDAFPGTDFIDALK	22.71	1319.66	880.107	13556	105.9	YOR142W
TDPAGYYVGYK	14.39	617.293	411.864	5281	39.7	YGL011C
TDPIGDEEQSINDTIFK	88.08	961.455	641.306	10237	70.4	YBL076C
TDSWFNETLIGGR	47.53	748.362	499.244	10456	71.8	YKL080W
TDTTYPAGFMDVITLDATNENFR	28.02	1296.6	864.736	11676	92.9	YJR145C
TEDLWDALADASGK	32.39	746.352	497.904	11853	80.7	YKL157W
TEELQTSSMK	26.02	577.274	385.185	2049	20	YJR045C
TELDGILPLVAR	51.06	648.88	432.922	11133	76.1	YAR015W
TESSLEWDAQR	23.24	661.305	441.205	4900	37.4	YLR300W
TETGIDLENDR	23.76	631.797	421.533	4057	32.3	YJR045C
TEWIADYGAAASGR	77.41	734.347	489.9	7429	52.9	YLR060W
TFEFLDEDVPDDSSNR	63.09	943.408	629.274	9475	65.7	YGR285C
TFESEAAHGTVTR	23.44	703.339	469.228	2466	22.5	YNL009W
TFITQGAYEDR	66.46	650.812	434.21	5104	38.6	YBR127C
TFSPQEISAMVLTK	70.88	776.408	517.941	11225	76.7	YNL209W
TFSPTPDYYPLQLVVESVVNEDER	25.45	1399.18	933.124	14467	112.2	YGL173C
TFSYAGFEQQPK	29.13	701.835	468.226	6765	48.8	YJL111W
TFTDCFNCLPIAAIIDEK	43.77	1064.51	710.008	12262	96.9	YER133W
TFTTCADNQTTVQFPVYQGER	67.88	1232.07	821.713	6745	58.1	YDL229W
TFTTVSDNQTTVQFPVYQGER	58.51	1209.58	806.724	7057	60.5	YNL209W
TFTVDVSSPTENGVFDPASYAK	64.98	1166.55	778.037	8805	73	YLR061W
TGAAPQTTFNVAPNSTPIVSTAATGLQHK	21.83	1440.75	960.833	8153	57.4	YDR129C
TGANVIEIDFEPLLELAR	20.14	1000.54	667.361	14028	109.2	YBR208C
TGDLAGTATTSSFTEAVIK	60.83	935.476	623.986	8442	59.2	YOR136W
TGELLCYDHYK	14.84	699.822	466.883	5245	39.5	YLR438W
TGETTLLSMSK	69.19	584.3	389.869	5881	43.4	YOR230W
TGHIAADGSVYNK	45.07	666.831	444.89	1559	17	YFR053C
TGHIAADGSVYNR	36.44	680.834	454.225	1813	18.5	YGL253W
TGIEAFAEALLVIPK	25.63	786.456	524.64	15309	103.4	YDR188W
TGIWAGVDASQPPATVWADILNK	77.49	1205.62	804.085	12214	96.6	YDR226W
TGKPLSVELGPGLMETIYDGIQRPLK	16.98	1406.77	938.181	12940	87.8	YDL185W
TGLDISDDAR	20.88	531.757	354.84	3968	31.7	YNL209W
TGLVSVDDDIYQK	31.95	726.864	484.912	6826	49.2	YNR016C
TGPFEVGVHVLPK	32.6	690.388	460.594	7396	52.7	YER043C
TGPSPQPESQGSFYQR	65.08	883.411	589.276	3864	31.1	YOR204W
TGTLTTSETAHNMK	83.7	746.359	497.908	1452	16.3	YOR133W
TGTTTNDVDYPIPPNHEMIFTTDDK	43.68	1411.64	941.432	8348	58.6	YAL038W
TGVFEPEFTADGK	21.88	699.333	466.558	7358	52.5	YGR094W
TGVIVGEDVHNLFTYAK	92.62	931.986	621.66	20935	149.7	YKL060C
THGAPTDEVR	30.89	541.765	361.512	946	13.2	YJR104C
THMIINVEWGSFDNELK	15.55	1016.99	678.331	10927	74.8	YCL040W
TIAETLAEELINAAK	80.33	793.935	529.626	14420	97.5	YJR123W
TIDEIYGVVK	18.87	568.813	379.545	7046	50.6	YNL220W
TIEEFETWLSNADTETLK	23.42	1064.01	709.676	11273	90.1	YNL247W
TIELLEDYIAHAVNIK	22.66	921.504	614.672	13513	91.5	YMR235C
TIFSNIQDIAEK	25.34	689.864	460.245	9899	68.3	YPL237W
TIFTVTPGSEQIR	37.78	724.891	483.596	7267	51.9	YLR304C
TIHLINEALDLEELQDTDLNAIALAK	36.49	1438.77	959.513	13596	92.1	YJR069C
TIIGSEDGLGVECLR	47.55	809.909	540.275	8423	59.1	YNR016C
TILATGGDDGIVNFWSLEK	22.44	1018.52	679.349	10940	87.8	YDR267C
TILSELSALEDPATNEGGVEAASEEK	20.29	1330.64	887.431	10442	84.4	YDR429C
TIQQIHEEEER	17.7	706.344	471.232	1766	18.2	YGR162W
TISTPFIEK	13.21	518.29	345.862	9947	68.6	YJR149W
TITLEVESSDTIDNVK	57.47	882.449	588.635	7761	55	YKR094C
TITPMGGFVHYGEIK	13.32	825.421	550.617	8214	57.8	YOR063W
TLAETAGLDVNEVLPNLYAAHNVTEPGAVK	36.74	1553.81	1036.21	9727	79.4	YJL008C
TLEDELEVTEGMR	57.94	761.359	507.908	8787	61.4	YLR259C
TLLALGQYQSQDPTSK	49.27	875.454	583.972	7447	53	YIL076W
TLLDYVSILDNLDLSPR	15.26	974.025	649.686	15834	107	YPL226W
TLMELLTQMDGFDNLGQTK	34.62	1078.02	719.018	13128	102.9	YOR259C
TLQEGQSEDPNFADSR	52.64	897.4	598.603	3934	31.5	YBL050W
TLQFVIQEK	35.23	553.316	369.213	7133	51.1	YNL007C
TLSDYNIQK	41.83	541.28	361.189	3508	28.9	YKR094C
TLSEYNNLLNR	30.07	668.846	446.233	6967	50.1	YPL273W
TLSSSAQTSVEIDSLFEGIDFYTSITR	77.66	1484.23	989.82	15253	117.8	YAL005C
TLSSVTQTTVEVDSLFDGEDFESSLTR	77.9	1482.2	988.472	12398	97.9	YDL229W
TLTFALADGGVPNNEGR	17.83	866.437	577.96	8443	59.2	YOR335C
TMNDEDANELIK	26.68	696.819	464.882	4953	37.7	YKL210W

TNIDNSTGQAGQANAQSANTVNNR	23.2	1223.57	816.048	1511	19.5	YNL098C
TNNPETLVALR	43.23	614.338	409.895	6457	46.9	YAL038W
TPFQLCSEVLSR	32.08	718.864	479.578	8869	61.9	YDR516C
TPGLSNATQVTDLNLTYASR	97.74	1061.54	708.031	7124	61	YNL241C
TPGPGGQAALR	43.54	512.78	342.189	1876	18.9	YCR031C
TPIGSFQGSLSSK	24.45	654.843	436.898	5869	43.3	YPL028W
TPLEPGLELTAIAK	32.67	726.919	484.948	9606	66.5	YDL126C
TPSELQEEQER	18.88	673.315	449.213	2029	19.9	YDR358W
TPSEYIQWR	49.57	590.293	393.865	6885	49.6	YLR249W
TPSIDTLDDLAQR	30.98	722.868	482.247	8281	58.2	YLR206W
TPTAAAWDSPESHIGVAK	39.79	919.458	613.307	5971	43.9	YGR155W
TPVFGICLGHQLIAR	14.93	841.464	561.312	9678	66.9	YJL130C
TQDLLLLDVAPLSLGIETAGGVMTK	45.06	1278.2	852.471	14393	111.7	YAL005C
TQDVLGENGR	32.81	544.77	363.516	2057	20	YNL178W
TQLLGADDDLNAQAQIIR	107.09	978.013	652.345	8742	61.1	YPL048W
TQLTGLQDDINEFLTGR	65.59	960.987	640.994	14021	94.9	YJL184W
TQWIDYEQCK	20.93	685.806	457.54	6017	44.2	YDR399W
TSAVAALTEVR	73.45	559.314	373.212	6202	45.4	YHL033C
TSDKPIWVLGEPK	25.13	735.404	490.605	7426	52.9	YOR230W
TSFFQALGVPTK	53.52	648.353	432.571	10630	72.9	YLR340W
TSGPIDLASLEALLGATGGVK	30.12	985.544	657.365	15016	101.5	YER089C
TSSGNEMPPQDAEGWFYK	44.24	1022.44	681.963	7044	60.4	YOL121C
TSYGWIECVGCADR	61.38	837.356	558.573	8739	61.1	YBR121C
TTEEQVENAVDR	67.17	695.826	464.22	4265	33.5	YLR354C
TTGIVLDSGDGVTHVVPIYAGFSLPHAILR	16.63	1553.34	1035.9	12342	83.9	YFL039C
TTLVANTSNMPVAAR	51.83	773.406	515.94	5155	39	YDL185W
TTPSFVAFTDTER	23.46	736.357	491.24	8231	57.9	YAL005C
TTPSFVGFTDTER	43.41	729.349	486.568	7688	54.5	YLL024C
TTPSYVAFTDTER	30.86	744.354	496.572	6491	47.1	YBL075C
TTQNPDELWEFIADSLK	76.45	1003.99	669.662	14190	110.3	YGL253W
TTVANFEPSLDYIVAK	29.5	884.462	589.977	10518	72.2	YJR109C
TTVEFTGESLR	39.53	620.314	413.879	5761	42.7	YBR127C
TTVLLDYTRPISDDPEVINK	33.28	1145.1	763.737	8763	61.2	YGL037C
TTVQVAEEAIVNAMR	19.19	816.425	544.619	12077	82.2	YFR050C
TTYVTQRPVYLGLPANLVDLNVPAK	23.24	1371.76	914.844	9707	79.3	YLR044C
TVASSGQELSVEER	100.32	746.368	497.914	3477	28.7	YER177W
TVAVAGNPTDWK	56.15	629.825	420.219	5393	40.4	YNL134C
TVAVDSVFEQNEMIDAIAVTK	29.79	1140.57	760.719	10169	82.5	YOR063W
TVAVLPPNWK	45.57	562.827	375.554	7237	51.8	YDR064W
TVESVNVIVSTYADEVLGDVQVYPAR	47.23	1412.22	941.819	14297	111	YOR133W
TVFESLDQAWSLLR	46.52	832.936	555.626	14645	99	YBR127C
TVFIQELINNIAK	55.97	751.932	501.624	14356	97.1	YJR121W
TVGAALTNDPR	45.91	557.796	372.2	2644	23.6	YPL061W
TVIFTHGVEPTVVVSSK	13.85	900.499	600.668	7000	50.3	YJR105W
TVIGEVLLEQAYGGMR	48.79	868.456	579.306	12540	85.2	YNR001C
TVLDYTIEFLDK	26.31	728.882	486.257	12856	87.2	YGR205W
TVLITGASAGIGK	54.06	594.353	396.571	5543	41.3	YMR226C
TVLVYGHYDVQPAQLEDGWDTEPFK	20.89	1454.2	969.799	11010	75.4	YFR044C
TVPFVPISGWNGDNMIEATTNAPWYK	48.25	1454.7	970.137	12124	96	YPR080W
TVPGFPLLENLNDISLK	22.43	935.52	624.016	14209	96.1	YGR061C
TVPGSSLTSVPGFFAAGDVQDSK	16.15	1134.06	756.378	10632	72.9	YDR353W
TVSQADFPGLEGVAK	38.02	759.894	506.931	7813	55.3	YIL078W
TVYVSVAAPR	25.48	531.801	354.87	4467	34.8	YPR163C
TWAPEIAQEILK	22.13	699.885	466.926	11262	77	YER134C
TWELMQELPK	44.89	637.826	425.553	10379	71.3	YOR120W
TWETYEMR	40.61	558.245	372.499	5851	43.2	YHL015W
TYAAEIAHNISAK	55.69	694.862	463.577	5434	40.7	YBL092W
TYCLQHVEK	28.15	589.287	393.194	2172	20.7	YFL045C
TYIGNLLALSISSDNLVNK	62.05	1018.06	679.04	11892	94.4	YGR180C
VAATLSPAMDILISSNFER	18.67	1018.03	679.022	11160	89.3	YCR053W
VAAVETLYQDMAAR	63.5	769.388	513.261	9789	67.6	YMR242C
VADVLSQIEAK	48.91	586.83	391.556	7515	53.5	YMR250W
VAFTVDQMR	63.89	533.771	356.183	6056	44.5	YOR133W
VAPEEHPVLLTEAPMNPK	20.09	986.514	658.012	6535	47.4	YFL039C
VASANATAAESDVAK	72.49	702.852	468.904	2094	20.3	YIL133C
VASSQATWVEVLPLTLCSHDENFK	15.85	1366.17	911.118	12112	82.4	YLR060W
VAVETGVDGVDVVIGTSK	39.65	872.97	582.316	8941	62.3	YDL131W
VAVIGDDVAVGR	42.03	585.827	390.887	5466	40.9	YML070W
VAVVAGYGDVGK	68.1	567.811	378.877	4487	34.9	YER043C
VCEFMISQLGLQK	20.03	776.897	518.267	10056	69.3	YNL244C
VCPAPCEGACTLGIIEDPVGIK	31.35	1178.57	786.05	8545	71.2	YDL171C
VDALEQETVYR	26.51	661.833	441.558	5319	40	YDL110C
VDCSELSEK	40.29	533.74	356.162	1870	18.9	YLL026W
VDDELLVAR	48.86	515.282	343.857	5693	42.2	YDR226W
VDIIANDQGNR	64.28	607.81	405.542	2983	25.7	YAL005C
VDPLVIELVTGAK	55.18	677.403	451.938	12372	84.1	YGL195W
VDTVTYDLTK	37.12	577.801	385.536	4985	37.9	YFL022C
VEEMNNIIAASR	64.3	673.84	449.563	6254	45.7	YMR194W
VEFGVLTSFAYPVIGSDEK	27.62	1029.53	686.686	11441	91.3	YGR094W
VEFSIGFER	32.77	542.277	361.854	8751	61.1	YPL160W
VEGAVGNLGNAVTVTEDGTVVTVVSTAK	35.01	1344.21	896.475	8683	72.1	YLR061W
VEGITEHVNR	18.28	577.302	385.204	1805	18.5	YBR035C
VELDALFNIAELK	33.39	737.911	492.277	13696	92.7	YPL218W
VELDDYVGLVAK	55.55	660.856	440.906	9715	67.2	YDR129C
VELTPVAIAAGR	22.35	598.853	399.571	7303	52.2	YPL091W
VENIISWGYGTPGAGAYDYIK	25.87	1137.56	758.707	9698	79.2	YLR179C
VESLGSPSGATK	45.23	566.796	378.2	1693	17.8	YDR155C
VETGVIKPGMVVTFAPAGVTTEVK	30.17	1215.67	810.782	7904	66.6	YPR080W
VEVDSFSGAK	19.21	519.759	346.842	3573	29.3	YGR148C
VFDALNDLEQLK	48.08	702.872	468.917	11021	75.4	YBR218C
VFEEEGAFIEALER	20.46	819.904	546.938	12162	82.7	YJR016C
VFLGIYYVDQIQDGVNTIK	31.5	1093.08	729.056	11573	92.2	YGR279C
VFNLPLFPTTTIGSFPQTK	64.61	1054.57	703.386	11922	94.6	YER091C
VFSLDPQYLVDDLRPEFAGYSK	43.75	1280.14	853.764	13658	92.5	YMR116C
VGDPFDESTFQGAQTSQMQLNK	26.05	1214.56	810.041	6988	60	YOR374W

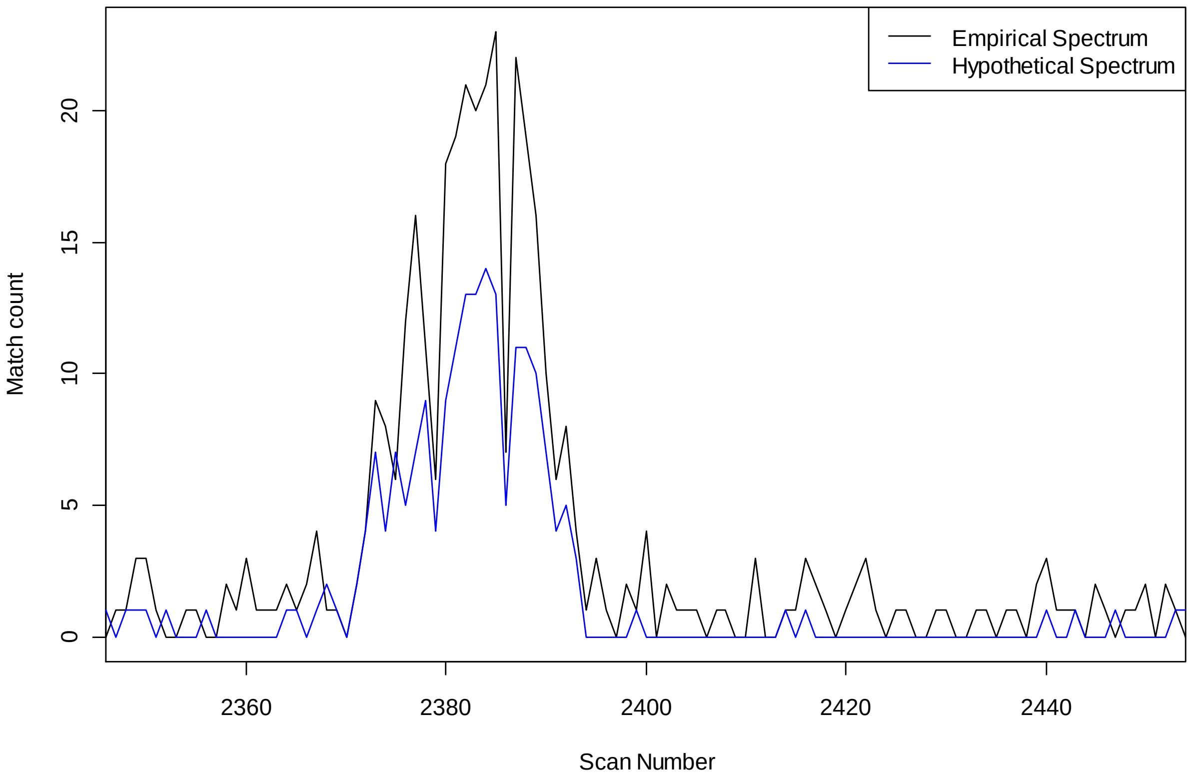
VGGASEVEVGEK	74.44	580.793	387.531	2140	20.5	YLR259C
VGHDNLVGEVIR	52.15	654.357	436.574	5560	41.4	YDL185W
VGIADTVGCANPR	31.78	665.333	443.891	4180	33	YDL131W
VGLIGSCTNSSYEDMSR	88.72	938.414	625.945	6607	47.8	YLR304C
VGQAVETVGQAGRPK	29.72	748.913	499.611	1820	18.6	YHR027C
VGQSLSIVSNDELSK	25.23	788.415	525.946	6549	47.5	YBR078W
VGSTSENITQK	48.54	582.299	388.535	1231	15	YOR204W
VIAIDINDPLAPK	44.75	689.901	460.27	9756	67.4	YBR011C
VIDDVNEEDWNLLEK	66.75	915.941	610.963	9978	68.8	YDL195W
VIDVDGNPVIEVQYLEETK	96.44	1080.56	720.707	9583	78.4	YDL229W
VIEQPITSETAMK	46.89	723.879	482.922	4677	36	YOL127W
VILFIGDGSLQLTVQEISTMIR	30.79	1217.17	811.786	17774	120.5	YLR044C
VINDAFGIEEGLMTTVHSLTATQK	43.65	1288.16	859.107	14444	97.7	YGR192C
VINDAFGIEEGLMTTVHSMTATQK	26.02	1297.14	865.093	13500	91.4	YJL052W
VISCLAELQQFEK	31.5	782.906	522.273	10008	69	YGL206C
VISDDYVTSDSGTGIVHNAPAFGEEDNAACLK	27.23	1676.77	1118.18	6727	58	YBL076C
VITLPDYPGVDADNIK	16.3	865.454	577.305	9309	64.6	YBR072W
VIYQSLEDLIDCCK	56.69	878.418	585.948	11692	79.7	YMR300C
VLDALFPCVQGGTTCIPGAFGCGK	21.19	1263.1	842.404	10128	82.2	YDL185W
VLDEVVVDNFDQK	39.3	760.386	507.259	8059	56.8	YLR259C
VLDTGGPISVPVGR	26.87	683.888	456.261	6921	49.8	YJR121W
VLEGGIVIEDR	48.54	600.335	400.559	6304	46	YML074C
VLEQLSGQTPVQSK	58.5	757.415	505.279	4333	33.9	YGR085C
VLGSVGEPISPDLWEWYHEK	24.65	1171.08	781.055	11327	77.4	YLR153C
VLLSICSLLTDANPDDPLVPEIAHIYK	69.09	1503.8	1002.87	13326	104.3	YBR082C
VLNEQVDESYGLR	72.53	761.381	507.923	5959	43.9	YER110C
VLVQDLLHPTAASEAR	43.58	860.473	573.984	7758	55	YHR021C
VNDNNDDDWNEPELK	38.52	966.398	644.601	5755	42.6	YCR088W
VNLDTDCQYAYLTGIR	74.37	951.457	634.64	9502	65.8	YKL060C
VNLENPIPIAVLDSYTPSTNEPYAR	49.01	1387.21	925.14	12696	86.2	YKL182W
VNPETGIIDYDTLEK	70.49	853.928	569.621	8343	58.6	YLR058C
VNQAIALLTIGAR	75.97	670.406	447.273	10169	70	YJR123W
VNQIGTLSESIK	48.43	644.859	430.242	6110	44.8	YGR254W
VNQNLLEDHSFINYK	20.68	917.46	611.976	7972	56.3	YLR304C
VNSSGPGSSFGELALMYNSPR	18.68	1085.52	724.013	8790	72.9	YIL033C
VNVVLGSQWGDEGK	56.19	744.378	496.588	7271	52	YNL220W
VPAINVNDSVTK	49.13	628.846	419.566	4551	35.3	YER043C
VPANFISEGLDQTR	44.81	773.897	516.267	8406	59	YBL076C
VPEQPVSVVEEAIDVAYETFK	31.82	1175.1	783.733	16627	127.6	YBR006W
VPFCPLVGSELYSVEVK	36.87	962	641.669	11585	79	YDR190C
VPFLQDISQLVR	50.91	707.906	472.273	13171	89.3	YGL195W
VPLSDNAIIEANLGK	37.51	777.43	518.623	8547	59.9	YGL076C
VPPTIAQFQYTLDR	29.9	824.938	550.295	9840	67.9	YHL033C
VPTVDVSVVDLTVK	90.4	735.924	490.952	9921	68.5	YGR192C
VQDDEVGDGTTSVTVLSAELLR	31.34	1152.58	768.724	10064	81.7	YIL142W
VQEQAILSCIEQTMVADAK	17.99	1067.53	712.022	11551	92	YDR395W
VQPVQPSQTSTYPGQGMPTPK	38.05	1114.55	743.372	4048	38	YNL007C
VQQLQQQQAQQELFQQQLQK	15.49	1235.15	823.766	5683	50.1	YNL243W
VQSEYLGIPEEGPFK	29.43	846.928	564.954	9305	64.6	YER043C
VQTVTTEDGETVK	33.61	703.854	469.572	2016	19.8	YER067W
VQVGDIVTVGQCRPISK	61.53	928.507	619.34	6375	46.4	YDR025W
VSPEVVYVAEK	36.81	610.332	407.224	5164	39	YCL030C
VSSASAAASESDVAK	87.42	690.336	460.56	1686	17.7	YNL069C
VSSVLSALEGK	69.29	545.311	363.877	8388	58.9	YOL039W
VSVEGVNVEK	42.97	530.288	353.861	3963	31.7	YLR448W
VSWGPNMKPAVSNSPSPSPSAPSLTTGLGAK	18.57	1511.77	1008.18	6579	56.9	YJL080C
VTAFVPNDGCLNFVDENDEVLLAGFGR	45.74	1484.71	990.143	14049	95.1	YGR118W
VTDGALVVVDTIEGVCVQTETVLR	71.8	1287.18	858.455	15569	105.2	YOR133W
VTNMEFQYPGTSKPQITDINFQCSLSSR	51.44	1624.77	1083.52	8110	68	YLR249W
VTTDSDGWCTFEAK	70.78	808.848	539.568	6919	49.8	YOR276W
VTVVEFQPQIGASMDGEVAK	27.51	1053.03	702.358	7612	64.5	YFL018C
VTYDITSKPPATVEWE	52.18	918.457	612.64	8598	60.2	YMR217W
VVDETDAEPK	20.53	551.767	368.18	1327	15.6	YJR025C
VVDISETSCIVELSAKPTR	16.5	1052.55	702.037	8310	58.4	YCL009C
VVDLEDAVPDSK	27.45	643.827	429.554	6230	45.5	YDL171C
VVDLIEYVAK	60.99	574.832	383.557	9694	67	YJL052W
VVDPETTLFLIASK	14.8	766.932	511.624	12332	83.8	YBR196C
VVEVCLADLQGSEDHSFR	38.7	1030.99	687.662	6708	57.8	YML063W
VVGLSSLPEIYEK	49.22	717.398	478.601	9546	66.1	YMR303C
VVGLSTLPEIYEK	41.64	724.406	483.273	9421	65.3	YOL086C
VVITAPSSSAPMFVVGVNHTK	13.33	1071.07	714.386	8447	59.3	YJL052W
VVITAPSSTAPMFVMGVNEEK	35.39	1104.06	736.374	8499	70.8	YGR192C
VVNEPTAAALAYGLEK	88.98	823.443	549.298	8819	61.6	YJR045C
VVNMEFPIDEATGK	29.7	775.382	517.257	8970	62.5	YOR361C
VVNVAVIGAGVVGSAFLDQLLAMK	43.22	1186.17	791.119	18293	124.4	YJR139C
VVNYNHLLPTR	32.69	663.37	442.582	5716	42.4	YHR010W
VVVFEDAPAGIAAGK	34.01	722.396	481.933	7561	53.7	YIL053W
VYEPLLLVGLDK	60.18	679.9	453.602	11909	81.1	YDL083C
VYYFQGGNNELGTAVGK	34.69	908.947	606.3	7594	53.9	YGL030W
WAGNANELNAAYAADGYAR	98.29	999.459	666.641	7687	54.5	YLR044C
WASLANSDVMSNIARPFLSFK	15.67	1177.6	785.404	13501	91.4	YKL081W
WEAWENLK	26.28	538.264	359.178	8029	56.6	YGR037C
WFFDASKPTLISSDSIIR	21.75	1042.05	695.033	11695	79.7	YNL160W
WGLKPYLFVLNNDGYTIEK	46.49	1135.6	757.4	10404	84.1	YLR044C
WSEVCHYIITDIPVEYGPGGDIAISGK	40.12	1488.73	992.82	11418	77.9	YLR179C
WSFEEVEVK	43.65	576.782	384.857	8837	61.7	YJR123W
WVNNILYEGAESER	34.45	840.405	560.606	8612	60.3	YLR270W
YAGEVSHDDK	45.73	560.749	374.168	832	12.5	YGR192C
YAPGTIVLYAER	16.06	676.864	451.578	8043	56.7	YNL178W
YAQDGAGIER	23.5	540.259	360.509	1739	18.1	YOR063W
YDCSSADINPIGGISK	43.81	848.896	566.266	6698	48.4	YHR074W
YDIDIDQK	26.67	505.245	337.166	4715	36.3	YDR516C
YDLEAWFPYQK	28.98	730.348	487.235	11599	79.1	YDR023W
YDNQIAVFGLDFQK	37.07	829.415	553.279	11317	77.3	YKL210W
YDSASDNVYMNAEQEEK	86.74	996.91	664.942	4941	37.7	YHR179W

YEELASLGNIIR	47.25	689.372	459.917	10143	69.8	YBR169C
YEFDGLIIVGGFEAFESLHQLER	21.85	1335.17	890.446	16321	110.3	YMR205C
YEIISQQPENVSNLSK	83.43	924.97	616.983	6536	47.4	YKL035W
YGADIVTHSATK	24.09	631.822	421.551	2399	22.1	YLR303W
YGANPHQKPAQAYVSQQDSLPFK	24.46	1287.64	858.763	5645	41.9	YMR120C
YGASAGNVGDEGGVAPNIQTAEEALDLIVDAIK	79.74	1629.31	1086.54	16781	128.8	YHR174W
YGATSTNPAK	28.02	505.251	337.17	996	13.5	YJL177W
YGCSVTDACIGWESTEQVLELLAEGVR	47.85	1521.71	1014.81	15307	118.2	YDR035W
YGEHSIEVPGAVK	25.28	693.357	462.573	4288	33.7	YIL053W
YGGVYVGTLSKPEVK	45.36	798.935	532.959	5463	40.8	YLR044C
YGHAEDFVPILESPEGK	17.77	944.46	629.976	8804	61.5	YLR438W
YGILSIDDLIHEIITVGPHFK	38.28	1190.65	794.102	17101	115.7	YGL076C
YGLENYNNECR	62.68	716.301	477.87	4074	32.4	YBL076C
YGLNHVVALIENK	21.64	735.409	490.609	8935	62.3	YHL033C
YGLNHVVSLIENK	40.87	743.407	495.94	8498	59.6	YLL045C
YGLTGEGQTVQMATLSEGQR	63.72	1063.51	709.344	6149	53.6	YER036C
YGPLLVDIIDPAK	16.58	707.403	471.938	12205	83	YKL127W
YGSFIVDALVDYK	71.82	745.382	497.257	12297	83.6	YNR016C
YGVIVHDIATPNLIDR	30.43	898.489	599.328	8531	59.8	YDL055C
YGVSITDACIGWETTEDVLR	33.25	1143.04	762.363	10536	85	YBR249C
YHGEVEIGCDGSVVEYYPGFR	17.49	1217.04	811.699	8989	62.6	YCL040W
YHIEEEGSR	45.89	560.257	373.84	1446	16.3	YCR012W
YIEDDQEPVQGGIFALSWLDSQK	14.39	1319.64	880.094	12282	97.1	YMR092C
YIEWLSSPK	20.63	561.795	374.866	8252	58	YPL226W
YINEGNSVGSVNFPEVSLK	14.92	1027.02	685.013	7682	65	YIL074C
YINESVNEFSR	34.35	679.323	453.218	5238	39.5	YIL041W
YIPGEPEFLPFVNELPK	41.02	995.022	663.684	13724	92.9	YDR023W
YIQTEQQIEIPEGVTVSIK	16.07	1088.08	725.723	8003	67.3	YNL067W
YIQTEQQIEVPEGVTVSIK	38.09	1081.07	721.051	7240	61.8	YGL147C
YLAAYLLLNAAGNTPDATK	26.5	990.525	660.686	11927	81.2	YOL039W
YLAAYLLLVQGGNAAPSAADIK	38.7	1110.11	740.407	12624	85.7	YDR382W
YLAEFSSGDAR	79.7	608.286	405.86	4893	37.4	YDR099W
YLDGMFAWTLYDAK	32.19	847.4	565.269	13365	90.6	YPR145W
YLGLKPGSIDAISQVINIAK	41.69	1050.61	700.74	12057	82	YKL182W
YLIENFSAQLQNPEGK	86.35	925.968	617.648	9594	66.4	YGR180C
YLPGITLPDNLVANPDLIDSVK	41.73	1184.14	789.765	11405	91	YDL022W
YLSEIDLPK	31.77	539.295	359.866	7261	51.9	YFL045C
YLTPSSLVAGNPK	26.54	673.869	449.582	6753	48.8	YDR129C
YNEIVNLTLPDGTVR	51.7	852.452	568.637	9711	67.1	YBR127C
YNLDYYLEVVEK	39.08	774.385	516.592	11651	79.4	YBR218C
YNPDDTIAPPQDATEESQTK	13.29	1110.5	740.669	3691	35.5	YOR230W
YNSDAQTYVLESTLEGHSDWVR	68.65	1285.59	857.398	10600	72.7	YLR208W
YPGQLNSDLR	31.2	581.796	388.2	4438	34.6	YFL037W
YPIEHGIVTNWDDMEK	64.02	973.951	649.637	8393	58.9	YFL039C
YPIVSIEDPFAEDDWEAWSHFFK	44.53	1414.65	943.434	15746	106.4	YGR254W
YPMGVVTSDIDK	22.58	662.826	442.22	11146	76.2	YBL020W
YQGYAEDVR	25.45	550.754	367.505	2773	24.4	YIL078W
YSYGQDLVSFYQDGPGYDMIR	28.22	1237.55	825.37	10476	84.6	YBR092C
YTNPVVIQGAGAGAAVTAAGVLGDVIK	102.22	1256.69	838.13	11489	91.6	YJR139C
YTVSFIEGDGIGPEISK	45.45	906.457	604.64	9856	68.1	YOR136W
YVDPNVLPETESLALVIDR	86.42	1072.07	715.048	10897	87.5	YKL152C
YVHIIEDSPVFPVIMDSK	23.32	1045.04	697.027	9172	75.6	YLR060W
YWGTPIPLWVSDDFEEVVCVGSIK	15.45	1398.68	932.791	15147	117	YBL076C
YYNAVNPFEFMEDVATAGK	84.39	1083.5	722.666	13284	104	YGR180C

Appendix Figure B.3

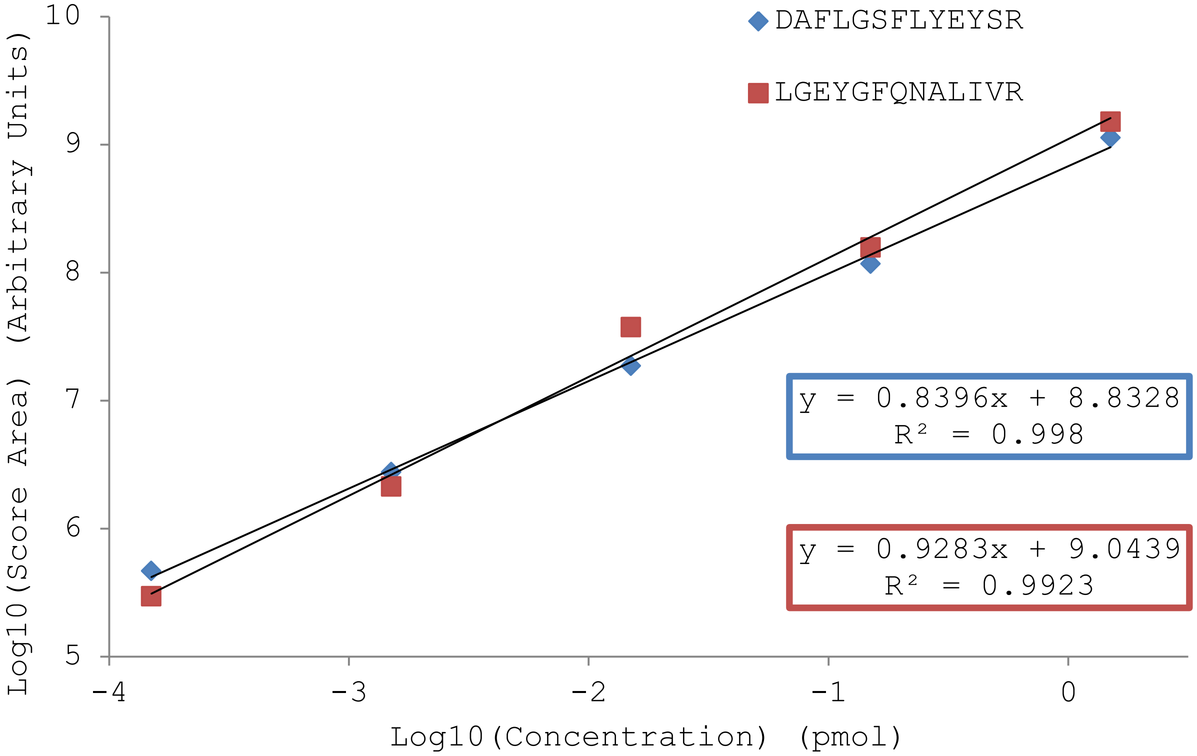


Appendix Figure B.4



Appendix Figure B.3 is a score chromatogram comparison of hypothetical vs. spectral library FT-ARM scored data. The calculation was normalized using the scalar dot-product. This shows that the FT-ARM process is compatible with spectral library data, with the caveat that it is acquired using a high resolution mass analyzer. In Appendix Figure 4, it is shown the difference in the number of matching peaks between the spectral data and the hypothetical spectrum. It is clear that the spectral data has approximately double the number of matching peaks for the peptide of interest. The peptide shown from yeast ENO_2, AVDDFLISLDGTANK.

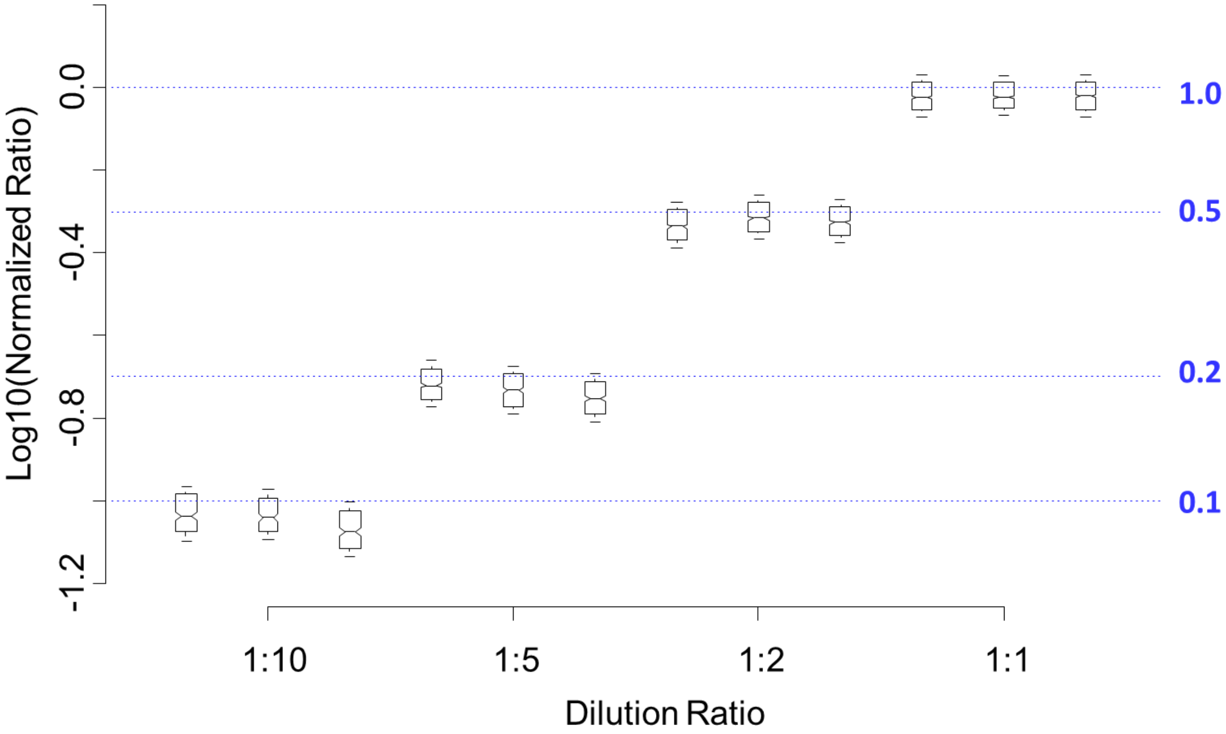
Appendix Figure B.5



Appendix Figure 5 was generated by processing the data presented in 6B without any normalization and by tracking accurate fragment masses with retention time constraints. This approach has not been exploited in any of the data presented in the manuscript simply because the authors performed this analysis subsequent to the review process. We intend to pursue this approach as it allows us to gain access to quantitative information at lower concentration, even levels that were only achievable with the triple quadrupole previously, and appears to have greater linearity.

Appendix Figure 6 was generated by normalizing each peptide score area to a reference acquisition in which no dilution was made or yeast background present. The data was then plotted on the log scale to indicate that relative error contributions and medians are centered very near to the expected ratios. This figure was generated subsequent to the review process.

Supplemental Figure B.6



1. Krokhin OV & Spicer V (2009) Peptide retention standards and hydrophobicity indexes in reversed-phase high-performance liquid chromatography of peptides. *Anal Chem* 81(22):9522-9530.

Appendix C: Supporting information for ReACT

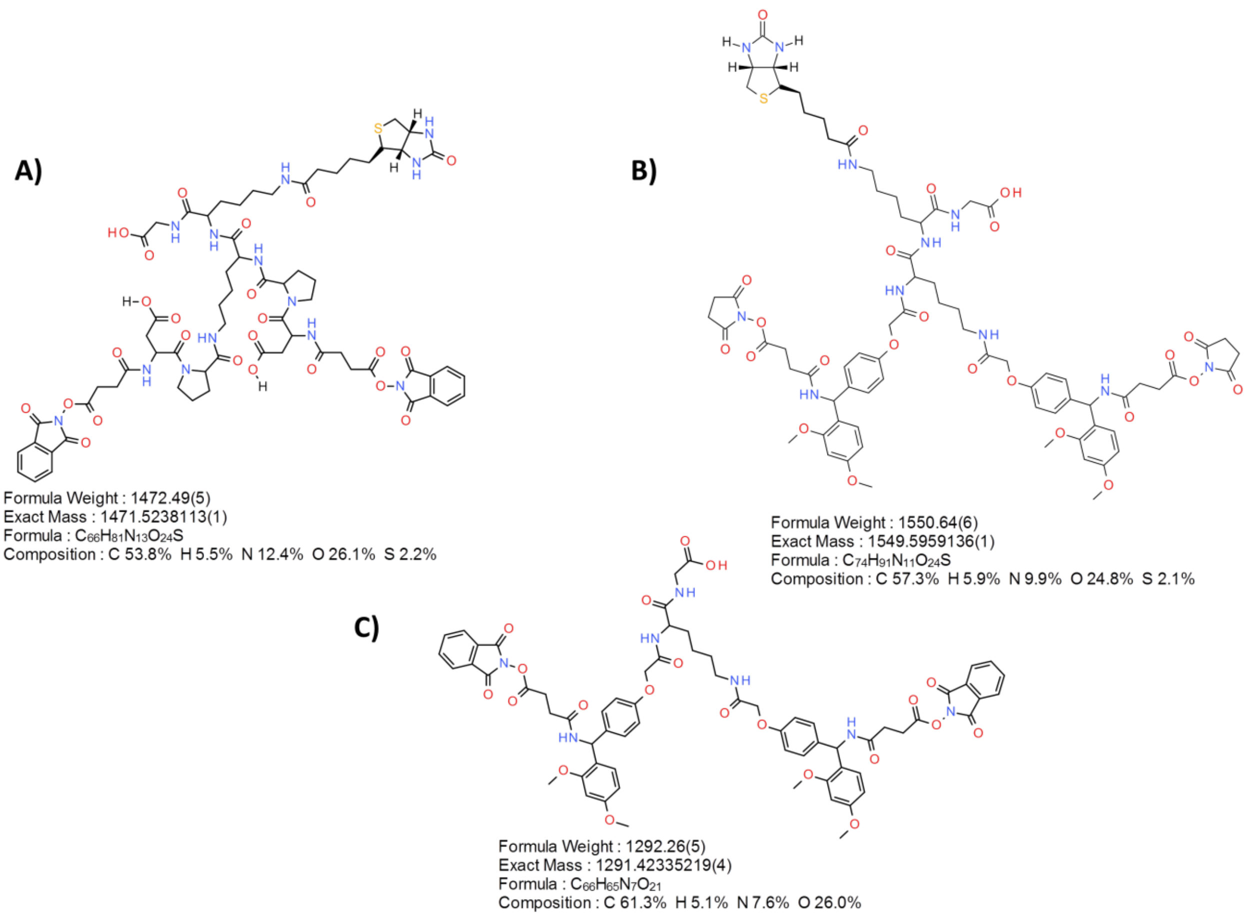
Singly charged ions often yield low quality peptide fragmentation patterns when analyzed with ion trap-based instrumentation. The REACT algorithm includes the ability to target higher charge state released peptides even if the signal-to-noise ratio of higher charge state ions is too low to be selected or even observable within the mass spectrum. It has been shown previously that quadrupole ion storage devices are prone to exclusion of low abundance ions if simultaneously accumulated with more abundant ions (1, 2). Instrument duty cycle has been reduced as mentioned previously. The analysis time liberated by using the real-time targeted approach can be utilized here in the accumulation of low abundance ions. The targeting of low abundance, higher charge ions in some cases results in a cross-linked peptide identification, which would otherwise not be obtainable with 1+ fragmentation patterns alone. This targeting feature of REACT is illustrated in **Appendix Figure C.2**, where the 2+ ion for the released peptide is observed at a low intensity near the noise level, while the 1+ ion is the base peak in the spectrum. By specifically targeting the 2+ ion for MS^3, a fragmentation spectrum useful for peptide sequence identification was acquired. However, MS^3 analysis of the 1+ ion of this peptide did not yield sufficient fragment ion information to obtain sequence identification.

A set of purified proteins were labeled to illustrate that REACT is useful for real-time analysis of PIR cross-linked peptides. The data resultant from this set of experiments is presented in **Appendix Table C.1**. Each protein is displayed with the number of fully identified relationships and unique relationships. Unique relationships are defined here as meaning two unique peptide sequences fully identified ($E<0.1$). An unambiguous α-β hemoglobin cross-link was observed as well as unambiguous homodimeric cross-links supporting protein dimerization of ribonuclease A and carbonic anhydrase. The presence of concentrated tryptic peptides from each protein, approximately 100 times more abundant than cross-linked products, provided a more appropriate test for the algorithm. Some examples within the data show cross-linked peptide products were identified with a signal-to-noise ratio of ~2. This illustrates the ability of ReACT to extract useful information, even from low intensity ions.

One important feature of REACT is that the algorithm is customizable for use with any mass spectrometry cleavable cross-linker including linkers with mono, bi, or higher order CID cleavage sites. To demonstrate this flexibility we analyzed a digest of Ribonuclease A (RNase A) sample that had been cross-linked using two different PIR molecules, 2Rink and BDP (3, 4). For this sample the respective reporter masses were entered into REACT so that ions matching either the mass relationship for 2Rink or for BDP would be identified as cross-linked peptide pairs and the released peptide ions would be selected for MS^3 analysis. The cross-linked peptide pairs from both 2Rink and BDP are listed in **Appendix Table C.S2**. If the 2Rink RNase A sample was run alone we detected 8 fully identified cross-linked relationships, 5 of which are unique. When we mixed the BDP and 2Rink labeled RibA digests in equimolar ratios we detected a total of four fully identified cross-linked products with 3 unique. Of the four, two are obtained from BDP and two are obtained from 2Rink. All four share a single cross-linking site with a different second site. One pair overlaps between the two linkers. Although this manuscript has focused on the initial description and application of REACT, one could employ REACT for analysis of a sample with varying linker arm distances to achieve finer granularity in distance constraints for protein topologies.

In **Supplemental Figure 3A**, the mass accuracy of all high confidence fully identified cross-links(<5% FDR) within E. coli is presented. From these data it is readily apparent that relationship mass error of identified species is significantly narrower than the applied 20 ppm threshold. To try understand better how mass accuracy effects PIR relationship false discovery, we conducted performed a Monte Carlo simulation in which we search previously acquired ReACT MS^2 data on a real E. coli sample against randomized reporter masses. The Figure 3B shows that when considering 1000 random reporter masses per mass accuracy threshold the rate relationship false discovery per MS^2 queried. We noticed that at 20 ppm we obtained approximately 5% false discoveries at this mass accuracy. But even at this relatively low rate, we still have to identify both MS^3 acquired at <5% FDR to obtain a completely false identification that would meet our cut-off criteria.

Reproducibility in using ReACT is comparable to intensity driven sampling processes like data-dependent acquisition (DDA). We found the reproducibility of fully identified unique cross-links between two technical replicates to be ~70% in our E. coli analysis(**Appendix Figure C.4**). The biological reproducibility of the overall cross-linking methodology as surveyed by the same metric, fully identified unique cross-links, is approximately 30-35%. This reproducibility includes all sources of variance, which includes, but is not limited to cell growth, lysis, effective cross-linker concentration, free-amine in labeling solution during labeling, and three separate stages of purification.

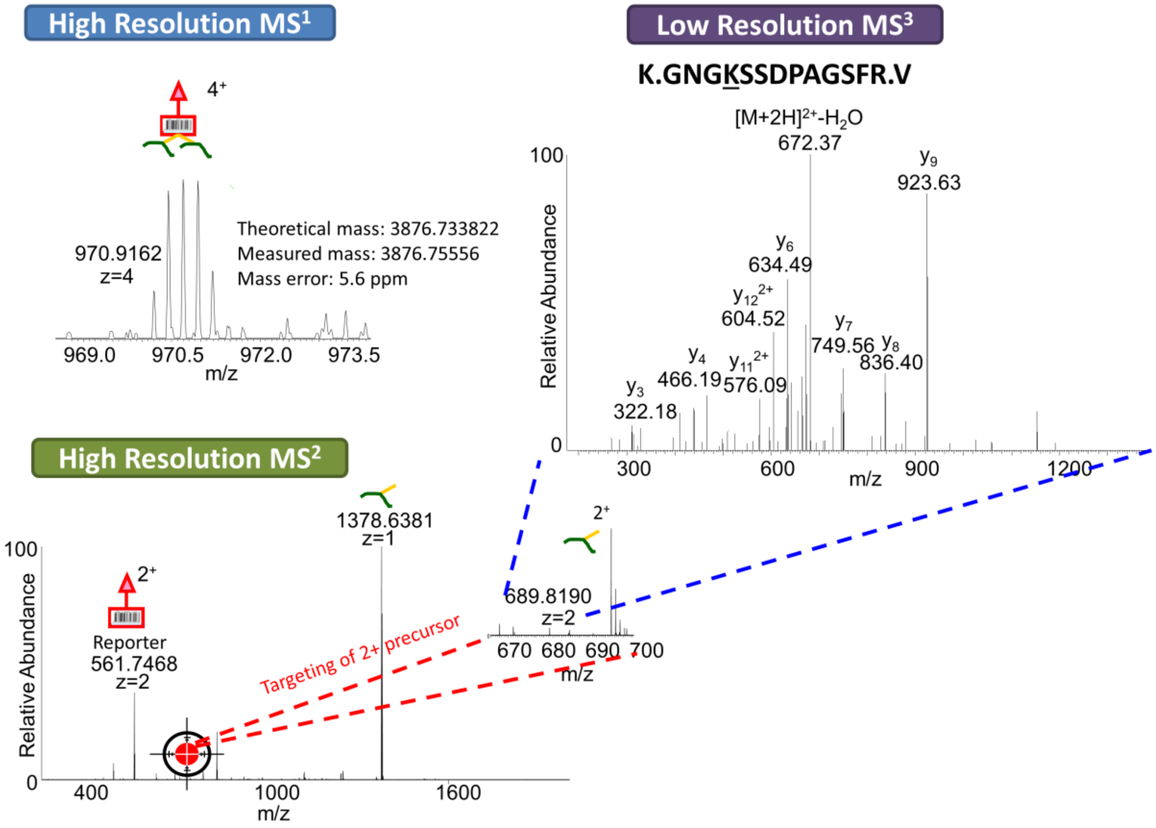


Formula Weight : 1472.49(5)
Exact Mass : 1471.5238113(1)
Formula : $C_{66}H_{81}N_{13}O_{24}S$
Composition : C 53.8% H 5.5% N 12.4% O 26.1% S 2.2%

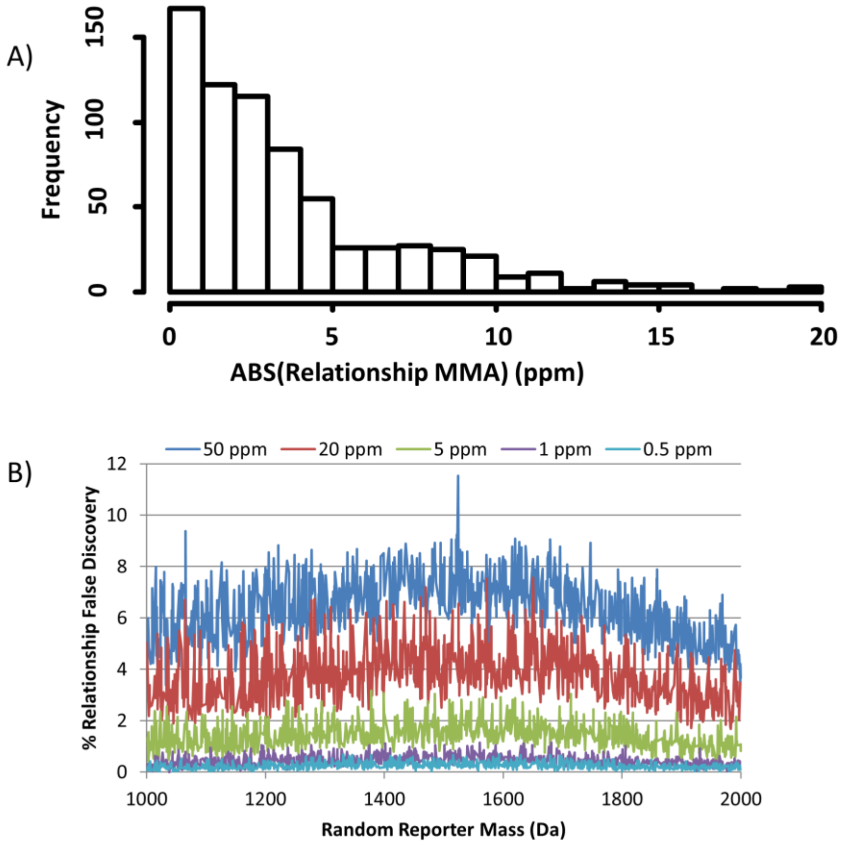
Formula Weight : 1550.64(6)
Exact Mass : 1549.5959136(1)
Formula : $C_{74}H_{91}N_{11}O_{24}S$
Composition : C 57.3% H 5.9% N 9.9% O 24.8% S 2.1%

Formula Weight : 1292.26(5)
Exact Mass : 1291.42335219(4)
Formula : $C_{66}H_{65}N_{7}O_{21}$
Composition : C 61.3% H 5.1% N 7.6% O 26.0%

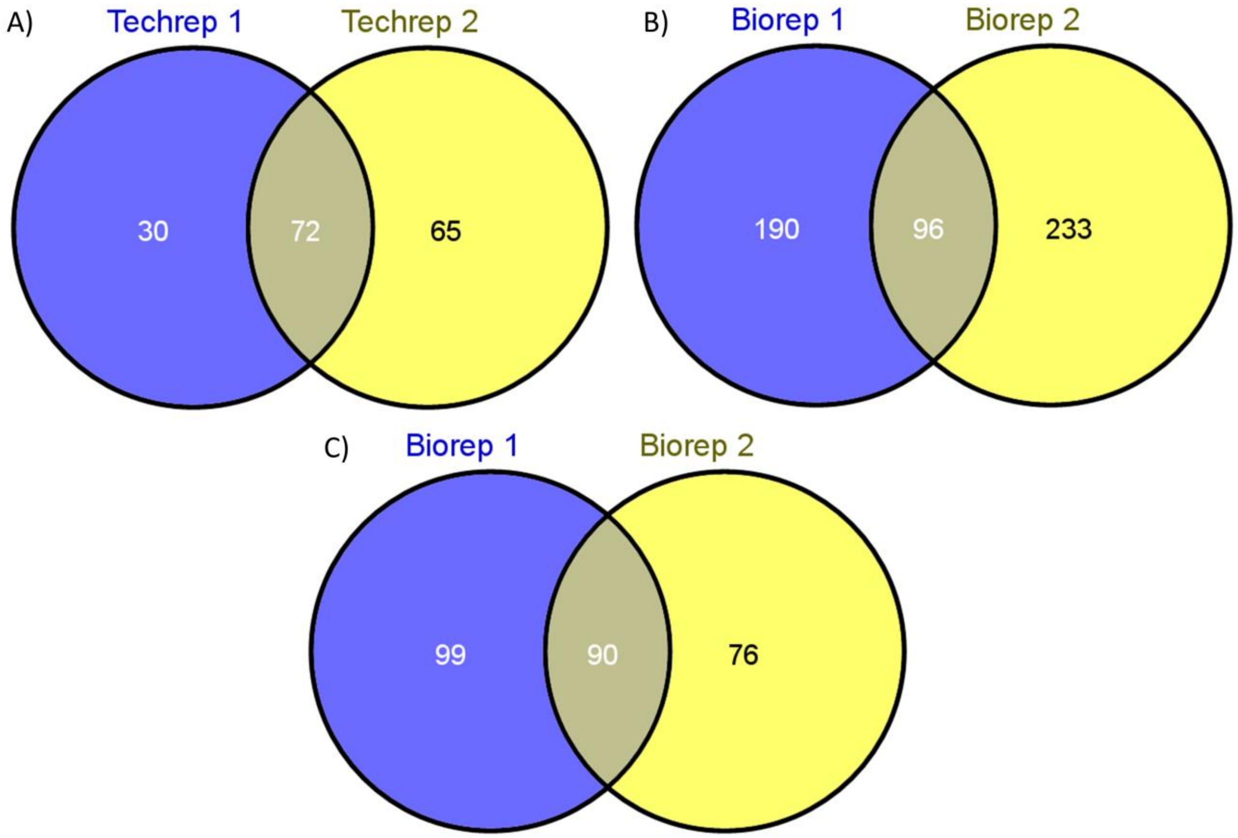
Appendix Figure C.1. Protein interaction reporter (PIR) molecules which have been used in this study. **A)** Biotin Aspartate Proline N-Hydroxyphlalamide (BDP-NHP) **B)** Biotin Rink N-Hydroxysuccinimide (BRink-NHS) **C)** Rink N-Hydroxysuccinimide (2Rink-NHS).



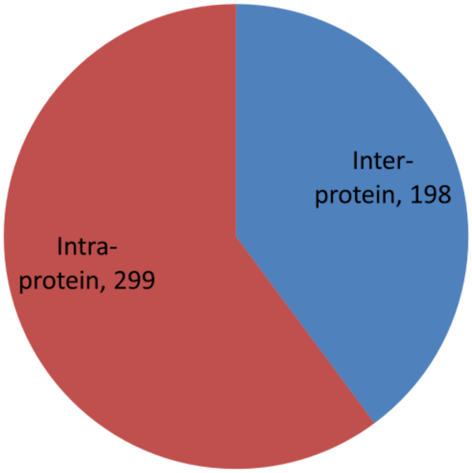
Appendix Figure C.2. REACT algorithm permits targeting of 2+ or greater low abundance peptide cleavage products to increase peptide identification probability. Example presented here includes the MS, MS2, and MS3 of a cross-linked peptide pair.



Appendix Figure C.3. A) Histogram of relationship mass error determined by ReACT for both E. coli B) Relationship false discovery rate estimated post acquisition by randomizing reporter mass and search all acquired MS^2 spectra for an entire run.



Appendix Figure C.4. Venn diagram showing overlapping identifications across technical and biological replicates. A) Technical reproducibility between two LC-ReACT acquisitions(80 mM salt fraction) B) Biological reproducibility between two separate *E. coli* PIR cross-linked samples C) Reproducibility of proteins found within identified cross-linked relationships



Appendix Figure C.5. The number of inter- and intra- protein cross-links found in the *E. coli* cellular cross-linking experiments.

1. Belov ME*, et al.* (2001) Dynamic range expansion applied to mass spectrometry based on data-dependent selective ion ejection in capillary liquid chromatography fourier transform ion cyclotron resonance for enhanced proteome characterization. *Anal Chem* 73(21):5052-5060.

2. Bruce JE, Anderson GA, & Smith RD (1996) "Colored" noise waveforms and quadrupole excitation for the dynamic range expansion of Fourier transform ion cyclotron resonance mass spectrometry. *Anal Chem* 68(3):534-541.

3. Tang X, Munske GR, Siems WF, & Bruce JE (2005) Mass spectrometry identifiable cross-linking strategy for studying protein-protein interactions. *Anal Chem* 77(1):311-318.

4. Zheng C*, et al.* (2011) Cross-linking Measurements of In Vivo Protein Complex Topologies. *Mol Cell Proteomics* 10(10):M110 006841.

Appendix Table C.1: Purified protein cross-linked sites

ms3 pep1	ms3 pep2	ms3 prot1	ms3 prot2
IWC[160.03]K[325.13]DDQNPHSSNIC[160.03]NISC[160.03]DK	K[325.13]ILDK	sp|P00711|LALBA_BOVIN	sp|P00711|LALBA_BOVIN
K[325.13]ILDK	VGINYWLAHK[325.13]ALC[160.03]SEK	sp|P00711|LALBA_BOVIN	sp|P00711|LALBA_BOVIN
EQLTK[325.13]C[160.03]EVFR	VGINYWLAHK[325.13]ALC[160.03]SEK	sp|P00711|LALBA_BOVIN	sp|P00711|LALBA_BOVIN
ALC[160.03]SEK[325.13]LDQWLC[160.03]EK	EQLTK[325.13]C[160.03]EVFR	sp|P00711|LALBA_BOVIN	sp|P00711|LALBA_BOVIN
EQLTK[325.13]C[160.03]EVFR	LDQWLC[160.03]EK[325.13]L	sp|P00711|LALBA_BOVIN	sp|P00711|LALBA_BOVIN
ELK[325.13]DLK	LDQWLC[160.03]EK[325.13]L	sp|P00711|LALBA_BOVIN	sp|P00711|LALBA_BOVIN
ALC[160.03]SEKLDQWLC[160.03]EK[325.13]L	EQLTK[325.13]C[160.03]EVFR	sp|P00711|LALBA_BOVIN	sp|P00711|LALBA_BOVIN
ALC[160.03]SEK[325.13]LDQWLC[160.03]EKL	EQLTK[325.13]C[160.03]EVFR	sp|P00711|LALBA_BOVIN	sp|P00711|LALBA_BOVIN
LDQWLC[160.03]EK[325.13]L	VGINYWLAHK[325.13]ALC[160.03]SEK	sp|P00711|LALBA_BOVIN	sp|P00711|LALBA_BOVIN
K[325.13]ETAAAK	K[325.13]ETAAAK	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
K[325.13]ETAAAK	SRNLTK[325.13]DR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
K[325.13]ETAAAK	K[325.13]SR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
K[325.13]ETAAAK	NLTK[325.13]DR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
K[325.13]ETAAAK	MK[325.13]SR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
KETAAAK[325.13]FER	NLTK[325.13]DR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
KETAAAK[325.13]FER	SRNLTK[325.13]DR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
ETGSSK[325.13]YPNC[160.03]AYK	SRNLTK[325.13]DR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
ETAAAK[325.13]FER	SRNLTK[325.13]DR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
K[325.13]ETAAAK	QHMDSSTSAASSSNYC[160.03]NQMMK[325.13]SR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
ETAAAK[325.13]FER	NLTK[325.13]DR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
ETGSSKYPNC[160.03]AYK[325.13]TTQANK	NVAC[160.03]K[325.13]NGQTNC[160.03]YQSYSTMSITDC[160.03]R	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
C[160.03]K[325.13]PVNTFVHESLADVQAVC[160.03]SQK	K[325.13]ETAAAK	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
C[160.03]K[325.13]PVNTFVHESLADVQAVC[160.03]SQK	NLTK[325.13]DR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN
HK[325.13]IPIK	KGHHEAELK[325.13]PLAQSHATK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
GHHEAELK[325.13]PLAQSHATK	HK[325.13]IPIK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
FDK[325.13]FK	GHHEAELKPLAQSHATK[325.13]HKIPIK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
FDKFK[325.13]HLK	HK[325.13]IPIK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
ASEDLKK[325.13]	FDK[325.13]FK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
HK[325.13]IPIK	NDIAAK[325.13]YK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
K[325.13]GHHEAELK[325.13]	PLAQSHATK[325.13]HKIPIK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
FK[325.13]HLK	LFTGHPETLEK[325.13]FDK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
K[325.13]HGTVVLTALGGILK	K[325.13]KGHHEAELKPLAQSHATK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
HGTVVLTALGGILK[325.13]K	K[325.13]GHHEAELKPLAQSHATK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
KK[325.13]GHHEAELKPLAQSHATK	K[325.13]HGTVVLTALGGILK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
FDKFK[325.13]HLK	YK[325.13]ELGFQG	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
FDKFK[325.13]HLK	K[325.13]HGTVVLTALGGILKK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
FK[325.13]HLK	K[325.13]HGTVVLTALGGILKK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
FDKFK[325.13]HLK	K[325.13]HGTVVLTALGGILK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
ASEDLKK[325.13]HGTVVLTALGGILK	FDKFK[325.13]HLK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE

FDK[325.13]FK	K[325.13]HGTVVLTALGGILKK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
K[325.13]HGTVVLTALGGILKK	LFTGHPETLEKFDK[325.13]FK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
HKIPIK[325.13]YLEF	YK[325.13]ELGFQG	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
HK[325.13]IPIKYLEFISDAIIHVLHSK	LFTGHPETLEK[325.13]FDK	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
ASEDLK[325.13]K	GLSDGEWQQVLNVWGK[325.13]VEADIAGHGQEVLIR	sp|P68082|MYG_HORSE	sp|P68082|MYG_HORSE
AHGK[325.13]K	GNPK[325.13]VK	sp|P68871|HBB_HUMAN	sp|P68871|HBB_HUMAN
K[325.13]VLGAFSDGLAHLDNLK	VK[325.13]AHGK	sp|P68871|HBB_HUMAN	sp|P68871|HBB_HUMAN
VHLTPEEK[325.13]SAVTALWGK	VVAGVANALAHK[325.13]YH	sp|P68871|HBB_HUMAN	sp|P68871|HBB_HUMAN
FFESFGDLSTPDAVM[147.04]GNPK[325.13]VK	K[325.13]VLGAFSDGLAHLDNLK	sp|P68871|HBB_HUMAN	sp|P68871|HBB_HUMAN
FFESFGDLSTPDAVMGNPK[325.13]VK	K[325.13]VLGAFSDGLAHLDNLK	sp|P68871|HBB_HUMAN	sp|P68871|HBB_HUMAN
AQVKGHGK[325.13]K	VLGAFSDGLAHLDNLK[325.13]GTFATLSELHC[160.03]DK	sp|P69905|HBA_HUMAN	sp|P68871|HBB_HUMAN
AAWGK[325.13]VGAHAGEYGAEALER	LLGNVLVC[160.03]VLAHHFGK[325.13]EFTPPVQAAYQK	sp|P69905|HBA_HUMAN	sp|P68871|HBB_HUMAN
VVAGVANALAHK[325.13]YH	VVAGVANALAHK[325.13]YH	sp|P68871|HBB_HUMAN	sp|P68871|HBB_HUMAN
VDPVNFK[325.13]LLSHC[160.03]LLVTLAAHLPAEFTPAVHASLDK	VLSPADK[325.13]TNVK	sp|P69905|HBA_HUMAN	sp|P69905|HBA_HUMAN
GGK[325.13]HK	GK[325.13]K	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
GGK[325.13]HK	K[325.13]ATNE	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
KK[325.13]TER	K[325.13]IFVQK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
AGIK[325.13]K	K[325.13]TER	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
GGK[325.13]HK	GKK[325.13]IFVQK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
GKK[325.13]IFVQK	KK[325.13]TER	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]K	K[325.13]YIPGTK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]TER	K[325.13]YIPGTK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]ATNE	K[325.13]TGQAPGFTYTDANKNK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
GGK[325.13]HKTGPNLHGLFGR	GKK[325.13]IFVQK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
GGK[325.13]HKTGPNLHGLFGR	K[325.13]ATNE	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]TER	M[147.04]IFAGIKK[325.13]	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]TER	M[147.04]IFAGIK[325.13]K	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
GGKHK[325.13]TGPNLHGLFGR	K[325.13]IFVQK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]YIPGTK	MIFAGIK[325.13]KK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]YIPGTK	MIFAGIKKK[325.13]	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]TER	MIFAGIK[325.13]K	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]YIPGTK	M[147.04]IFAGIK[325.13]K	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]IFVQK	MIFAGIK[325.13]KK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]IFVQK	MIFAGIK[325.13]K	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]IFVQK	M[147.04]IFAGIK[325.13]K	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
HK[325.13]TGPNLHGLFGR	K[325.13]IFVQK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]YIPGTK	MIFAGIK[325.13]K	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
EDLIAYLK[325.13]K	K[325.13]TGQAPGFTYTDANKNK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
EETLMEYLENPK[325.13]K	K[325.13]KTER	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
EDLIAYLK[325.13]K	K[325.13]TGQAPGFTYTDANK	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
K[325.13]TEREDLIAYLK	MIFAGIK[325.13]K	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE

EETLMEYLENPK[325.13]KYIPGTK	MIFAGIKK[325.13]K	sp|P00004|CYC_HORSE	sp|P00004|CYC_HORSE
M[147.04]EK[325.13]GQIVGR	SPIK[325.13]VVGLSTLPEIYEK	sp|P00330|ADH1_YEAST	sp|P00330|ADH1_YEAST
YDDSQDK[325.13]	DDSQDK[325.13]	sp|P00921|CAH2_BOVIN	sp|P00921|CAH2_BOVIN

Appendix Table C.2: Multiple cross-linkers applied to Ribonuclease A

ms3 pep1	**ms3 pep2**	**ms3 prot1**	**ms3 prot2**	**Cross-linker**
ETGSSKYPNCAYK	NLTKDR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN	BDP
ETAAAKFER	NLTKDR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN	BDP
ETAAAKFER	NLTKDR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN	2RINK
CKPVNTFVHESLADVQAVCSQK	NLTKDR	sp|P61823|RNAS1_BOVIN	sp|P61823|RNAS1_BOVIN	2RINK

Appendix Table C.3: High confidence *E. coli* cross-linked sites

ms3 pep1	ms3 pep2	ms3 prot1	prot1 red	ms3 prot2	prot2 red
AEFEK[325.13]AAASR	LDQLPADK[325.13]K	sp|P00448|SODM_ECOLI	0	sp|P00448|SODM_ECOLI	0
INLDK[325.13]IHR	K[325.13]LLNEAK	sp|P00452|RIR1_ECOLI	0	sp|P77434|YFDZ_ECOLI	0
INLDK[325.13]IHR	VDILAK[325.13]DR	sp|P00452|RIR1_ECOLI	0	sp|P76481|YFBK_ECOLI	0
GYVSIK[325.13]ASK	QLEGK[325.13]YLVQNR	sp|P00452|RIR1_ECOLI	0	sp|P00452|RIR1_ECOLI	0
DLLTAYK[325.13]FGVK	FPSGK[325.13]VPMQQLLK	sp|P00452|RIR1_ECOLI	0	sp|P00452|RIR1_ECOLI	0
K[325.13]AEQYLLENETTK	K[325.13]AEQYLLENETTK	sp|P00509|AAT_ECOLI	0	sp|P00509|AAT_ECOLI	0
NAGFINK[325.13]R	YVDEQAPWVVAK[325.13]QEGR	sp|P00959|SYM_ECOLI	0	sp|P00959|SYM_ECOLI	0
TLDAAAALAAANK[325.13]R	VSNILAK[325.13]SDEVLSDR	sp|P00961|SYGB_ECOLI	0	sp|P00961|SYGB_ECOLI	0
IK[325.13]FAEHHQTGNK	K[325.13]LNLLVTDK	sp|P00962|SYQ_ECOLI	1	sp|P00962|SYQ_ECOLI	0
TK[325.13]HAVTEASPMVK	nM[147.04]R	sp|P02358|RS6_ECOLI	0	sp|P02358|RS6_ECOLI	0
K[325.13]ILPDPK	K[325.13]VGLR	sp|P02359|RS7_ECOLI	0	sp|P0A7X3|RS9_ECOLI	0
GQK[325.13]SR	QK[325.13]R	sp|P02413|RL15_ECOLI	0	sp|P0AD65|PBP2_ECOLI	24
K[325.13]AAITAEIR	VTK[325.13]GAR	sp|P02413|RL15_ECOLI	0	sp|P02413|RL15_ECOLI	0
GIGSGLGK[325.13]TGGR	GQK[325.13]SR	sp|P02413|RL15_ECOLI	0	sp|P02413|RL15_ECOLI	0
GHK[325.13]GQK	GIGSGLGK[325.13]TGGR	sp|P02413|RL15_ECOLI	0	sp|P02413|RL15_ECOLI	0
AGK[325.13]R	GHK[325.13]GQK	sp|P02413|RL15_ECOLI	0	sp|P02413|RL15_ECOLI	5
K[325.13]AGEGAK	LSK[325.13]EEAR	sp|P02925|RBSB_ECOLI	0	sp|P23882|FMT_ECOLI	0
IAGDYIAK[325.13]K	LVVK[325.13]Q	sp|P02925|RBSB_ECOLI	5	sp|P02925|RBSB_ECOLI	0
GEK[325.13]VQAK	GVETADK[325.13]VLK	sp|P02925|RBSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
K[325.13]AGEGAK	YPVDLK[325.13]LVVK	sp|P02925|RBSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
DGAQK[325.13]EADK	IAGDYIAK[325.13]K	sp|P02925|RBSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
IAGDYIAK[325.13]K	YPVDLK[325.13]LVVK	sp|P02925|RBSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
AVNDGK[325.13]LAATIAQLPDQIGAK	LVVK[325.13]Q	sp|P02925|RBSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
AVNDGK[325.13]LAATIAQLPDQIGAK	K[325.13]AGEGAK	sp|P02925|RBSB_ECOLI	6	sp|P02925|RBSB_ECOLI	0
GEK[325.13]VQAK	LAATIAQLPDQIGAK[325.13]GVETADK	sp|P02925|RBSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
AVNDGK[325.13]LAATIAQLPDQIGAK	IAGDYIAK[325.13]K	sp|P02925|RBSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
QATK[325.13]GEVVSHIASDNVLGGK	VQAK[325.13]YPVDLK	sp|P02925|RBSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
GEGFQQAVAAHK[325.13]FNVLASQPADFDR	IAGDYIAK[325.13]K	sp|P02925|RBSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
ILLINPTDSDAVGNAVK[325.13]MANQANIPVITLDR	QATK[325.13]GEVVSHIASDNVLGGK	sp|P02925|RBSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
FLK[325.13]GQGQGWITAEYGM[147.04]LPR	nMAHRPR	sp|P03842|RNPH_ECOLI	0	sp|P12996|BIOB_ECOLI	0
AHVIK[325.13]SHHNVGGLPK	K[325.13]LIGR	sp|P04079|GUAA_ECOLI	0	sp|P0AER0|GLPF_ECOLI	0
AK[325.13]HAIR	VYTGK[325.13]VTR	sp|P05055|PNP_ECOLI	0	sp|P05055|PNP_ECOLI	0
AK[325.13]HAIR	IHTIK[325.13]INPDK	sp|P05055|PNP_ECOLI	0	sp|P05055|PNP_ECOLI	0
K[325.13]FQYGQHTVTLETGMMAR	nMLNPIVR	sp|P05055|PNP_ECOLI	0	sp|P05055|PNP_ECOLI	0
IAEM[147.04]EAM[147.04]K[325.13]R	IK[325.13]ELAVK	sp|P05704|MCP3_ECOLI	0	sp|P0AFG6|ODO2_ECOLI	0
K[325.13]HAPLR	TNEK[325.13]GYIVVDK	sp|P06715|GSHR_ECOLI	0	sp|P06715|GSHR_ECOLI	0
IHTSYENVLGK[325.13]NNVDVIK	VYK[325.13]SSFTAMYTAVTTHR	sp|P06715|GSHR_ECOLI	0	sp|P06715|GSHR_ECOLI	0
LK[325.13]LR	VAK[325.13]R	sp|P06846|EBGR_ECOLI	0	sp|P16916|RHSA_ECOLI	0
IQK[325.13]ISGANLSR	VK[325.13]GTGR	sp|P06959|ODP2_ECOLI	0	sp|P06959|ODP2_ECOLI	0
EFGVNLAK[325.13]VK	IQK[325.13]ISGANLSR	sp|P06959|ODP2_ECOLI	0	sp|P06959|ODP2_ECOLI	0
EFGVNLAK[325.13]VK	K[325.13]FTSSLVAPFVR	sp|P06959|ODP2_ECOLI	0	sp|Q9JMR6|YUAY_ECOLI	0

EDVQAYVK[325.13]EAIK	IQK[325.13]ISGANLSR	sp|P06959|ODP2_ECOLI	0	sp|P06959|ODP2_ECOLI	0
IQK[325.13]ISGANLSR	VDFSK[325.13]FGEIEEVELGR	sp|P06959|ODP2_ECOLI	0	sp|P06959|ODP2_ECOLI	0
AEAPAAAPAAK[325.13]AEGK	VDFSK[325.13]FGEIEEVELGR	sp|P06959|ODP2_ECOLI	0	sp|P06959|ODP2_ECOLI	0
AEGK[325.13]SEFAENDAYVHATPLIR	EFGVNLAK[325.13]VK	sp|P06959|ODP2_ECOLI	0	sp|P06959|ODP2_ECOLI	0
AEGK[325.13]SEFAENDAYVHATPLIR	IQK[325.13]ISGANLSR	sp|P06959|ODP2_ECOLI	0	sp|P06959|ODP2_ECOLI	0
AEAAPAATGGGIPGMLPWPK[325.13]VDFSK	IQK[325.13]ISGANLSR	sp|P06959|ODP2_ECOLI	0	sp|P06959|ODP2_ECOLI	0
EAIK[325.13]R	IQK[325.13]ISGANLSR	sp|P06959|ODP2_ECOLI	1	sp|P06959|ODP2_ECOLI	0
LVPHATMPHPVK[325.13]DVR	VVALGVK[325.13]K	sp|P06992|KSGA_ECOLI	0	sp|P69811|PTFAH_ECOLI	0
IK[325.13]PYLLNNGQNPPAR	IK[325.13]PYLLNNGQNPPAR	sp|P07014|DHSB_ECOLI	0	sp|P07014|DHSB_ECOLI	0
APEAVIAK[325.13]ER	IENK[325.13]LANEGFVAR	sp|P07118|SYV_ECOLI	0	sp|P07118|SYV_ECOLI	0
AEANPALHPGQSAAIYLK[325.13]GER	FLK[325.13]QFK	sp|P07395|SYFB_ECOLI	0	sp|P08312|SYFA_ECOLI	0
GNIMK[325.13]FTEGAFK	K[325.13]LR	sp|P08200|IDH_ECOLI	0	sp|P00968|CARB_ECOLI	92
K[325.13]AELESAALNAR	K[325.13]LDLNGR	sp|P08312|SYFA_ECOLI	0	sp|P07395|SYFB_ECOLI	0
K[325.13]AELESAALNAR	VEYLGK[325.13]K	sp|P08312|SYFA_ECOLI	0	sp|P08312|SYFA_ECOLI	0
ADK[325.13]IK	K[325.13]LGLTNTTFQTVHGLDAPGQFSTAR	sp|P08506|DACC_ECOLI	0	sp|P08506|DACC_ECOLI	0
DADWK[325.13]IR	M[147.04]QTQIK[325.13]VR	sp|P08997|MASY_ECOLI	0	sp|P77712|TESC_ECOLI	0
QQAAQLK[325.13]QANR	QQAAQLK[325.13]QANR	sp|P09127|HEMX_ECOLI	0	sp|P09127|HEMX_ECOLI	0
K[325.13]SGVLTGLPDAYGR	K[325.13]TGNTPDGR	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
K[325.13]IFTEYR	K[325.13]SGVLTGLPDAYGR	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
K[325.13]SGVLTGLPDAYGR	MIEGSC[160.03]K[325.13]AYNR	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
K[325.13]SGVLTGLPDAYGR	VALYGIDYLMK[325.13]DK	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
K[325.13]SGVLTGLPDAYGR	VALYGIDYLM[147.04]K[325.13]DK	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
DAIPTQSVLTITSNVVYGK[325.13]K	LPLNFK[325.13]K	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
K[325.13]SGVLTGLPDAYGR	TMLYAINGGVDEK[325.13]LK	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
ALIPFGGIK[325.13]MIEGSC[160.03]K	K[325.13]SGVLTGLPDAYGR	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
ALIPFGGIK[325.13]M[147.04]IEGSC[160.03]K	K[325.13]SGVLTGLPDAYGR	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
ANLAK[325.13]TMLYAINGGVDEK	K[325.13]SGVLTGLPDAYGR	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
FM[147.04]K[325.13]K	IQK[325.13]LHTYR	sp|P09373|PFLB_ECOLI	0	sp|P09373|PFLB_ECOLI	0
K[325.13]VQTYPGR	K[325.13]YGYTGK	sp|P09394|GLPQ_ECOLI	0	sp|P09394|GLPQ_ECOLI	0
FPMGK[325.13]SDFR	TLEVLK[325.13]K	sp|P09394|GLPQ_ECOLI	0	sp|P09394|GLPQ_ECOLI	0
FPMGK[325.13]SDFR	K[325.13]VQTYPGR	sp|P09394|GLPQ_ECOLI	0	sp|P09394|GLPQ_ECOLI	0
FPMGK[325.13]SDFR	FTEGFDIENGK[325.13]K	sp|P09394|GLPQ_ECOLI	0	sp|P09394|GLPQ_ECOLI	0
K[325.13]PLK	TK[325.13]TNAR	sp|P09832|GLTD_ECOLI	0	sp|P0A7S9|RS13_ECOLI	0
K[325.13]YIVALDQGTTSSR	nM[147.04]NELDGIK	sp|P0A6F3|GLPK_ECOLI	0	sp|P0A867|TALA_ECOLI	0
DVK[325.13]FGNDAR	VK[325.13]MLR	sp|P0A6F5|CH60_ECOLI	0	sp|P0A6F5|CH60_ECOLI	0
K[325.13]ISNIR	K[325.13]QLDHGQK	sp|P0A6F5|CH60_ECOLI	0	sp|P0ABB0|ATPA_ECOLI	0
K[325.13]ISNIR	VGGAAQTK[325.13]IM[147.04]K	sp|P0A6F5|CH60_ECOLI	0	sp|P0ABB0|ATPA_ECOLI	0
GVNVLADAVK[325.13]VTLGPK	VK[325.13]MLR	sp|P0A6F5|CH60_ECOLI	0	sp|P0A6F5|CH60_ECOLI	0
AVAAGMNPMDLK[325.13]R	K[325.13]LAAQLNLTDDIR	sp|P0A6F5|CH60_ECOLI	0	sp|P39410|YJJJ_ECOLI	0
GVNVLADAVK[325.13]VTLGPK	GVNVLADAVK[325.13]VTLGPK	sp|P0A6F5|CH60_ECOLI	0	sp|P0A6F5|CH60_ECOLI	0
K[325.13]EVETK	VIVK[325.13]R	sp|P0A6F9|CH10_ECOLI	0	sp|P0A6F9|CH10_ECOLI	0
VIVK[325.13]R	nMNIRPLHDR	sp|P0A6F9|CH10_ECOLI	0	sp|P0A6F9|CH10_ECOLI	0
K[325.13]EVETK	nMNIRPLHDR	sp|P0A6F9|CH10_ECOLI	0	sp|P0A6F9|CH10_ECOLI	0

K[325.13]AMAR	K[325.13]TGAR	sp|P0A6H1|CLPX_ECOLI	0	sp|P0A6H1|CLPX_ECOLI	0
EIVSELDK[325.13]HIIGQDNAK	K[325.13]AIEQDAK	sp|P0A6H5|HSLU_ECOLI	0	sp|P0AEE5|DGAL_ECOLI	0
EGFK[325.13]K	HAK[325.13]QSGGR	sp|P0A6M8|EFG_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
IAFVNK[325.13]MDR	SLTK[325.13]GR	sp|P0A6M8|EFG_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
LAK[325.13]EDPSFR	TK[325.13]ADQEK	sp|P0A6M8|EFG_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
EEIK[325.13]EVR	IVQMHANK[325.13]R	sp|P0A6M8|EFG_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
IAFVNK[325.13]MDR	LAK[325.13]EDPSFR	sp|P0A6M8|EFG_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
IAFVNK[325.13]MDR	MGANFLK[325.13]VVNQIK	sp|P0A6M8|EFG_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
IAFVNK[325.13]MDR	M[147.04]GANFLK[325.13]VVNQIK	sp|P0A6M8|EFG_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
IAFVNK[325.13]M[147.04]DR	MGANFLK[325.13]VVNQIK	sp|P0A6M8|EFG_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
EK[325.13]FER	K[325.13]LLDEGR	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
K[325.13]LLDEGR	K[325.13]LLDEGR	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
K[325.13]LLDEGR	QYEEK[325.13]IR	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A759|NAGB_ECOLI	0
ETQK[325.13]STC[160.03]TGVEMFR	GIK[325.13]R	sp|P0A6N1|EFTU_ECOLI	1	sp|P0A6N1|EFTU_ECOLI	0
AFDQIDNAPEEK[325.13]AR	EK[325.13]FER	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
K[325.13]LLDEGR	VPGSIGQNQTPGK[325.13]VFK	sp|P0A6N1|EFTU_ECOLI	0	sp|P60438|RL3_ECOLI	0
K[325.13]LLDEGR	VGEEVEIVGIK[325.13]ETQK	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
ETQK[325.13]STC[160.03]TGVEMFR	K[325.13]LLDEGR	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
EK[325.13]FER	TK[325.13]PHVNVGTIGHVDHGK	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
EK[325.13]FER	VM[147.04]DVAAAPGSK[325.13]TTQISAR	sp|P0A6N1|EFTU_ECOLI	0	sp|P76273|RSMF_ECOLI	0
FESEVYILSK[325.13]DEGGR	K[325.13]LLDEGR	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
K[325.13]LLDEGR	TK[325.13]PHVNVGTIGHVDHGK	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
TK[325.13]PHVNVGTIGHVDHGK	VLGK[325.13]AGAAR	sp|P0A6N1|EFTU_ECOLI	0	sp|P60422|RL2_ECOLI	0
TK[325.13]PHVNVGTIGHVDHGK	VAVIK[325.13]AVR	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
AIDK[325.13]PFLLPIEDVFSISGR	EK[325.13]FER	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
AIDK[325.13]PFLLPIEDVFSISGR	K[325.13]LLDEGR	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
AFDQIDNAPEEK[325.13]AR	AFDQIDNAPEEK[325.13]AR	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
AFDQIDNAPEEK[325.13]AR	FESEVYILSK[325.13]DEGGR	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
AFDQIDNAPEEK[325.13]AR	TK[325.13]PHVNVGTIGHVDHGK	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
AFDQIDNAPEEK[325.13]AR	TTLTAAITTVLAK[325.13]TYGGAAR	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
TK[325.13]PHVNVGTIGHVDHGK	TK[325.13]PHVNVGTIGHVDHGK	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
GIK[325.13]R	TK[325.13]PHVNVGTIGHVDHGK	sp|P0A6N1|EFTU_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
K[325.13]AGNVAADGVIK	K[325.13]SGAIK	sp|P0A6P1|EFTS_ECOLI	0	sp|P0A6P1|EFTS_ECOLI	0
K[325.13]AGNVAADGVIK	SGAIK[325.13]AAK	sp|P0A6P1|EFTS_ECOLI	0	sp|P0A6P1|EFTS_ECOLI	0
EIAEK[325.13]MVEGR	EYQVQLDIAMQSGK[325.13]PK	sp|P0A6P1|EFTS_ECOLI	0	sp|P0A6P1|EFTS_ECOLI	0
AAK[325.13]K	K[325.13]SGAIK	sp|P0A6P1|EFTS_ECOLI	11	sp|P0A6P1|EFTS_ECOLI	0
M[147.04]K[325.13]K	TVGQLLK[325.13]EHNAEVTGFIR	sp|P0A6P1|EFTS_ECOLI	0	sp|P0A6P1|EFTS_ECOLI	0
DGDK[325.13]SR	FLGK[325.13]GVTK	sp|P0A6P9|ENO_ECOLI	0	sp|P0A6P9|ENO_ECOLI	0
FLGK[325.13]GVTK	IVK[325.13]IIGR	sp|P0A6P9|ENO_ECOLI	0	sp|P0A6P9|ENO_ECOLI	0
IEEALGEK[325.13]APYNGR	K[325.13]EIK	sp|P0A6P9|ENO_ECOLI	0	sp|P0A6P9|ENO_ECOLI	1
DGDK[325.13]SR	MGSEVFHHLAK[325.13]VLK	sp|P0A6P9|ENO_ECOLI	0	sp|P0A6P9|ENO_ECOLI	0
MGSEVFHHLAK[325.13]VLK	TVK[325.13]EAIR	sp|P0A6P9|ENO_ECOLI	0	sp|P0A6P9|ENO_ECOLI	0
M[147.04]GSEVFHHLAK[325.13]VLK	TVK[325.13]EAIR	sp|P0A6P9|ENO_ECOLI	0	sp|P0A6P9|ENO_ECOLI	0

FLGK[325.13]GVTK	MGSEVFHHLAK[325.13]VLK	sp|P0A6P9|ENO_ECOLI	0	sp|P0A6P9|ENO_ECOLI	0
IAGLEVK[325.13]R	QATK[325.13]DAGR	sp|P0A6Y8|DNAK_ECOLI	0	sp|P0A6Y8|DNAK_ECOLI	0
HMNIK[325.13]VTR	MPMVQK[325.13]K	sp|P0A6Y8|DNAK_ECOLI	0	sp|P0A6Y8|DNAK_ECOLI	0
AK[325.13]LESLVEDLVNR	MPMVQK[325.13]K	sp|P0A6Y8|DNAK_ECOLI	0	sp|P0A6Y8|DNAK_ECOLI	0
AK[325.13]LESLVEDLVNR	HM[147.04]NIK[325.13]VTR	sp|P0A6Y8|DNAK_ECOLI	0	sp|P0A6Y8|DNAK_ECOLI	0
NALTK[325.13]R	TINEM[147.04]SSYTPHMK[325.13]VNR	sp|P0A6Z3|HTPG_ECOLI	0	sp|Q9JMS7|YUAM_ECOLI	0
AARPK[325.13]K	GNK[325.13]HAESK	sp|P0A705|IF2_ECOLI	5	sp|P0A705|IF2_ECOLI	0
EAAEQAK[325.13]R	EAAEQAK[325.13]R	sp|P0A705|IF2_ECOLI	0	sp|P0A705|IF2_ECOLI	0
K[325.13]GNK	NAK[325.13]AARPK	sp|P0A705|IF2_ECOLI	2	sp|P0A705|IF2_ECOLI	0
QYEEK[325.13]IR	TK[325.13]PHVNVGTIGHVDHGK	sp|P0A759|NAGB_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
LPK[325.13]R	YLK[325.13]R	sp|P0A776|RPPH_ECOLI	1	sp|P77334|GMR_ECOLI	1
GK[325.13]WVK	LVAVPHSK[325.13]LSK	sp|P0A7A9|IPYR_ECOLI	0	sp|P0A7A9|IPYR_ECOLI	0
DLEK[325.13]GK	LVAVPHSK[325.13]LSK	sp|P0A7A9|IPYR_ECOLI	0	sp|P0A7A9|IPYR_ECOLI	0
GAK[325.13]AIGTTGR	YQGGHNAGHTLVINGEK[325.13]TVLHLIPSGILR	sp|P0A7D4|PURA_ECOLI	0	sp|P0A7D4|PURA_ECOLI	0
EK[325.13]AR	GAK[325.13]AIGTTGR	sp|P0A7D4|PURA_ECOLI	4	sp|P0A7D4|PURA_ECOLI	0
AAGSLVK[325.13]R	GK[325.13]AK	sp|P0A7D7|PUR7_ECOLI	0	sp|P0A7D7|PUR7_ECOLI	5
AAGSLVK[325.13]R	AAGSLVK[325.13]R	sp|P0A7D7|PUR7_ECOLI	0	sp|P0A7D7|PUR7_ECOLI	0
AAVEEK[325.13]YR	K[325.13]LLDEGR	sp|P0A7F9|QUEA_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
EIK[325.13]DPR	SLLGK[325.13]AMR	sp|P0A7G2|RBFA_ECOLI	2	sp|P0A7G2|RBFA_ECOLI	0
GVTVDK[325.13]MTELR	K[325.13]AGR	sp|P0A7J3|RL10_ECOLI	0	sp|P0A7J3|RL10_ECOLI	3
LFK[325.13]EFAK	VAVIK[325.13]AVR	sp|P0A7J3|RL10_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
ANAK[325.13]FEVK	LFK[325.13]EFAK	sp|P0A7J3|RL10_ECOLI	0	sp|P0A7J3|RL10_ECOLI	0
ANAK[325.13]FEVK	ANAK[325.13]FEVK	sp|P0A7J3|RL10_ECOLI	0	sp|P0A7J3|RL10_ECOLI	0
EFAK[325.13]ANAK	GVTVDK[325.13]MTELR	sp|P0A7J3|RL10_ECOLI	0	sp|P0A7J3|RL10_ECOLI	0
GVTVDK[325.13]MTELR	LFK[325.13]EFAK	sp|P0A7J3|RL10_ECOLI	5	sp|P0A7J3|RL10_ECOLI	0
ANAK[325.13]FEVK	GVTVDK[325.13]MTELR	sp|P0A7J3|RL10_ECOLI	0	sp|P0A7J3|RL10_ECOLI	0
TPPAAVLLK[325.13]K	VGK[325.13]ISR	sp|P0A7J7|RL11_ECOLI	0	sp|P0A7J7|RL11_ECOLI	0
K[325.13]AAGIK	SFTFVTK[325.13]TPPAAVLLK	sp|P0A7J7|RL11_ECOLI	0	sp|P0A7J7|RL11_ECOLI	0
AQLQEIAQTK[325.13]AADMTGADIEAMTR	TPPAAVLLK[325.13]K	sp|P0A7J7|RL11_ECOLI	0	sp|P0A7J7|RL11_ECOLI	0
VAVIK[325.13]AVR	VAVIK[325.13]AVR	sp|P0A7K2|RL7_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
AAGANK[325.13]VAVIK	VAVIK[325.13]AVR	sp|P0A7K2|RL7_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
GATGLGLK[325.13]EAK	VAVIK[325.13]AVR	sp|P0A7K2|RL7_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
VAVIK[325.13]AVR	nMNELVQILK	sp|P0A7K2|RL7_ECOLI	0	sp|P32672|PTFC2_ECOLI	0
AAGANK[325.13]VAVIK	GATGLGLK[325.13]EAK	sp|P0A7K2|RL7_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
K[325.13]ALEEAGAEVEVK	VAVIK[325.13]AVR	sp|P0A7K2|RL7_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
EAK[325.13]DLVESAPAALK	VAVIK[325.13]AVR	sp|P0A7K2|RL7_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
EAK[325.13]DLVESAPAALK	ILVK[325.13]PGQK	sp|P0A7K2|RL7_ECOLI	0	sp|P0AFS9|YEBA_ECOLI	0
EAK[325.13]DLVESAPAALK	LIAQGK[325.13]IR	sp|P0A7K2|RL7_ECOLI	0	sp|P76234|YEAE_ECOLI	0
EAK[325.13]DLVESAPAALK	VIK[325.13]AVLLR	sp|P0A7K2|RL7_ECOLI	0	sp|P05523|FPG_ECOLI	0
AAGANK[325.13]VAVIK	EAK[325.13]DLVESAPAALK	sp|P0A7K2|RL7_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
EAK[325.13]DLVESAPAALK	EAK[325.13]DLVESAPAALK	sp|P0A7K2|RL7_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
GATGLGLK[325.13]EAK	M[147.04]LEEISSVK[325.13]HIPEFVR	sp|P0A7K2|RL7_ECOLI	0	sp|P0ABH7|CISY_ECOLI	0
AK[325.13]LYYLR	TGK[325.13]AAR	sp|P0A7K6|RL19_ECOLI	0	sp|P0A7K6|RL19_ECOLI	0

K[325.13]ISNGEGVER	TGK[325.13]AAR	sp|P0A7K6|RL19_ECOLI	1	sp|P0A7K6|RL19_ECOLI	0
K[325.13]ISNGEGVER	VWVVEGSK[325.13]K	sp|P0A7K6|RL19_ECOLI	0	sp|P0A7K6|RL19_ECOLI	0
EK[325.13]VDATK	LTK[325.13]R	sp|P0A7L0|RL1_ECOLI	1	sp|P0A7L0|RL1_ECOLI	0
GLMPNPK[325.13]VGTVTPNVAEAVK	NAK[325.13]AGQVR	sp|P0A7L0|RL1_ECOLI	0	sp|P0A7L0|RL1_ECOLI	0
GLMPNPK[325.13]VGTVTPNVAEAVK	K[325.13]SDQNVR	sp|P0A7L0|RL1_ECOLI	0	sp|P0A7L0|RL1_ECOLI	0
DSEAK[325.13]R	LGVK[325.13]R	sp|P0A7L8|RL27_ECOLI	0	sp|P0A7L8|RL27_ECOLI	0
GTK[325.13]FHAGANVGC[160.03]GR	LGVK[325.13]R	sp|P0A7L8|RL27_ECOLI	0	sp|P0A7L8|RL27_ECOLI	0
VIDK[325.13]K	VSAK[325.13]GMR	sp|P0A7M2|RL28_ECOLI	0	sp|P0A7M2|RL28_ECOLI	0
SHALNATK[325.13]R	VSAK[325.13]GMR	sp|P0A7M2|RL28_ECOLI	0	sp|P0A7M2|RL28_ECOLI	0
K[325.13]GIDTVLAELR	VSAK[325.13]GMR	sp|P0A7M2|RL28_ECOLI	131	sp|P0A7M2|RL28_ECOLI	0
SHALNATK[325.13]R	VC[160.03]QVTGK[325.13]RPVTGNNR	sp|P0A7M2|RL28_ECOLI	0	sp|P0A7M2|RL28_ECOLI	0
MQAASGQLQQSHLLK[325.13]QVR	VK[325.13]TLLNEK	sp|P0A7M6|RL29_ECOLI	0	sp|P0A7M6|RL29_ECOLI	0
M[147.04]QAASGQLQQSHLLK[325.13]QVR	VK[325.13]TLLNEK	sp|P0A7M6|RL29_ECOLI	0	sp|P0A7M6|RL29_ECOLI	0
GAAK[325.13]R	K[325.13]TGK	sp|P0A7Q1|RL35_ECOLI	1	sp|P0A7Q1|RL35_ECOLI	0
GAAK[325.13]R	IK[325.13]TVR	sp|P0A7Q1|RL35_ECOLI	0	sp|P0A7Q1|RL35_ECOLI	0
HILTK[325.13]K	TAK[325.13]R	sp|P0A7Q1|RL35_ECOLI	0	sp|P20343|CYSX_ECOLI	0
GGFK[325.13]HK	HILTK[325.13]K	sp|P0A7Q1|RL35_ECOLI	0	sp|P0A7Q1|RL35_ECOLI	0
HK[325.13]HANLR	IK[325.13]TVR	sp|P0A7Q1|RL35_ECOLI	0	sp|P0A7Q1|RL35_ECOLI	0
HK[325.13]HANLR	TGK[325.13]GGFK	sp|P0A7Q1|RL35_ECOLI	0	sp|P0A7Q1|RL35_ECOLI	0
HILTK[325.13]K	HK[325.13]HANLR	sp|P0A7Q1|RL35_ECOLI	0	sp|P0A7Q1|RL35_ECOLI	0
FK[325.13]K	GAAK[325.13]R	sp|P0A7Q1|RL35_ECOLI	0	sp|P0A7Q1|RL35_ECOLI	0
VANLGSLGDQVNVK[325.13]AGYAR	nMQVILLDK	sp|P0A7R1|RL9_ECOLI	0	sp|P0A7R1|RL9_ECOLI	0
LK[325.13]AFDHR	VK[325.13]NGER	sp|P0A7R5|RS10_ECOLI	0	sp|P77561|YDEP_ECOLI	0
LVDIVEPTEK[325.13]TVDALMR	nMQNQR	sp|P0A7R5|RS10_ECOLI	0	sp|P0A7R5|RS10_ECOLI	0
LK[325.13]AFDHR	TK[325.13]PHVNVGTIGHVDHGK	sp|P0A7R5|RS10_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
K[325.13]ER	LK[325.13]AFDHR	sp|P0A7R5|RS10_ECOLI	27	sp|P0A7R5|RS10_ECOLI	0
K[325.13]PNSALR	K[325.13]VC[160.03]R	sp|P0A7S3|RS12_ECOLI	0	sp|P0A7S3|RS12_ECOLI	0
K[325.13]VAK	K[325.13]VC[160.03]R	sp|P0A7S3|RS12_ECOLI	0	sp|P0A7S3|RS12_ECOLI	0
K[325.13]QAR	K[325.13]VC[160.03]R	sp|P0A7S3|RS12_ECOLI	0	sp|P0A7S3|RS12_ECOLI	0
K[325.13]QAR	SK[325.13]YGVK	sp|P0A7S3|RS12_ECOLI	1	sp|P0A7S3|RS12_ECOLI	0
K[325.13]GPR	TK[325.13]TNAR	sp|P0A7S9|RS13_ECOLI	4	sp|P0A7S9|RS13_ECOLI	0
AK[325.13]YQR	LAK[325.13]R	sp|P0A7T7|RS18_ECOLI	0	sp|P75770|YBHN_ECOLI	9
AK[325.13]YQR	K[325.13]FC[160.03]R	sp|P0A7T7|RS18_ECOLI	0	sp|P0A7T7|RS18_ECOLI	0
AK[325.13]YQR	TK[325.13]HAVTEASPMVK	sp|P0A7T7|RS18_ECOLI	0	sp|P02358|RS6_ECOLI	0
K[325.13]HNASR	TFIK[325.13]K	sp|P0A7U7|RS20_ECOLI	0	sp|P0A7U7|RS20_ECOLI	0
AIQSEK[325.13]AR	K[325.13]HNASR	sp|P0A7U7|RS20_ECOLI	0	sp|P0A7U7|RS20_ECOLI	0
K[325.13]HNASR	QAAK[325.13]GLIHK	sp|P0A7U7|RS20_ECOLI	0	sp|P0A7U7|RS20_ECOLI	0
GLIHK[325.13]NK	HK[325.13]ANLTAQINK	sp|P0A7U7|RS20_ECOLI	0	sp|P0A7U7|RS20_ECOLI	0
HK[325.13]ANLTAQINK	QAAK[325.13]GLIHK	sp|P0A7U7|RS20_ECOLI	0	sp|P0A7U7|RS20_ECOLI	0
ELEK[325.13]LENSLGGIK	K[325.13]EALMR	sp|P0A7V0|RS2_ECOLI	0	sp|P0A7V0|RS2_ECOLI	0
DMLK[325.13]AGVHFGHQTR	nMM[147.04]VIR	sp|P0A7V0|RS2_ECOLI	0	sp|P76544|YFFM_ECOLI	0
MK[325.13]PFIFGAR	NK[325.13]VHIINLEK	sp|P0A7V0|RS2_ECOLI	0	sp|P0A7V0|RS2_ECOLI	0
AASEAVK[325.13]DAALSC[160.03]DQFFVNHR	ILFVGTK[325.13]R	sp|P0A7V0|RS2_ECOLI	0	sp|P0A7V0|RS2_ECOLI	0

<table>
<tr><td>LGAK[325.13]GIK</td><td>MAK[325.13]R</td><td>sp|P0A7V3|RS3_ECOLI</td><td>0</td><td>sp|P0ACT2|ENVR_ECOLI</td><td>5</td></tr>
<tr><td>AMK[325.13]R</td><td>K[325.13]PELDAK</td><td>sp|P0A7V3|RS3_ECOLI</td><td>0</td><td>sp|P0A7V3|RS3_ECOLI</td><td>0</td></tr>
<tr><td>AMK[325.13]R</td><td>GIK[325.13]VEVSGR</td><td>sp|P0A7V3|RS3_ECOLI</td><td>0</td><td>sp|P0A7V3|RS3_ECOLI</td><td>0</td></tr>
<tr><td>ELAK[325.13]ASVSR</td><td>K[325.13]PELDAK</td><td>sp|P0A7V3|RS3_ECOLI</td><td>0</td><td>sp|P0A7V3|RS3_ECOLI</td><td>0</td></tr>
<tr><td>GIK[325.13]VEVSGR</td><td>IAEM[147.04]EAM[147.04]K[325.13]R</td><td>sp|P0A7V3|RS3_ECOLI</td><td>0</td><td>sp|P05704|MCP3_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]PER</td><td>MEGTFK[325.13]R</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td></tr>
<tr><td>EK[325.13]QK</td><td>NYYK[325.13]EAAR</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td></tr>
<tr><td>EGTDLFLK[325.13]SGVR</td><td>YLGPK[325.13]LK</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]PER</td><td>LK[325.13]GNTGENLLALLEGR</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td></tr>
<tr><td>LK[325.13]GNTGENLLALLEGR</td><td>NYYK[325.13]EAAR</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td></tr>
<tr><td>EK[325.13]AK</td><td>K[325.13]QSR</td><td>sp|P0A7V8|RS4_ECOLI</td><td>3</td><td>sp|P0A7V8|RS4_ECOLI</td><td>3</td></tr>
<tr><td>K[325.13]QSR</td><td>VK[325.13]AALELAEQR</td><td>sp|P0A7V8|RS4_ECOLI</td><td>3</td><td>sp|P0A7V8|RS4_ECOLI</td><td>0</td></tr>
<tr><td>AMEK[325.13]AR</td><td>VSK[325.13]TVK</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td></tr>
<tr><td>VGFGYGK[325.13]AR</td><td>VSK[325.13]TVK</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td></tr>
<tr><td>AMEK[325.13]AR</td><td>VGFGYGK[325.13]AR</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td></tr>
<tr><td>EVPAAIQK[325.13]AMEK</td><td>VGFGYGK[325.13]AR</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td></tr>
<tr><td>ATIDGLENMNSPEMVAAK[325.13]R</td><td>GK[325.13]SVEEILGK</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td></tr>
<tr><td>NMINVALNNGTLQHPVK[325.13]GVHTGSR</td><td>YLK[325.13]R</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td><td>sp|P77334|GMR_ECOLI</td><td>1</td></tr>
<tr><td>K[325.13]DELPK</td><td>LYK[325.13]R</td><td>sp|P0A7W7|RS8_ECOLI</td><td>0</td><td>sp|P63284|CLPB_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]VGLR</td><td>RPQFSK[325.13]R</td><td>sp|P0A7X3|RS9_ECOLI</td><td>0</td><td>sp|P0A7X3|RS9_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]AGFVTR</td><td>K[325.13]ILPDPK</td><td>sp|P0A7X3|RS9_ECOLI</td><td>0</td><td>sp|P02359|RS7_ECOLI</td><td>0</td></tr>
<tr><td>IK[325.13]VQR</td><td>nMQGSVTEFLKPR</td><td>sp|P0A7Z4|RPOA_ECOLI</td><td>0</td><td>sp|P0A7Z4|RPOA_ECOLI</td><td>0</td></tr>
<tr><td>TQISK[325.13]IR</td><td>TQISK[325.13]IR</td><td>sp|P0A805|RRF_ECOLI</td><td>0</td><td>sp|P0A805|RRF_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]DAEVR</td><td>MDK[325.13]C[160.03]VEAFK</td><td>sp|P0A805|RRF_ECOLI</td><td>0</td><td>sp|P0A805|RRF_ECOLI</td><td>0</td></tr>
<tr><td>MDK[325.13]C[160.03]VEAFK</td><td>TQISK[325.13]IR</td><td>sp|P0A805|RRF_ECOLI</td><td>0</td><td>sp|P0A805|RRF_ECOLI</td><td>0</td></tr>
<tr><td>GFK[325.13]EAEAK</td><td>MLK[325.13]R</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>GGSEELYK[325.13]K</td><td>YAEGYPGK[325.13]R</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>GFK[325.13]EAEAK</td><td>TYQQQVAK[325.13]NAK</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>GGSEELYK[325.13]K</td><td>NLTGK[325.13]EADAALGR</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>NLTGK[325.13]EADAALGR</td><td>YAEGYPGK[325.13]R</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>ANITVNK[325.13]NSVPNDPK</td><td>GGSEELYK[325.13]K</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>GGSEELYK[325.13]K</td><td>GK[325.13]WGTLVNTLC[160.03]SFK</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P28629|ADIA_ECOLI</td><td>0</td></tr>
<tr><td>ANITVNK[325.13]NSVPNDPK</td><td>NFIENM[147.04]K[325.13]K</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P32690|YJBI_ECOLI</td><td>0</td></tr>
<tr><td>ANITVNK[325.13]NSVPNDPK</td><td>YAEGYPGK[325.13]R</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>ANITVNK[325.13]NSVPNDPK</td><td>YGK[325.13]DTQDVK</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0AF34|YIIR_ECOLI</td><td>0</td></tr>
<tr><td>EAMEPEFK[325.13]TYQQQVAK</td><td>GFK[325.13]EAEAK</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>5</td></tr>
<tr><td>GGSEELYK[325.13]K</td><td>NSVPNDPK[325.13]SPFVTSGIR</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>NSVPNDPK[325.13]SPFVTSGIR</td><td>YAEGYPGK[325.13]R</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>ANITVNK[325.13]NSVPNDPK</td><td>NLTGK[325.13]EADAALGR</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>NLTGK[325.13]EADAALGR</td><td>NSVPNDPK[325.13]SPFVTSGIR</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]LNSAVFPGGQGGPLMHVIAGK</td><td>YAEGYPGK[325.13]R</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>GK[325.13]AGGVK</td><td>nMNLHEYQAK</td><td>sp|P0A836|SUCC_ECOLI</td><td>0</td><td>sp|P0A836|SUCC_ECOLI</td><td>0</td></tr>
<tr><td>LGLEGK[325.13]LVQQFTK</td><td>MVGGVTPGK[325.13]GGTTHLGLPVFNTVR</td><td>sp|P0A836|SUCC_ECOLI</td><td>0</td><td>sp|P0AGE9|SUCD_ECOLI</td><td>0</td></tr>
</table>

<table>
<tr><td>LGLEGK[325.13]LVQQFTK</td><td>QM[147.04]SLC[160.03]ILIFLALVNK[325.13]VSENTK</td><td>sp|P0A836|SUCC_ECOLI</td><td>0</td><td>sp|P75908|YCDT_ECOLI</td><td>0</td></tr>
<tr><td>ELK[325.13]SAIR</td><td>VK[325.13]SQAIEGLVK</td><td>sp|P0A850|TIG_ECOLI</td><td>0</td><td>sp|P0A850|TIG_ECOLI</td><td>0</td></tr>
<tr><td>VIEPVK[325.13]R</td><td>nMENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>HFTAK[325.13]LK</td><td>VIEPVK[325.13]R</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>HFTAK[325.13]LK</td><td>HFTAK[325.13]LK</td><td>sp|P0A853|TNAA_ECOLI</td><td>2</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>HVK[325.13]ENAANIK</td><td>nMENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>DPK[325.13]TGK</td><td>YADMLAMSAK[325.13]K</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>GLTFTYEPK[325.13]VLR</td><td>LK[325.13]EV</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>HFTAK[325.13]LK</td><td>HVK[325.13]ENAANIK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>FAENAYFIK[325.13]QR</td><td>nMENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>FAENAYFIK[325.13]QR</td><td>nM[147.04]ENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>DPK[325.13]TGK</td><td>NVYIK[325.13]EAFDTGVR</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>FAENAYFIK[325.13]QR</td><td>VIEPVK[325.13]R</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>AMYSIAK[325.13]K</td><td>FAENAYFIK[325.13]QR</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>5</td></tr>
<tr><td>NVYIK[325.13]EAFDTGVR</td><td>VIEPVK[325.13]R</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>MENFK[325.13]HLPEPFR</td><td>VIEPVK[325.13]R</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>EAEYK[325.13]DWTIEQITR</td><td>nMENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>EAEYK[325.13]DWTIEQITR</td><td>nM[147.04]ENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>GLTFTYEPK[325.13]VLR</td><td>HVK[325.13]ENAANIK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>FAENAYFIK[325.13]QR</td><td>YADMLAMSAK[325.13]K</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>FAENAYFIK[325.13]QR</td><td>NVYIK[325.13]EAFDTGVR</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>GLTFTYEPK[325.13]VLR</td><td>TGK[325.13]QLPC[160.03]PAELLR</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>FAENAYFIK[325.13]QR</td><td>MENFK[325.13]HLPEPFR</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>GAEQIYIPVLIK[325.13]K</td><td>GAEQIYIPVLIK[325.13]K</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>ATYTQTHMDFIIEAFK[325.13]HVK</td><td>nMENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>ATYTQTHMDFIIEAFK[325.13]HVK</td><td>nM[147.04]ENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>NVYIK[325.13]EAFDTGVR</td><td>TGK[325.13]QLPC[160.03]PAELLR</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>ATYTQTHM[147.04]DFIIEAFK[325.13]HVK</td><td>nM[147.04]ENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>EAEYK[325.13]DWTIEQITR</td><td>FAENAYFIK[325.13]QR</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>LLPHIPADQFPAQALAC[160.03]ELYK[325.13]VAGIR</td><td>nMENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>SYYALAESVK[325.13]NIFGYQYTIPTHQGR</td><td>nMENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>LLPHIPADQFPAQALAC[160.03]ELYK[325.13]VAGIR</td><td>nM[147.04]ENFK</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td><td>sp|P0A853|TNAA_ECOLI</td><td>0</td></tr>
<tr><td>ESDELIAK[325.13]K</td><td>TYHK[325.13]ESDELIAK</td><td>sp|P0A858|TPIS_ECOLI</td><td>0</td><td>sp|P0A858|TPIS_ECOLI</td><td>0</td></tr>
<tr><td>LEEAAK[325.13]R</td><td>NEK[325.13]IGFK</td><td>sp|P0A8M3|SYT_ECOLI</td><td>0</td><td>sp|P0A8M3|SYT_ECOLI</td><td>0</td></tr>
<tr><td>DSLPEGVYNDQFK[325.13]K</td><td>IMGK[325.13]ASFVTLQDVGGR</td><td>sp|P0A8N5|SYK2_ECOLI</td><td>0</td><td>sp|P0A8N5|SYK2_ECOLI</td><td>1</td></tr>
<tr><td>ALRPLPDK[325.13]FHGLQDQEVR</td><td>YLDLIANDK[325.13]SR</td><td>sp|P0A8N5|SYK2_ECOLI</td><td>0</td><td>sp|P0A8N5|SYK2_ECOLI</td><td>0</td></tr>
<tr><td>AITGSNK[325.13]RPLK</td><td>VAK[325.13]ER</td><td>sp|P0A8T7|RPOC_ECOLI</td><td>0</td><td>sp|P0AEL6|FEPB_ECOLI</td><td>0</td></tr>
<tr><td>GLADTALK[325.13]TANSGYLTR</td><td>K[325.13]AISK</td><td>sp|P0A8T7|RPOC_ECOLI</td><td>0</td><td>sp|P0A8T7|RPOC_ECOLI</td><td>1</td></tr>
<tr><td>LK[325.13]R</td><td>SVVK[325.13]K</td><td>sp|P0A8T7|RPOC_ECOLI</td><td>0</td><td>sp|P00954|SYW_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]DDGNTIMVVQK</td><td>K[325.13]DDGNTIMVVQK</td><td>sp|P0A905|SLYB_ECOLI</td><td>0</td><td>sp|P0A905|SLYB_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]DDGNTIMVVQK</td><td>K[325.13]DDGNTIM[147.04]VVQK</td><td>sp|P0A905|SLYB_ECOLI</td><td>0</td><td>sp|P0A905|SLYB_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]ESAR</td><td>K[325.13]ESAR</td><td>sp|P0A908|MIPA_ECOLI</td><td>0</td><td>sp|P0A908|MIPA_ECOLI</td><td>0</td></tr>
<tr><td>AK[325.13]DSGDHQMR</td><td>K[325.13]ESAR</td><td>sp|P0A908|MIPA_ECOLI</td><td>0</td><td>sp|P0A908|MIPA_ECOLI</td><td>0</td></tr>
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GIPADK[325.13]ISAR	VLAQK[325.13]AVR	sp|P0A910|OMPA_ECOLI	1	sp|P77717|YBAY_ECOLI	0
GIPADK[325.13]ISAR	VEIEVK[325.13]GIK	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
GIPADK[325.13]ISAR	GIPADK[325.13]ISAR	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
GIPADK[325.13]ISAR	LDNMATK[325.13]YR	sp|P0A910|OMPA_ECOLI	0	sp|P69776|LPP_ECOLI	0
GIK[325.13]DVVTQPQA	HFTLK[325.13]SDVLFNFNK	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
GIPADK[325.13]ISAR	GMGESNPVTGNTC[160.03]DNVK[325.13]QR	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	5
GMGESNPVTGNTC[160.03]DNVK[325.13]QR	LDNMATK[325.13]YR	sp|P0A910|OMPA_ECOLI	1	sp|P69776|LPP_ECOLI	0
FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	VEIEVK[325.13]GIK	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	GIPADK[325.13]ISAR	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	LDNMATK[325.13]YR	sp|P0A910|OMPA_ECOLI	0	sp|P69776|LPP_ECOLI	0
FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	GIK[325.13]DVVTQPQA	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
GMGESNPVTGNTC[160.03]DNVK[325.13]QR	GMGESNPVTGNTC[160.03]DNVK[325.13]QR	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	MYLQGK[325.13]GVSADQISIVSYGK	sp|P0A910|OMPA_ECOLI	0	sp|P0A912|PAL_ECOLI	0
FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
EK[325.13]PAVLGHDEAAYSK	SNPSYK[325.13]VTVEGHADER	sp|P0A912|PAL_ECOLI	0	sp|P0A912|PAL_ECOLI	0
HITAGAK[325.13]K	K[325.13]LR	sp|P0A9B2|G3P1_ECOLI	0	sp|P00968|CARB_ECOLI	0
K[325.13]HITAGAK	K[325.13]VVMTGPSK	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
K[325.13]HITAGAK	TVDGPSHK[325.13]DWR	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
FDGTVEVK[325.13]DGHLIVNGK	K[325.13]LR	sp|P0A9B2|G3P1_ECOLI	0	sp|Q57261|TRUD_ECOLI	92
AVGK[325.13]VLPELNGK	TVDGPSHK[325.13]DWR	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
K[325.13]HITAGAK	VVMTGPSK[325.13]DNTPMFVK	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
GASQNIIPSSTGAAK[325.13]AVGK	K[325.13]HITAGAK	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
AATYEQIK[325.13]AAVK	TVDGPSHK[325.13]DWR	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
TVDGPSHK[325.13]DWR	TVDGPSHK[325.13]DWR	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
AVGK[325.13]VLPELNGK	VVMTGPSK[325.13]DNTPMFVK	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
TVDGPSHK[325.13]DWR	VVMTGPSK[325.13]DNTPMFVK	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
GASQNIIPSSTGAAK[325.13]AVGK	TVDGPSHK[325.13]DWR	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
GASQNIIPSSTGAAK[325.13]AVGK	VVMTGPSK[325.13]DNTPMFVK	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
FNTMTK[325.13]K	IPVVSSPK[325.13]AR	sp|P0A9C5|GLNA_ECOLI	0	sp|P0A9C5|GLNA_ECOLI	0
FNTMTK[325.13]K	K[325.13]NAIMMVDFALEAQR	sp|P0A9C5|GLNA_ECOLI	0	sp|P76399|MDTC_ECOLI	0
IPVVSSPK[325.13]AR	K[325.13]NAIMMVDFALEAQR	sp|P0A9C5|GLNA_ECOLI	0	sp|P76399|MDTC_ECOLI	0
EQHVTIPAHQVNAEFFEEGK[325.13]MFDGSSIGGWK	IPVVSSPK[325.13]AR	sp|P0A9C5|GLNA_ECOLI	0	sp|P0A9C5|GLNA_ECOLI	0
GK[325.13]VGINELLR	YFDK[325.13]VPMK	sp|P0A9D8|DAPD_ECOLI	0	sp|P0A9D8|DAPD_ECOLI	0
GK[325.13]VGINELLR	YFDK[325.13]VPM[147.04]K	sp|P0A9D8|DAPD_ECOLI	0	sp|P0A9D8|DAPD_ECOLI	0
K[325.13]AALAAER	NTK[325.13]SGLR	sp|P0A9K3|PHOL_ECOLI	0	sp|P0A9K3|PHOL_ECOLI	0
K[325.13]AALAAER	QQELDK[325.13]WK	sp|P0A9K3|PHOL_ECOLI	0	sp|P77354|YAFU_ECOLI	0
K[325.13]HQFAQSLNYEIAK	NTNITGVIVNK[325.13]LNAPVDEQGR	sp|P0A9M8|PTA_ECOLI	0	sp|P0A9M8|PTA_ECOLI	0
NTNITGVIVNK[325.13]LNAPVDEQGR	NTNITGVIVNK[325.13]LNAPVDEQGR	sp|P0A9M8|PTA_ECOLI	0	sp|P0A9M8|PTA_ECOLI	0
GILEQYGHK[325.13]VMF	HLTK[325.13]K	sp|P0A9N4|PFLA_ECOLI	0	sp|P32721|ALSA_ECOLI	0
K[325.13]APAEPQR	VFTK[325.13]R	sp|P0A9P0|DLDH_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
K[325.13]HYFDPK	VK[325.13]GTGR	sp|P0A9P0|DLDH_ECOLI	0	sp|P06959|ODP2_ECOLI	0
K[325.13]HYFDPK	VDK[325.13]QLR	sp|P0A9P0|DLDH_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
EK[325.13]VINQLTGGLAGMAK	ISK[325.13]K	sp|P0A9P0|DLDH_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	1

VFTK[325.13]R	VINQLTGGLAGMAK[325.13]GR	sp|P0A9P0|DLDH_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
EK[325.13]VINQLTGGLAGMAK	VFTK[325.13]R	sp|P0A9P0|DLDH_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
GVHEGHVAAEVIAGK[325.13]K	LIFDK[325.13]ESHR	sp|P0A9P0|DLDH_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
FNLMLETK[325.13]VTAVEAK	VPNGK[325.13]NLDAGK	sp|P0A9P0|DLDH_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
FNLM[147.04]LETK[325.13]VTAVEAK	VPNGK[325.13]NLDAGK	sp|P0A9P0|DLDH_ECOLI	5	sp|P0A9P0|DLDH_ECOLI	0
FNLM[147.04]LETK[325.13]VTAVEAK	M[147.04]IEFK[325.13]NVSK	sp|P0A9P0|DLDH_ECOLI	0	sp|P10346|GLNQ_ECOLI	1
ISK[325.13]K	VFTK[325.13]R	sp|P0A9P0|DLDH_ECOLI	1	sp|P0A9P0|DLDH_ECOLI	0
ISK[325.13]K	K[325.13]APAEPQR	sp|P0A9P0|DLDH_ECOLI	1	sp|P0A9P0|DLDH_ECOLI	0
ISK[325.13]K	VINQLTGGLAGMAK[325.13]GR	sp|P0A9P0|DLDH_ECOLI	1	sp|P0A9P0|DLDH_ECOLI	0
HLINK[325.13]K	HLINK[325.13]K	sp|P0A9Q7|ADHE_ECOLI	0	sp|P0A9Q7|ADHE_ECOLI	0
TDK[325.13]VYYHHTGHIGGIK	VAVTGNK[325.13]R	sp|P0AA10|RL13_ECOLI	0	sp|P0AA10|RL13_ECOLI	0
FGGK[325.13]VVAVQNQQGK	FGGK[325.13]VVAVQNQQGK	sp|P0AA91|YEAY_ECOLI	0	sp|P0AA91|YEAY_ECOLI	0
AQNVIVFK[325.13]R	ISSK[325.13]PLMLPNR	sp|P0AB67|PNTB_ECOLI	0	sp|P0AB67|PNTB_ECOLI	0
APVIVQFSNGGASFIAGK[325.13]GVK	K[325.13]YYDPR	sp|P0AB71|ALF_ECOLI	0	sp|P0AB71|ALF_ECOLI	0
APVIVQFSNGGASFIAGK[325.13]GVK	MSK[325.13]SHPR	sp|P0AB71|ALF_ECOLI	0	sp|P75770|YBHN_ECOLI	0
APVIVQFSNGGASFIAGK[325.13]GVK	GEDQPNK[325.13]K	sp|P0AB71|ALF_ECOLI	0	sp|P0AB71|ALF_ECOLI	0
LC[160.03]K[325.13]AK	LC[160.03]K[325.13]AK	sp|P0AB77|KBL_ECOLI	0	sp|P0AB77|KBL_ECOLI	0
AEGLFK[325.13]EER	LC[160.03]K[325.13]AK	sp|P0AB77|KBL_ECOLI	0	sp|P0AB77|KBL_ECOLI	0
AEGLFK[325.13]EER	VDIITGTLGK[325.13]ALGGASGGYTAAR	sp|P0AB77|KBL_ECOLI	0	sp|P0AB77|KBL_ECOLI	0
LK[325.13]ELTR	YGIEK[325.13]PYEK	sp|P0AB89|PUR8_ECOLI	0	sp|P0AB89|PUR8_ECOLI	0
GVSK[325.13]LEVNR	YGDK[325.13]VSALR	sp|P0AB89|PUR8_ECOLI	0	sp|P0AB89|PUR8_ECOLI	0
ILK[325.13]GNDDR	K[325.13]AIHK	sp|P0AB91|AROG_ECOLI	0	sp|P0AB91|AROG_ECOLI	0
AHK[325.13]DLDLAK	ASATDQLK[325.13]K	sp|P0ABA0|ATPF_ECOLI	0	sp|P0ABA0|ATPF_ECOLI	0
AK[325.13]AEAQVIIEQANK	ASATDQLK[325.13]K	sp|P0ABA0|ATPF_ECOLI	0	sp|P0ABA0|ATPF_ECOLI	0
AHK[325.13]DLDLAK	AK[325.13]AEAQVIIEQANK	sp|P0ABA0|ATPF_ECOLI	0	sp|P0ABA0|ATPF_ECOLI	0
AK[325.13]AEAQVIIEQANK	M[147.04]NAVLSVQGASAPVK[325.13]K	sp|P0ABA0|ATPF_ECOLI	0	sp|P04737|PIL1_ECOLI	0
AEAQVIIEQANK[325.13]R	SQILDEAK[325.13]AEAEQER	sp|P0ABA0|ATPF_ECOLI	0	sp|P0ABA0|ATPF_ECOLI	0
K[325.13]LSGGIR	K[325.13]QLDHGQK	sp|P0ABB0|ATPA_ECOLI	0	sp|P0ABB0|ATPA_ECOLI	0
K[325.13]LSGGIR	LK[325.13]GILDSFK	sp|P0ABB0|ATPA_ECOLI	0	sp|P0ABB0|ATPA_ECOLI	0
K[325.13]LSGGIR	VGGAAQTK[325.13]IMK	sp|P0ABB0|ATPA_ECOLI	0	sp|P0ABB0|ATPA_ECOLI	0
K[325.13]LSGGIR	VGGAAQTK[325.13]IM[147.04]K	sp|P0ABB0|ATPA_ECOLI	0	sp|P0ABB0|ATPA_ECOLI	0
K[325.13]QLDHGQK	LK[325.13]GILDSFK	sp|P0ABB0|ATPA_ECOLI	0	sp|P0ABB0|ATPA_ECOLI	0
DLEHPIEVPVGK[325.13]ATLGR	EIAEK[325.13]MVEGR	sp|P0ABB4|ATPB_ECOLI	0	sp|P0A6P1|EFTS_ECOLI	0
LSK[325.13]QK	RPEPYK[325.13]GK	sp|P0ABB8|ATMA_ECOLI	0	sp|P0AG55|RL6_ECOLI	0
YMK[325.13]TPTSATR	YMK[325.13]TPTSATR	sp|P0ABC3|HFLC_ECOLI	0	sp|P0ABC3|HFLC_ECOLI	0
GGNAPAAK[325.13]SDNGASNLLR	GGNAPAAK[325.13]SDNGASNLLR	sp|P0ABC7|HFLK_ECOLI	0	sp|P0ABC7|HFLK_ECOLI	0
EK[325.13]DK	LDNMATK[325.13]YR	sp|P0ABC9|BETT_ECOLI	1	sp|P69776|LPP_ECOLI	0
DK[325.13]NDSFR	MLEEISSVK[325.13]HIPEFVR	sp|P0ABH7|CISY_ECOLI	0	sp|P0ABH7|CISY_ECOLI	0
DK[325.13]NDSFR	GDDILK[325.13]ALNGEENVAINR	sp|P0ABH7|CISY_ECOLI	0	sp|P0AEC8|DCUS_ECOLI	0
GDFEK[325.13]R	TK[325.13]PHVNVGTIGHVDHGK	sp|P0ABH9|CLPA_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
AAFDQWVAK[325.13]AK	FK[325.13]AIATPDR	sp|P0ABJ1|CYOA_ECOLI	0	sp|P0ABJ1|CYOA_ECOLI	0
LGPSSLK[325.13]TGR	SK[325.13]IEETR	sp|P0ABJ9|CYDA_ECOLI	0	sp|P0ABK2|CYDB_ECOLI	0
SFNTQK[325.13]VFSGLEVAYR	nM[147.04]DVR	sp|P0ABP3|DCUC_ECOLI	0	sp|Q46938|KDUI_ECOLI	0

LVK[325.13]SK	NDVSDSEK[325.13]K	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
K[325.13]ATVELLNR	LVK[325.13]SK	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
K[325.13]ATVELLNR	SK[325.13]ATNLLYTR	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
AVQLGGVALGTTQVINSK[325.13]TPLK	LVK[325.13]SK	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
AVQLGGVALGTTQVINSK[325.13]TPLK	K[325.13]LAGNLK	sp|P0ABT2|DPS_ECOLI	0	sp|P0A7G6|RECA_ECOLI	0
AVQLGGVALGTTQVINSK[325.13]TPLK	K[325.13]ATVELLNR	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
SK[325.13]ATNLLYTR	TPLK[325.13]SYPLDIHNVQDHLK	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
AVQLGGVALGTTQVINSK[325.13]TPLK	SK[325.13]ATNLLYTR	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
GESK[325.13]NISVTEVHAR	K[325.13]GDIVGPIR	sp|P0ABZ6|SURA_ECOLI	0	sp|P0ABZ6|SURA_ECOLI	0
AAFSDFSK[325.13]LVR	K[325.13]LR	sp|P0AC02|YFIO_ECOLI	0	sp|P22523|MUKB_ECOLI	0
AAFSDFSK[325.13]LVR	LVFLK[325.13]DR	sp|P0AC02|YFIO_ECOLI	0	sp|P0AC02|YFIO_ECOLI	0
LK[325.13]ER	TGK[325.13]AAR	sp|P0AC33|FUMA_ECOLI	9	sp|P0A7K6|RL19_ECOLI	0
ALLTPGK[325.13]LK	NYLVEK[325.13]MR	sp|P0AC33|FUMA_ECOLI	1	sp|P0AC33|FUMA_ECOLI	0
AAAMANK[325.13]ELQTIPK	EYSPLAVK[325.13]K	sp|P0AC38|ASPA_ECOLI	0	sp|P0AC38|ASPA_ECOLI	0
EAAGSALK[325.13]GDR	K[325.13]SYQMNPMNR	sp|P0ACB2|HEM2_ECOLI	0	sp|P0ACB2|HEM2_ECOLI	0
ALK[325.13]DAVK	NPQTGK[325.13]EITIAAAK	sp|P0ACF0|DBHA_ECOLI	0	sp|P0ACF4|DBHB_ECOLI	0
EK[325.13]GVNR	GLTPK[325.13]MLTEANLNSLR	sp|P0ACI3|XYLR_ECOLI	0	sp|Q46851|YGHZ_ECOLI	0
MK[325.13]QAGIITGAR	MK[325.13]QAGIITGAR	sp|P0ACI6|ASNC_ECOLI	0	sp|P0ACI6|ASNC_ECOLI	0
NPQVAAMLK[325.13]NK	TPPAAVLLK[325.13]K	sp|P0ACT6|UIDR_ECOLI	0	sp|P0A7J7|RL11_ECOLI	0
EHLK[325.13]AHGGENIHIISK	K[325.13]LR	sp|P0AD61|KPYK1_ECOLI	0	sp|P0AD61|KPYK1_ECOLI	92
K[325.13]LR	LDAPLIVVATQGGK[325.13]SAR	sp|P0AD61|KPYK1_ECOLI	92	sp|P0AD61|KPYK1_ECOLI	0
AQVAQIAGK[325.13]PSSEVSMIHAR	K[325.13]GMSR	sp|P0ADB1|OSME_ECOLI	0	sp|P0ADB1|OSME_ECOLI	0
AQVAQIAGK[325.13]PSSEVSMIHAR	VLAQK[325.13]AVR	sp|P0ADB1|OSME_ECOLI	0	sp|P77717|YBAY_ECOLI	0
AQVAQIAGK[325.13]PSSEVSMIHAR	GIPADK[325.13]ISAR	sp|P0ADB1|OSME_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
AQVAQIAGK[325.13]PSSEVSMIHAR	GIK[325.13]DVVTQPQA	sp|P0ADB1|OSME_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
AQVAQIAGK[325.13]PSSEVSMIHAR	DQFVQPVVK[325.13]DVK	sp|P0ADB1|OSME_ECOLI	0	sp|P0ADB1|OSME_ECOLI	0
AQVAQIAGK[325.13]PSSEVSM[147.04]IHAR	DQFVQPVVK[325.13]DVK	sp|P0ADB1|OSME_ECOLI	0	sp|P0ADB1|OSME_ECOLI	0
AQVAQIAGK[325.13]PSSEVSMIHAR	AQVAQIAGK[325.13]PSSEVSM[147.04]IHAR	sp|P0ADB1|OSME_ECOLI	0	sp|P0ADB1|OSME_ECOLI	0
AQVAQIAGK[325.13]PSSEVSMIHAR	FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	sp|P0ADB1|OSME_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
DFQK[325.13]AER	LK[325.13]EIIHQQMGGLR	sp|P0ADG7|IMDH_ECOLI	0	sp|P0ADG7|IMDH_ECOLI	0
IK[325.13]RPK	YFDNK[325.13]HYPR	sp|P0ADN2|YIFE_ECOLI	0	sp|P0ADN2|YIFE_ECOLI	0
K[325.13]LGPVYSVR	K[325.13]LGPVYSVR	sp|P0ADS6|YGGE_ECOLI	0	sp|P0ADS6|YGGE_ECOLI	0
TAWIPLK[325.13]QLSTEPSLR	TAWIPLK[325.13]QLSTEPSLR	sp|P0ADT8|YGIM_ECOLI	0	sp|P0ADT8|YGIM_ECOLI	0
DASGTINVDIDHK[325.13]R	K[325.13]VNP	sp|P0ADU5|YGIW_ECOLI	0	sp|P0ADU5|YGIW_ECOLI	0
GGDFAALAK[325.13]EK	YSIIQTK[325.13]TEDEAK	sp|P0ADY1|PPID_ECOLI	5	sp|P0ADY1|PPID_ECOLI	0
ITIK[325.13]EAIPR	K[325.13]GDVLK	sp|P0ADY3|RL14_ECOLI	0	sp|P0ADY3|RL14_ECOLI	0
ITIK[325.13]EAIPR	VMC[160.03]IK[325.13]VLGGSHR	sp|P0ADY3|RL14_ECOLI	0	sp|P0ADY3|RL14_ECOLI	0
GK[325.13]VK	K[325.13]GDVLK	sp|P0ADY3|RL14_ECOLI	4	sp|P0ADY3|RL14_ECOLI	0
MHK[325.13]GR	TK[325.13]FR	sp|P0ADY7|RL16_ECOLI	0	sp|P0ADY7|RL16_ECOLI	0
QGK[325.13]IWIR	VAK[325.13]R	sp|P0ADY7|RL16_ECOLI	0	sp|P16916|RHSA_ECOLI	0
LAAAK[325.13]LPIK	VAK[325.13]R	sp|P0ADY7|RL16_ECOLI	0	sp|P16916|RHSA_ECOLI	0
EAFK[325.13]LAAAK	LPIK[325.13]TTFVTK	sp|P0ADY7|RL16_ECOLI	0	sp|P0ADY7|RL16_ECOLI	0
EAFK[325.13]LAAAK	GLAQGTDVSFGSFGLK[325.13]AVGR	sp|P0ADY7|RL16_ECOLI	0	sp|P0ADY7|RL16_ECOLI	0

GLAQGTDVSFGSFGLK[325.13]AVGR	LPIK[325.13]TTFVTK	sp|P0ADY7|RL16_ECOLI	0	sp|P0ADY7|RL16_ECOLI	0
K[325.13]AYVTLK	LLK[325.13]VLR	sp|P0ADZ0|RL23_ECOLI	0	sp|P0ADZ0|RL23_ECOLI	0
K[325.13]AYVTLK	nM[147.04]SAIEVK	sp|P0ADZ0|RL23_ECOLI	0	sp|P37774|YECC_ECOLI	0
DATK[325.13]AEIK	K[325.13]AYVTLK	sp|P0ADZ0|RL23_ECOLI	0	sp|P0ADZ0|RL23_ECOLI	0
K[325.13]AYVTLK	SNTIVLK[325.13]VAK	sp|P0ADZ0|RL23_ECOLI	0	sp|P0ADZ0|RL23_ECOLI	0
APHVSEK[325.13]ASTAMEK	LLK[325.13]VLR	sp|P0ADZ0|RL23_ECOLI	0	sp|P0ADZ0|RL23_ECOLI	0
APHVSEK[325.13]ASTAMEK	K[325.13]AYVTLK	sp|P0ADZ0|RL23_ECOLI	0	sp|P0ADZ0|RL23_ECOLI	0
K[325.13]DVAR	K[325.13]LLDYLK	sp|P0ADZ4|RS15_ECOLI	0	sp|P0ADZ4|RS15_ECOLI	0
GTMK[325.13]AL	LMDSIAK[325.13]GDEVLTNGGLVGR	sp|P0ADZ7|YAJC_ECOLI	0	sp|P0ADZ7|YAJC_ECOLI	0
DFVAAVLPK[325.13]GTMK	LMDSIAK[325.13]GDEVLTNGGLVGR	sp|P0ADZ7|YAJC_ECOLI	0	sp|P0ADZ7|YAJC_ECOLI	0
IAEVRPQVSGIILK[325.13]R	INLAYTK[325.13]VTSPISGR	sp|P0AE06|ACRA_ECOLI	0	sp|P0AE06|ACRA_ECOLI	0
SPTK[325.13]TETVSK	SQWLQDK[325.13]NIR	sp|P0AE22|APHA_ECOLI	0	sp|P0AE22|APHA_ECOLI	0
K[325.13]LLTWGFR	TFK[325.13]GR	sp|P0AEB2|DACA_ECOLI	0	sp|P0AEB2|DACA_ECOLI	0
AGK[325.13]FK	ASLGVDK[325.13]DVYLTIPR	sp|P0AEB2|DACA_ECOLI	0	sp|P0AEB2|DACA_ECOLI	0
K[325.13]ALDSYDK	TTYVIK[325.13]ELNDK	sp|P0AEE5|DGAL_ECOLI	0	sp|P0AEE5|DGAL_ECOLI	0
ELNDK[325.13]GIK	GAADGTNWK[325.13]IDNK	sp|P0AEE5|DGAL_ECOLI	0	sp|P0AEE5|DGAL_ECOLI	0
K[325.13]AIEQDAK	QNDQIDVLLAK[325.13]GVK	sp|P0AEE5|DGAL_ECOLI	0	sp|P0AEE5|DGAL_ECOLI	0
AYYVGTDSK[325.13]ESGIIQGDLIAK	K[325.13]ALDSYDK	sp|P0AEE5|DGAL_ECOLI	0	sp|P0AEE5|DGAL_ECOLI	0
ILK[325.13]SDDDLEPVVIGR	K[325.13]MAGQMGNER	sp|P0AEH3|ELAA_ECOLI	0	sp|P60438|RL3_ECOLI	0
AK[325.13]QAVYR	AK[325.13]QAVYR	sp|P0AEH5|ELAB_ECOLI	0	sp|P0AEH5|ELAB_ECOLI	0
AK[325.13]QAVYR	LGETGDAIAK[325.13]QTR	sp|P0AEH5|ELAB_ECOLI	0	sp|P64581|YQJD_ECOLI	0
AMMK[325.13]K	LSK[325.13]AVMR	sp|P0AEK2|FABG_ECOLI	0	sp|P0AEK2|FABG_ECOLI	0
K[325.13]MLAHC[160.03]EAVTPIR	TLAASGIK[325.13]DFR	sp|P0AEK4|FABI_ECOLI	0	sp|P0AEK4|FABI_ECOLI	0
EGAELAFTYQNDK[325.13]LK	TLAASGIK[325.13]DFR	sp|P0AEK4|FABI_ECOLI	0	sp|P0AEK4|FABI_ECOLI	0
EGAELAFTYQNDK[325.13]LK	K[325.13]ILADIAVFDK	sp|P0AEK4|FABI_ECOLI	0	sp|P0A7L3|RL20_ECOLI	0
EGAELAFTYQNDK[325.13]LK	IIWAPDK[325.13]HLGR	sp|P0AEK4|FABI_ECOLI	0	sp|P11458|NADA_ECOLI	0
SGTGSVDYAK[325.13]ANIK	TK[325.13]DLR	sp|P0AEQ3|GLNH_ECOLI	0	sp|P0AEQ3|GLNH_ECOLI	0
GK[325.13]VYIR	LIEK[325.13]IAELVK	sp|P0AES4|GYRA_ECOLI	0	sp|P0AES4|GYRA_ECOLI	0
LQK[325.13]LTGLEHEK	LQK[325.13]LTGLEHEK	sp|P0AES4|GYRA_ECOLI	0	sp|P0AES4|GYRA_ECOLI	0
NPQK[325.13]NLYTFK	VIEYC[160.03]K[325.13]K	sp|P0AET2|HDEB_ECOLI	0	sp|P0AET2|HDEB_ECOLI	0
GGDTVTLNETDLTQIPK[325.13]VIEYC[160.03]K	K[325.13]NPQK	sp|P0AET2|HDEB_ECOLI	0	sp|P0AET2|HDEB_ECOLI	0
LQSMK[325.13]AGSDR	MK[325.13]K	sp|P0AEU7|SKP_ECOLI	0	sp|P0AEU7|SKP_ECOLI	0
K[325.13]LQSMK	METDLQAK[325.13]MK	sp|P0AEU7|SKP_ECOLI	0	sp|P0AEU7|SKP_ECOLI	0
GK[325.13]LVTR	TGVSNTLENEFK[325.13]GR	sp|P0AEU7|SKP_ECOLI	0	sp|P0AEU7|SKP_ECOLI	0
LEK[325.13]DVMAQR	TALAM[147.04]TQK[325.13]AAIGK	sp|P0AEU7|SKP_ECOLI	0	sp|P52598|YGBI_ECOLI	0
QTFAQK[325.13]AQAFEQDR	TGVSNTLENEFK[325.13]GR	sp|P0AEU7|SKP_ECOLI	0	sp|P0AEU7|SKP_ECOLI	0
DITADVLK[325.13]QVK	IAIVNMGSLFQQVAQK[325.13]TGVSNTLENEFK	sp|P0AEU7|SKP_ECOLI	0	sp|P0AEU7|SKP_ECOLI	0
DK[325.13]PLGAVALK	VTVEHPDK[325.13]LEEK	sp|P0AEX9|MALE_ECOLI	0	sp|P0AEX9|MALE_ECOLI	0
FGGYAQSGLLAEITPDK[325.13]AFQDK	YENGK[325.13]YDIK	sp|P0AEX9|MALE_ECOLI	0	sp|P0AEX9|MALE_ECOLI	0
NAK[325.13]R	NAK[325.13]VGK	sp|P0AF18|NAGA_ECOLI	0	sp|P32132|TYPA_ECOLI	0
K[325.13]SER	STFQQLPGTGVK[325.13]PDQFHSQTR	sp|P0AFG0|NUSG_ECOLI	0	sp|P0AFG3|ODO1_ECOLI	0
FPGAK[325.13]R	VAK[325.13]IYGDR	sp|P0AFG3|ODO1_ECOLI	0	sp|P0AFG3|ODO1_ECOLI	0
STFQQLPGTGVK[325.13]PDQFHSQTR	nMQNSALK	sp|P0AFG3|ODO1_ECOLI	0	sp|P0AFG3|ODO1_ECOLI	0

<table>
<tr><td>IK[325.13]ELAVK</td><td>LAK[325.13]DASR</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG3|ODO1_ECOLI</td><td>0</td></tr>
<tr><td>EDVEK[325.13]HLAK</td><td>SEK[325.13]R</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>3</td></tr>
<tr><td>HLAK[325.13]APAK</td><td>IK[325.13]ELAVK</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>EDVEK[325.13]HLAK</td><td>IK[325.13]ELAVK</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>IK[325.13]ELAVK</td><td>K[325.13]QYGEAFEK</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>IK[325.13]ELAVK</td><td>QYGEAFEK[325.13]R</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>IK[325.13]ELAVK</td><td>SEEK[325.13]ASTPAQR</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>HLAK[325.13]APAK</td><td>SEEK[325.13]ASTPAQR</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>IK[325.13]ELAVK</td><td>NYWLAFGEK[325.13]R</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|Q46837|ACFD_ECOLI</td><td>0</td></tr>
<tr><td>DVDTLGMADIEK[325.13]K</td><td>IK[325.13]ELAVK</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>EGNSAGK[325.13]ETSAK</td><td>SEEK[325.13]ASTPAQR</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>APAK[325.13]ESAPAAAAPAAQPALAAR</td><td>DTK[325.13]R</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P76547|YFFP_ECOLI</td><td>1</td></tr>
<tr><td>LLAEHNLDASAIK[325.13]GTGVGGR</td><td>VDK[325.13]QLR</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0A9P0|DLDH_ECOLI</td><td>0</td></tr>
<tr><td>IK[325.13]ELAVK</td><td>LLAEHNLDASAIK[325.13]GTGVGGR</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>HLAK[325.13]APAK</td><td>LLAEHNLDASAIK[325.13]GTGVGGR</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>APAK[325.13]ESAPAAAAPAAQPALAAR</td><td>K[325.13]HYFDPK</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0A9P0|DLDH_ECOLI</td><td>0</td></tr>
<tr><td>EDVEK[325.13]HLAK</td><td>LLAEHNLDASAIK[325.13]GTGVGGR</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>APAK[325.13]ESAPAAAAPAAQPALAAR</td><td>EDVEK[325.13]HLAK</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>APAK[325.13]ESAPAAAAPAAQPALAAR</td><td>SEEK[325.13]ASTPAQR</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td></tr>
<tr><td>GGHDPK[325.13]K</td><td>K[325.13]DTSGK</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>GGHDPK[325.13]K</td><td>K[325.13]AQETK</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]AQETK</td><td>K[325.13]IYAAFK</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>GGHDPK[325.13]K</td><td>IYAAFK[325.13]K</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>ALNVMLK[325.13]NK</td><td>SIK[325.13]DR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>GGHDPK[325.13]K</td><td>SK[325.13]DGAYVR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>3</td></tr>
<tr><td>K[325.13]MNMDGVR</td><td>SK[325.13]DGAYVR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>FLK[325.13]YLEHR</td><td>GLK[325.13]DTSK</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]VVADAIAK</td><td>LETIEGSK[325.13]GK</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>ALNVMLK[325.13]NK</td><td>K[325.13]MNMDGVR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>GYGMGDAAEGK[325.13]NIAHQVK</td><td>K[325.13]MNMDGVR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>GYGMGDAAEGK[325.13]NIAHQVK</td><td>K[325.13]M[147.04]NMDGVR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>GYGM[147.04]GDAAEGK[325.13]NIAHQVK</td><td>K[325.13]MNMDGVR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]MNMDGVR</td><td>SHPEK[325.13]M[147.04]AFSYSYALSR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|Q02885|YUBO_ECOLI</td><td>0</td></tr>
<tr><td>ALNVMLK[325.13]NK</td><td>GYGMGDAAEGK[325.13]NIAHQVK</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>GGHDPK[325.13]K</td><td>LIQLM[147.04]NETVDGDYQTFK[325.13]SK</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>ATVILAHTIK[325.13]GYGMGDAAEGK</td><td>K[325.13]MNMDGVR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>STDISVK[325.13]TDQK</td><td>VK[325.13]AALVDHDNIK</td><td>sp|P0AFH8|OSMY_ECOLI</td><td>0</td><td>sp|P0AFH8|OSMY_ECOLI</td><td>0</td></tr>
<tr><td>AWAEK[325.13]NPAAAK</td><td>K[325.13]FYR</td><td>sp|P0AFM2|PROX_ECOLI</td><td>0</td><td>sp|P0AFM2|PROX_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]QLTR</td><td>MK[325.13]K</td><td>sp|P0AFM6|PSPA_ECOLI</td><td>0</td><td>sp|P0AFM6|PSPA_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]LNANR</td><td>K[325.13]SVR</td><td>sp|P0AG16|PUR1_ECOLI</td><td>0</td><td>sp|P0AG16|PUR1_ECOLI</td><td>2</td></tr>
<tr><td>IVK[325.13]FR</td><td>K[325.13]HYR</td><td>sp|P0AG48|RL21_ECOLI</td><td>0</td><td>sp|P0AG48|RL21_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]HYR</td><td>K[325.13]QQGHR</td><td>sp|P0AG48|RL21_ECOLI</td><td>1</td><td>sp|P0AG48|RL21_ECOLI</td><td>0</td></tr>
<tr><td>GK[325.13]GVR</td><td>TK[325.13]EAK</td><td>sp|P0AG55|RL6_ECOLI</td><td>0</td><td>sp|P0AG55|RL6_ECOLI</td><td>0</td></tr>
</table>

RPEPYK[325.13]GK	TK[325.13]EAK	sp|P0AG55|RL6_ECOLI	0	sp|P0AG55|RL6_ECOLI	0
GADK[325.13]QVIGQVAADLR	VAK[325.13]APVVVPAGVDVK	sp|P0AG55|RL6_ECOLI	0	sp|P0AG55|RL6_ECOLI	0
K[325.13]FGLSR	LK[325.13]VR	sp|P0AG59|RS14_ECOLI	0	sp|P16431|HYCE_ECOLI	0
EVK[325.13]R	VALADK[325.13]YFAK	sp|P0AG59|RS14_ECOLI	0	sp|P0AG59|RS14_ECOLI	0
FIK[325.13]R	FVK[325.13]HPIYGK	sp|P0AG63|RS17_ECOLI	2	sp|P0AG63|RS17_ECOLI	0
K[325.13]GAIVTGK	K[325.13]NR	sp|P0AG67|RS1_ECOLI	0	sp|P0AG67|RS1_ECOLI	24
VIK[325.13]LDQK	VLK[325.13]FDR	sp|P0AG67|RS1_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
VIK[325.13]LDQK	VK[325.13]GGFTVELNGIR	sp|P0AG67|RS1_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
ANPWQQFAETHNK[325.13]GDR	K[325.13]NR	sp|P0AG67|RS1_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
GAIVTGK[325.13]VTAVDAK	GGSEELYK[325.13]K	sp|P0AG67|RS1_ECOLI	0	sp|P0A825|GLYA_ECOLI	0
K[325.13]GAIVTGK	TK[325.13]PHVNVGTIGHVDHGK	sp|P0AG67|RS1_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
AYEDAETVTGVINGK[325.13]VK	VIK[325.13]LDQK	sp|P0AG67|RS1_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
ANPWQQFAETHNK[325.13]GDR	K[325.13]GAIVTGK	sp|P0AG67|RS1_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
VLK[325.13]FDR	VSLGLK[325.13]QLGEDPWVAIAK	sp|P0AG67|RS1_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
K[325.13]GAIVTGK	VTAVDAK[325.13]GATVELADGVEGYLR	sp|P0AG67|RS1_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
ISLGVK[325.13]QLAEDPFNNWVALNK	K[325.13]GAIVTGK	sp|P0AG67|RS1_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
EK[325.13]AK	LDQK[325.13]R	sp|P0AG67|RS1_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
EK[325.13]AK	VIK[325.13]LDQK	sp|P0AG67|RS1_ECOLI	3	sp|P0AG67|RS1_ECOLI	0
K[325.13]NR	VTAVDAK[325.13]GATVELADGVEGYLR	sp|P0AG67|RS1_ECOLI	24	sp|P0AG67|RS1_ECOLI	0
ETADNLK[325.13]K	IVVNYAK[325.13]R	sp|P0AGA2|SECY_ECOLI	0	sp|P0AGA2|SECY_ECOLI	0
K[325.13]GSQVYIEGQLR	K[325.13]WTDQSGQDR	sp|P0AGE0|SSB_ECOLI	0	sp|P0AGE0|SSB_ECOLI	0
IGIQPGHIHK[325.13]PGK	LEGNNAELGAK[325.13]K	sp|P0AGE9|SUCD_ECOLI	0	sp|P0A836|SUCC_ECOLI	0
IGIQPGHIHK[325.13]PGK	LADSGLNIIAAK[325.13]GLTDAAQQVVAAVEGK	sp|P0AGE9|SUCD_ECOLI	0	sp|P0A836|SUCC_ECOLI	0
ALEK[325.13]GIK	YTGNK[325.13]DAAAAVGK	sp|P0C018|RL18_ECOLI	0	sp|P0C018|RL18_ECOLI	0
AIAEQLK[325.13]YTGNK	DAAAAVGK[325.13]AVAER	sp|P0C018|RL18_ECOLI	0	sp|P0C018|RL18_ECOLI	0
GQAHWEGDIK[325.13]R	HLTK[325.13]K	sp|P0C0L2|OSMC_ECOLI	0	sp|P32721|ALSA_ECOLI	0
VK[325.13]EDK	VK[325.13]EDK	sp|P0C0S1|MSCS_ECOLI	0	sp|P0C0S1|MSCS_ECOLI	0
MVGK[325.13]DPR	NLTSQMVEYGQVK[325.13]R	sp|P0C0V0|DEGP_ECOLI	0	sp|P0C0V0|DEGP_ECOLI	0
K[325.13]FDAK	SDIALIQIQNPK[325.13]NLTAIK	sp|P0C0V0|DEGP_ECOLI	0	sp|P0C0V0|DEGP_ECOLI	0
AGDVITSLNGK[325.13]PISSFAALR	K[325.13]FDAK	sp|P0C0V0|DEGP_ECOLI	0	sp|P0C0V0|DEGP_ECOLI	0
GK[325.13]DQGVVVNNVK	K[325.13]GDVIIGANQQAVK	sp|P0C0V0|DEGP_ECOLI	0	sp|P0C0V0|DEGP_ECOLI	0
DGK[325.13]SYK	LNTSNNTK[325.13]VR	sp|P10100|RLPA_ECOLI	0	sp|P10100|RLPA_ECOLI	0
LLK[325.13]ER	LLK[325.13]ER	sp|P11458|NADA_ECOLI	4	sp|P11458|NADA_ECOLI	4
ATDESK[325.13]ELFEGR	FAPLNSWPDNVSLDK[325.13]AR	sp|P13029|KATG_ECOLI	0	sp|P13029|KATG_ECOLI	0
SGYLEQGK[325.13]R	SYDDNNK[325.13]GIYAGQPR	sp|P13036|FECA_ECOLI	0	sp|P13036|FECA_ECOLI	0
C[160.03]VIELDIAK[325.13]GK	SK[325.13]EELSK	sp|P14294|TOP3_ECOLI	0	sp|P64581|YQJD_ECOLI	0
C[160.03]VIELDIAK[325.13]GK	YPQATIK[325.13]LR	sp|P14294|TOP3_ECOLI	0	sp|P31463|YIDZ_ECOLI	0
C[160.03]VIELDIAK[325.13]GK	LGETGDAIAK[325.13]QTR	sp|P14294|TOP3_ECOLI	0	sp|P64581|YQJD_ECOLI	0
ILIVDAK[325.13]YYK	VVMTGPSK[325.13]DNTPMFVK	sp|P15006|MCRC_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
AALIAK[325.13]SR	LAGAK[325.13]TEAK	sp|P15288|PEPD_ECOLI	0	sp|P15288|PEPD_ECOLI	0
VK[325.13]TLHPK	VK[325.13]TLHPK	sp|P15639|PUR9_ECOLI	0	sp|P15639|PUR9_ECOLI	0
NHK[325.13]DVAIVVK	nMQQR	sp|P15639|PUR9_ECOLI	0	sp|P15639|PUR9_ECOLI	0
TLHPK[325.13]VHGGILGR	nMQQR	sp|P15639|PUR9_ECOLI	0	sp|P15639|PUR9_ECOLI	0

<table>
<tr><td>ITAAK[325.13]QNVR</td><td>VYSAK[325.13]IAGIK</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td></tr>
<tr><td>VYSAK[325.13]IAGIK</td><td>VYSAK[325.13]IAGIK</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td></tr>
<tr><td>TLHPK[325.13]VHGGILGR</td><td>VK[325.13]TLHPK</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td></tr>
<tr><td>TLHPK[325.13]VHGGILGR</td><td>TLHPK[325.13]VHGGILGR</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td></tr>
<tr><td>AADEGLEVK[325.13]GSSMASDAFFPFR</td><td>VYSAK[325.13]IAGIK</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td></tr>
<tr><td>EASVATATQVQGK[325.13]ALSYNNIADTDAALEC[160.03]VK</td><td>ITAAK[325.13]QNVR</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td><td>sp|P15639|PUR9_ECOLI</td><td>5</td></tr>
<tr><td>LK[325.13]VR</td><td>VEK[325.13]R</td><td>sp|P16431|HYCE_ECOLI</td><td>0</td><td>sp|Q06065|ATOC_ECOLI</td><td>0</td></tr>
<tr><td>VAK[325.13]R</td><td>VAK[325.13]R</td><td>sp|P16916|RHSA_ECOLI</td><td>10</td><td>sp|P16916|RHSA_ECOLI</td><td>10</td></tr>
<tr><td>VAK[325.13]R</td><td>YAGWK[325.13]K</td><td>sp|P16916|RHSA_ECOLI</td><td>10</td><td>sp|P0A6F3|GLPK_ECOLI</td><td>0</td></tr>
<tr><td>THAM[147.04]TDHIIFDGK[325.13]R</td><td>VK[325.13]QLTK</td><td>sp|P17444|BETA_ECOLI</td><td>0</td><td>sp|P45472|YHBQ_ECOLI</td><td>0</td></tr>
<tr><td>EK[325.13]QQC[160.03]SLVDGK</td><td>NTFSAK[325.13]YQQEPGVSGPLK</td><td>sp|P19926|AGP_ECOLI</td><td>0</td><td>sp|P19926|AGP_ECOLI</td><td>0</td></tr>
<tr><td>IPSINVSK[325.13]HR</td><td>IPSINVSK[325.13]HR</td><td>sp|P21599|KPYK2_ECOLI</td><td>0</td><td>sp|P21599|KPYK2_ECOLI</td><td>0</td></tr>
<tr><td>IAGK[325.13]K</td><td>VTDTGK[325.13]LR</td><td>sp|P23845|CYSN_ECOLI</td><td>1</td><td>sp|P71242|WCAK_ECOLI</td><td>0</td></tr>
<tr><td>AK[325.13]EIR</td><td>ILK[325.13]C[160.03]GFR</td><td>sp|P24183|FDNG_ECOLI</td><td>0</td><td>sp|P0AG44|RL17_ECOLI</td><td>0</td></tr>
<tr><td>AK[325.13]EIR</td><td>HEIIK[325.13]TTLPK</td><td>sp|P24183|FDNG_ECOLI</td><td>0</td><td>sp|P0AG44|RL17_ECOLI</td><td>0</td></tr>
<tr><td>APGLAVVLVGSNPASQIYVASK[325.13]R</td><td>IIDGK[325.13]TIAQQVR</td><td>sp|P24186|FOLD_ECOLI</td><td>0</td><td>sp|P24186|FOLD_ECOLI</td><td>0</td></tr>
<tr><td>LTK[325.13]SGK</td><td>VTK[325.13]PVFVR</td><td>sp|P27248|GCST_ECOLI</td><td>0</td><td>sp|P27248|GCST_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]AVDNALR</td><td>nMNIRPLHDR</td><td>sp|P27298|OPDA_ECOLI</td><td>0</td><td>sp|P0A6F9|CH10_ECOLI</td><td>0</td></tr>
<tr><td>GK[325.13]WGTLVNTLC[160.03]SFK</td><td>NLTGK[325.13]EADAALGR</td><td>sp|P28629|ADIA_ECOLI</td><td>0</td><td>sp|P0A825|GLYA_ECOLI</td><td>0</td></tr>
<tr><td>DLLAGIVAK[325.13]HYAR</td><td>DSK[325.13]VIPTQR</td><td>sp|P28903|NRDD_ECOLI</td><td>0</td><td>sp|P28903|NRDD_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]VGVQNGTTHQK</td><td>YTSVDQLK[325.13]GK</td><td>sp|P30859|ARTI_ECOLI</td><td>0</td><td>sp|P30859|ARTI_ECOLI</td><td>0</td></tr>
<tr><td>EISC[160.03]VDSAELGK[325.13]ASR</td><td>EISC[160.03]VDSAELGK[325.13]ASR</td><td>sp|P31120|GLMM_ECOLI</td><td>0</td><td>sp|P31120|GLMM_ECOLI</td><td>0</td></tr>
<tr><td>AAK[325.13]PK</td><td>IGK[325.13]PK</td><td>sp|P32053|INTA_ECOLI</td><td>0</td><td>sp|P67697|YDCQ_ECOLI</td><td>0</td></tr>
<tr><td>GK[325.13]GGK</td><td>NAK[325.13]R</td><td>sp|P32057|WCAI_ECOLI</td><td>9</td><td>sp|P0AF18|NAGA_ECOLI</td><td>0</td></tr>
<tr><td>EGK[325.13]FVTSR</td><td>LNK[325.13]ELVHNVALR</td><td>sp|P32132|TYPA_ECOLI</td><td>0</td><td>sp|P32132|TYPA_ECOLI</td><td>5</td></tr>
<tr><td>K[325.13]GNK</td><td>K[325.13]IVR</td><td>sp|P32153|FRVX_ECOLI</td><td>0</td><td>sp|P10121|FTSY_ECOLI</td><td>0</td></tr>
<tr><td>DMK[325.13]K</td><td>FGAK[325.13]SISTIAESK</td><td>sp|P32694|YJBM_ECOLI</td><td>0</td><td>sp|P69910|DCEB_ECOLI</td><td>0</td></tr>
<tr><td>AK[325.13]IIGNGAK</td><td>NAK[325.13]AGQVR</td><td>sp|P32717|YJCS_ECOLI</td><td>0</td><td>sp|P0A7L0|RL1_ECOLI</td><td>0</td></tr>
<tr><td>HLTK[325.13]K</td><td>QTPESFAFTLK[325.13]R</td><td>sp|P32721|ALSA_ECOLI</td><td>0</td><td>sp|P32131|HEMN_ECOLI</td><td>0</td></tr>
<tr><td>AYWNNLK[325.13]TPFK</td><td>INEVTATAVK[325.13]R</td><td>sp|P33136|OPGG_ECOLI</td><td>0</td><td>sp|P33136|OPGG_ECOLI</td><td>0</td></tr>
<tr><td>EQK[325.13]VK</td><td>VK[325.13]MLR</td><td>sp|P33230|YDAC_ECOLI</td><td>0</td><td>sp|P0A6F5|CH60_ECOLI</td><td>0</td></tr>
<tr><td>INEK[325.13]K</td><td>K[325.13]DLLR</td><td>sp|P33346|YEHI_ECOLI</td><td>0</td><td>sp|P0AGM7|URAA_ECOLI</td><td>0</td></tr>
<tr><td>SGGK[325.13]R</td><td>VLGK[325.13]AGAAR</td><td>sp|P36548|AMIA_ECOLI</td><td>0</td><td>sp|P60422|RL2_ECOLI</td><td>0</td></tr>
<tr><td>SGGK[325.13]R</td><td>TDK[325.13]FIVR</td><td>sp|P36548|AMIA_ECOLI</td><td>0</td><td>sp|P60422|RL2_ECOLI</td><td>0</td></tr>
<tr><td>TIK[325.13]TAYR</td><td>TIK[325.13]TAYR</td><td>sp|P36659|CBPA_ECOLI</td><td>0</td><td>sp|P36659|CBPA_ECOLI</td><td>0</td></tr>
<tr><td>ALYK[325.13]VLAQR</td><td>ALYK[325.13]VLAQR</td><td>sp|P37051|PURU_ECOLI</td><td>0</td><td>sp|P37051|PURU_ECOLI</td><td>0</td></tr>
<tr><td>FGGK[325.13]VINVINGK</td><td>FGGK[325.13]VINVINGK</td><td>sp|P37194|SLP_ECOLI</td><td>0</td><td>sp|P37194|SLP_ECOLI</td><td>0</td></tr>
<tr><td>GSLAK[325.13]ALSTASNAR</td><td>GSLAK[325.13]ALSTASNAR</td><td>sp|P37636|MDTE_ECOLI</td><td>0</td><td>sp|P37636|MDTE_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]IDGIPALLDR</td><td>K[325.13]IDGIPALLDR</td><td>sp|P37769|KDUD_ECOLI</td><td>0</td><td>sp|P37769|KDUD_ECOLI</td><td>0</td></tr>
<tr><td>VPSYTASK[325.13]SGVMGVTR</td><td>VPSYTASK[325.13]SGVMGVTR</td><td>sp|P37769|KDUD_ECOLI</td><td>0</td><td>sp|P37769|KDUD_ECOLI</td><td>0</td></tr>
<tr><td>VHVHVEEGSPK[325.13]DR</td><td>VHVHVEEGSPK[325.13]DR</td><td>sp|P37903|USPF_ECOLI</td><td>0</td><td>sp|P37903|USPF_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]ALTSVK</td><td>K[325.13]ATVELLNR</td><td>sp|P39276|YJDL_ECOLI</td><td>0</td><td>sp|P0ABT2|DPS_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]ALTSVK</td><td>SK[325.13]ATNLLYTR</td><td>sp|P39276|YJDL_ECOLI</td><td>0</td><td>sp|P0ABT2|DPS_ECOLI</td><td>0</td></tr>
</table>

INNPLK[325.13]Q	VAMVSMTGSVSAGEK[325.13]IMATAAK	sp|P39347|INTB_ECOLI	0	sp|P25553|ALDA_ECOLI	0
VIIVPDGEHAGK[325.13]R	VIK[325.13]LDQK	sp|P39356|YJHU_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
ESK[325.13]R	HLAK[325.13]APAK	sp|P39874|YBEM_ECOLI	1	sp|P0AFG6|ODO2_ECOLI	0
ESK[325.13]R	LLAEHNLDASAIK[325.13]GTGVGGR	sp|P39874|YBEM_ECOLI	1	sp|P0AFG6|ODO2_ECOLI	0
IGK[325.13]R	IGK[325.13]R	sp|P43676|PITB_ECOLI	0	sp|P43676|PITB_ECOLI	0
IGK[325.13]R	LQSHPLK[325.13]R	sp|P43676|PITB_ECOLI	0	sp|P0A821|SELA_ECOLI	0
VK[325.13]SSAQAK	VK[325.13]SSAQAK	sp|P45523|FKBA_ECOLI	0	sp|P45523|FKBA_ECOLI	0
EQEK[325.13]LGIK	VK[325.13]SSAQAK	sp|P45523|FKBA_ECOLI	5	sp|P45523|FKBA_ECOLI	0
SELK[325.13]R	TK[325.13]SWTLVR	sp|P54901|CSIE_ECOLI	0	sp|P0AG63|RS17_ECOLI	0
TDK[325.13]FIVR	VLGK[325.13]AGAAR	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
GK[325.13]PFAPLLEK	NSK[325.13]SGGR	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
HPVTPWGVQTK[325.13]GK	K[325.13]TR	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	27
VLGK[325.13]AGAAR	YILAPK[325.13]GLK	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
HIGGGHK[325.13]QAYR	NSK[325.13]SGGR	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
IVDFK[325.13]R	NK[325.13]DGIPAVVER	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
HIGGGHK[325.13]QAYR	IVDFK[325.13]R	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
HIGGGHK[325.13]QAYR	VLGK[325.13]AGAAR	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
HIGGGHK[325.13]QAYR	YILAPK[325.13]GLK	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
GK[325.13]PFAPLLEK	HIGGGHK[325.13]QAYR	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
HIGGGHK[325.13]QAYR	NK[325.13]DGIPAVVER	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
GK[325.13]PFAPLLEK	HVVK[325.13]VVNPELHK	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
IVDFK[325.13]R	NIPVGSTVHNVEMK[325.13]PGK	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
IVDFK[325.13]R	NIPVGSTVHNVEM[147.04]K[325.13]PGK	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
HIGGGHK[325.13]QAYR	HVVK[325.13]VVNPELHK	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
NIPVGSTVHNVEMK[325.13]PGK	VLGK[325.13]AGAAR	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
HVVK[325.13]VVNPELHK	K[325.13]VGVQNGTTHQK	sp|P60422|RL2_ECOLI	1	sp|P30859|ARTI_ECOLI	0
K[325.13]VEADC[160.03]R	NIPVGSTVHNVEMK[325.13]PGK	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
HVVK[325.13]VVNPELHK	SK[325.13]AEVYHIIQLK	sp|P60422|RL2_ECOLI	0	sp|P52123|YFJH_ECOLI	0
AGDQIQSGVDAAIK[325.13]PGNTLPMR	YILAPK[325.13]GLK	sp|P60422|RL2_ECOLI	0	sp|P60422|RL2_ECOLI	0
K[325.13]TR	SNK[325.13]R	sp|P60422|RL2_ECOLI	27	sp|P60422|RL2_ECOLI	0
K[325.13]MAGQMGNER	VFK[325.13]GK	sp|P60438|RL3_ECOLI	0	sp|P60438|RL3_ECOLI	0
GFAGTVK[325.13]R	K[325.13]VDVTGTSK	sp|P60438|RL3_ECOLI	0	sp|P60438|RL3_ECOLI	0
AIQVTTGAK[325.13]K	VTK[325.13]PEAGHFAK	sp|P60438|RL3_ECOLI	0	sp|P60438|RL3_ECOLI	0
HQK[325.13]PVPALNQPGGIVEK	VIVEGINLVK[325.13]K	sp|P60624|RL24_ECOLI	0	sp|P60624|RL24_ECOLI	0
K[325.13]PWR	VNK[325.13]K	sp|P60723|RL4_ECOLI	0	sp|P60723|RL4_ECOLI	0
AQK[325.13]TR	VNK[325.13]K	sp|P60723|RL4_ECOLI	0	sp|P60723|RL4_ECOLI	4
AQK[325.13]TR	LK[325.13]VR	sp|P60723|RL4_ECOLI	0	sp|P16431|HYCE_ECOLI	0
AQK[325.13]TR	K[325.13]PWR	sp|P60723|RL4_ECOLI	0	sp|P60723|RL4_ECOLI	0
AQK[325.13]TR	SGSIK[325.13]SPIWR	sp|P60723|RL4_ECOLI	0	sp|P60723|RL4_ECOLI	0
GALK[325.13]SILSELVR	NVK[325.13]K	sp|P60723|RL4_ECOLI	0	sp|P69054|DHSC_ECOLI	3
FSVEAPK[325.13]TK	LLAQK[325.13]LK	sp|P60723|RL4_ECOLI	0	sp|P60723|RL4_ECOLI	0
LLAQK[325.13]LK	TK[325.13]PHVNVGTIGHVDHGK	sp|P60723|RL4_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
K[325.13]MYR	SGGVTFAARPQDHSQK[325.13]VNK	sp|P60723|RL4_ECOLI	0	sp|P60723|RL4_ECOLI	0

IAMQK[325.13]SGR	IAMQK[325.13]SGR	sp|P60757|HIS1_ECOLI	0	sp|P60757|HIS1_ECOLI	0
METIAK[325.13]HR	SSAQK[325.13]VR	sp|P61175|RL22_ECOLI	0	sp|P61175|RL22_ECOLI	0
AAVLVK[325.13]K	VSQALDILTYTNK[325.13]K	sp|P61175|RL22_ECOLI	0	sp|P61175|RL22_ECOLI	0
K[325.13]AAVLVK	K[325.13]VLESAIANAEHNDGADIDDLK	sp|P61175|RL22_ECOLI	0	sp|P61175|RL22_ECOLI	0
AK[325.13]GR	IIK[325.13]R	sp|P61175|RL22_ECOLI	0	sp|P76071|INSH5_ECOLI	0
AK[325.13]GR	SSAQK[325.13]VR	sp|P61175|RL22_ECOLI	0	sp|P61175|RL22_ECOLI	0
GAFAYISDQQK[325.13]VYAR	LK[325.13]LK	sp|P61320|LOLB_ECOLI	0	sp|P00968|CARB_ECOLI	10
HGISNLK[325.13]LK	HGISNLK[325.13]LK	sp|P61517|CAN_ECOLI	0	sp|P61517|CAN_ECOLI	0
K[325.13]PGMDR	K[325.13]PGMDR	sp|P61889|MDH_ECOLI	0	sp|P61889|MDH_ECOLI	0
K[325.13]PGMDR	K[325.13]PGM[147.04]DR	sp|P61889|MDH_ECOLI	0	sp|P61889|MDH_ECOLI	0
IQNAGTEVVEAK[325.13]AGGGSATLSMGQAAAR	K[325.13]PGMDR	sp|P61889|MDH_ECOLI	0	sp|P61889|MDH_ECOLI	0
AAAVANQGK[325.13]AK	HYGALQGLNK[325.13]AETAEK	sp|P62707|GPMA_ECOLI	0	sp|P62707|GPMA_ECOLI	0
HYGALQGLNK[325.13]AETAEK	YGDEQVK[325.13]QWR	sp|P62707|GPMA_ECOLI	0	sp|P62707|GPMA_ECOLI	0
HGESQWNK[325.13]ENR	HYGALQGLNK[325.13]AETAEK	sp|P62707|GPMA_ECOLI	0	sp|P62707|GPMA_ECOLI	0
LYK[325.13]R	NMINVALNNGTLQHPVK[325.13]GVHTGSR	sp|P63284|CLPB_ECOLI	0	sp|P0A7W1|RS5_ECOLI	0
LLGIEPK[325.13]VR	MGK[325.13]TYQQPK	sp|P64429|YPFJ_ECOLI	0	sp|P64429|YPFJ_ECOLI	0
SK[325.13]AEQALK	VK[325.13]SSAQAK	sp|P64581|YQJD_ECOLI	0	sp|P45523|FKBA_ECOLI	0
AEQALK[325.13]QSR	SK[325.13]EELSK	sp|P64581|YQJD_ECOLI	0	sp|P64581|YQJD_ECOLI	0
AEQALK[325.13]QSR	AK[325.13]QAVYR	sp|P64581|YQJD_ECOLI	0	sp|P0AEH5|ELAB_ECOLI	0
SK[325.13]AEQALK	YPQATIK[325.13]LR	sp|P64581|YQJD_ECOLI	0	sp|P31463|YIDZ_ECOLI	0
AEQALK[325.13]QSR	AEQALK[325.13]QSR	sp|P64581|YQJD_ECOLI	0	sp|P64581|YQJD_ECOLI	0
AEQALK[325.13]QSR	YPQATIK[325.13]LR	sp|P64581|YQJD_ECOLI	0	sp|P31463|YIDZ_ECOLI	0
AEQALK[325.13]QSR	C[160.03]VIELDIAK[325.13]GK	sp|P64581|YQJD_ECOLI	0	sp|P14294|TOP3_ECOLI	0
AEQALK[325.13]QSR	LGETGDAIAK[325.13]QTR	sp|P64581|YQJD_ECOLI	0	sp|P64581|YQJD_ECOLI	0
LGETGDAIAK[325.13]QTR	LGETGDAIAK[325.13]QTR	sp|P64581|YQJD_ECOLI	0	sp|P64581|YQJD_ECOLI	0
MWLK[325.13]K	VK[325.13]VVNGLGK	sp|P67153|YQFA_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
GQIEYIPFPDK[325.13]LK	GQIEYIPFPDK[325.13]LK	sp|P67910|HLDD_ECOLI	0	sp|P67910|HLDD_ECOLI	0
ASAVK[325.13]R	HAK[325.13]K	sp|P68679|RS21_ECOLI	0	sp|P68679|RS21_ECOLI	0
HPYK[325.13]PK	VK[325.13]AQDVQR	sp|P68919|RL25_ECOLI	0	sp|P68919|RL25_ECOLI	0
K[325.13]NYIR	K[325.13]NYIR	sp|P69222|IF1_ECOLI	0	sp|P69222|IF1_ECOLI	0
AAVK[325.13]SGSELGK	K[325.13]DDQEETVR	sp|P69441|KAD_ECOLI	0	sp|P69441|KAD_ECOLI	3
AAVK[325.13]SGSELGK	IILLGAPGAGK[325.13]GTQAQFIMEK	sp|P69441|KAD_ECOLI	0	sp|P69441|KAD_ECOLI	0
LDNMATK[325.13]YR	VLAQK[325.13]AVR	sp|P69776|LPP_ECOLI	0	sp|P77717|YBAY_ECOLI	0
LDNMATK[325.13]YR	SDVQAAK[325.13]DDAAR	sp|P69776|LPP_ECOLI	0	sp|P69776|LPP_ECOLI	0
AISTIAESK[325.13]R	ASLK[325.13]YLSDHPK	sp|P69908|DCEA_ECOLI	0	sp|P69908|DCEA_ECOLI	1
AISTIAESK[325.13]R	MDQK[325.13]LLTDFR	sp|P69908|DCEA_ECOLI	0	sp|P69908|DCEA_ECOLI	0
FGAK[325.13]AISTIAESK	MDQK[325.13]LLTDFR	sp|P69908|DCEA_ECOLI	0	sp|P69908|DCEA_ECOLI	0
ASLK[325.13]YLSDHPK	LQGIAQQNSFK[325.13]HT	sp|P69908|DCEA_ECOLI	0	sp|P69908|DCEA_ECOLI	0
YLSDHPK[325.13]LQGIAQQNSFK	YLSDHPK[325.13]LQGIAQQNSFK	sp|P69908|DCEA_ECOLI	1	sp|P69908|DCEA_ECOLI	1
FGAK[325.13]SISTIAESK	nMFPK	sp|P69910|DCEB_ECOLI	0	sp|P0AAP1|ADRA_ECOLI	0
FGAK[325.13]SISTIAESK	K[325.13]QVTDLR	sp|P69910|DCEB_ECOLI	0	sp|P69910|DCEB_ECOLI	0
NIVNDPSVVFDDIVTNEQIQK[325.13]R	nM[147.04]NILLAFK	sp|P69924|RIR2_ECOLI	0	sp|Q46908|YGCR_ECOLI	0
LAK[325.13]R	TK[325.13]HAVTEASPMVK	sp|P75770|YBHN_ECOLI	0	sp|P02358|RS6_ECOLI	0

SAQDK[325.13]LR	SAQDK[325.13]LR	sp|P75777|YBHG_ECOLI	0	sp|P75777|YBHG_ECOLI	0
K[325.13]LAAAGK	LK[325.13]ER	sp|P75794|PFLE_ECOLI	0	sp|P0AC33|FUMA_ECOLI	0
AGLEEPK[325.13]NWQQLLDVAQK	K[325.13]EALMR	sp|P76042|YCJN_ECOLI	0	sp|P0A7V0|RS2_ECOLI	0
IIK[325.13]R	SSAQK[325.13]VR	sp|P76071|INSH5_ECOLI	0	sp|P61175|RL22_ECOLI	0
LAGQK[325.13]LVAR	LAGQK[325.13]LVAR	sp|P76076|YDBL_ECOLI	0	sp|P76076|YDBL_ECOLI	0
QNATAK[325.13]G	VAGEMNLSK[325.13]TQLR	sp|P76235|YEAH_ECOLI	0	sp|P45577|PROQ_ECOLI	0
NNK[325.13]SMLLLFFSLLIISTAK	VAVIK[325.13]AVR	sp|P76507|YFDI_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
K[325.13]LR	VK[325.13]GTGR	sp|P76542|INTZ_ECOLI	0	sp|P06959|ODP2_ECOLI	0
QFLNK[325.13]INELR	nMYAVFQSGGK	sp|P76543|YFFL_ECOLI	0	sp|P0AG48|RL21_ECOLI	0
AYK[325.13]YTAR	IQK[325.13]LGLQIK	sp|P76558|MAO2_ECOLI	0	sp|P76558|MAO2_ECOLI	0
TNLFMK[325.13]PIFSQAR	nMDDQLK	sp|P76558|MAO2_ECOLI	0	sp|P76558|MAO2_ECOLI	0
AATAAANK[325.13]K	LETIEGSK[325.13]GK	sp|P76573|YFGI_ECOLI	0	sp|P0AFG8|ODP1_ECOLI	0
AGK[325.13]LR	EALHDSLK[325.13]R	sp|P76577|PBPC_ECOLI	0	sp|P0A9T4|TAS_ECOLI	0
AGEK[325.13]TPPDALEK	IK[325.13]ELAVK	sp|P77218|EUTD_ECOLI	0	sp|P0AFG6|ODO2_ECOLI	0
K[325.13]RPK	K[325.13]RPK	sp|P77293|GTRB_ECOLI	1	sp|P77293|GTRB_ECOLI	1
DAFNLAWK[325.13]LALVIQGK	GLTFTYEPK[325.13]VLR	sp|P77397|MHPA_ECOLI	0	sp|P0A853|TNAA_ECOLI	0
EEK[325.13]K	TK[325.13]PHVNVGTIGHVDHGK	sp|P77609|FLXA_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
K[325.13]EEK	TK[325.13]PHVNVGTIGHVDHGK	sp|P77609|FLXA_ECOLI	4	sp|P0A6N1|EFTU_ECOLI	0
VLAQK[325.13]AVR	VLAQK[325.13]AVR	sp|P77717|YBAY_ECOLI	0	sp|P77717|YBAY_ECOLI	0
TEGK[325.13]QSPFSFVLSFNPADVQPNAR	VLAQK[325.13]AVR	sp|P77717|YBAY_ECOLI	0	sp|P77717|YBAY_ECOLI	0
HK[325.13]VK	nMENFK	sp|Q46829|BGLA_ECOLI	0	sp|P0A853|TNAA_ECOLI	5
EGNK[325.13]VR	GLTPK[325.13]MLTEANLNSLR	sp|Q46851|YGHZ_ECOLI	1	sp|Q46851|YGHZ_ECOLI	0

Appendix Table C.4: Low confidence *E. coli* cross-linked sites

ms3 pep1	ms3 pep2	ms3 prot1	prot 1 red	ms3 prot2	prot 2 red
*GK[325.13]PTRPVK	TEGK[325.13]QSPFSFVLSFNPADVQPNAR	*sp|P02919|PBPB_ECOLI	0	sp|P77717|YBAY_ECOLI	0
*MDVSYLLDSLNDK[325.13]QR	EDAELVGELVTPVIK[325.13]K	*sp|P03018|UVRD_ECOLI	0	sp|P75970|VXIS_ECOLI	0
*VM[147.04]ALVGENGAGK[325.13]STM[147.04]MK	TLAASGIK[325.13]DFR	*sp|P04983|RBSA_ECOLI	0	sp|P0AEK4|FABI_ECOLI	0
*K[325.13]LM[147.04]DSAGASGK	M[147.04]LEEISSVK[325.13]HIPEFVR	*sp|P06720|AGAL_ECOLI	0	sp|P0ABH7|CISY_ECOLI	0
*ILNK[325.13]QK	AVQLGGVALGTTQVINSK[325.13]TPLK	*sp|P06971|FHUA_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
*LELVAEVGEVK[325.13]SR	K[325.13]HGGIR	*sp|P07023|TYRA_ECOLI	0	sp|P0AEP7|GCL_ECOLI	0
*LNK[325.13]LC[160.03]QIGVK	IAGDYIAK[325.13]K	*sp|P07330|CHEB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
*QLALEAK[325.13]GETPSAVTR	K[325.13]MAGQMGNER	*sp|P07363|CHEA_ECOLI	0	sp|P60438|RL3_ECOLI	0
*QVNPK[325.13]AMISVK	DK[325.13]VGK	*sp|P09831|GLTB_ECOLI	0	sp|P0A7J7|RL11_ECOLI	2
*GLMK[325.13]K	NMINVALNNGTLQHPVK[325.13]GVHTGSR	*sp|P0A6I3|COAA_ECOLI	0	sp|P0A7W1|RS5_ECOLI	0
*YVPHFK[325.13]PGK	VAVIK[325.13]AVR	*sp|P0A6Y1|IHFB_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
*NALTK[325.13]R	TINEM[147.04]SSYTPHMK[325.13]VNR	*sp|P0A6Z3|HTPG_ECOLI	0	sp|Q9JMS7|YUAM_ECOLI	0
*QYEEK[325.13]IR	TK[325.13]PHVNVGTIGHVDHGK	*sp|P0A759|NAGB_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*NFLVPQGK[325.13]AVPATK	AIAMLNEPEIIK[325.13]K	*sp|P0A7R1|RL9_ECOLI	0	sp|P27128|RFAI_ECOLI	0
*LRPMTGLDK[325.13]PVAAFLDR	LLNDTDMAIIDK[325.13]R	*sp|P0A894|YHBJ_ECOLI	0	sp|P0A717|KPRS_ECOLI	0
*GVSAPK[325.13]APR	TEGK[325.13]QSPFSFVLSFNPADVQPNAR	*sp|P0A8P6|XERC_ECOLI	0	sp|P77717|YBAY_ECOLI	0
*K[325.13]NIFK	VINQLTGGLAGMAK[325.13]GR	*sp|P0A932|GFCE_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*K[325.13]NIFK	K[325.13]APAEPQR	*sp|P0A932|GFCE_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*AVGHGK[325.13]K	VLDAAVAGK[325.13]ITDVEVLK	*sp|P0A9H5|BTUR_ECOLI	0	sp|P0A6P1|EFTS_ECOLI	0
*QVLNMPTK[325.13]R	AEQALK[325.13]QSR	*sp|P0AAB4|UBID_ECOLI	0	sp|P64581|YQJD_ECOLI	0
*MTTK[325.13]K	HAK[325.13]QSGGR	*sp|P0AB80|ILVE_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
*AIDGTLSVMVGGDK[325.13]AIFDK	K[325.13]SGVLTGLPDAYGR	*sp|P0ABQ2|GARR_ECOLI	0	sp|P09373|PFLB_ECOLI	0
*LANQVIVALNIAAM[147.04]SEALTLATK[325.13]AGVNPDLVYQAIR	IK[325.13]SAATR	*sp|P0ABQ2|GARR_ECOLI	0	sp|P09546|PUTA_ECOLI	0
*IK[325.13]QAVALR	GATGLGLK[325.13]EAK	*sp|P0AED9|DCM_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
*MFVK[325.13]LLR	GEFFAK[325.13]SVK	*sp|P0AEE3|DEGS_ECOLI	0	sp|P62768|YAEH_ECOLI	0
*LDITESTVK[325.13]VHVK	SFGAPTITK[325.13]DGVSVAR	*sp|P0AF28|NARL_ECOLI	0	sp|P0A6F5|CH60_ECOLI	0
*K[325.13]SER	APAK[325.13]ESAPAAAAPAAQPALAAR	*sp|P0AFG0|NUSG_ECOLI	1	sp|P0AFG6|ODO2_ECOLI	0
*K[325.13]SER	LLAEHNLDASAIK[325.13]GTGVGGR	*sp|P0AFG0|NUSG_ECOLI	1	sp|P0AFG6|ODO2_ECOLI	0
*K[325.13]SER	STFQQLPGTGVK[325.13]PDQFHSQTR	*sp|P0AFG0|NUSG_ECOLI	1	sp|P0AFG3|ODO1_ECOLI	0
*K[325.13]LLSPEVANDK	DK[325.13]VGK	*sp|P0AFK9|POTD_ECOLI	0	sp|P0A7J7|RL11_ECOLI	2
*ILVK[325.13]PGQK	EAK[325.13]DLVESAPAALK	*sp|P0AFS9|YEBA_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
*IVK[325.13]FR	VGTYK[325.13]SAVEPFIR	*sp|P0AG48|RL21_ECOLI	0	sp|P08395|SPPA_ECOLI	0
*K[325.13]LSSGR	VINQLTGGLAGMAK[325.13]GR	*sp|P0AG71|RMUC_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*ILIVDAK[325.13]YYK	VVMTGPSK[325.13]DNTPMFVK	*sp|P15006|MCRC_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
*VLSK[325.13]LK	NVVLDK[325.13]SFGAPTITK	*sp|P19926|AGP_ECOLI	0	sp|P0A6F5|CH60_ECOLI	0
*DC[160.03]ELVTQIFHK[325.13]TEIM[147.04]PFLLER	M[147.04]HEK[325.13]R	*sp|P21189|DPO2_ECOLI	0	sp|P0ADG7|IMDH_ECOLI	0
*DC[160.03]ELVTQIFHK[325.13]TEIM[147.04]PFLLER	VALYGIDYLMK[325.13]DK	*sp|P21189|DPO2_ECOLI	0	sp|P09373|PFLB_ECOLI	0
*LK[325.13]YR	NMINVALNNGTLQHPVK[325.13]GVHTGSR	*sp|P21889|SYD_ECOLI	0	sp|P0A7W1|RS5_ECOLI	0
*K[325.13]LDDLPK	VAMVSMTGSVSAGEK[325.13]IMATAAK	*sp|P23865|PRC_ECOLI	0	sp|P25553|ALDA_ECOLI	0
*IAK[325.13]LAEQNQLR	M[147.04]IPGFEDGIK[325.13]GHK	*sp|P27129|RFAJ_ECOLI	0	sp|P0A850|TIG_ECOLI	0
*GGFIK[325.13]K	EK[325.13]VINQLTGGLAGMAK	*sp|P27241|RFAZ_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0

*AIEILK[325.13]HIYGEGK	SFGAPTITK[325.13]DGVSVAR	*sp|P27242|WAAU_ECOLI	0	sp|P0A6F5|CH60_ECOLI	0
*QAM[147.04]LK[325.13]AVALAFK	EGAELAFTYQNDK[325.13]LK	*sp|P27294|INAA_ECOLI	0	sp|P0AEK4|FABI_ECOLI	0
*MAALM[147.04]K[325.13]QR	AFDQIDNAPEEK[325.13]AR	*sp|P27302|TKT1_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*MAALM[147.04]K[325.13]QR	TK[325.13]PHVNVGTIGHVDHGK	*sp|P27302|TKT1_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*LGLK[325.13]G	APVVVK[325.13]NYPK	*sp|P27830|RFFG_ECOLI	0	sp|P0A8M0|SYN_ECOLI	0
*SHHQAYAWLLTPHPK[325.13]AMTTDAQK	K[325.13]SGVLTGLPDAYGR	*sp|P30958|MFD_ECOLI	0	sp|P09373|PFLB_ECOLI	0
*SHHQAYAWLLTPHPK[325.13]AMTTDAQK	VALYGIDYLMK[325.13]DK	*sp|P30958|MFD_ECOLI	0	sp|P09373|PFLB_ECOLI	0
*DMK[325.13]K	FGAK[325.13]SISTIAESK	*sp|P32694|YJBM_ECOLI	0	sp|P69910|DCEB_ECOLI	0
*VNLNK[325.13]ATLQNINLIDSK	LLNDTDMAIIDK[325.13]R	*sp|P32704|YJCF_ECOLI	0	sp|P0A717|KPRS_ECOLI	0
*NEK[325.13]SGK	DMLK[325.13]AGVHFGHQTR	*sp|P33228|RECT_ECOLI	0	sp|P0A7V0|RS2_ECOLI	0
*AHK[325.13]VLGVK	LLK[325.13]TLSHEPGK	*sp|P33570|TKT2_ECOLI	0	sp|P69228|BAER_ECOLI	0
*VGNGLAFNVVAK[325.13]GDPR	AK[325.13]AEAQVIIEQANK	*sp|P33666|YDBA_ECOLI	0	sp|P0ABA0|ATPF_ECOLI	0
*DPQQK[325.13]VAATR	FNLMLETK[325.13]VTAVEAK	*sp|P33940|MQO_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*SLAVVIK[325.13]NR	AGDQIQSGVDAAIK[325.13]PGNTLPMR	*sp|P37349|DHAM_ECOLI	0	sp|P60422|RL2_ECOLI	0
*TAK[325.13]GQVTAK	HFTAK[325.13]LK	*sp|P37906|PUUB_ECOLI	0	sp|P0A853|TNAA_ECOLI	0
*NVSDDELHWK[325.13]R	K[325.13]GNK	*sp|P39206|CAIE_ECOLI	0	sp|P0A705|IF2_ECOLI	2
*NGATEAFK[325.13]K	TK[325.13]PHVNVGTIGHVDHGK	*sp|P39265|ALSB_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*GIYLVNLDEK[325.13]IDMDNLK	ILLINPTDSDAVGNAVK[325.13]MANQANIPVITLDR	*sp|P39265|ALSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
*EAGAPIK[325.13]R	K[325.13]FQYGQHTVTLETGMMAR	*sp|P39452|RIR3_ECOLI	0	sp|P05055|PNP_ECOLI	0
*ESK[325.13]R	APAK[325.13]ESAPAAAAPAAQPALAAR	*sp|P39874|YBEM_ECOLI	1	sp|P0AFG6|ODO2_ECOLI	0
*TALNEC[160.03]K[325.13]K	AFDQIDNAPEEK[325.13]AR	*sp|P42588|PAT_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*MPLLPALK[325.13]SYLSLK	TK[325.13]PHVNVGTIGHVDHGK	*sp|P45537|YHFK_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*INSLSEIK[325.13]K	IGIQPGHIHK[325.13]PGK	*sp|P63204|GADE_ECOLI	0	sp|P0AGE9|SUCD_ECOLI	0
*LYK[325.13]R	NMINVALNNGTLQHPVK[325.13]GVHTGSR	*sp|P63284|CLPB_ECOLI	0	sp|P0A7W1|RS5_ECOLI	0
*IIQLK[325.13]LEQQALM[147.04]K	TK[325.13]PHVNVGTIGHVDHGK	*sp|P63284|CLPB_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*IIQLK[325.13]LEQQALM[147.04]K	EK[325.13]FER	*sp|P63284|CLPB_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*MWLK[325.13]K	K[325.13]VVADAIAK	*sp|P67153|YQFA_ECOLI	0	sp|P0AFG8|ODP1_ECOLI	0
*LLK[325.13]TLSHEPGK	VVMTGPSK[325.13]DNTPMFVK	*sp|P69228|BAER_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
*LK[325.13]MQK	VINQLTGGLAGMAK[325.13]GR	*sp|P71239|WCAE_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*LEEK[325.13]Q	LK[325.13]QR	*sp|P75704|YKIA_ECOLI	0	sp|P0AFL6|PPX_ECOLI	6
*IITTDAMGC[160.03]QK[325.13]DIAEK	NAGELDTVLAK[325.13]FPHVK	*sp|P75741|YBFL_ECOLI	2	sp|P0AEW4|ICC_ECOLI	0
*YISM[147.04]NVTQK[325.13]PFDNPK	AELEAK[325.13]LAEVLAAANAR	*sp|P75797|GSIB_ECOLI	0	sp|P0A7R1|RL9_ECOLI	0
*QSM[147.04]FGSSK[325.13]VLR	IK[325.13]ELAVK	*sp|P75831|MACB_ECOLI	0	sp|P0AFG6|ODO2_ECOLI	0
*M[147.04]LGQM[147.04]SK[325.13]GK	LK[325.13]GNTGENLLALLEGR	*sp|P75864|RLML_ECOLI	0	sp|P0A7V8|RS4_ECOLI	0
*AK[325.13]PVSLLR	EAK[325.13]DLVESAPAALK	*sp|P75969|INTE_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
*K[325.13]SDGVTEIDDVLLIETQGETAQALAIR	GIK[325.13]DVVTQPQA	*sp|P76083|PAAH_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
*GFLSLDK[325.13]FISSGPDAQTWADR	K[325.13]GAIVTGK	*sp|P76205|ARPB_ECOLI	0	sp|P0AG67|RS1_ECOLI	0
*LIAQGK[325.13]IR	GATGLGLK[325.13]EAK	*sp|P76234|YEAE_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
*ELFHK[325.13]QNATAK	SK[325.13]YGVK	*sp|P76235|YEAH_ECOLI	0	sp|P0A7S3|RS12_ECOLI	0
*GDTVQK[325.13]VAHTLGYDSTTAFITMFK	VALYGIDYLMK[325.13]DK	*sp|P76241|YEAM_ECOLI	0	sp|P09373|PFLB_ECOLI	0
*K[325.13]EGVTLMVEAIHASPGSEFTVTK	DLGK[325.13]LVAEQIEAAGGVAK	*sp|P76387|WZC_ECOLI	0	sp|P05791|ILVD_ECOLI	0
*MTAK[325.13]R	HAK[325.13]QSGGR	*sp|P76393|YEGI_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
*ASIDK[325.13]LR	VTAVDAK[325.13]GATVELADGVEGYLR	*sp|P76481|YFBK_ECOLI	0	sp|P0AG67|RS1_ECOLI	0

*FAK[325.13]PGK	VINQLTGGLAGMAK[325.13]GR	*sp|P76520|YFDX_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*FAK[325.13]PGK	EK[325.13]VINQLTGGLAGMAK	*sp|P76520|YFDX_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*K[325.13]GDEPPLSVPPAPALK	AK[325.13]AEAQVIIEQANK	*sp|P76559|YPFG_ECOLI	0	sp|P0ABA0|ATPF_ECOLI	0
*EIQQEK[325.13]QR	TGYDGAAPPK[325.13]GETHR	*sp|P76573|YFGI_ECOLI	0	sp|P12994|YBHB_ECOLI	0
*LEELAQNWK[325.13]GR	ANITVNK[325.13]NSVPNDPK	*sp|P76577|PBPC_ECOLI	0	sp|P0A825|GLYA_ECOLI	0
*LLTK[325.13]R	DLSDVTLGQFAGK[325.13]R	*sp|P76577|PBPC_ECOLI	0	sp|P0A862|TPX_ECOLI	0
*K[325.13]GYR	GK[325.13]VPMNIVAQR	*sp|P76639|YGEH_ECOLI	1	sp|P0A850|TIG_ECOLI	0
*QQVDAK[325.13]VTK	GHLVK[325.13]EVDALGGLM[147.04]AK	*sp|P77172|YFGF_ECOLI	0	sp|P0A6U3|MNMG_ECOLI	0
*M[147.04]IFSVDK[325.13]VR	FNLMLETK[325.13]VTAVEAK	*sp|P77444|SUFS_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*VNLIALTPDGK[325.13]R	VINDNFGIIEGLMTTVHATTATQK[325.13]TVDGPSHK	*sp|P77561|YDEP_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
*LLANK[325.13]ALIGIC[160.03]VPSYR	GAEQIYIPVLIK[325.13]K	*sp|P77698|YBCK_ECOLI	0	sp|P0A853|TNAA_ECOLI	0
*TYGGAVLNTAMLTENIHFYK[325.13]R	APVIVQFSNGGASFIAGK[325.13]GVK	*sp|P77721|YDJF_ECOLI	0	sp|P0AB71|ALF_ECOLI	0
*M[147.04]NDYK[325.13]M[147.04]TPGER	IIDGK[325.13]TIAQQVR	*sp|P77726|YAJR_ECOLI	0	sp|P24186|FOLD_ECOLI	0
*K[325.13]ISFR	VINQLTGGLAGMAK[325.13]GR	*sp|P77746|YBDO_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*QLIIDNFPK[325.13]LNR	AVAAGMNPMDLK[325.13]R	*sp|P77748|YDIJ_ECOLI	0	sp|P0A6F5|CH60_ECOLI	0
*GK[325.13]HNR	K[325.13]IGNEK	*sp|Q00037|TNPA_ECOLI	0	sp|P27550|ACSA_ECOLI	0
*K[325.13]VALEK	K[325.13]VVADAIAK	*sp|Q46811|YGFK_ECOLI	0	sp|P0AFG8|ODP1_ECOLI	0
*M[147.04]YLSK[325.13]VIIAR	K[325.13]AAITAEIR	*sp|Q46897|YGCH_ECOLI	0	sp|P02413|RL15_ECOLI	0
WDVK[325.13]LVK	*AIGHK[325.13]LAK	sp|P00490|PHSM_ECOLI	0	sp|P75822|YBJT_ECOLI	0
*NTSVK[325.13]R	K[325.13]VVADAIAK	sp|P00509|AAT_ECOLI	0	sp|P0AFG8|ODP1_ECOLI	0
AFSQMK[325.13]AAIR	*NAINAGVVALSTTNTGVWTLAK[325.13]K	sp|P00509|AAT_ECOLI	0	sp|Q46906|YGCP_ECOLI	0
*DDLSGK[325.13]DVMR	AQVAQIAGK[325.13]PSSEVSMIHAR	sp|P00562|AK2H_ECOLI	0	sp|P0ADB1|OSME_ECOLI	0
*MPK[325.13]K	LK[325.13]DLVNQDGGENWAK	sp|P00579|RPOD_ECOLI	2	sp|P00363|FRDA_ECOLI	0
SVVK[325.13]K	*LK[325.13]R	sp|P00954|SYW_ECOLI	0	sp|P67662|AAER_ECOLI	0
ALGK[325.13]IIGNGHLHK	*K[325.13]ASR	sp|P00956|SYI_ECOLI	1	sp|P06720|AGAL_ECOLI	0
VTGATDLSNK[325.13]SLR	*QK[325.13]ETTATTR	sp|P00957|SYA_ECOLI	0	sp|P39838|YOJN_ECOLI	0
*LK[325.13]LK	GAFAYISDQQK[325.13]VYAR	sp|P00968|CARB_ECOLI	10	sp|P61320|LOLB_ECOLI	0
*K[325.13]HGR	K[325.13]GQAHWEGDIK	sp|P00968|CARB_ECOLI	0	sp|P0C0L2|OSMC_ECOLI	0
*GTAVK[325.13]K	MAEANK[325.13]AFAHYR	sp|P02359|RS7_ECOLI	0	sp|P02359|RS7_ECOLI	0
SGK[325.13]SELEAFEVALENVRPTVEVK	*MQK[325.13]LK	sp|P02359|RS7_ECOLI	0	sp|P39306|ULAF_ECOLI	0
*AGK[325.13]R	GQK[325.13]SR	sp|P02413|RL15_ECOLI	7	sp|P02413|RL15_ECOLI	0
*AGK[325.13]R	LNTLSPAEGSK[325.13]K	sp|P02413|RL15_ECOLI	7	sp|P02413|RL15_ECOLI	0
*K[325.13]AGK	GQK[325.13]SR	sp|P02413|RL15_ECOLI	3	sp|P02413|RL15_ECOLI	0
*AGK[325.13]R	GHK[325.13]GQK	sp|P02413|RL15_ECOLI	0	sp|P02413|RL15_ECOLI	0
K[325.13]AGEGAK	*ISK[325.13]GGTNR	sp|P02925|RBSB_ECOLI	0	sp|P77555|ALLD_ECOLI	0
IAGDYIAK[325.13]K	*AAVEGIPALK[325.13]K	sp|P02925|RBSB_ECOLI	0	sp|P02919|PBPB_ECOLI	0
IAGDYIAK[325.13]K	*TNIM[147.04]SPLK[325.13]IPIADYFQLNANDEFMGK	sp|P02925|RBSB_ECOLI	0	sp|P71296|YAGM_ECOLI	0
*HTTDGLLK[325.13]LK	K[325.13]AGFVTR	sp|P03841|MALM_ECOLI	0	sp|P0A7X3|RS9_ECOLI	0
*K[325.13]MGIK	LPVIK[325.13]K	sp|P03960|ATKB_ECOLI	0	sp|P76197|YDIM_ECOLI	0
AK[325.13]PGQDFFPLTVNYQER	*MGK[325.13]LTGK	sp|P05055|PNP_ECOLI	1	sp|P37440|UCPA_ECOLI	0
*EK[325.13]GIDK	LVAVPHSK[325.13]LSK	sp|P05458|PTRA_ECOLI	0	sp|P0A7A9|IPYR_ECOLI	0
*LHK[325.13]HSVSAEPR	GIPADK[325.13]ISAR	sp|P05704|MCP3_ECOLI	5	sp|P0A910|OMPA_ECOLI	0
*EAIK[325.13]R	GVHEGHVAAEVIAGK[325.13]K	sp|P06959|ODP2_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0

<table>
<tr><td>K[325.13]IDVK</td><td>*K[325.13]GHLTLQM[147.04]TTLR</td><td>sp|P06968|DUT_ECOLI</td><td>0</td><td>sp|P08312|SYFA_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]VTWEDGK</td><td>TK[325.13]PHVNVGTIGHVDHGK</td><td>sp|P07024|USHA_ECOLI</td><td>4</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td></tr>
<tr><td>*MPGDAWQK[325.13]FANLR</td><td>GVTVDK[325.13]MTELR</td><td>sp|P07762|GLGB_ECOLI</td><td>0</td><td>sp|P0A7J3|RL10_ECOLI</td><td>0</td></tr>
<tr><td>YAGQDK[325.13]VNPGSIILSAEM[147.04]MLR</td><td>*SK[325.13]PNR</td><td>sp|P08200|IDH_ECOLI</td><td>0</td><td>sp|P31474|HSRA_ECOLI</td><td>0</td></tr>
<tr><td>*LPAFK[325.13]DALR</td><td>VYNNPK[325.13]YAGER</td><td>sp|P08202|ARAA_ECOLI</td><td>0</td><td>sp|P69797|PTNAB_ECOLI</td><td>0</td></tr>
<tr><td>*M[147.04]K[325.13]ASK</td><td>GK[325.13]LNGIGFAQK</td><td>sp|P08369|CRED_ECOLI</td><td>0</td><td>sp|P31473|RAVA_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]LGLTNTTFQTVHGLDAPGQFSTAR</td><td>*ADK[325.13]IK</td><td>sp|P08506|DACC_ECOLI</td><td>0</td><td>sp|P08506|DACC_ECOLI</td><td>0</td></tr>
<tr><td>*VELENVLLHK[325.13]LPVK</td><td>K[325.13]GTSM[147.04]AAESR</td><td>sp|P09152|NARG_ECOLI</td><td>0</td><td>sp|P0ACH1|SFSB_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]SGVLTGLPDAYGR</td><td>*M[147.04]DVSYLLDSLNDK[325.13]QR</td><td>sp|P09373|PFLB_ECOLI</td><td>0</td><td>*sp|P03018|UVRD_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]SGVLTGLPDAYGR</td><td>*VAPSTQK[325.13]YHM[147.04]EDVHR</td><td>sp|P09373|PFLB_ECOLI</td><td>0</td><td>*sp|P05791|ILVD_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]SGVLTGLPDAYGR</td><td>*FYGAGFVTFTDQAK[325.13]MK</td><td>sp|P09373|PFLB_ECOLI</td><td>0</td><td>*sp|P31131|YDEJ_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]SGVLTGLPDAYGR</td><td>*DDAAVFGFIDK[325.13]EQLDK</td><td>sp|P09373|PFLB_ECOLI</td><td>0</td><td>*sp|P42592|YGJK_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]SGVLTGLPDAYGR</td><td>*ALIPFGGIK[325.13]MIEGSC[160.03]K</td><td>sp|P09373|PFLB_ECOLI</td><td>0</td><td>sp|P09373|PFLB_ECOLI</td><td>0</td></tr>
<tr><td>LTGMVQDAQQNK[325.13]LVVHPYTVR</td><td>*M[147.04]HNDK</td><td>sp|P09394|GLPQ_ECOLI</td><td>0</td><td>sp|P60752|MSBA_ECOLI</td><td>0</td></tr>
<tr><td>*SSDVK[325.13]ALLGHR</td><td>IVDFK[325.13]R</td><td>sp|P09831|GLTB_ECOLI</td><td>0</td><td>sp|P60422|RL2_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]PLK</td><td>*K[325.13]GPR</td><td>sp|P09832|GLTD_ECOLI</td><td>0</td><td>sp|P0A7S9|RS13_ECOLI</td><td>0</td></tr>
<tr><td>*nM[147.04]LK</td><td>AVQLGGVALGTTQVINSK[325.13]TPLK</td><td>sp|P0A6E9|BIOD2_ECOLI</td><td>0</td><td>sp|P0ABT2|DPS_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]YIVALDQGTTSSR</td><td>*K[325.13]C[160.03]PTGTDR</td><td>sp|P0A6F3|GLPK_ECOLI</td><td>0</td><td>*sp|P16919|RHSD_ECOLI</td><td>0</td></tr>
<tr><td>*AVK[325.13]R</td><td>LEK[325.13]LAAQDPLK</td><td>sp|P0A6F3|GLPK_ECOLI</td><td>9</td><td>sp|P46125|YEDI_ECOLI</td><td>0</td></tr>
<tr><td>*AVK[325.13]R</td><td>YAGWK[325.13]K</td><td>sp|P0A6F3|GLPK_ECOLI</td><td>0</td><td>sp|P0A6F3|GLPK_ECOLI</td><td>0</td></tr>
<tr><td>*AVK[325.13]R</td><td>ETQK[325.13]STC[160.03]TGVEMFR</td><td>sp|P0A6F3|GLPK_ECOLI</td><td>0</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td></tr>
<tr><td>*AVK[325.13]R</td><td>AIDK[325.13]PFLLPIEDVFSISGR</td><td>sp|P0A6F3|GLPK_ECOLI</td><td>0</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td></tr>
<tr><td>VTLGPK[325.13]GR</td><td>*TIPLTLNPMK[325.13]QSK</td><td>sp|P0A6F5|CH60_ECOLI</td><td>0</td><td>*sp|P75672|YAFS_ECOLI</td><td>0</td></tr>
<tr><td>VASK[325.13]LADLR</td><td>*LDITESTVK[325.13]VHVK</td><td>sp|P0A6F5|CH60_ECOLI</td><td>0</td><td>*sp|P0AF28|NARL_ECOLI</td><td>0</td></tr>
<tr><td>VASK[325.13]LADLR</td><td>*QLIIDNFPK[325.13]LNR</td><td>sp|P0A6F5|CH60_ECOLI</td><td>0</td><td>*sp|P77748|YDIJ_ECOLI</td><td>0</td></tr>
<tr><td>VASK[325.13]LADLR</td><td>*K[325.13]LAAQLNLTDDIR</td><td>sp|P0A6F5|CH60_ECOLI</td><td>0</td><td>sp|P39410|YJJJ_ECOLI</td><td>0</td></tr>
<tr><td>*VIVK[325.13]R</td><td>MNIRPLHDR</td><td>sp|P0A6F9|CH10_ECOLI</td><td>0</td><td>sp|P0A6F9|CH10_ECOLI</td><td>0</td></tr>
<tr><td>MNIRPLHDR</td><td>*IAVK[325.13]TNDK</td><td>sp|P0A6F9|CH10_ECOLI</td><td>0</td><td>sp|P0AFF6|NUSA_ECOLI</td><td>1</td></tr>
<tr><td>*VQAIEK[325.13]NR</td><td>LGIVK[325.13]PWNSTWFANTK</td><td>sp|P0A6H5|HSLU_ECOLI</td><td>0</td><td>sp|P0A7V3|RS3_ECOLI</td><td>0</td></tr>
<tr><td>*EIVSELDK[325.13]HIIGQDNAK</td><td>SSIPVFGVDALPEALALVK[325.13]SGALAGTVLNDANNQAK</td><td>sp|P0A6H5|HSLU_ECOLI</td><td>0</td><td>sp|P0AEE5|DGAL_ECOLI</td><td>0</td></tr>
<tr><td>HAK[325.13]QSGGR</td><td>*TIIHGDALAELK[325.13]K</td><td>sp|P0A6M8|EFG_ECOLI</td><td>0</td><td>*sp|P28638|YHDJ_ECOLI</td><td>0</td></tr>
<tr><td>*IVQM[147.04]HANK[325.13]R</td><td>FNLMLETK[325.13]VTAVEAK</td><td>sp|P0A6M8|EFG_ECOLI</td><td>0</td><td>sp|P0A9P0|DLDH_ECOLI</td><td>0</td></tr>
<tr><td>*EEIK[325.13]EVR</td><td>IVQMHANK[325.13]R</td><td>sp|P0A6M8|EFG_ECOLI</td><td>0</td><td>sp|P0A6M8|EFG_ECOLI</td><td>0</td></tr>
<tr><td>NIGISAHIDAGK[325.13]TTTTER</td><td>*MK[325.13]LAVYSTK</td><td>sp|P0A6M8|EFG_ECOLI</td><td>0</td><td>sp|P52643|LDHD_ECOLI</td><td>0</td></tr>
<tr><td>*EEIK[325.13]EVR</td><td>AGDIAAAIGLK[325.13]DVTTGDTLC[160.03]DPDAPIILER</td><td>sp|P0A6M8|EFG_ECOLI</td><td>0</td><td>sp|P0A6M8|EFG_ECOLI</td><td>0</td></tr>
<tr><td>*MK[325.13]R</td><td>EFNVEANVGK[325.13]PQVAYR</td><td>sp|P0A6M8|EFG_ECOLI</td><td>78</td><td>sp|P0A6M8|EFG_ECOLI</td><td>0</td></tr>
<tr><td>MK[325.13]R</td><td>*K[325.13]LGHK</td><td>sp|P0A6M8|EFG_ECOLI</td><td>0</td><td>sp|P0A6V1|GLGC_ECOLI</td><td>0</td></tr>
<tr><td>TK[325.13]PHVNVGTIGHVDHGK</td><td>*AAVEEK[325.13]YR</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td><td>*sp|P0A7F9|QUEA_ECOLI</td><td>0</td></tr>
<tr><td>TK[325.13]PHVNVGTIGHVDHGK</td><td>*MAALM[147.04]K[325.13]QR</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td><td>*sp|P27302|TKT1_ECOLI</td><td>0</td></tr>
<tr><td>TK[325.13]PHVNVGTIGHVDHGK</td><td>*MMGAEGLK[325.13]K</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td><td>*sp|P33195|GCSP_ECOLI</td><td>0</td></tr>
<tr><td>TK[325.13]PHVNVGTIGHVDHGK</td><td>*QYEEK[325.13]IR</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td><td>*sp|P0A759|NAGB_ECOLI</td><td>0</td></tr>
<tr><td>TK[325.13]PHVNVGTIGHVDHGK</td><td>*MPLLPALK[325.13]SYLSLK</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td><td>*sp|P45537|YHFK_ECOLI</td><td>0</td></tr>
<tr><td>TK[325.13]PHVNVGTIGHVDHGK</td><td>*NGATEAFK[325.13]K</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td><td>*sp|P39265|ALSB_ECOLI</td><td>0</td></tr>
</table>

TK[325.13]PHVNVGTIGHVDHGK	*GK[325.13]VEC[160.03]TLR	sp|P0A6N1|EFTU_ECOLI	0	*sp|P23839|YICC_ECOLI	0
EK[325.13]FER	*K[325.13]VTWEDGK	sp|P0A6N1|EFTU_ECOLI	0	*sp|P07024|USHA_ECOLI	0
K[325.13]LLDEGR	*MAALM[147.04]K[325.13]QR	sp|P0A6N1|EFTU_ECOLI	0	*sp|P27302|TKT1_ECOLI	0
EK[325.13]FER	*VTFK[325.13]HVR	sp|P0A6N1|EFTU_ECOLI	0	sp|P76440|YEIT_ECOLI	0
K[325.13]LLDEGR	*M[147.04]QK[325.13]QLK	sp|P0A6N1|EFTU_ECOLI	0	sp|Q9JMR7|YUAX_ECOLI	0
K[325.13]LLDEGR	*ALGMPLK[325.13]R	sp|P0A6N1|EFTU_ECOLI	0	sp|P04395|3MG2_ECOLI	0
K[325.13]LLDEGR	*AGVSK[325.13]ATVSR	sp|P0A6N1|EFTU_ECOLI	1	sp|P24242|ASCG_ECOLI	0
K[325.13]LLDEGR	*NINLK[325.13]IPAGK	sp|P0A6N1|EFTU_ECOLI	0	sp|P60752|MSBA_ECOLI	0
TK[325.13]PHVNVGTIGHVDHGK	*AVK[325.13]R	sp|P0A6N1|EFTU_ECOLI	0	sp|P0ABY7|FLHC_ECOLI	0
GIIK[325.13]VGEEVEIVGIK	*K[325.13]GVDM[147.04]AM[147.04]R	sp|P0A6N1|EFTU_ECOLI	0	sp|P09546|PUTA_ECOLI	0
EK[325.13]FER	*VHTQK[325.13]QAYILQNEDK	sp|P0A6N1|EFTU_ECOLI	0	sp|P13035|GLPD_ECOLI	0
TK[325.13]PHVNVGTIGHVDHGK	*K[325.13]ASTVSR	sp|P0A6N1|EFTU_ECOLI	0	sp|P39295|YJFM_ECOLI	0
TK[325.13]PHVNVGTIGHVDHGK	*K[325.13]AGFVDK	sp|P0A6N1|EFTU_ECOLI	0	sp|P76066|YDAW_ECOLI	0
GSALK[325.13]ALEGDAEWEAK	*IDVK[325.13]ILDPR	sp|P0A6N1|EFTU_ECOLI	0	sp|P06968|DUT_ECOLI	0
TK[325.13]PHVNVGTIGHVDHGK	*HLTVK[325.13]LMPHLR	sp|P0A6N1|EFTU_ECOLI	0	sp|P37147|FXSA_ECOLI	0
GIK[325.13]R	*MPLLPALK[325.13]SYLSLK	sp|P0A6N1|EFTU_ECOLI	0	sp|P45537|YHFK_ECOLI	0
GIK[325.13]R	*LLTGK[325.13]AALTPEM[147.04]AIK	sp|P0A6N1|EFTU_ECOLI	0	sp|P67699|YDDM_ECOLI	1
GIK[325.13]R	*IIQLK[325.13]LEQQALM[147.04]K	sp|P0A6N1|EFTU_ECOLI	0	sp|P63284|CLPB_ECOLI	0
EYQVQLDIAMQSGK[325.13]PK	*MK[325.13]K	sp|P0A6P1|EFTS_ECOLI	0	sp|P0A6P1|EFTS_ECOLI	141
TVGQLLK[325.13]EHNAEVTGFIR	*MK[325.13]K	sp|P0A6P1|EFTS_ECOLI	0	sp|P0A6P1|EFTS_ECOLI	141
K[325.13]AGNVAADGVIK	*QLVK[325.13]NIR	sp|P0A6P1|EFTS_ECOLI	0	*sp|P37596|NORW_ECOLI	0
K[325.13]AGNVAADGVIK	*ITK[325.13]EIIR	sp|P0A6P1|EFTS_ECOLI	0	sp|P77721|YDJF_ECOLI	0
TGAGMMDC[160.03]K[325.13]K	*IQAIIEDIK[325.13]ER	sp|P0A6P1|EFTS_ECOLI	0	sp|P10408|SECA_ECOLI	4
TVGQLLK[325.13]EHNAEVTGFIR	*K[325.13]M[147.04]K	sp|P0A6P1|EFTS_ECOLI	0	sp|P0A6Y8|DNAK_ECOLI	0
TGAGM[147.04]MDC[160.03]K[325.13]K	*EAIEEAGLIVK[325.13]R	sp|P0A6P1|EFTS_ECOLI	0	sp|Q93K97|ADPP_ECOLI	1
*MK[325.13]K	EYQVQLDIAMQSGK[325.13]PK	sp|P0A6P1|EFTS_ECOLI	141	sp|P0A6P1|EFTS_ECOLI	0
*AAK[325.13]K	K[325.13]SGAIK	sp|P0A6P1|EFTS_ECOLI	0	sp|P0A6P1|EFTS_ECOLI	0
DAK[325.13]DQAGIDK	*AVK[325.13]PR	sp|P0A6P9|ENO_ECOLI	0	sp|P37690|YIBP_ECOLI	0
FLGK[325.13]GVTK	*DGDK[325.13]SR	sp|P0A6P9|ENO_ECOLI	0	sp|P0A6P9|ENO_ECOLI	5
*DGDK[325.13]SR	MGSEVFHHLAK[325.13]VLK	sp|P0A6P9|ENO_ECOLI	0	sp|P0A6P9|ENO_ECOLI	0
K[325.13]EIK	*TAIK[325.13]VIMTYDFDE	sp|P0A6P9|ENO_ECOLI	1	*sp|P77539|YDJL_ECOLI	0
*MSNVPAELK[325.13]YSK	MSNVPAELK[325.13]YSK	sp|P0A6T9|GCSH_ECOLI	0	sp|P0A6T9|GCSH_ECOLI	0
*VQK[325.13]M[147.04]IIANR	AEQALK[325.13]QSR	sp|P0A6X1|HEM1_ECOLI	0	sp|P64581|YQJD_ECOLI	0
*M[147.04]AK[325.13]GQSLQDPFLNALR	DAATAK[325.13]K	sp|P0A6X3|HFQ_ECOLI	0	sp|P0ADS6|YGGE_ECOLI	0
IAGLEVK[325.13]R	*K[325.13]HNLR	sp|P0A6Y8|DNAK_ECOLI	0	sp|P45428|DCUD_ECOLI	0
IAGLEVK[325.13]R	*MANIEIR	sp|P0A6Y8|DNAK_ECOLI	0	sp|P0A6Y8|DNAK_ECOLI	0
SGTK[325.13]SFLESLGSDQAK	*K[325.13]GDIVGPIR	sp|P0A6Z3|HTPG_ECOLI	0	*sp|P0ABZ6|SURA_ECOLI	0
*K[325.13]GNK	NAK[325.13]AARPK	sp|P0A705|IF2_ECOLI	2	sp|P0A705|IF2_ECOLI	0
GQK[325.13]PLEK	*MLK[325.13]LFAK	sp|P0A769|MNTH_ECOLI	0	sp|P77682|GTRA_ECOLI	6
GNVK[325.13]K	*SAIGAGLGSLVGAGIGALSSSK[325.13]K	sp|P0A7B8|HSLV_ECOLI	0	*sp|P37665|YIAD_ECOLI	0
*K[325.13]LAGNLK	SK[325.13]ATNLLYTR	sp|P0A7G6|RECA_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
*LMATM[147.04]K[325.13]EASAGK	IK[325.13]ELAVK	sp|P0A7J3|RL10_ECOLI	0	sp|P0AFG6|ODO2_ECOLI	0
EFAK[325.13]ANAK	*K[325.13]IAPGLYK	sp|P0A7J3|RL10_ECOLI	1	sp|P31663|PANC_ECOLI	1

EFAK[325.13]ANAK	*IK[325.13]APIVHALR	sp|P0A7J3|RL10_ECOLI	0	sp|P07003|POXB_ECOLI	0
ANAK[325.13]FEVK	*GDQDM[147.04]ILLLSK[325.13]K	sp|P0A7J3|RL10_ECOLI	0	sp|P0A9E5|FNR_ECOLI	0
GVTVDK[325.13]MTELR	*IK[325.13]APIVHALR	sp|P0A7J3|RL10_ECOLI	0	sp|P07003|POXB_ECOLI	2
*K[325.13]AGR	LNTLSPAEGSK[325.13]K	sp|P0A7J3|RL10_ECOLI	3	sp|P02413|RL15_ECOLI	0
K[325.13]AAGIK	*WWIK[325.13]DGGR	sp|P0A7J7|RL11_ECOLI	0	*sp|P76159|LYSQ_ECOLI	0
TPPAAVLLK[325.13]K	*QVNPK[325.13]AMISVK	sp|P0A7J7|RL11_ECOLI	0	*sp|P09831|GLTB_ECOLI	0
VGK[325.13]ISR	*SK[325.13]SFFDGVK	sp|P0A7J7|RL11_ECOLI	0	*sp|P08622|DNAJ_ECOLI	0
VGK[325.13]ISR	*NPQVAAMLK[325.13]NK	sp|P0A7J7|RL11_ECOLI	0	sp|P0ACT6|UIDR_ECOLI	0
K[325.13]AAGIK	*NVSNNAK[325.13]NR	sp|P0A7J7|RL11_ECOLI	0	sp|P64624|YHEO_ECOLI	0
VGK[325.13]ISR	*HFINSDK[325.13]R	sp|P0A7J7|RL11_ECOLI	0	sp|P08201|NIRB_ECOLI	5
VGK[325.13]ISR	*QVNPK[325.13]AMISVK	sp|P0A7J7|RL11_ECOLI	0	sp|P09831|GLTB_ECOLI	0
VAVIK[325.13]AVR	*NTVLPSGLLFVAHK[325.13]YDPTTPWINAR	sp|P0A7K2|RL7_ECOLI	0	*sp|P34211|YUAR_ECOLI	0
VAVIK[325.13]AVR	*M[147.04]GK[325.13]TEIIAETGAGQHGVASALASALLGLK	sp|P0A7K2|RL7_ECOLI	0	*sp|P0A879|TRPB_ECOLI	0
*nM[147.04]SITK	LEK[325.13]LANATM[147.04]R	sp|P0A7K2|RL7_ECOLI	0	sp|P76128|DDPA_ECOLI	0
VAVIK[325.13]AVR	*VK[325.13]SNIPMQR	sp|P0A7K2|RL7_ECOLI	0	sp|P52037|YGFF_ECOLI	0
VAVIK[325.13]AVR	*QENQIK[325.13]AVR	sp|P0A7K2|RL7_ECOLI	0	sp|P39325|YTFQ_ECOLI	0
AAGANK[325.13]VAVIK	*GATGLGLK[325.13]EAK	sp|P0A7K2|RL7_ECOLI	0	sp|P0A7K2|RL7_ECOLI	2
*VAVIK[325.13]AVR	EAK[325.13]DLVESAPAALK	sp|P0A7K2|RL7_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
EAK[325.13]DLVESAPAALK	*K[325.13]LPVVVVR	sp|P0A7K2|RL7_ECOLI	0	sp|P45756|GSPA_ECOLI	0
EAK[325.13]DLVESAPAALK	*LPVAVK[325.13]TVAGWIR	sp|P0A7K2|RL7_ECOLI	0	sp|P69425|TATB_ECOLI	0
VAVIK[325.13]AVR	*HPLLK[325.13]AVEYWITPPLFEK	sp|P0A7K2|RL7_ECOLI	0	sp|P46890|YBAE_ECOLI	0
VAVIK[325.13]AVR	*VIAGIM[147.04]QQILASHQVTLK[325.13]IK	sp|P0A7K2|RL7_ECOLI	0	sp|P33595|SGRR_ECOLI	0
VAVIK[325.13]AVR	*MNSLRPELLELTPQALTALSNAGFVK	sp|P0A7K2|RL7_ECOLI	0	sp|P33353|YEHQ_ECOLI	0
*TGK[325.13]AAR	LEGK[325.13]R	sp|P0A7K6|RL19_ECOLI	0	sp|P0AFR2|YCHM_ECOLI	0
K[325.13]SDQNVR	*FSGK[325.13]ELATPLLK	sp|P0A7L0|RL1_ECOLI	0	sp|P23325|ARPA_ECOLI	0
HK[325.13]K	*ILK[325.13]QAK	sp|P0A7L3|RL20_ECOLI	0	sp|P0A7L3|RL20_ECOLI	0
*VIDK[325.13]K	K[325.13]LQSMK	sp|P0A7M2|RL28_ECOLI	0	sp|P0AEU7|SKP_ECOLI	0
SHALNATK[325.13]R	*MGLVIK	sp|P0A7M2|RL28_ECOLI	0	sp|P0ACX0|YDGC_ECOLI	4
HK[325.13]HANLR	*FK[325.13]K	sp|P0A7Q1|RL35_ECOLI	0	sp|P0A7Q1|RL35_ECOLI	4
*ATK[325.13]R	HLRPK[325.13]AMVSK	sp|P0A7Q1|RL35_ECOLI	0	sp|P0A7Q1|RL35_ECOLI	0
*FK[325.13]K	GAAK[325.13]R	sp|P0A7Q1|RL35_ECOLI	0	sp|P0A7Q1|RL35_ECOLI	0
LIDQATAEIVETAK[325.13]R	*K[325.13]ER	sp|P0A7R5|RS10_ECOLI	0	sp|P0A7R5|RS10_ECOLI	27
K[325.13]VC[160.03]R	*ELNK[325.13]AAQR	sp|P0A7S3|RS12_ECOLI	0	sp|P76616|YGAQ_ECOLI	0
K[325.13]VC[160.03]R	*FAVENK[325.13]TLSALNIR	sp|P0A7S3|RS12_ECOLI	0	sp|P41066|TRAK1_ECOLI	0
*K[325.13]GPR	TK[325.13]TNAR	sp|P0A7S9|RS13_ECOLI	0	sp|P0A7S9|RS13_ECOLI	0
K[325.13]HNASR	*K[325.13]PAEELGR	sp|P0A7U7|RS20_ECOLI	0	sp|P33224|AIDB_ECOLI	0
AIQSEK[325.13]AR	*LK[325.13]ENGFIK	sp|P0A7U7|RS20_ECOLI	0	sp|P00959|SYM_ECOLI	0
K[325.13]EALMR	*EK[325.13]DVSFSATASMLLELGLR	sp|P0A7V0|RS2_ECOLI	0	*sp|P10026|TRAM1_ECOLI	0
NK[325.13]VHIINLEK	*ALLTPGK[325.13]LK	sp|P0A7V0|RS2_ECOLI	0	sp|P0AC33|FUMA_ECOLI	0
DMLK[325.13]AGVHFGHQTR	*K[325.13]NQM[147.04]K	sp|P0A7V0|RS2_ECOLI	0	sp|P37330|MASZ_ECOLI	4
NK[325.13]VHIINLEK	*K[325.13]LAVLTAFVK	sp|P0A7V0|RS2_ECOLI	0	sp|Q00037|TNPA_ECOLI	0
*ILFVGTK[325.13]R	TQLVESINM[147.04]AK[325.13]LLQR	sp|P0A7V0|RS2_ECOLI	0	sp|P32712|NRFG_ECOLI	0
K[325.13]EALMR	*MAGK[325.13]TM[147.04]IPLLAFAAWSGTGK	sp|P0A7V0|RS2_ECOLI	0	sp|P32125|MOBB_ECOLI	0

*MGQK[325.13]VHPNGIR	QQAAQLK[325.13]QANR	sp|P0A7V3|RS3_ECOLI	5	sp|P09127|HEMX_ECOLI	0
EK[325.13]AK	*K[325.13]QSR	sp|P0A7V8|RS4_ECOLI	0	sp|P0A7V8|RS4_ECOLI	0
NMINVALNNGTLQHPVK[325.13]GVHTGSR	*LMK[325.13]LK	sp|P0A7W1|RS5_ECOLI	0	sp|P32106|YIBG_ECOLI	0
K[325.13]AGFVTR	*IK[325.13]NHILK	sp|P0A7X3|RS9_ECOLI	0	sp|P76104|YDCP_ECOLI	0
K[325.13]VGLR	*ISPFEVVK[325.13]R	sp|P0A7X3|RS9_ECOLI	1	*sp|P0ABP3|DCUC_ECOLI	0
K[325.13]VGLR	*AQNVIVFK[325.13]R	sp|P0A7X3|RS9_ECOLI	1	*sp|P0AB67|PNTB_ECOLI	0
GGSEELYK[325.13]K	*K[325.13]GEETPTLSYM[147.04]LPK	sp|P0A825|GLYA_ECOLI	0	*sp|P21513|RNE_ECOLI	0
NLTGK[325.13]EADAALGR	*TQMPAALAFPLQGK[325.13]R	sp|P0A825|GLYA_ECOLI	0	*sp|P17444|BETA_ECOLI	0
NLTGK[325.13]EADAALGR	*DIGK[325.13]HFSVNQMINK	sp|P0A825|GLYA_ECOLI	0	*sp|P0AGJ9|SYY_ECOLI	0
NLTGK[325.13]EADAALGR	*NSVPNDPK[325.13]SPFVTSGIR	sp|P0A825|GLYA_ECOLI	0	sp|P0A825|GLYA_ECOLI	0
GK[325.13]AGGVK	*ALSQLPAC[160.03]IAPK[325.13]PHLYLR	sp|P0A836|SUCC_ECOLI	0	*sp|P75948|THIK_ECOLI	0
NAK[325.13]YK	*NQVLEK[325.13]LGLNSEEQK	sp|P0A847|TGT_ECOLI	0	sp|P18390|YJJA_ECOLI	0
*NAK[325.13]YK	K[325.13]YNWAHLDIAGTAWR	sp|P0A847|TGT_ECOLI	0	sp|P68767|AMPA_ECOLI	0
EAEYK[325.13]DWTIEQITR	*K[325.13]HGGIR	sp|P0A853|TNAA_ECOLI	0	*sp|P0AEP7|GCL_ECOLI	0
GLTFTYEPK[325.13]VLR	*MDTHAK[325.13]AIDGYTPR	sp|P0A853|TNAA_ECOLI	0	*sp|P25718|AMY1_ECOLI	0
GLTFTYEPK[325.13]VLR	*GTK[325.13]AGAHTVTASMTGGK	sp|P0A853|TNAA_ECOLI	0	*sp|P76347|YEEJ_ECOLI	0
GLTFTYEPK[325.13]VLR	*TGK[325.13]M[147.04]LHALFSHYR	sp|P0A853|TNAA_ECOLI	0	sp|P22564|RIHC_ECOLI	0
NVYIK[325.13]EAFDTGVR	*DPK[325.13]TGK	sp|P0A853|TNAA_ECOLI	0	sp|P0A853|TNAA_ECOLI	6
FAENAYFIK[325.13]QR	*VVIGPVK[325.13]GK	sp|P0A853|TNAA_ECOLI	0	sp|P29131|FTSN_ECOLI	0
*GLTFTYEPK[325.13]VLR	TGK[325.13]QLPC[160.03]PAELLR	sp|P0A853|TNAA_ECOLI	0	sp|P0A853|TNAA_ECOLI	0
*GAEQIYIPVLIK[325.13]K	GAEQIYIPVLIK[325.13]K	sp|P0A853|TNAA_ECOLI	0	sp|P0A853|TNAA_ECOLI	0
GQLAQAK[325.13]NVFAELDVSWDK	*IK[325.13]GSY	sp|P0A8G0|UVRC_ECOLI	1	sp|P76469|KDRA_ECOLI	0
*LIVQDK[325.13]ASAMFR	GGDTVTLNETDLTQIPK[325.13]VIEYC[160.03]K	sp|P0A8S9|FLHD_ECOLI	0	sp|P0AET2|HDEB_ECOLI	0
TFK[325.13]PER	*GAAK[325.13]LMPSELSGGM[147.04]AR	sp|P0A8T7|RPOC_ECOLI	0	*sp|P63386|YRBF_ECOLI	0
LHQC[160.03]GLPK[325.13]K	*K[325.13]AYK	sp|P0A8T7|RPOC_ECOLI	0	sp|P08622|DNAJ_ECOLI	1
IVK[325.13]VYLAVK	*FK[325.13]R	sp|P0A8V2|RPOB_ECOLI	0	sp|P0A9H7|CFA_ECOLI	0
GIK[325.13]DVVTQPQA	*MSAGIALQWM[147.04]SPLGPLVFSYAQPFK[325.13]K	sp|P0A910|OMPA_ECOLI	0	*sp|P0A940|YAET_ECOLI	0
*GIPADK[325.13]ISAR	FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
GIPADK[325.13]ISAR	*GIPADK[325.13]ISAR	sp|P0A910|OMPA_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
VEIEVK[325.13]GIK	*M[147.04]LK[325.13]LFAK	sp|P0A910|OMPA_ECOLI	0	sp|P77682|GTRA_ECOLI	0
GIPADK[325.13]ISAR	*WLEK[325.13]APVIK	sp|P0A910|OMPA_ECOLI	0	sp|P24218|INTD_ECOLI	0
GMGESNPVTGNTC[160.03]DNVK[325.13]QR	*IMK[325.13]K	sp|P0A910|OMPA_ECOLI	0	sp|P0ABB0|ATPA_ECOLI	0
GMGESNPVTGNTC[160.03]DNVK[325.13]QR	*AELGIPK[325.13]SIR	sp|P0A910|OMPA_ECOLI	0	sp|P0A9Q7|ADHE_ECOLI	0
FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	*K[325.13]DAVLSPAAER	sp|P0A910|OMPA_ECOLI	0	sp|P52696|YBHD_ECOLI	1
FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	*ADILSPVK[325.13]ETGTLLGVVSSQAAELC[160.03]GLK	sp|P0A910|OMPA_ECOLI	0	sp|P77432|LSRK_ECOLI	0
MAMK[325.13]K	*LSK[325.13]AVMR	sp|P0A940|YAET_ECOLI	0	sp|P0AEK2|FABG_ECOLI	0
*K[325.13]LGFSVEGELMHEFFINGQYR	INEVTATAVK[325.13]R	sp|P0A951|ATDA_ECOLI	0	sp|P33136|OPGG_ECOLI	0
VVMTGPSK[325.13]DNTPMFVK	*ILIVDAK[325.13]YYK	sp|P0A9B2|G3P1_ECOLI	0	*sp|P15006|MCRC_ECOLI	0
TVDGPSHK[325.13]DWR	*K[325.13]QLQAPR	sp|P0A9B2|G3P1_ECOLI	0	*sp|P0AB20|HSPQ_ECOLI	0
TVDGPSHK[325.13]DWR	*ILIVDAK[325.13]YYK	sp|P0A9B2|G3P1_ECOLI	0	*sp|P15006|MCRC_ECOLI	0
K[325.13]HITAGAK	*TVDGPSHK[325.13]DWR	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0
FDGTVEVK[325.13]DGHLIVNGK	*K[325.13]LR	sp|P0A9B2|G3P1_ECOLI	0	sp|P75931|MVIM_ECOLI	92
TVDGPSHK[325.13]DWR	*AVGK[325.13]VLPELNGK	sp|P0A9B2|G3P1_ECOLI	0	sp|P0A9B2|G3P1_ECOLI	0

IPVVSSPK[325.13]AR	*K[325.13]NAIMMVDFALEAQR	sp|P0A9C5|GLNA_ECOLI	0	sp|P76399|MDTC_ECOLI	0
*nM[147.04]IPEK	LHC[160.03]AK[325.13]R	sp|P0A9E5|FNR_ECOLI	0	sp|P31806|YJEF_ECOLI	0
K[325.13]AGK	*FTK[325.13]AL	sp|P0A9M8|PTA_ECOLI	3	*sp|P16691|PHNO_ECOLI	0
*K[325.13]GVR	IGIQPGHIHK[325.13]PGK	sp|P0A9M8|PTA_ECOLI	7	sp|P0AGE9|SUCD_ECOLI	0
VINQLTGGLAGMAK[325.13]GR	*K[325.13]DGTR	sp|P0A9P0|DLDH_ECOLI	0	*sp|P77286|YDEU_ECOLI	0
*VFTK[325.13]R	VINQLTGGLAGMAK[325.13]GR	sp|P0A9P0|DLDH_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*VFTK[325.13]R	EK[325.13]VINQLTGGLAGMAK	sp|P0A9P0|DLDH_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
VPNGK[325.13]NLDAGK	*NLTADEVATLEYLLK[325.13]K	sp|P0A9P0|DLDH_ECOLI	0	*sp|P27245|MARR_ECOLI	0
VINQLTGGLAGMAK[325.13]GR	*GDAGK[325.13]K	sp|P0A9P0|DLDH_ECOLI	0	sp|P21499|RNR_ECOLI	0
FNLMLETK[325.13]VTAVEAK	*IVQM[147.04]HANK[325.13]R	sp|P0A9P0|DLDH_ECOLI	0	sp|P0A6M8|EFG_ECOLI	0
GVHEGHVAAEVIAGK[325.13]K	*VVK[325.13]K	sp|P0A9P0|DLDH_ECOLI	0	sp|P16916|RHSA_ECOLI	0
*ISK[325.13]K	EK[325.13]VINQLTGGLAGMAK	sp|P0A9P0|DLDH_ECOLI	1	sp|P0A9P0|DLDH_ECOLI	0
*ISK[325.13]K	EDGIYVTMEGK[325.13]K	sp|P0A9P0|DLDH_ECOLI	1	sp|P0A9P0|DLDH_ECOLI	0
*ISK[325.13]K	VINQLTGGLAGMAK[325.13]GR	sp|P0A9P0|DLDH_ECOLI	1	sp|P0A9P0|DLDH_ECOLI	0
ISK[325.13]K	*LGK[325.13]SSR	sp|P0A9P0|DLDH_ECOLI	1	sp|P24205|MSBB_ECOLI	0
*ISK[325.13]K	K[325.13]APAEPQR	sp|P0A9P0|DLDH_ECOLI	5	sp|P0A9P0|DLDH_ECOLI	0
K[325.13]AQR	*K[325.13]EVK	sp|P0A9Q7|ADHE_ECOLI	2	sp|P23847|DPPA_ECOLI	2
K[325.13]GTGLK	*M[147.04]LHK	sp|P0A9V5|YIAG_ECOLI	0	sp|P39172|ZNUA_ECOLI	0
*IIDQEVK[325.13]ALIER	TDK[325.13]FIVR	sp|P0AAI3|FTSH_ECOLI	1	sp|P60422|RL2_ECOLI	0
*K[325.13]GAAADK	AVNDGK[325.13]LAATIAQLPDQIGAK	sp|P0AB58|YCIM_ECOLI	0	sp|P02925|RBSB_ECOLI	0
APVIVQFSNGGASFIAGK[325.13]GVK	*K[325.13]YYDPR	sp|P0AB71|ALF_ECOLI	0	sp|P0AB71|ALF_ECOLI	0
SFLVSEK[325.13]N	*EGK[325.13]FVTSR	sp|P0AB85|APBE_ECOLI	0	sp|P32132|TYPA_ECOLI	0
QLANAVK[325.13]AR	*YAK[325.13]AQGM[147.04]WR	sp|P0AB91|AROG_ECOLI	0	sp|P25516|ACON1_ECOLI	0
ASATDQLK[325.13]K	*GAVSVLDNLSPIK[325.13]AER	sp|P0ABA0|ATPF_ECOLI	0	*sp|P75949|NAGZ_ECOLI	0
K[325.13]LSGGIR	*WEEYLK[325.13]K	sp|P0ABB0|ATPA_ECOLI	0	*sp|P42592|YGJK_ECOLI	0
K[325.13]LSGGIR	*VLK[325.13]AC[160.03]VTADK	sp|P0ABB0|ATPA_ECOLI	0	*sp|P06149|DLD_ECOLI	0
K[325.13]LSGGIR	*M[147.04]K[325.13]GIGGFTK	sp|P0ABB0|ATPA_ECOLI	1	sp|P0AB98|ATP6_ECOLI	0
K[325.13]LSGGIR	*VGGAAQTK[325.13]IMK	sp|P0ABB0|ATPA_ECOLI	0	sp|P0ABB0|ATPA_ECOLI	0
K[325.13]LSGGIR	*VEK[325.13]DLQLMK	sp|P0ABB0|ATPA_ECOLI	0	sp|P06864|BGA2_ECOLI	0
LK[325.13]GILDSFK	*K[325.13]FLAATNNK	sp|P0ABB0|ATPA_ECOLI	0	sp|P37751|YEFI_ECOLI	0
IPFIETVK[325.13]MLDAR	*K[325.13]SQGK	sp|P0ABC3|HFLC_ECOLI	0	sp|P77538|YFHR_ECOLI	5
*K[325.13]LFR	VGGAAQTK[325.13]IMK	sp|P0ABF1|PCNB_ECOLI	0	sp|P0ABB0|ATPA_ECOLI	0
*GLVALIEASDAM[147.04]VK[325.13]AAR	GLMPNPK[325.13]VGTVTPNVAEAVK	sp|P0ABF4|EUTM_ECOLI	0	sp|P0A7L0|RL1_ECOLI	0
MLEEISSVK[325.13]HIPEFVR	*EK[325.13]DPSLSFR	sp|P0ABH7|CISY_ECOLI	0	*sp|P07014|DHSB_ECOLI	0
MLEEISSVK[325.13]HIPEFVR	*TIK[325.13]NSTDSGR	sp|P0ABH7|CISY_ECOLI	0	*sp|P77188|MATC_ECOLI	0
*LVK[325.13]SK	NDVSDSEK[325.13]K	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
*LVK[325.13]SK	K[325.13]ATVELLNR	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
TPLK[325.13]SYPLDIHNVQDHLK	*MVR	sp|P0ABT2|DPS_ECOLI	0	sp|P0A6Y8|DNAK_ECOLI	0
*LVK[325.13]SK	AVQLGGVALGTTQVINSK[325.13]TPLK	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
*K[325.13]ATVELLNR	AVQLGGVALGTTQVINSK[325.13]TPLK	sp|P0ABT2|DPS_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
*AVK[325.13]R	VGEEVEIVGIK[325.13]ETQK	sp|P0ABY7|FLHC_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
GESK[325.13]NISVTEVHAR	*LSLPPSIK[325.13]R	sp|P0ABZ6|SURA_ECOLI	0	sp|P76349|YEEL_ECOLI	0
*LIM[147.04]DQIILQM[147.04]GQK[325.13]M[147.04]GVK	ILLINPTDSDAVGNAVK[325.13]MANQANIPVITLDR	sp|P0ABZ6|SURA_ECOLI	0	sp|P02925|RBSB_ECOLI	0

*nMSNNIR	K[325.13]IIGEQLGVK	sp|P0AC38|ASPA_ECOLI	1	sp|P0A6A8|ACP_ECOLI	0
*MSK[325.13]IC[160.03]NDLR	AQVAQIAGK[325.13]PSSEVSM[147.04]IHAR	sp|P0AC38|ASPA_ECOLI	0	sp|P0ADB1|OSME_ECOLI	0
*K[325.13]HATR	WLGGMLTNWK[325.13]TVR	sp|P0ACB4|HEMG_ECOLI	6	sp|P0A7V0|RS2_ECOLI	0
M[147.04]YSDLPK[325.13]VLHTLAGK	*LK[325.13]LH	sp|P0ACC7|GLMU_ECOLI	0	sp|P00393|DHNA_ECOLI	0
ALK[325.13]DAVK	*MPFK[325.13]K	sp|P0ACF0|DBHA_ECOLI	0	sp|P71244|WCAM_ECOLI	0
IAAGADISK[325.13]AAAGR	*MTIEYTK	sp|P0ACF4|DBHB_ECOLI	0	sp|P33129|HTRE_ECOLI	0
*AASVLVELAK[325.13]EYSSYNGC[160.03]R	M[147.04]GLK	sp|P0ACQ7|TDCA_ECOLI	0	sp|P10443|DPO3A_ECOLI	0
*NPQVAAMLK[325.13]NK	TPPAAVLLK[325.13]K	sp|P0ACT6|UIDR_ECOLI	0	sp|P0A7J7|RL11_ECOLI	0
SANK[325.13]GM[147.04]PILLLTALGTIEHR	*VAVIK[325.13]AVR	sp|P0ACZ8|CUSR_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
*EK[325.13]WDELSLR	FGQGEAAPVVAPAPAPAPEVQTK[325.13]HFTLK	sp|P0AD35|YFDO_ECOLI	0	sp|P0A910|OMPA_ECOLI	0
LDAPLIVVATQGGK[325.13]SAR	*K[325.13]LR	sp|P0AD61|KPYK1_ECOLI	0	sp|P0AD61|KPYK1_ECOLI	92
EHLK[325.13]AHGGENIHIISK	*K[325.13]LR	sp|P0AD61|KPYK1_ECOLI	1	sp|P0AD61|KPYK1_ECOLI	1
*K[325.13]LR	LDAPLIVVATQGGK[325.13]SAR	sp|P0AD61|KPYK1_ECOLI	92	sp|P0AD61|KPYK1_ECOLI	0
*K[325.13]LR	GNIMK[325.13]FTEGAFK	sp|P0AD61|KPYK1_ECOLI	0	sp|P08200|IDH_ECOLI	0
M[147.04]SAGSPK	*SDWM[147.04]EMEK[325.13]QR	sp|P0ADA3|NLPD_ECOLI	0	sp|P0A7I4|RF3_ECOLI	0
K[325.13]GMSR	*MAGMAIDGK[325.13]DK	sp|P0ADB1|OSME_ECOLI	0	sp|P0AFD6|NUOI_ECOLI	0
AQVAQIAGK[325.13]PSSEVSMIHAR	*WLEK[325.13]APVIK	sp|P0ADB1|OSME_ECOLI	0	sp|P24218|INTD_ECOLI	0
*M[147.04]HEK[325.13]R	VALYGIDYLMK[325.13]DK	sp|P0ADG7|IMDH_ECOLI	1	sp|P09373|PFLB_ECOLI	0
K[325.13]DISSANLR	*SLK[325.13]EDAEEFLQRPIK	sp|P0ADS6|YGGE_ECOLI	1	sp|P77319|HSCC_ECOLI	1
K[325.13]DISSANLR	*YLENPANAQAFAQLK[325.13]K	sp|P0ADS6|YGGE_ECOLI	1	sp|P37661|EPTB_ECOLI	0
*DK[325.13]AR	K[325.13]DISSANLR	sp|P0ADS6|YGGE_ECOLI	0	sp|P0ADS6|YGGE_ECOLI	0
*K[325.13]VNP	DASGTINVDIDHK[325.13]R	sp|P0ADU5|YGIW_ECOLI	0	sp|P0ADU5|YGIW_ECOLI	0
*M[147.04]K[325.13]FK	IQK[325.13]LHTYR	sp|P0ADV1|LPTA_ECOLI	2	sp|P09373|PFLB_ECOLI	1
K[325.13]EAK	*K[325.13]QSR	sp|P0ADY1|PPID_ECOLI	0	sp|P0A7V8|RS4_ECOLI	0
K[325.13]MHK	*K[325.13]PNSALR	sp|P0ADY7|RL16_ECOLI	0	sp|P0A7S3|RS12_ECOLI	2
TK[325.13]FR	*K[325.13]RPQTR	sp|P0ADY7|RL16_ECOLI	0	sp|P0A9J0|RNG_ECOLI	0
TK[325.13]FR	*VEGNK[325.13]VR	sp|P0ADY7|RL16_ECOLI	0	sp|P21179|CATE_ECOLI	0
LAAAK[325.13]LPIK	*K[325.13]VLP	sp|P0ADY7|RL16_ECOLI	0	sp|P27245|MARR_ECOLI	0
MHK[325.13]GR	*VK[325.13]GIDPR	sp|P0ADY7|RL16_ECOLI	0	sp|P15286|FLK_ECOLI	6
TK[325.13]FR	*VK[325.13]GIDPR	sp|P0ADY7|RL16_ECOLI	3	*sp|P15286|FLK_ECOLI	0
TK[325.13]FR	*MAK[325.13]APIR	sp|P0ADY7|RL16_ECOLI	3	*sp|P0A7R9|RS11_ECOLI	0
*AVK[325.13]R	LAAAK[325.13]LPIK	sp|P0ADY7|RL16_ECOLI	0	sp|P0ADY7|RL16_ECOLI	1
APHVSEK[325.13]ASTAMEK	*K[325.13]HNLR	sp|P0ADZ0|RL23_ECOLI	0	*sp|P45428|DCUD_ECOLI	0
GK[325.13]VK	*WLPK[325.13]LGIVQK	sp|P0ADZ0|RL23_ECOLI	4	*sp|P32709|NRFD_ECOLI	0
GK[325.13]VK	*IPVDK[325.13]LIQVR	sp|P0ADZ0|RL23_ECOLI	4	*sp|P52636|YCCM_ECOLI	0
LGVDVYAVSTDTHFTHK[325.13]AWHSSSETIAK	*VIDQGTGETM[147.04]GDM[147.04]TK[325.13]HGQR	sp|P0AE08|AHPC_ECOLI	0	*sp|P42641|OBG_ECOLI	0
IK[325.13]AAQYVASHPGEVC[160.03]PAK	*EVM[147.04]EK[325.13]LIR	sp|P0AE08|AHPC_ECOLI	0	sp|P69902|FCTA_ECOLI	0
IK[325.13]AAQYVASHPGEVC[160.03]PAK	*GK[325.13]VLDIC[160.03]AR	sp|P0AE08|AHPC_ECOLI	0	sp|P0A825|GLYA_ECOLI	0
K[325.13]YGR	*LK[325.13]ELAAATSSADEGASVAYK	sp|P0AE82|CPXA_ECOLI	0	sp|P32162|YIIS_ECOLI	0
*IK[325.13]QAVALR	EAK[325.13]DLVESAPAALK	sp|P0AED9|DCM_ECOLI	2	sp|P0A7K2|RL7_ECOLI	0
K[325.13]AIEQDAK	*AK[325.13]LNGIPSIAWPEK	sp|P0AEE5|DGAL_ECOLI	0	sp|P75990|YCGF_ECOLI	0
VTVPLFEGVQK[325.13]TQTIR	*IK[325.13]QAVALR	sp|P0AEG4|DSBA_ECOLI	0	sp|P0AED9|DCM_ECOLI	0
EMK[325.13]AIWC[160.03]AK	*EMK[325.13]AIWC[160.03]AK	sp|P0AEG6|DSBC_ECOLI	0	sp|P0AEG6|DSBC_ECOLI	0

<table>
<tr><td>AK[325.13]QAVYR</td><td>*IWMETTK[325.13]GGSK</td><td>sp|P0AEH5|ELAB_ECOLI</td><td>0</td><td>sp|P0AGM0|YHHT_ECOLI</td><td>0</td></tr>
<tr><td>AMMK[325.13]K</td><td>*LSK[325.13]AVMR</td><td>sp|P0AEK2|FABG_ECOLI</td><td>1</td><td>sp|P0AEK2|FABG_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]HGGIR</td><td>EVHIEGYTPEDK[325.13]K</td><td>sp|P0AEP7|GCL_ECOLI</td><td>0</td><td>sp|P0A8P3|FETP_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]LIGR</td><td>AHVIK[325.13]SHHNVGGLPK</td><td>sp|P0AER0|GLPF_ECOLI</td><td>0</td><td>sp|P04079|GUAA_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]NPQK</td><td>GGDTVTLNETDLTQIPK[325.13]VIEYC[160.03]K</td><td>sp|P0AET2|HDEB_ECOLI</td><td>0</td><td>sp|P0AET2|HDEB_ECOLI</td><td>0</td></tr>
<tr><td>GGDTVTLNETDLTQIPK[325.13]VIEYC[160.03]K</td><td>*M[147.04]IDPK</td><td>sp|P0AET2|HDEB_ECOLI</td><td>0</td><td>sp|Q46868|YQIC_ECOLI</td><td>1</td></tr>
<tr><td>K[325.13]LQSMK</td><td>*TALAM[147.04]TQK[325.13]AAIGK</td><td>sp|P0AEU7|SKP_ECOLI</td><td>0</td><td>*sp|P52598|YGBI_ECOLI</td><td>0</td></tr>
<tr><td>*TK[325.13]LEK</td><td>LQSMK[325.13]AGSDR</td><td>sp|P0AEU7|SKP_ECOLI</td><td>0</td><td>sp|P0AEU7|SKP_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]LQSMK</td><td>*NLAGM[147.04]ILEK[325.13]TGR</td><td>sp|P0AEU7|SKP_ECOLI</td><td>0</td><td>sp|P77439|PTFX1_ECOLI</td><td>0</td></tr>
<tr><td>LQSMK[325.13]AGSDR</td><td>*TAIK[325.13]PWLMDNK</td><td>sp|P0AEU7|SKP_ECOLI</td><td>0</td><td>sp|P05523|FPG_ECOLI</td><td>0</td></tr>
<tr><td>TGVSNTLENEFK[325.13]GR</td><td>*SK[325.13]PFSDM[147.04]YFLAAEK</td><td>sp|P0AEU7|SKP_ECOLI</td><td>0</td><td>sp|P0ADP0|YIGB_ECOLI</td><td>0</td></tr>
<tr><td>*MK[325.13]K</td><td>LQSMK[325.13]AGSDR</td><td>sp|P0AEU7|SKP_ECOLI</td><td>0</td><td>sp|P0AEU7|SKP_ECOLI</td><td>0</td></tr>
<tr><td>NSK[325.13]R</td><td>*K[325.13]TR</td><td>sp|P0AEX7|LIVH_ECOLI</td><td>0</td><td>sp|P60422|RL2_ECOLI</td><td>48</td></tr>
<tr><td>*M[147.04]LFPQQK[325.13]AIDSPEAK</td><td>K[325.13]GAIVTGK</td><td>sp|P0AEY1|MARC_ECOLI</td><td>5</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td></tr>
<tr><td>*MAGMAIDGK[325.13]DK</td><td>VLAQK[325.13]AVR</td><td>sp|P0AFD6|NUOI_ECOLI</td><td>0</td><td>sp|P77717|YBAY_ECOLI</td><td>0</td></tr>
<tr><td>STFQQLPGTGVK[325.13]PDQFHSQTR</td><td>*ESK[325.13]R</td><td>sp|P0AFG3|ODO1_ECOLI</td><td>0</td><td>sp|P39874|YBEM_ECOLI</td><td>1</td></tr>
<tr><td>HK[325.13]EHLGTGDVK</td><td>*TSK[325.13]VK</td><td>sp|P0AFG3|ODO1_ECOLI</td><td>0</td><td>sp|P00550|PTM3C_ECOLI</td><td>0</td></tr>
<tr><td>IK[325.13]ELAVK</td><td>*NTSM[147.04]TSVLK[325.13]DK</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>*sp|P32135|YIHN_ECOLI</td><td>0</td></tr>
<tr><td>LLAEHNLDASAIK[325.13]GTGVGGR</td><td>*K[325.13]FDPVVR</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>*sp|P0A7N9|RL33_ECOLI</td><td>0</td></tr>
<tr><td>IK[325.13]ELAVK</td><td>*AGEK[325.13]TPPDALEK</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|P77218|EUTD_ECOLI</td><td>0</td></tr>
<tr><td>IK[325.13]ELAVK</td><td>*NYWLAFGEK[325.13]R</td><td>sp|P0AFG6|ODO2_ECOLI</td><td>0</td><td>sp|Q46837|ACFD_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]MNMDGVR</td><td>*GGFSSSSGYELAK[325.13]QMLAR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>*sp|P06846|EBGR_ECOLI</td><td>0</td></tr>
<tr><td>LETIEGSK[325.13]GK</td><td>*QTPATAK[325.13]K</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|Q46861|YGIQ_ECOLI</td><td>0</td></tr>
<tr><td>*ASK[325.13]K</td><td>K[325.13]HNASR</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td><td>sp|P0A7U7|RS20_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]AIK</td><td>GMLPK[325.13]GPLGR</td><td>sp|P0AFL6|PPX_ECOLI</td><td>2</td><td>sp|P0AA10|RL13_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]FYR</td><td>AWAEK[325.13]NPAAAK</td><td>sp|P0AFM2|PROX_ECOLI</td><td>0</td><td>sp|P0AFM2|PROX_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]LAPEVK</td><td>*VFTK[325.13]R</td><td>sp|P0AFS3|FOLM_ECOLI</td><td>0</td><td>sp|P0A9P0|DLDH_ECOLI</td><td>0</td></tr>
<tr><td>TGDTISGK[325.13]IRPPK</td><td>*M[147.04]HK</td><td>sp|P0AG30|RHO_ECOLI</td><td>0</td><td>sp|P02924|ARAF_ECOLI</td><td>0</td></tr>
<tr><td>QMK[325.13]ALNK</td><td>*EIK[325.13]QANK</td><td>sp|P0AG34|RHTB_ECOLI</td><td>0</td><td>*sp|P00490|PHSM_ECOLI</td><td>0</td></tr>
<tr><td>MYAVFQSGGK</td><td>*QFLNK[325.13]INELR</td><td>sp|P0AG48|RL21_ECOLI</td><td>0</td><td>sp|P76543|YFFL_ECOLI</td><td>0</td></tr>
<tr><td>MYAVFQSGGK</td><td>*DSHLPISGSIK[325.13]AR</td><td>sp|P0AG48|RL21_ECOLI</td><td>0</td><td>sp|P00926|SDHD_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]HYR</td><td>*K[325.13]YETGR</td><td>sp|P0AG48|RL21_ECOLI</td><td>0</td><td>sp|P75967|YMFD_ECOLI</td><td>0</td></tr>
<tr><td>*INGQVITIK[325.13]GK</td><td>GIPADK[325.13]ISAR</td><td>sp|P0AG55|RL6_ECOLI</td><td>6</td><td>sp|P0A910|OMPA_ECOLI</td><td>0</td></tr>
<tr><td>*EVK[325.13]R</td><td>LK[325.13]VR</td><td>sp|P0AG59|RS14_ECOLI</td><td>0</td><td>sp|P16431|HYCE_ECOLI</td><td>0</td></tr>
<tr><td>*EVK[325.13]R</td><td>YFAK[325.13]R</td><td>sp|P0AG59|RS14_ECOLI</td><td>5</td><td>sp|P0AG59|RS14_ECOLI</td><td>0</td></tr>
<tr><td>*FIK[325.13]R</td><td>FVK[325.13]HPIYGK</td><td>sp|P0AG63|RS17_ECOLI</td><td>0</td><td>sp|P0AG63|RS17_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]GAIVTGK</td><td>*TSLGSLLDHTGAFGESEK[325.13]YAAR</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td><td>*sp|P28629|ADIA_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]GAIVTGK</td><td>*NDGC[160.03]HLLFIQC[160.03]PVC[160.03]AEK[325.13]YK</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td><td>*sp|P24188|YCEA_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]GAIVTGK</td><td>*WQSLSIFGC[160.03]FLC[160.03]K[325.13]M[147.04]TLFR</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td><td>*sp|P77607|YAGL_ECOLI</td><td>0</td></tr>
<tr><td>VTAVDAK[325.13]GATVELADGVEGYLR</td><td>*K[325.13]NR</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td><td>sp|P0AG67|RS1_ECOLI</td><td>24</td></tr>
<tr><td>K[325.13]GAIVTGK</td><td>*K[325.13]GIR</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td><td>sp|P35340|AHPF_ECOLI</td><td>0</td></tr>
<tr><td>VIK[325.13]LDQK</td><td>*MVK[325.13]NPDIVAGVAALK</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td><td>sp|P0ABQ0|COABC_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]GAIVTGK</td><td>*M[147.04]LQEELC[160.03]SVVEASGASLEK[325.13]GR</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td><td>sp|P76508|YFDL_ECOLI</td><td>0</td></tr>
</table>

<table>
<tr><td>*K[325.13]NR</td><td>K[325.13]GAIVTGK</td><td>sp|P0AG67|RS1_ECOLI</td><td>24</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]NR</td><td>ANPWQQFAETHNK[325.13]GDR</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td><td>sp|P0AG67|RS1_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]AGLDPEQPPK</td><td>IYAAFK[325.13]K</td><td>sp|P0AG80|UGPB_ECOLI</td><td>0</td><td>sp|P0AFG8|ODP1_ECOLI</td><td>0</td></tr>
<tr><td>M[147.04]SEK[325.13]LQVVTLLGSLR</td><td>*K[325.13]LVATAPR</td><td>sp|P0AGE6|YIEF_ECOLI</td><td>0</td><td>sp|P76043|YCJQ_ECOLI</td><td>0</td></tr>
<tr><td>IGIQPGHIHK[325.13]PGK</td><td>*K[325.13]ISI</td><td>sp|P0AGE9|SUCD_ECOLI</td><td>0</td><td>sp|P43533|FLGN_ECOLI</td><td>0</td></tr>
<tr><td>IGIQPGHIHK[325.13]PGK</td><td>*LNGLIK[325.13]TR</td><td>sp|P0AGE9|SUCD_ECOLI</td><td>0</td><td>sp|P39321|YTFN_ECOLI</td><td>1</td></tr>
<tr><td>*IWMETTK[325.13]GGSK</td><td>LGETGDAIAK[325.13]QTR</td><td>sp|P0AGM0|YHHT_ECOLI</td><td>0</td><td>sp|P64581|YQJD_ECOLI</td><td>0</td></tr>
<tr><td>GQAHWEGDIK[325.13]R</td><td>*K[325.13]HGR</td><td>sp|P0C0L2|OSMC_ECOLI</td><td>0</td><td>sp|P00968|CARB_ECOLI</td><td>1</td></tr>
<tr><td>GQAHWEGDIK[325.13]R</td><td>*YK[325.13]GK</td><td>sp|P0C0L2|OSMC_ECOLI</td><td>0</td><td>*sp|P0ADA3|NLPD_ECOLI</td><td>1</td></tr>
<tr><td>GQAHWEGDIK[325.13]R</td><td>*K[325.13]GYK</td><td>sp|P0C0L2|OSMC_ECOLI</td><td>0</td><td>*sp|P76190|YDHO_ECOLI</td><td>1</td></tr>
<tr><td>*MTIHK[325.13]K</td><td>VLC[160.03]VTALGHTVAEAQK[325.13]R</td><td>sp|P0C0L2|OSMC_ECOLI</td><td>1</td><td>sp|P15640|PUR2_ECOLI</td><td>0</td></tr>
<tr><td>*MVGK[325.13]DPR</td><td>NLTSQMVEYGQVK[325.13]R</td><td>sp|P0C0V0|DEGP_ECOLI</td><td>0</td><td>sp|P0C0V0|DEGP_ECOLI</td><td>0</td></tr>
<tr><td>*DGK[325.13]SYK</td><td>LNTSNNTK[325.13]VR</td><td>sp|P10100|RLPA_ECOLI</td><td>0</td><td>sp|P10100|RLPA_ECOLI</td><td>0</td></tr>
<tr><td>GGGK[325.13]LAPENTLASIDVGAK</td><td>*VYELM[147.04]QEGK[325.13]SK</td><td>sp|P10908|UGPQ_ECOLI</td><td>0</td><td>*sp|P0ABM9|CCMH_ECOLI</td><td>0</td></tr>
<tr><td>*IIWAPDK[325.13]HLGR</td><td>EGAELAFTYQNDK[325.13]LK</td><td>sp|P11458|NADA_ECOLI</td><td>0</td><td>sp|P0AEK4|FABI_ECOLI</td><td>0</td></tr>
<tr><td>GK[325.13]TR</td><td>*VC[160.03]LHNAVTLC[160.03]NWVWPMTVSPLK[325.13]SR</td><td>sp|P13036|FECA_ECOLI</td><td>2</td><td>*sp|P76192|YDHV_ECOLI</td><td>0</td></tr>
<tr><td>*C[160.03]VIELDIAK[325.13]GK</td><td>IWIENLSK[325.13]DK</td><td>sp|P14294|TOP3_ECOLI</td><td>0</td><td>sp|P30863|DKGB_ECOLI</td><td>0</td></tr>
<tr><td>*C[160.03]VIELDIAK[325.13]GK</td><td>YPQATIK[325.13]LR</td><td>sp|P14294|TOP3_ECOLI</td><td>0</td><td>sp|P31463|YIDZ_ECOLI</td><td>0</td></tr>
<tr><td>C[160.03]VIELDIAK[325.13]GK</td><td>*C[160.03]VIELDIAK[325.13]GK</td><td>sp|P14294|TOP3_ECOLI</td><td>0</td><td>sp|P14294|TOP3_ECOLI</td><td>0</td></tr>
<tr><td>C[160.03]VIELDIAK[325.13]GK</td><td>*IWIENLSK[325.13]DK</td><td>sp|P14294|TOP3_ECOLI</td><td>0</td><td>*sp|P30863|DKGB_ECOLI</td><td>0</td></tr>
<tr><td>*C[160.03]VIELDIAK[325.13]GK</td><td>AK[325.13]QAVYR</td><td>sp|P14294|TOP3_ECOLI</td><td>0</td><td>sp|P0AEH5|ELAB_ECOLI</td><td>0</td></tr>
<tr><td>*C[160.03]VIELDIAK[325.13]GK</td><td>LGETGDAIAK[325.13]QTR</td><td>sp|P14294|TOP3_ECOLI</td><td>0</td><td>sp|P64581|YQJD_ECOLI</td><td>0</td></tr>
<tr><td>DTALK[325.13]ALHER</td><td>*TLLYAINGGVDEK[325.13]LK</td><td>sp|P14376|RCSC_ECOLI</td><td>0</td><td>*sp|P42632|TDCE_ECOLI</td><td>0</td></tr>
<tr><td>*ELIDAGK[325.13]ELPQYIK</td><td>AK[325.13]AEAQVIIEQANK</td><td>sp|P14407|FUMB_ECOLI</td><td>0</td><td>sp|P0ABA0|ATPF_ECOLI</td><td>0</td></tr>
<tr><td>SGK[325.13]K</td><td>*K[325.13]GVHTR</td><td>sp|P15032|RECE_ECOLI</td><td>0</td><td>sp|P0AA80|GARP_ECOLI</td><td>0</td></tr>
<tr><td>FM[147.04]LQDLLGVVSPGLK[325.13]R</td><td>*K[325.13]VNP</td><td>sp|P15078|CSTA_ECOLI</td><td>0</td><td>sp|P0ADU5|YGIW_ECOLI</td><td>0</td></tr>
<tr><td>ITAAK[325.13]QNVR</td><td>*M[147.04]SDQLQM[147.04]TDGM[147.04]HIIVEALK[325.13]QNNIDTIYGVVGIPVTDMAR</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td><td>*sp|P0AFI0|OXC_ECOLI</td><td>0</td></tr>
<tr><td>VYSAK[325.13]IAGIK</td><td>*TTLLK[325.13]SISAR</td><td>sp|P15639|PUR9_ECOLI</td><td>0</td><td>sp|P16678|PHNK_ECOLI</td><td>0</td></tr>
<tr><td>VAK[325.13]R</td><td>*VAK[325.13]R</td><td>sp|P16916|RHSA_ECOLI</td><td>0</td><td>sp|P16916|RHSA_ECOLI</td><td>0</td></tr>
<tr><td>VAK[325.13]R</td><td>*IIK[325.13]R</td><td>sp|P16916|RHSA_ECOLI</td><td>0</td><td>sp|P76071|INSH5_ECOLI</td><td>0</td></tr>
<tr><td>*VVK[325.13]K</td><td>GVHEGHVAAEVIAGK[325.13]K</td><td>sp|P16916|RHSA_ECOLI</td><td>0</td><td>sp|P0A9P0|DLDH_ECOLI</td><td>0</td></tr>
<tr><td>*DK[325.13]LDVPIK</td><td>QDGGK[325.13]ALK</td><td>sp|P18775|DMSA_ECOLI</td><td>0</td><td>sp|P32141|YIHT_ECOLI</td><td>0</td></tr>
<tr><td>LK[325.13]ER</td><td>*TGK[325.13]AAR</td><td>sp|P19323|FHLA_ECOLI</td><td>0</td><td>sp|P0A7K6|RL19_ECOLI</td><td>0</td></tr>
<tr><td>*AHELGLK[325.13]PR</td><td>M[147.04]PKPGILK</td><td>sp|P21151|FADA_ECOLI</td><td>0</td><td>sp|P0AB43|YCGL_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]IDK</td><td>STK[325.13]QQEATQPDDVIR</td><td>sp|P21177|FADB_ECOLI</td><td>0</td><td>sp|P76116|YNCE_ECOLI</td><td>0</td></tr>
<tr><td>*VEGNK[325.13]VR</td><td>K[325.13]NIGPK</td><td>sp|P21179|CATE_ECOLI</td><td>1</td><td>sp|P32136|YIHO_ECOLI</td><td>0</td></tr>
<tr><td>QGNK[325.13]PLSQALK</td><td>*NGVK[325.13]AVVFDR</td><td>sp|P21189|DPO2_ECOLI</td><td>0</td><td>sp|P09832|GLTD_ECOLI</td><td>0</td></tr>
<tr><td>*AENK[325.13]A</td><td>K[325.13]NVELLTGFSNR</td><td>sp|P21362|YCIF_ECOLI</td><td>0</td><td>sp|P76236|YEAI_ECOLI</td><td>0</td></tr>
<tr><td>HGFLPLK[325.13]EIAR</td><td>*AVK[325.13]PR</td><td>sp|P21513|RNE_ECOLI</td><td>0</td><td>sp|P37690|YIBP_ECOLI</td><td>6</td></tr>
<tr><td>IPSINVSK[325.13]HR</td><td>*K[325.13]LTLM[147.04]VGFNR</td><td>sp|P21599|KPYK2_ECOLI</td><td>0</td><td>sp|P75931|MVIM_ECOLI</td><td>0</td></tr>
<tr><td>SQLNYSEENLK[325.13]QAR</td><td>*SQLNYSEENLK[325.13]QAR</td><td>sp|P21888|SYC_ECOLI</td><td>0</td><td>sp|P21888|SYC_ECOLI</td><td>0</td></tr>
<tr><td>*FSGK[325.13]ELATPLLK</td><td>ENLEALLVALK[325.13]K</td><td>sp|P23325|ARPA_ECOLI</td><td>0</td><td>sp|P0A7L0|RL1_ECOLI</td><td>0</td></tr>
<tr><td>NK[325.13]HQQHLAQLPK</td><td>*K[325.13]FR</td><td>sp|P23830|PSS_ECOLI</td><td>0</td><td>sp|P25666|HTRL_ECOLI</td><td>0</td></tr>
</table>

<table>
<tr><td>K[325.13]LAIAASSLWK</td><td>*GK[325.13]IIK</td><td>sp|P23843|OPPA_ECOLI</td><td>0</td><td>*sp|P28916|YBFD_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]GVK</td><td>*K[325.13]AVIPVAGLGTR</td><td>sp|P23847|DPPA_ECOLI</td><td>2</td><td>*sp|P0AEP3|GALU_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]GVK</td><td>*WLPK[325.13]LGIVQK</td><td>sp|P23847|DPPA_ECOLI</td><td>2</td><td>*sp|P32709|NRFD_ECOLI</td><td>0</td></tr>
<tr><td>MK[325.13]NK</td><td>*LNK[325.13]R</td><td>sp|P23908|ARGE_ECOLI</td><td>0</td><td>sp|P38134|ETK_ECOLI</td><td>0</td></tr>
<tr><td>*YK[325.13]R</td><td>SDVQAAK[325.13]DDAAR</td><td>sp|P23910|ARAJ_ECOLI</td><td>0</td><td>sp|P69776|LPP_ECOLI</td><td>0</td></tr>
<tr><td>*MGK[325.13]K</td><td>GMGESNPVTGNTC[160.03]DNVK[325.13]QR</td><td>sp|P24183|FDNG_ECOLI</td><td>0</td><td>sp|P0A910|OMPA_ECOLI</td><td>0</td></tr>
<tr><td>*VPGK[325.13]QGSLLQAK</td><td>VVMTGPSK[325.13]DNTPMFVK</td><td>sp|P24192|HYPD_ECOLI</td><td>0</td><td>sp|P0A9B2|G3P1_ECOLI</td><td>0</td></tr>
<tr><td>VLAYGEAK[325.13]R</td><td>*LSK[325.13]S</td><td>sp|P24230|RECG_ECOLI</td><td>0</td><td>sp|P0A9L8|P5CR_ECOLI</td><td>1</td></tr>
<tr><td>*ELLTTLNLK[325.13]LEPADDFR</td><td>SK[325.13]QADVQASAVSENNK</td><td>sp|P24251|CRL_ECOLI</td><td>0</td><td>sp|P37197|YHJA_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]QLV</td><td>HMNIK[325.13]VTR</td><td>sp|P24255|RP54_ECOLI</td><td>1</td><td>sp|P0A6Y8|DNAK_ECOLI</td><td>0</td></tr>
<tr><td>*MK[325.13]LNDSNLFR</td><td>AEQALK[325.13]QSR</td><td>sp|P25526|GABD_ECOLI</td><td>0</td><td>sp|P64581|YQJD_ECOLI</td><td>0</td></tr>
<tr><td>*VEQK[325.13]VAR</td><td>VAMVSMTGSVSAGEK[325.13]IMATAAK</td><td>sp|P25553|ALDA_ECOLI</td><td>0</td><td>sp|P25553|ALDA_ECOLI</td><td>0</td></tr>
<tr><td>*VEQK[325.13]VAR</td><td>VAM[147.04]VSMTGSVSAGEK[325.13]IMATAAK</td><td>sp|P25553|ALDA_ECOLI</td><td>0</td><td>sp|P25553|ALDA_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]NNPK</td><td>*VYFEK[325.13]PR</td><td>sp|P25907|YDBD_ECOLI</td><td>0</td><td>sp|P00888|AROF_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]DGPGK</td><td>*AVEK[325.13]AIVK</td><td>sp|P26266|FEPE_ECOLI</td><td>0</td><td>sp|P08956|T1RK_ECOLI</td><td>0</td></tr>
<tr><td>*AIAMLNEPEIIK[325.13]K</td><td>SFGAPTITK[325.13]DGVSVAR</td><td>sp|P27128|RFAI_ECOLI</td><td>0</td><td>sp|P0A6F5|CH60_ECOLI</td><td>0</td></tr>
<tr><td>*AIEAGLPK[325.13]R</td><td>INLDK[325.13]IHR</td><td>sp|P27253|SBM_ECOLI</td><td>0</td><td>sp|P00452|RIR1_ECOLI</td><td>0</td></tr>
<tr><td>*nMAFK</td><td>FIK[325.13]QR</td><td>sp|P28635|METQ_ECOLI</td><td>0</td><td>sp|P42909|PTPB1_ECOLI</td><td>0</td></tr>
<tr><td>*nMPPR</td><td>FIK[325.13]QR</td><td>sp|P30011|NADC_ECOLI</td><td>5</td><td>sp|P42909|PTPB1_ECOLI</td><td>0</td></tr>
<tr><td>MGK[325.13]IVAIK</td><td>*LC[160.03]RPSEVVLEILPDAQK[325.13]GAFSK</td><td>sp|P30131|HYPF_ECOLI</td><td>0</td><td>*sp|P0AB96|ARSC_ECOLI</td><td>0</td></tr>
<tr><td>*EYYGSANTSTK[325.13]R</td><td>NGQAANK[325.13]AAVTMPSSK</td><td>sp|P30192|YCHG_ECOLI</td><td>0</td><td>sp|P0A7W7|RS8_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]VGVQNGTTHQK</td><td>HVVK[325.13]VVNPELHK</td><td>sp|P30859|ARTI_ECOLI</td><td>0</td><td>sp|P60422|RL2_ECOLI</td><td>0</td></tr>
<tr><td>*nMEVNK</td><td>VIEYC[160.03]K[325.13]K</td><td>sp|P31061|NOHA_ECOLI</td><td>0</td><td>sp|P0AET2|HDEB_ECOLI</td><td>0</td></tr>
<tr><td>GK[325.13]FPR</td><td>*MQLSISAPQAWLK[325.13]YK</td><td>sp|P31466|YIEG_ECOLI</td><td>0</td><td>sp|P76655|YQIG_ECOLI</td><td>0</td></tr>
<tr><td>*WK[325.13]PLR</td><td>GESK[325.13]NISVTEVHAR</td><td>sp|P31600|NFRA_ECOLI</td><td>0</td><td>sp|P0ABZ6|SURA_ECOLI</td><td>0</td></tr>
<tr><td>AAK[325.13]PK</td><td>*IGK[325.13]PK</td><td>sp|P32053|INTA_ECOLI</td><td>0</td><td>sp|P67697|YDCQ_ECOLI</td><td>0</td></tr>
<tr><td>GK[325.13]GGK</td><td>*QGK[325.13]R</td><td>sp|P32057|WCAI_ECOLI</td><td>0</td><td>sp|P76215|ASTE_ECOLI</td><td>0</td></tr>
<tr><td>GK[325.13]GGK</td><td>*K[325.13]VLR</td><td>sp|P32057|WCAI_ECOLI</td><td>0</td><td>sp|P05458|PTRA_ECOLI</td><td>0</td></tr>
<tr><td>GK[325.13]GGK</td><td>*ANIK[325.13]GGK</td><td>sp|P32057|WCAI_ECOLI</td><td>0</td><td>sp|P52143|YPJA_ECOLI</td><td>0</td></tr>
<tr><td>*QTPESFAFTLK[325.13]R</td><td>HLTK[325.13]K</td><td>sp|P32131|HEMN_ECOLI</td><td>1</td><td>sp|P32721|ALSA_ECOLI</td><td>0</td></tr>
<tr><td>NAK[325.13]VGK</td><td>*IALHQK[325.13]DLNLALQSAK</td><td>sp|P32132|TYPA_ECOLI</td><td>0</td><td>sp|P77161|GLXR_ECOLI</td><td>2</td></tr>
<tr><td>*IGPK[325.13]GK</td><td>ITAFIYK[325.13]K</td><td>sp|P32137|YIHP_ECOLI</td><td>0</td><td>sp|P76177|YDGH_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]GQQLSSFAQLR</td><td>QASLLK[325.13]TNYVSR</td><td>sp|P32176|FDOG_ECOLI</td><td>0</td><td>sp|P37636|MDTE_ECOLI</td><td>0</td></tr>
<tr><td>*WLPK[325.13]LGIVQK</td><td>ITIK[325.13]EAIPR</td><td>sp|P32709|NRFD_ECOLI</td><td>1</td><td>sp|P0ADY3|RL14_ECOLI</td><td>0</td></tr>
<tr><td>*QPK[325.13]IPVK</td><td>ELAK[325.13]ASVSR</td><td>sp|P32712|NRFG_ECOLI</td><td>0</td><td>sp|P0A7V3|RS3_ECOLI</td><td>0</td></tr>
<tr><td>*LAGTLGM[147.04]LSK[325.13]VMR</td><td>EK[325.13]GIPYTTVR</td><td>sp|P32715|MDTO_ECOLI</td><td>0</td><td>sp|P0AG90|SECD_ECOLI</td><td>0</td></tr>
<tr><td>*M[147.04]VIK[325.13]K</td><td>K[325.13]HNASR</td><td>sp|P33014|YEED_ECOLI</td><td>1</td><td>sp|P0A7U7|RS20_ECOLI</td><td>0</td></tr>
<tr><td>*MMGAEGLK[325.13]K</td><td>TK[325.13]PHVNVGTIGHVDHGK</td><td>sp|P33195|GCSP_ECOLI</td><td>4</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td></tr>
<tr><td>*SVK[325.13]LPPLK</td><td>TEGK[325.13]QSPFSFVLSFNPADVQPNAR</td><td>sp|P33225|TORA_ECOLI</td><td>0</td><td>sp|P77717|YBAY_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]EAGVSR</td><td>*K[325.13]DYPAR</td><td>sp|P33230|YDAC_ECOLI</td><td>0</td><td>*sp|P33599|NUOCD_ECOLI</td><td>0</td></tr>
<tr><td>LK[325.13]TLR</td><td>*THK[325.13]GVK</td><td>sp|P33345|MOLR_ECOLI</td><td>0</td><td>sp|P32153|FRVX_ECOLI</td><td>0</td></tr>
<tr><td>*GVM[147.04]LNFK[325.13]K</td><td>K[325.13]IAAGDTSNLGDTSTLADPGVVEK</td><td>sp|P33666|YDBA_ECOLI</td><td>0</td><td>sp|P27550|ACSA_ECOLI</td><td>0</td></tr>
<tr><td>*ALK[325.13]R</td><td>K[325.13]DSHLPISGSIK</td><td>sp|P33940|MQO_ECOLI</td><td>0</td><td>sp|P00926|SDHD_ECOLI</td><td>0</td></tr>
</table>

*K[325.13]GIR	K[325.13]NQMK	sp|P35340|AHPF_ECOLI	0	sp|P37330|MASZ_ECOLI	0
*K[325.13]GIR	TK[325.13]PHVNVGTIGHVDHGK	sp|P35340|AHPF_ECOLI	2	sp|P0A6N1|EFTU_ECOLI	0
*K[325.13]QIR	EALHDSLK[325.13]R	sp|P36655|DSBD_ECOLI	1	sp|P0A9T4|TAS_ECOLI	0
*TK[325.13]IPK	AVNDGK[325.13]LAATIAQLPDQIGAK	sp|P36667|WBBL_ECOLI	0	sp|P02925|RBSB_ECOLI	0
GFSLAQK[325.13]MVGR	*LLSK[325.13]MPTMAAMC[160.03]YK	sp|P36683|ACON2_ECOLI	0	sp|P0ABH7|CISY_ECOLI	0
*K[325.13]LMK	MPLPGSVVASVSPDELLK[325.13]TLPK	sp|P37016|YADK_ECOLI	0	sp|P76104|YDCP_ECOLI	0
VK[325.13]TSSPDLAIGR	*IWMETTK[325.13]GGSK	sp|P37388|XYLG_ECOLI	0	sp|P0AGM0|YHHT_ECOLI	0
*MGK[325.13]AVIAIHGGAGAISR	GYIK[325.13]AK	sp|P37595|IAAA_ECOLI	5	sp|P32176|FDOG_ECOLI	0
TK[325.13]TM[147.04]PR	*GVVK[325.13]HLQLR	sp|P37650|BCSC_ECOLI	0	sp|P0A6T3|GAL1_ECOLI	0
*AVK[325.13]PR	ANNVGELEK[325.13]HK	sp|P37690|YIBP_ECOLI	0	sp|P0AG27|YIBN_ECOLI	0
*DSLASK[325.13]AHR	K[325.13]YGDK	sp|P37747|GLF_ECOLI	0	sp|P37747|GLF_ECOLI	0
VPSYTASK[325.13]SGVM[147.04]GVTR	*MTK[325.13]QPPIAK	sp|P37769|KDUD_ECOLI	0	sp|P33228|RECT_ECOLI	0
*GIYLVNLDEK[325.13]IDMDNLK	GEK[325.13]VQAK	sp|P39265|ALSB_ECOLI	0	sp|P02925|RBSB_ECOLI	1
*GIYLVNLDEK[325.13]IDMDNLK	VQAK[325.13]YPVDLK	sp|P39265|ALSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
*GIYLVNLDEK[325.13]IDMDNLK	ILLINPTDSDAVGNAVK[325.13]M[147.04]ANQANIPVITLDR	sp|P39265|ALSB_ECOLI	0	sp|P02925|RBSB_ECOLI	0
*K[325.13]ALTSVK	NDVSDSEK[325.13]K	sp|P39276|YJDL_ECOLI	5	sp|P0ABT2|DPS_ECOLI	0
*K[325.13]ALTSVK	SK[325.13]ATNLLYTR	sp|P39276|YJDL_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
*K[325.13]ALTSVK	AVQLGGVALGTTQVINSK[325.13]TPLK	sp|P39276|YJDL_ECOLI	0	sp|P0ABT2|DPS_ECOLI	0
VQSTSK[325.13]TAPQAK	*SQLEEIIK[325.13]K	sp|P39279|YJEJ_ECOLI	0	*sp|P37903|USPF_ECOLI	0
*AK[325.13]AVAAK	MIEQIEK[325.13]VAIK	sp|P39297|YJFO_ECOLI	0	sp|P38035|RTCR_ECOLI	0
*NIK[325.13]TIR	GM[147.04]INK[325.13]M[147.04]SADLLIVPFIDK	sp|P39404|BGLJ_ECOLI	0	sp|P0AAB8|USPD_ECOLI	0
*ATIAK[325.13]HR	FGGK[325.13]VINVINGK	sp|P39405|FHUF_ECOLI	3	sp|P37194|SLP_ECOLI	0
*DGLDVGSQLLLSTLTPHTK[325.13]GK	VAVIK[325.13]AVR	sp|P39406|RSMC_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
*ESK[325.13]R	STFQQLPGTGVK[325.13]PDQFHSQTR	sp|P39874|YBEM_ECOLI	1	sp|P0AFG3|ODO1_ECOLI	0
*M[147.04]SK[325.13]VLVLK	LK[325.13]ALAHPTK	sp|P41407|AZOR_ECOLI	0	sp|P19768|INSJ_ECOLI	0
*nMEIASNK	K[325.13]TAVEAAIAR	sp|P42628|YHAO_ECOLI	1	sp|P77611|RNFC_ECOLI	0
*DAK[325.13]NK	VINQLTGGLAGMAK[325.13]GR	sp|P42640|YHBX_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
IGK[325.13]R	*IGK[325.13]R	sp|P43676|PITB_ECOLI	1	sp|P43676|PITB_ECOLI	0
*IGK[325.13]R	K[325.13]LLDEGR	sp|P43676|PITB_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
GK[325.13]VVVMGM[147.04]GK	*FFSIDGTK[325.13]LPDAVEEAIEAEM[147.04]EK	sp|P45395|KDSD_ECOLI	0	*sp|P31120|GLMM_ECOLI	0
VK[325.13]SSAQAK	*LPFNK[325.13]VR	sp|P45523|FKBA_ECOLI	0	sp|P43340|YCAK_ECOLI	0
*EQEK[325.13]LGIK	VK[325.13]SSAQAK	sp|P45523|FKBA_ECOLI	0	sp|P45523|FKBA_ECOLI	0
AAFK[325.13]NDDQK	*MSLHSPGK[325.13]AFR	sp|P45523|FKBA_ECOLI	0	sp|P77541|PRPB_ECOLI	0
*MPLLPALK[325.13]SYLSLK	K[325.13]LLDEGR	sp|P45537|YHFK_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*MPLLPALK[325.13]SYLSLK	ETQK[325.13]STC[160.03]TGVEMFR	sp|P45537|YHFK_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
LK[325.13]QDLAR	*K[325.13]FDR	sp|P45543|FRLD_ECOLI	0	sp|P33643|RLUD_ECOLI	0
DPK[325.13]R	*K[325.13]M[147.04]VIDR	sp|P45804|YHGE_ECOLI	0	sp|P13669|MNGR_ECOLI	0
LEK[325.13]LAAQDPLK	*MPK[325.13]LR	sp|P46125|YEDI_ECOLI	0	sp|P37666|GHRB_ECOLI	1
K[325.13]ASISGVQR	*QYQQVIDNYPK[325.13]LSATLR	sp|P46889|FTSK_ECOLI	0	sp|P39285|YJEP_ECOLI	1
*LISGK[325.13]K	LTQPGK[325.13]R	sp|P52134|YPJK_ECOLI	0	sp|P75966|RLUE_ECOLI	0
*TALAM[147.04]TQK[325.13]AAIGK	QTFAQK[325.13]AQAFEQDR	sp|P52598|YGBI_ECOLI	0	sp|P0AEU7|SKP_ECOLI	0
QFAMSGAFSGALPLWLNNEK[325.13]WIVK	*K[325.13]MPK	sp|P52645|YDBH_ECOLI	0	sp|P45769|YHDZ_ECOLI	0
HIGGGHK[325.13]QAYR	*IIQLK[325.13]LEQQALM[147.04]K	sp|P60422|RL2_ECOLI	0	*sp|P63284|CLPB_ECOLI	0

<table>
<tr><td>*IVDFK[325.13]R</td><td>HIGGGHK[325.13]QAYR</td><td>sp|P60422|RL2_ECOLI</td><td>0</td><td>sp|P60422|RL2_ECOLI</td><td>0</td></tr>
<tr><td>HIGGGHK[325.13]QAYR</td><td>*NSK[325.13]SGGR</td><td>sp|P60422|RL2_ECOLI</td><td>0</td><td>sp|P60422|RL2_ECOLI</td><td>0</td></tr>
<tr><td>HVVK[325.13]VVNPELHK</td><td>*AANFASFDK[325.13]LR</td><td>sp|P60422|RL2_ECOLI</td><td>0</td><td>*sp|Q46833|YGHE_ECOLI</td><td>0</td></tr>
<tr><td>IVDFK[325.13]R</td><td>*TVFPNM[147.04]K[325.13]LSK</td><td>sp|P60422|RL2_ECOLI</td><td>0</td><td>sp|P76159|LYSQ_ECOLI</td><td>0</td></tr>
<tr><td>HIGGGHK[325.13]QAYR</td><td>*K[325.13]VGVQNGTTHQK</td><td>sp|P60422|RL2_ECOLI</td><td>0</td><td>sp|P30859|ARTI_ECOLI</td><td>0</td></tr>
<tr><td>HIGGGHK[325.13]QAYR</td><td>*SK[325.13]AEVYHIIQLK</td><td>sp|P60422|RL2_ECOLI</td><td>0</td><td>sp|P52123|YFJH_ECOLI</td><td>0</td></tr>
<tr><td>HVVK[325.13]VVNPELHK</td><td>*MLDK[325.13]IDPLAAALR</td><td>sp|P60422|RL2_ECOLI</td><td>0</td><td>sp|P77658|YNAA_ECOLI</td><td>0</td></tr>
<tr><td>IVDFK[325.13]R</td><td>*ELAEK[325.13]AQLPTTMTLMALGMLPK</td><td>sp|P60422|RL2_ECOLI</td><td>0</td><td>sp|P08142|ILVB_ECOLI</td><td>0</td></tr>
<tr><td>MIGLVGK[325.13]K</td><td>*M[147.04]VIATVK[325.13]GDVHDIGK</td><td>sp|P60438|RL3_ECOLI</td><td>0</td><td>*sp|P13009|METH_ECOLI</td><td>0</td></tr>
<tr><td>GFAGTVK[325.13]R</td><td>*ILK[325.13]SDDDLEPVVIGR</td><td>sp|P60438|RL3_ECOLI</td><td>0</td><td>sp|P0AEH3|ELAA_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]MYR</td><td>*FLPQFC[160.03]AK[325.13]AP</td><td>sp|P60723|RL4_ECOLI</td><td>0</td><td>*sp|P32718|ALSK_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]MYR</td><td>*K[325.13]SGLGVYDWR</td><td>sp|P60723|RL4_ECOLI</td><td>0</td><td>*sp|P76083|PAAH_ECOLI</td><td>0</td></tr>
<tr><td>AQK[325.13]TR</td><td>*AQK[325.13]TR</td><td>sp|P60723|RL4_ECOLI</td><td>0</td><td>sp|P60723|RL4_ECOLI</td><td>0</td></tr>
<tr><td>*AQK[325.13]TR</td><td>SGSIK[325.13]SPIWR</td><td>sp|P60723|RL4_ECOLI</td><td>0</td><td>sp|P60723|RL4_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]MYR</td><td>*M[147.04]AIDIFQSLK</td><td>sp|P60723|RL4_ECOLI</td><td>0</td><td>sp|Q9JMR6|YUAY_ECOLI</td><td>0</td></tr>
<tr><td>K[325.13]PGMDR</td><td>*APGAK[325.13]DAK</td><td>sp|P61889|MDH_ECOLI</td><td>0</td><td>sp|P30130|FIMD_ECOLI</td><td>0</td></tr>
<tr><td>*YGDEQVK[325.13]QWR</td><td>HYGALQGLNK[325.13]AETAEK</td><td>sp|P62707|GPMA_ECOLI</td><td>0</td><td>sp|P62707|GPMA_ECOLI</td><td>0</td></tr>
<tr><td>YGDEQVK[325.13]QWR</td><td>*FTGFVFK[325.13]IQANM[147.04]DPK</td><td>sp|P62707|GPMA_ECOLI</td><td>0</td><td>sp|P0A7I4|RF3_ECOLI</td><td>0</td></tr>
<tr><td>*IIQLK[325.13]LEQQALM[147.04]K</td><td>VGEEVEIVGIK[325.13]ETQK</td><td>sp|P63284|CLPB_ECOLI</td><td>0</td><td>sp|P0A6N1|EFTU_ECOLI</td><td>0</td></tr>
<tr><td>*LYK[325.13]R</td><td>AVLEVAGVHNVLAK[325.13]AYGSTNPINVVR</td><td>sp|P63284|CLPB_ECOLI</td><td>0</td><td>sp|P0A7W1|RS5_ECOLI</td><td>0</td></tr>
<tr><td>*LEK[325.13]EMEK</td><td>K[325.13]DHHSR</td><td>sp|P63389|YHES_ECOLI</td><td>1</td><td>sp|P0ADZ4|RS15_ECOLI</td><td>0</td></tr>
<tr><td>*VQQQAMIDK[325.13]LDHLQR</td><td>K[325.13]ANR</td><td>sp|P64426|YDDW_ECOLI</td><td>0</td><td>sp|P0A6I9|COAE_ECOLI</td><td>0</td></tr>
<tr><td>*DEDAVAFHK[325.13]TTPHYK</td><td>IATSYPHLLK[325.13]R</td><td>sp|P64461|LSRG_ECOLI</td><td>0</td><td>sp|P60757|HIS1_ECOLI</td><td>0</td></tr>
<tr><td>*M[147.04]QIK[325.13]VIYSLIDNMVNFK</td><td>K[325.13]VLP</td><td>sp|P64490|YOAC_ECOLI</td><td>0</td><td>sp|P27245|MARR_ECOLI</td><td>0</td></tr>
<tr><td>SK[325.13]EELSK</td><td>*C[160.03]VIELDIAK[325.13]GK</td><td>sp|P64581|YQJD_ECOLI</td><td>0</td><td>sp|P14294|TOP3_ECOLI</td><td>0</td></tr>
<tr><td>SK[325.13]EELSK</td><td>*M[147.04]SK[325.13]LPTGVEIR</td><td>sp|P64581|YQJD_ECOLI</td><td>0</td><td>*sp|P76056|INTR_ECOLI</td><td>0</td></tr>
<tr><td>AEQALK[325.13]QSR</td><td>*VQK[325.13]M[147.04]IIANR</td><td>sp|P64581|YQJD_ECOLI</td><td>0</td><td>*sp|P0A6X1|HEM1_ECOLI</td><td>0</td></tr>
<tr><td>SK[325.13]AEQALK</td><td>*ITLIENK[325.13]MK</td><td>sp|P64581|YQJD_ECOLI</td><td>0</td><td>sp|P0A6T5|GCH1_ECOLI</td><td>0</td></tr>
<tr><td>SK[325.13]EELSK</td><td>*VQSTSK[325.13]TAPQAK</td><td>sp|P64581|YQJD_ECOLI</td><td>0</td><td>sp|P39279|YJEJ_ECOLI</td><td>0</td></tr>
<tr><td>*HTEPK[325.13]R</td><td>HTEPK[325.13]R</td><td>sp|P67143|YHGN_ECOLI</td><td>0</td><td>sp|P67143|YHGN_ECOLI</td><td>0</td></tr>
<tr><td>HTEPK[325.13]R</td><td>*NK[325.13]ESLFFMSVM[147.04]ELR</td><td>sp|P67143|YHGN_ECOLI</td><td>0</td><td>sp|P39279|YJEJ_ECOLI</td><td>0</td></tr>
<tr><td>*K[325.13]PELEVNHGAV</td><td>VK[325.13]VLK</td><td>sp|P69212|MDTJ_ECOLI</td><td>5</td><td>sp|P0AC53|G6PD_ECOLI</td><td>0</td></tr>
<tr><td>MQINASK[325.13]MK</td><td>*MGVK[325.13]ITGLDK</td><td>sp|P69411|RCSF_ECOLI</td><td>0</td><td>sp|Q9JMR7|YUAX_ECOLI</td><td>6</td></tr>
<tr><td>LDNMATK[325.13]YR</td><td>*GATAEQLLEHLGNGK[325.13]SFDSVAQAWDAAM[147.04]ADAK</td><td>sp|P69776|LPP_ECOLI</td><td>0</td><td>*sp|P08192|FOLC_ECOLI</td><td>0</td></tr>
<tr><td>LDNMATK[325.13]YR</td><td>*YLDHLK[325.13]MEYAFWMDGAESLIPNQAYR</td><td>sp|P69776|LPP_ECOLI</td><td>0</td><td>*sp|P62601|TREF_ECOLI</td><td>0</td></tr>
<tr><td>*LDNMATK[325.13]YR</td><td>GM[147.04]GESNPVTGNTC[160.03]DNVK[325.13]QR</td><td>sp|P69776|LPP_ECOLI</td><td>0</td><td>sp|P0A910|OMPA_ECOLI</td><td>0</td></tr>
<tr><td>MK[325.13]VSLVLVHAQDHLMTSM[147.04]LAR</td><td>*K[325.13]LGHK</td><td>sp|P69791|PTQA_ECOLI</td><td>0</td><td>sp|P0A6V1|GLGC_ECOLI</td><td>0</td></tr>
<tr><td>EVM[147.04]EK[325.13]LIR</td><td>*K[325.13]ISTLM[147.04]R</td><td>sp|P69902|FCTA_ECOLI</td><td>0</td><td>sp|P76035|YCIW_ECOLI</td><td>0</td></tr>
<tr><td>*VTDTGK[325.13]LR</td><td>IAGK[325.13]K</td><td>sp|P71242|WCAK_ECOLI</td><td>0</td><td>sp|P23845|CYSN_ECOLI</td><td>1</td></tr>
<tr><td>*LAALK[325.13]K</td><td>AVNDGK[325.13]LAATIAQLPDQIGAK</td><td>sp|P71311|YAIS_ECOLI</td><td>0</td><td>sp|P02925|RBSB_ECOLI</td><td>0</td></tr>
<tr><td>GDVK[325.13]YR</td><td>*YM[147.04]ATM[147.04]PPVVLPAPAGAWAK[325.13]HK</td><td>sp|P75691|YAHK_ECOLI</td><td>0</td><td>sp|P76464|YFAS_ECOLI</td><td>0</td></tr>
<tr><td>*LAK[325.13]R</td><td>AK[325.13]YQR</td><td>sp|P75770|YBHN_ECOLI</td><td>9</td><td>sp|P0A7T7|RS18_ECOLI</td><td>0</td></tr>
<tr><td>*LAK[325.13]R</td><td>K[325.13]FC[160.03]R</td><td>sp|P75770|YBHN_ECOLI</td><td>0</td><td>sp|P0A7T7|RS18_ECOLI</td><td>0</td></tr>
</table>

M[147.04]NLTLK[325.13]ESLVTR	*ITAIM[147.04]GPSGIGK[325.13]TTLLR	sp|P75785|YBIP_ECOLI	0	sp|P63386|YRBF_ECOLI	0
M[147.04]LNYVIK[325.13]R	*LAFALSK[325.13]TGSLNLYVMDLASGQIR	sp|P75798|GSIC_ECOLI	0	*sp|P0A855|TOLB_ECOLI	0
VK[325.13]AK	*K[325.13]VAK	sp|P75942|FLGJ_ECOLI	0	sp|P0A7S3|RS12_ECOLI	0
*AK[325.13]PVSLLR	GATGLGLK[325.13]EAK	sp|P75969|INTE_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
*LLGVK[325.13]R	LMEK[325.13]LITYTR	sp|P76046|YCJX_ECOLI	1	sp|P76594|YFIQ_ECOLI	0
*VK[325.13]TLK	M[147.04]K[325.13]LAVVTGQIVC[160.03]TVR	sp|P76071|INSH5_ECOLI	0	sp|P0AEJ8|EUTN_ECOLI	0
IIK[325.13]R	*M[147.04]NTLK[325.13]AEFASQVR	sp|P76071|INSH5_ECOLI	0	sp|P77399|FADJ_ECOLI	0
LAGQK[325.13]LVAR	*LAGQK[325.13]LVAR	sp|P76076|YDBL_ECOLI	0	sp|P76076|YDBL_ECOLI	0
*K[325.13]LAR	TK[325.13]HAVTEASPM[147.04]VK	sp|P76102|YDCM_ECOLI	0	sp|P02358|RS6_ECOLI	0
*VLM[147.04]TLK[325.13]YGNK	IYAAFK[325.13]K	sp|P76137|YDET_ECOLI	0	sp|P0AFG8|ODP1_ECOLI	0
*VQFK[325.13]LTYPAR	NVK[325.13]VWIR	sp|P76150|YNEK_ECOLI	0	sp|P0A9N4|PFLA_ECOLI	0
*K[325.13]VISK	DAK[325.13]DQAGIDK	sp|P76164|YDFW_ECOLI	1	sp|P0A6P9|ENO_ECOLI	0
FSGNYGNMTEVSYQVAK[325.13]R	*AAK[325.13]K	sp|P76177|YDGH_ECOLI	0	sp|P76177|YDGH_ECOLI	0
K[325.13]DAK	*AAK[325.13]AK	sp|P76177|YDGH_ECOLI	0	sp|P76177|YDGH_ECOLI	0
*AAK[325.13]AK	AAK[325.13]PK	sp|P76177|YDGH_ECOLI	0	sp|P32053|INTA_ECOLI	0
*QNATAK[325.13]G	TK[325.13]PHVNVGTIGHVDHGK	sp|P76235|YEAH_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*K[325.13]TLTSATK	MLSPLLK	sp|P76251|TTUC_ECOLI	0	sp|P75870|YCCS_ECOLI	0
K[325.13]VIISTGSK	*VQWALTK[325.13]AALWNETK	sp|P76257|YOAA_ECOLI	0	sp|P0AAH0|PSTB_ECOLI	0
*ADK[325.13]NNVLVK	VEK[325.13]ILNR	sp|P76339|YEDV_ECOLI	0	sp|P77546|YDAV_ECOLI	0
*K[325.13]NAIMMVDFALEAQR	FNTMTK[325.13]K	sp|P76399|MDTC_ECOLI	0	sp|P0A9C5|GLNA_ECOLI	0
*K[325.13]NAIMMVDFALEAQR	IPVVSSPK[325.13]AR	sp|P76399|MDTC_ECOLI	0	sp|P0A9C5|GLNA_ECOLI	0
NAGM[147.04]TNAK[325.13]PAILLM[147.04]IR	*K[325.13]M[147.04]GLNALAR	sp|P76399|MDTC_ECOLI	0	*sp|P78271|YFES_ECOLI	0
*AK[325.13]TEAR	ITVK[325.13]DGIR	sp|P76459|ATOA_ECOLI	0	sp|P38097|YEGE_ECOLI	0
*QM[147.04]LITVAK[325.13]DVK	EIWK[325.13]QK	sp|P76481|YFBK_ECOLI	0	sp|P24218|INTD_ECOLI	0
*NNK[325.13]SMLLLFFSLLIISTAK	VAVIK[325.13]AVR	sp|P76507|YFDI_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
LEK[325.13]K	*IM[147.04]PNK[325.13]LPTNK	sp|P76539|YPEA_ECOLI	0	*sp|P33342|YEHC_ECOLI	0
*FM[147.04]DK[325.13]PLSASAILK	K[325.13]EAK	sp|P76542|INTZ_ECOLI	0	sp|P0ADY1|PPID_ECOLI	0
K[325.13]LR	*EIK[325.13]R	sp|P76542|INTZ_ECOLI	0	sp|P0A9H3|LDCI_ECOLI	0
APK[325.13]NEETK	*THK[325.13]GVK	sp|P76543|YFFL_ECOLI	0	sp|P32153|FRVX_ECOLI	0
*EWVNPNPK[325.13]K	FNLM[147.04]LETK[325.13]VTAVEAK	sp|P76550|YFFS_ECOLI	0	sp|P0A9P0|DLDH_ECOLI	0
*MALNLTGEK[325.13]TPLTPK	AHK[325.13]DLDLAK	sp|P76578|YFHM_ECOLI	0	sp|P0ABA0|ATPF_ECOLI	0
*K[325.13]SGK	LASK[325.13]AQK	sp|P76578|YFHM_ECOLI	0	sp|P40711|YAEJ_ECOLI	0
*IALHQK[325.13]DLNLALQSAK	GK[325.13]GGK	sp|P77161|GLXR_ECOLI	0	sp|P32057|WCAI_ECOLI	0
*AGEK[325.13]TPPDALEK	IK[325.13]ELAVK	sp|P77218|EUTD_ECOLI	0	sp|P0AFG6|ODO2_ECOLI	0
*MTQDDAADK[325.13]AAK	M[147.04]DELAK[325.13]LVGQSSVQK	sp|P77304|TPPB_ECOLI	0	sp|P0ABY2|FLIT_ECOLI	0
YLK[325.13]R	*LPK[325.13]R	sp|P77334|GMR_ECOLI	0	sp|P0A776|RPPH_ECOLI	1
LAIFWLVFGLC[160.03]WK[325.13]VLEK	*K[325.13]VYLSSADWMTR	sp|P77338|KEFA_ECOLI	0	*sp|P0A7B1|PPK_ECOLI	0
DGLK[325.13]R	*GHAK[325.13]AR	sp|P77354|YAFU_ECOLI	0	sp|P0A8H6|YIHI_ECOLI	0
*LPAK[325.13]VTPR	EAK[325.13]DLVESAPAALK	sp|P77374|YNFE_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
K[325.13]LLNEAK	*GVQLEDGPAAFK[325.13]TIK	sp|P77434|YFDZ_ECOLI	0	*sp|P37765|RLUB_ECOLI	0
*K[325.13]LLNEAK	INLDK[325.13]IHR	sp|P77434|YFDZ_ECOLI	0	sp|P00452|RIR1_ECOLI	0
*TLK[325.13]K	AVAK[325.13]HLLSEK	sp|P77455|MAOC_ECOLI	5	sp|P77455|MAOC_ECOLI	0
*C[160.03]INLLK[325.13]AVPDATINFDFAAM[147.04]R	APVIVQFSNGGASFIAGK[325.13]GVK	sp|P77468|SFMD_ECOLI	0	sp|P0AB71|ALF_ECOLI	0

*LAPSHVTAPFK[325.13]TVAEWR	K[325.13]AIEQDAK	sp|P77546|YDAV_ECOLI	0	sp|P0AEE5|DGAL_ECOLI	0
*K[325.13]VGLTHPK	MLSK[325.13]FK	sp|P77608|MHPD_ECOLI	5	sp|P23830|PSS_ECOLI	0
*EEK[325.13]K	TK[325.13]PHVNVGTIGHVDHGK	sp|P77609|FLXA_ECOLI	1	sp|P0A6N1|EFTU_ECOLI	0
*K[325.13]EEK	TK[325.13]PHVNVGTIGHVDHGK	sp|P77609|FLXA_ECOLI	0	sp|P0A6N1|EFTU_ECOLI	0
*K[325.13]EEK	TTLTAAITTVLAK[325.13]TYGGAAR	sp|P77609|FLXA_ECOLI	5	sp|P0A6N1|EFTU_ECOLI	0
INK[325.13]LLC[160.03]YLTNR	*K[325.13]VGVVGIGGLGHMGIK	sp|P77657|YAGK_ECOLI	0	*sp|P75691|YAHK_ECOLI	0
*VLAQK[325.13]AVR	TEGK[325.13]QSPFSFVLSFNPADVQPNAR	sp|P77717|YBAY_ECOLI	0	sp|P77717|YBAY_ECOLI	0
K[325.13]TMIR	*FVVK[325.13]NVDNSDSYLR	sp|P77721|YDJF_ECOLI	0	*sp|P76621|CSID_ECOLI	0
K[325.13]TYPLQLTGFHYK	*MELK[325.13]ATTLGK	sp|P77783|YNFF_ECOLI	0	sp|P15038|HELD_ECOLI	0
*LWLDVK[325.13]R	K[325.13]ATK	sp|P77808|CINAL_ECOLI	2	sp|P0A7Q1|RL35_ECOLI	1
TLK[325.13]DLDQAALLLAR	*GLFIK[325.13]GIYGR	sp|Q00037|TNPA_ECOLI	0	sp|P07913|TDH_ECOLI	0
MDVR	*SGSIGSAAK[325.13]ELGLTQPAVSK	sp|Q06067|ATOS_ECOLI	0	sp|P0ACQ7|TDCA_ECOLI	1
*NK[325.13]LLSR	NK[325.13]LLSR	sp|Q2EES9|TORI_ECOLI	0	sp|Q2EES9|TORI_ECOLI	0
*QVLDVAAALK[325.13]ALR	EAK[325.13]DLVESAPAALK	sp|Q46803|YGEW_ECOLI	0	sp|P0A7K2|RL7_ECOLI	0
*ILTALEK[325.13]I	FGANSVLK[325.13]PEIK	sp|Q46814|XDHD_ECOLI	0	sp|P13035|GLPD_ECOLI	0
GLTPK[325.13]MLTEANLNSLR	*SK[325.13]FYR	sp|Q46851|YGHZ_ECOLI	0	sp|P22523|MUKB_ECOLI	0
HYLAPSDK[325.13]LDHK	*K[325.13]GYK	sp|Q47146|FADE_ECOLI	0	sp|P76190|YDHO_ECOLI	0