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Novel protein identification method by observation of metastable ions in matrix-assisted laser desorption ionization mass spectrometry

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Abstract

Peptide mass fingerprinting (PMF) is one strategy for protein identification by mass spectrometry (MS) analysis. The input data used in the PMF are mass lists of an enzymatic-digested protein extracted from matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) MS spectra. The MALDI process can lead to post-source decay (PSD) fragmentation, which occurs after the acceleration region of the ionization source. The PSD corresponds to the fragmentation of metastable ions. Herein, we present an enhanced PMF method by introducing a metastable ion relative C-terminal amino acid truncation of peptides derived from LysN protein digested peptides. In comparison to conventional PMF, highly reliable identification of this new method was verified by using three parameters of C-terminal amino acid sequence, N-terminal Lys and mass for database search. A non-probability-based sequence database search algorithm was developed for protein identification, especially for protein mixture, which showed advantageous in a way to common probability-based sequence database search algorithm. Because of its highly desirable property, the novel method could support the conventional PMF to find more applications in the analysis of protein identification.

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1 Chapter I: General Introduction and Aims

1.1 Mass Spectrometry

Mass spectrometry (MS) is an analytical technology that ionizes chemical substances and systematizes the ions based on the mass-to-charge ratio (m/z). MS is applied to many different fields and is acted on pure sample or complex mixtures as well. A mass spectrum is a plot of the intensity of ion signal on the basis of m/z . These spectra are used to identify the masses of particles or molecules, to measure the elements or isotopes, and to illustrate the chemical structures of molecules.

MS was invented by J.J. Thomson at the Cavendish Laboratory in the University of Cambridge. Thomson first used his apparatus to measure m/z of electrons in 1897, and he received the 1906 Nobel Prize in Physics by this work in “discovering” the electron. He established the foundation of the MS field according to his early work on cathode. The first mass spectrometer to measure the m/z of charged atoms was built by Thomson and F. Aston. Mass spectrometers were redesigned by Aston and others in order to improve the resolution in the early decades of the 20th century. Under their efforts on the development of mass spectrometers, elemental isotopes were proved to be existed and separated by MS. Furthermore, MS became a remarkable analytical tool really during the World War II, since the isotopes played significant roles developed by E.O. Lawrence in the Manhattan Project. (Griffiths 2008)

Commercial mass spectrometers were launched in the 1940s, and MS was still dominated by physicists and industrial chemists as a useful technique. K. Biemann made great contributions to apply the MS to chemistry field. He used

MS to determine the structure of complex molecules, founded basic regulation for peptide fragmentation; even designed an early peptide sequencing method. Consequently, A. Marshall and M.Comisarow first applied Fourier transform (TF) to ion cyclotron resonance (ICR) MS. FTICR MS is one of the most important technologies for complex mixture analysis since its ultrahigh resolution power. Then, in 1988, electrospray ionization (ESI) and matrix-assisted laser desorption/ionization (MALDI) appeared on the MS field. These ionization techniques revolutionized biological MS and are served as the predominant types of ionization sources for macromolecule at present (Griffiths 2008).

A common mass spectrometer consists of three main modules: ion source, analyzer, and detector (Figure. 1). Ion source is a device to ionize the analyte molecules to form charged ions by laser, electrospray, plasma, etc. As above mentioned, ESI and MALDI are the most common ion sources used in proteomics. Various analyzers can connect to ion sources to assemble the core part of mass spectrometers, such as time-of-flight (TOF), quadrupole (Q), ion trap (IT) and FTICR. The ion source generated charged ions are separated according to their m/z in the analyzer, and the ion intensity at different m/z values are recorded by detector. A visual mass spectrum are output by computer finally.

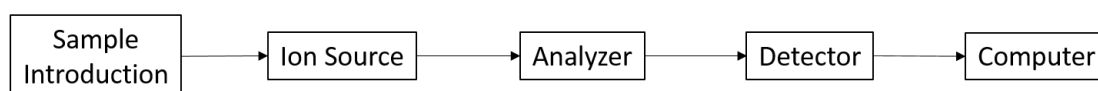


Figure. 1 Simplest form of MS.

1.1.1 Ion Source

1.1.1.1 Matrix-Assisted Laser Desorption Ionization (MALDI).

Matrix-assisted ultraviolet laser desorption/ionization (MALDI) was presented by Karas and Hillenkamp in 1984, which can rapidly measure the masses of non-volatile biological compounds with a TOF mass spectrometer (Karas et al. 1987, Karas, Gluckmann & Schafer 2000). It has become a widely used and strong technique to ionize a series molecules including proteins, peptides, DNA, RNA, polymers and large inorganic compounds in the gas-phase. One feature of MALDI to be different with other ionization technique is the use of MALDI matrix, which support the desorption and ionization of MALDI. Note that Tanaka and colleagues firstly acquired large proteins' mass spectra by using a combination of nano-metal particles and glycerol, instead of the MALDI matrix, in laser-desorption ionization TOFMS (Tanaka et al. 1988). The advantages of MALDI are the easy sample preparation, fast speed for data analysis, and a good tolerance to contamination (Stump et al. 2002, Chen, Carroll & Beavis 1998).

As to the full name of MALDI, “matrix” indicates a basic characteristic of MALDI MS, which is the appropriate matrix materials supported ionization on analytes. The success of MALDI ionization depends on good sample preparation, thus the matrix selection and the sample preparation optimization control the quality of the ionization results. Several substances have been measured as MALDI matrices. The wavelength of laser used in the MALDI determines the selection of suitable matrix. Small organic molecules with a wavelength absorption in the range of 266-355 nm are the most frequently used matrices in MALDI. α -Cyano-4-hydroxycinnamic acid (CHCA) is one of the most common matrices for peptides/proteins analysis by MALDI (Beavis, 1992).

The process of MALDI is separated into two steps. There are two ways of the first step, dropping the analyte, which is dissolved in a matrix containing solvent,

on a MALDI plate before analysis till the mixture is dried; or dropping the solution of matrix on the plate first, then dropping the sample compound on the dried matrix. After drying, the analyte-matrix mixture form crystals named “solid solution”. The analyte molecules are isolated from each other completed by embedding the matrix all over. In the second step, the majority of the “solid solution” is desorbed by strong laser impulse in the vacuum inside the ion source of MS in a short time (Knochenmuss 2002, Karas, Krüger 2003). The excitation of the matrix leads to the large energy accumulation in the condensed phase, consequently rapid heating of the crystals is induced by irradiation of the laser pulse. Then the matrix is sublimated and expanded into the gas phase caused by the rapid heating, along with the desorption of the surface of crystals. Finally, the analyte is entrained with the gaseous matrix and joins the expanding matrix plume (Dreisewerd 2003).

There are many different pathways, either chemical or physical, to explain the origin of ions generated in MALDI, such as excited state proton transfer, gas-phase photo ionization, desorption of preformed ions and in-molecule reactions, but is not completely understood yet. (Zenobi, Knochenmuss 1998, Knochenmuss, Zenobi 2003). Proton transfer and gas-phase photoionization are two most widely accepted mechanisms of ion formation in MALDI. The differences between these two mechanisms are the time. The former occurs in the solid phase, and the latter proceeds in the sublimated matrix plume. An electrostatic field supplied by high voltage accelerate the gas-phase ions towards the analyzer (Figure. 2). In comparison to other laser ionization techniques, MALDI is more sensitive and general. The highly increased sensitivity reflects on two points. The first point is the formation of analyte sample clusters are prevented by a huge number of matrix molecules separate the embedded analyte molecules exhaustively. Second, since the matrix absorb most of the energy from the incident laser pulse, the damage to the samples is

decreased, and prompt the laser transfer energy to the analyte efficiently. As to the generalizability, there are also two aspects. First, since the matrix molecules absorb the laser pulse, the adjustment of wavelength of laser to match the absorption range of every sample molecules is unnecessary. In the second place, macromolecules with high masses around 100,000 Da can be allowed by MALDI because the ionization process does not depends on the properties of analyte, such as absorption and size (Spengler, Cotter 1990).

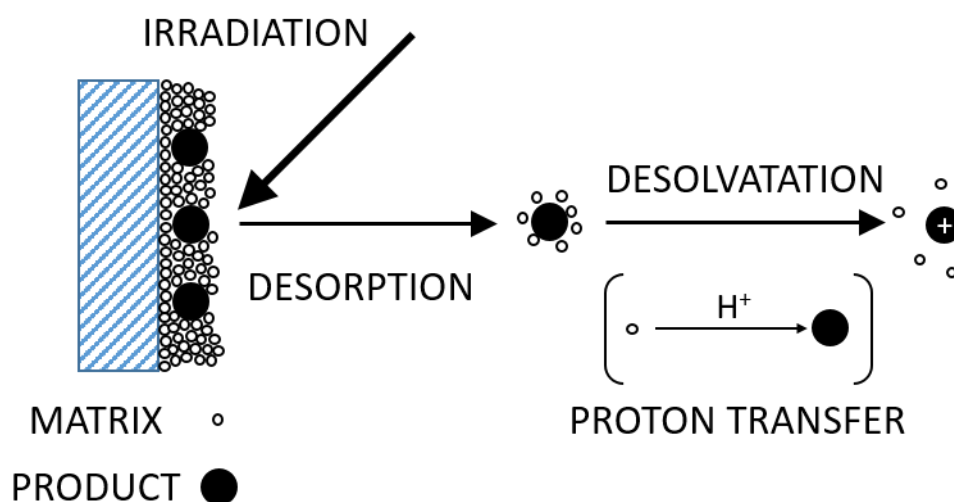


Fig. 2 Diagram of the principle of MALDI.

1.1.1.2 Electrospray Ionization (ESI)

ESI was first described by J. B. Fenn and colleagues who showed that the low molecular weight (low to 2000 Th) of multiply charged ions generated from proteins can be measured with instruments (Fenn et al. 1989). In the early stage, ESI was considered to ionize protein for proteomics, then the application field was expanded to the small polar molecules, polymers and biopolymers.

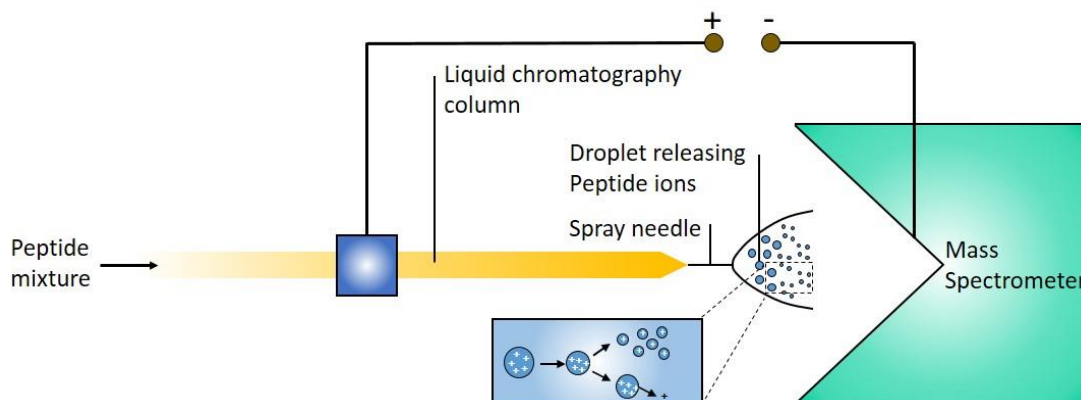


Figure. 3 Diagram of electrospray ionization (ESI)

Figure. 3 describes the structure of ESI. A biomolecules containing solution is pumped through a needle with a very large voltage applied to it (2-5 kV). This forms small, highly charged droplets of solvent upon exit of the needle. As the droplet travels towards the orifice of the mass spectrometer, the solvent evaporates aided by the drying gas, and it shrinks and the surface charge density increase. This causes the droplet to blow apart and the process repeats itself until charged biomolecules emerge.

The peptides containing liquid effluent is electrostatically dispersed by eluting from a syringe or HPLC eluent through a needle with a high voltage (several kV) applied to it. It forms highly charged droplets of solvent departure the needle. The solvent evaporates easily by the aid of drying gas during the droplets travel to the orifice, it increases the surface charge density of the droplets and decreases their size. High electrical fields allow the desorption of analyte ions on the surface of droplet to generate desolvated ions, and repetitive droplet fission, which sustain to each droplet contains only one analyte ion averagely, leads to the formation of tiny droplets.

1.1.2 Analyzer

1.1.2.1 Time-of-Flight (TOF)

The time-of-flight (TOF) analyzer was first come up with in 1946 by W. E. Stephens (Anonymous 1946). The linear TOF mass spectrometer was designed in 1955 and became the first commercial instrument later(Wiley, McLaren 1955). Since the end of 1980s, the development of MALDI settled new applications for both biomolecules and synthetic polymers. The basic principle of separation for TOF analyzer is based on velocities (flight time) of ions.

1.1.2.1.1 Linear Time-of-Flight Mass Spectrometer

Ions are separated by the TOF analyzer according to their velocity that depends on their m/z ratios when they travel through a free-field region (flight tube), after the electrostatic field induced acceleration followed by their formation during a laser pulse (Figure. 4). One advantage of TOF spectrometer is that it is suitable for soft ionization techniques, such as masses above 300 kDa samples can be observed by MALDI-TOF (Imrie, Pentney & Cottrell 1995, Moniatte et al. 1996), due to there is no limit for the upper mass range of it. Another benefit is the very high sensitivity results from their high transmission efficiency. For example, 10^{-15} mol of gramicidin (Lange et al. 1986) and 10^{-16} mol of protein mixture (Onnerfjord et al. 1998) have been detected by TOF analyzers. The third advantage is the analysis speed of TOF is very fast, a spectrum can be obtained in micro-seconds.

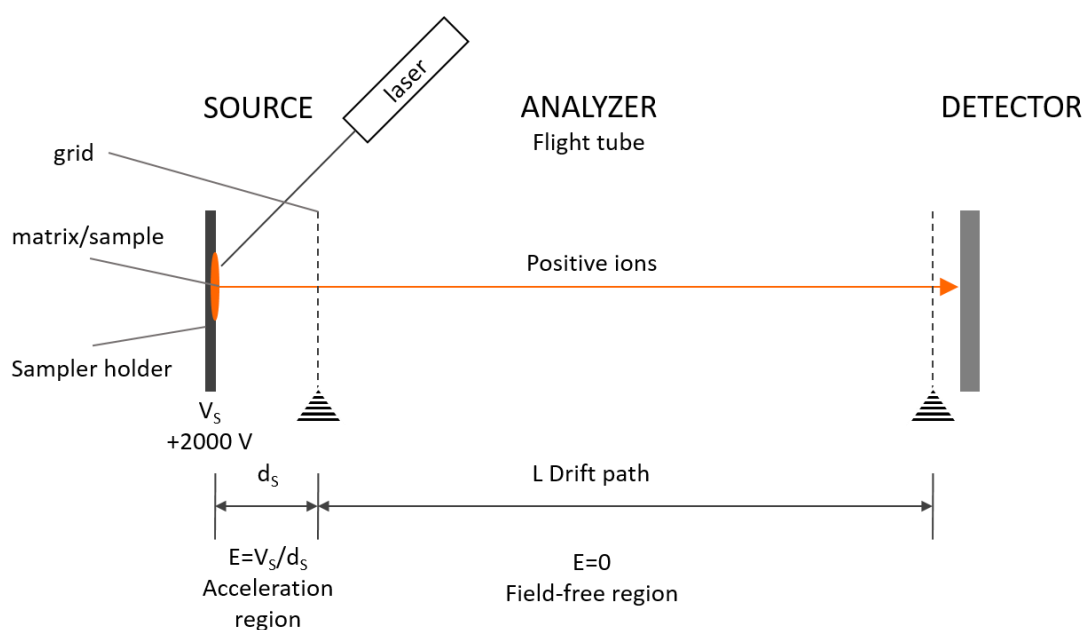


Figure. 4 Diagram of Linear TOF

1.1.1.1.2 Reflectron Time-of-Flight Mass Spectrometer

Electrostatic reflector, or reflection, is another way to improve mass resolution of TOF spectrometer. It was first described by Mamyrin (Mamyrin et al. 1973). The basic principle of reflectron is the ions are deflected by an ion mirror (retarding field) and are sent back through the field-free region. The reflectron is set at the end of the flight tube and the detector is set on the opposite side of the reflectron to receive the ions reflected from the reflectron (Figure. 5). The kinetic energy of the ions with the same m/z are corrected by reflectron thereby they can fly along different pathways in the reflectron. The distance penetrated in the reflectron of ions with less kinetic energy and less velocity is shallower than ions with more kinetic energy. Accordingly, the time cost in the reflectron by slower ions is short than the faster ions, and they arrive at the detector simultaneously.

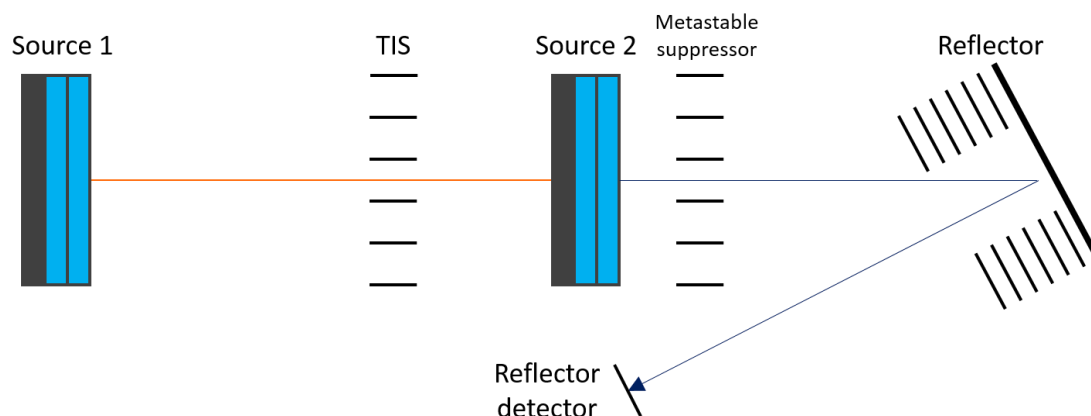


Figure. 5 Diagram of Reflectron TOF. Ion source 1: MALDI ion source. Ion source 2: re-acceleration cell. TIS: Timed ion selector.

1.2 Proteomics

The Human Genome Project (HGP) aiming to sequence the entire human genome was initiated by the US Department of Energy and National Institute of Health (NIH) from the late 1980 (Venter et al. 2001), and it has been achieved almost in 2003 by sequencing the human complete genome (Dunham et al. 1999). One major objective of HGP is to reveal and understand the linkage between genes and their related proteins by sequencing of the complete human genome. Whenever we mention the features of a protein, always including localization, expression, modification, interaction, domain structure, and activity. For an organism, not all encoded proteins express from genome at any time, and the protein expression changes at different stages of development, while the genome of each cell is almost same. For a single cell, different stimuli may change the dynamic proteome. The word “PROTEOME” is defined as the “total PROTEin complement of a genOME” (Wasinger et al. 1995), and “PROTEOMICS” started to attract enormous attention after the completion of HGP (Figure. 6). The goal of proteomics is obtaining complete characterization of all proteins, understanding the protein-protein interactions, and illustrating the functions of those proteins. Proteomics is the bridge

connected genomics and biology, the relationship between the proteome to physiological changes under the healthy or diseased conditions became one popular topic in modern biomedical research.



Figure. 6 Proteomics is a study of how the genome is expressed in proteins, and of how these proteins function and interaction.

1.1.2 Protein Identification

Analysis of the protein expression in organisms is one of the tasks of proteomics research. The 2D gel electrophoresis (2DE) is the first analysis tool in proteomics, proteins can be separated along two dimensions according to molecular masses and isoelectric points by gel electrophoresis (Bienvenut et al. 1999). With the development of MS, the 2DE-MS has been used for protein identification. 2DE resolved proteins can be addressed by in-gel digestion or membrane digestion (on immobilized trypsin containing membranes). Trypsin is the most commonly used protease in proteomics research, which cleaves at the C-terminal of lysine (Lys) and arginine (Arg). In addition, other proteases like AspN which cleaves before aspartate (Asp), GluC (V8) which cleave after glutamic acid (Glu) and LysC which cleave after Lys specifically are also used. The results of mass spectrometric analysis depend on the quality of the digestion, the digestion with high specificity and high cleavage efficiency lead to a good identification of protein. The development of newly engineered proteases promotes the improvement of cleavage methods (Willett et al. 1995). Moreover, the protein identification strategies of bottom-up sequencing and top-

down sequencing are developed by measurement of intact proteins and peptide fragments together by MS.

1.1.2.1 Peptide Mass Fingerprinting

Peptide mass fingerprinting (PMF) is an analytical technology for protein identification. PMF was developed by many groups independently in 1993 (Henzel et al. 1993, James et al. 1993, Mann, Hojrup & Roepstorff 1993, Pappin, Hojrup & Bleasby 1993, Yates et al. 1993), and it is still the most common way of identifying proteins separated by 2DE or one-dimensional SDS-PAGE. Basically, the unknown proteins of interest are commonly digested by trypsin into smaller peptides, which cleaves at the C-terminal end of Lys and Arg specifically. The experimental data in the PMF based protein identification strategy is the mass list derived from MALDI-TOF or ESI-TOF mass spectrum of the enzymatic-digested protein. The experimental masses of the resulting tryptic peptides from unknown proteins are calculated to compare the theoretical peptide masses of each protein in a database *in silico* for acquiring a best match. MALDI-TOF is commonly used for PMF since in the spectrum of MALDI-TOF MS, the peptides display as singly charged ions, which is simple to interpret. However, an ESI mass spectrum appears peptides as multiply charged ions, the peptides masses should be deconvoluted for every search (Yates et al. 1993b). It is why ESI spectra is seldom used for PMF, though PMF can be used for protein identification by ESI. Another reason is that as the preferred instrument for PMF, MALDI-TOF has the ability to analyze several proteins in a single MS experiment by its high sample throughput.

Many database search software can be used for PMF searches (Perkins et al. 1999, Zhang, Chait 2000). The outcome output from those software is usually a ranked list of proteins according to the size of database, the size of input experimental data, the abundance of a specific peptide mass derived from a

certain protein, the tolerance to the molecular mass, the allowed number of missed cleavages in one peptide sequence, the expected modifications, and other possible parameters. The protein ranks at the first place is the unknown protein in the sample with the highest reliability. On the other hand, the algorithm design is also important for the database search result. Probability-based database search algorithm is popular used in many software. The ranking list of proteins can be produced after a series complicated calculation and computational modification.

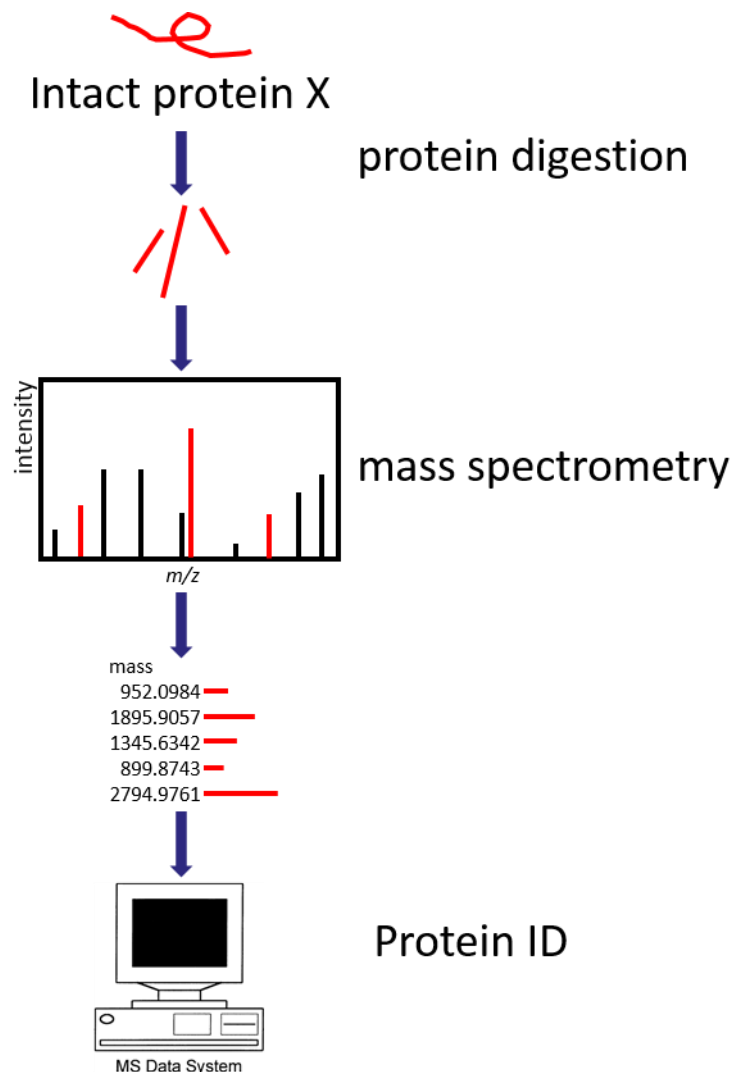


Figure. 7 Scheme of PMF. 1. Make proteolytic peptide fragments. 2. Measure peptide masses. 3. Match peptide masses to protein or nucleotide sequence database.

1.2 Aims

In the present study, I demonstrate a MALDI-based post-source fragmentation method that allows the C-terminal amino acid sequence in peptide sequences can be inferred for the digested peptides, which are produced by LysN or AspN proteases, to be performed. The data obtained for the constitute peptides are molecular masses, N-terminal amino acid sequences and C-terminal amino acid sequences are unique in the present method. Here I present an enhanced PMF approach based on the new method that employs MALDI-TOF/TOF-MS of protein digest by LysN, and demonstrate to be useful for reliable identification, of either single protein or those in a mixture.

2 Chapter II: C-terminal Fragmentation of Peptides

2.1 Introduction

2.1.1 In-Source Decay (ISD) and Post-Source Decay (PSD)

In the MALDI, the excess energy transfers to the analyte during the ionization desorption process can lead to the ion fragmentation. In MALDI spectra, fragment ions are generated by different types of fragmentations, which are distinguished from the different places they occur.

In general, the types of fragmentation consist of in-source decay (ISD) and post-source decay (PSD). Moreover, ISD contains prompt fragmentation and fast fragmentation. ISD is a kind of fragmentation taking place in the source and can be separated to two steps by time scale. First, the fragmentation occurs is before or during the desorption is prompt fragmentation; secondly, fragmentation occurs in the source after the desorption but before the acceleration is fast fragmentation. PSD is a type of fragmentation that occurs in the field-free region after the acceleration region of the MALDI. It corresponds to the fragmentation of metastable ions. Metastable ions, as the name suggests, are not “stable”. They are stable enough to leave the source after ionization like the normal molecule ions, but due to the excess energy they received from laser pulse, they can fragment in the field free region of analyzer (Figure. 8).

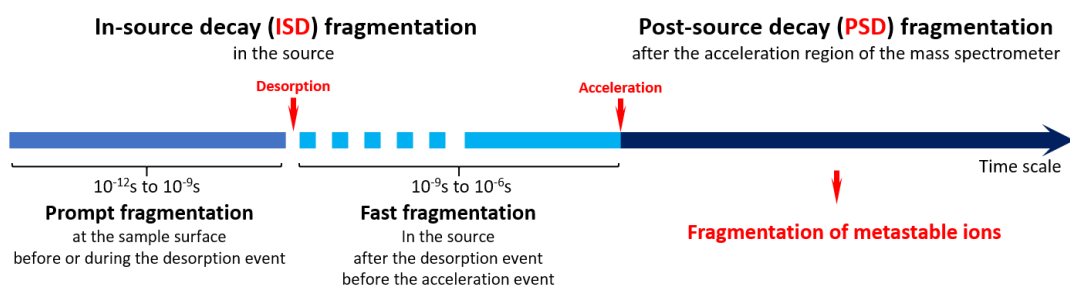


Figure. 8 Diagram of the fragmentation of MALDI.

Tandem mass spectrometry (MS/MS) is a type of spectrometer with additional analyzer(s) connect to the first analyzer to measure the fragment ions further. In the MALDI-TOF MS with a linear TOF analyzer, an extra reflectron time-of-flight instruments can be used to construct a MALDI-TOF-TOF MS/MS (Figure. 9). Fragment ions and neutral fragments can be fragmented by acquiring enough internal energy by ions.



Figure. 9 Simplest form of MS/MS

Since the ISD occurs before acceleration in MALDI, the ISD induced fragment ions (ISD fragment ions) have the same kinetic energy to the molecule ions (precursor ions) from the static electric field, thus they have the different velocities according to their m/z ratio. The different velocities allow both of the precursor ions and ISD fragment ions to be analyzed by linear TOF and reflectron TOF respectively. However, if a device named "timed ion selector" (TIS) is equipped, they cannot be analyzed in one experiment because they cannot pass the TIS in the same time.

On the other way, the velocity of the PSD induced fragment ions (PSD ions) and precursor ions are same because the PSD occurs after acceleration, and the kinetic energy of them are different. If the fragment ions have the same velocity to the precursor ions, the kinetic energy of the fragment ions is less than the precursors due to the less masses of the fragment ions. Thus they have the same flight time in TOF 1. Therefore, in TOF1, although the precursor ions and their PSD fragment ions have different kinetic energies, they can pass the TIS at the same time. Consequently, the precursor ions and their TOF 1

produced PSD fragment ions are reaccelerated in Ion Source 2, the kinetic energies of TOF 1 produced PSD fragment ions increase significantly to reach the kinetic energies of precursor ions, thus the velocity of the TOF 1 produced PSD fragment ions become faster than the precursors due to their lower masses. In the following field-free region (TOF 2), PSD occurs on precursor ions again, as well as in TOF 1. The TOF 2 produced PSD fragment ions have the same velocity as their precursor due to their lower kinetic energies and lower masses as mentioned above. The TOF 1 produced PSD fragment ions reach to the reflectron firstly, followed with the precursor ions and TOF 2 produced fragment ions. Since the precursor ions and TOF 1 produced PSD fragment ions are reaccelerated in Ion Source 2 together, they share a similar orbit in reflectron. However, the TOF 2 produced PSD fragment ions with less masses penetrate the reflectron shallower and spend less time than the precursor ions, thus the TOF 2 produced PSD fragment ions reached to the detector before the precursor ions. Because the velocities of TOF 1 produced PSD fragment ions are faster than the precursor ions, the TOF 1 produced PSD fragment ions reach to the detector before the precursor ions too (Figure 10). These ions reach the detector according to their m/z by different time of flight, and due to the reacceleration and refocusing of TOF 1 produced PSD fragment ions, the TOF 1 and TOF 2 produced PSD fragment ions perform as different type of peaks in the mass spectra.

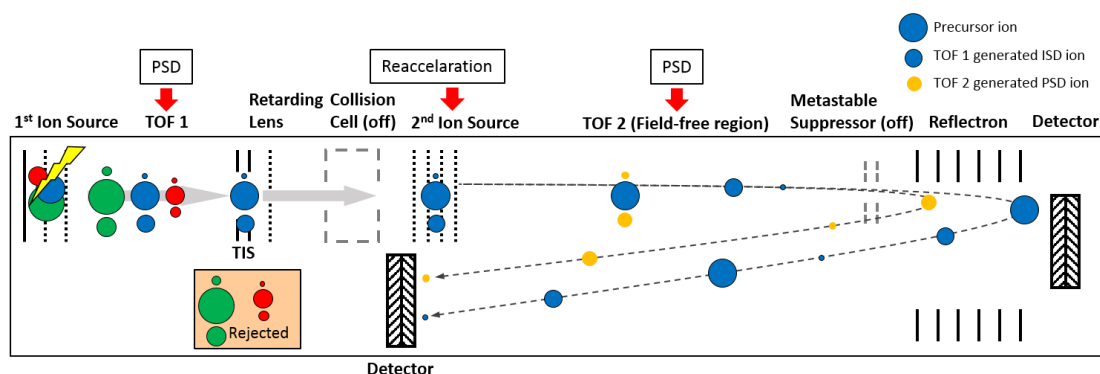


Figure. 10 Diagram of MALDI-TOF/TOF MS.

2.1.2 Collision Induced Dissociation (CID)

MS/MS requires the first analyzer to select fragment ions of precursor ions towards the second analyzer to measure the fragment ions. Collision Induced Dissociation (CID) is a technology to induce ion fragmentation in gas phase (Sleno, Volmer 2004, Mitchell Wells, McLuckey 2005). In a MALDI-TOF-TOF MS/MS, CID is usually equipped between TOF 1 and ion source 2 to increase the probability of ion fragmentation. The gas-phase precursor ions enter the CID cell which is full of collision gas (nitrogen, helium or argon) and then are activated by high electrical potential. Those ions collide with the neutral molecules of the collision gas and fragment to form small fragment ions. These accelerated fragment ions can then be analyzed by TOF 2 (Figure. 11).

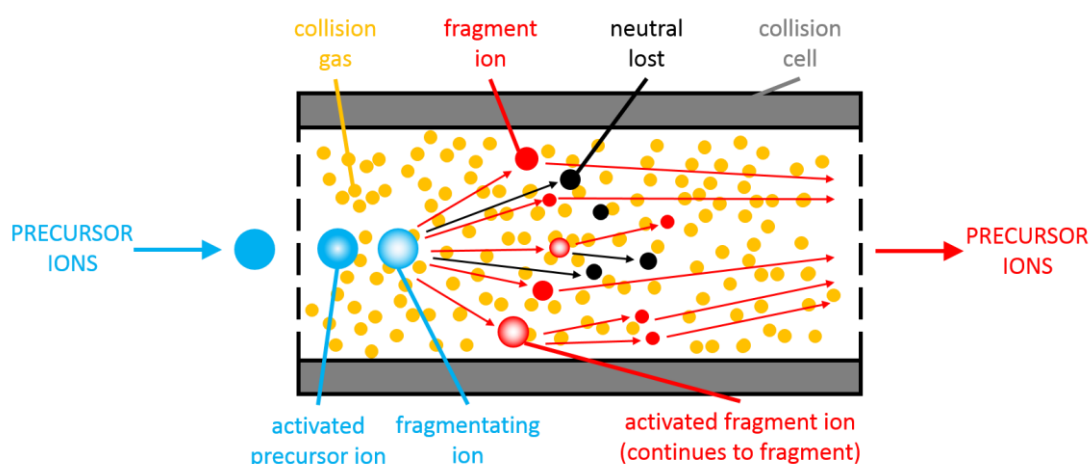


Figure. 11 Diagram of CID.

Figure. 12 shows the fragmentation specifics (the Roepstorff–Fohlmann–Biemann nomenclature) on the chemical structure of a peptide backbone by transmitting energy into the molecule (Roepstorff, Fohlman 1984, Biemann 1992). In the mass spectrometers for proteomics research, peptide fragmentation is induced by CID, and bond breakage mainly occurs at the amide bonds, where is the pathway with the lowest energy. If the charge retains on the N-terminal fragment, so called “b ions” are generated; if the charge retains on the C-terminal fragment, another kind of “y ion” are produced.

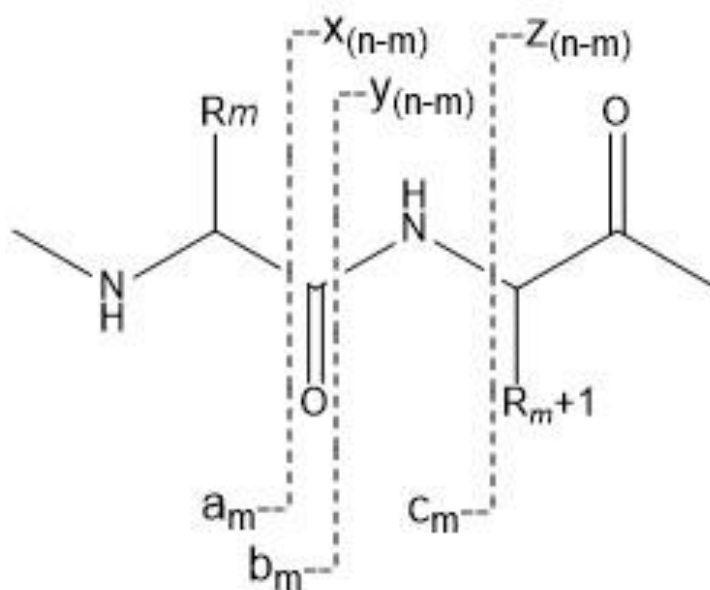


Fig. 12 Diagram of Roepstorff–Fohlmann–Biemann nomenclature.

2.1.3 C-terminal Rearrangement of Peptides.

Previous reports showed and illustrated a phenomenon of C-terminal rearrangement ions $[b_{n-1}+H_2O]$ (n is the total number of amino acid residues in peptides) are frequently observed from internal Arg-containing peptides in PSD spectra (Takao et al. 1993, Gonzalez et al. 1996, Fang et al. 2000). (Renner, Spiteller 1988, Tang et al. 1988, Grese, Cerny & Gross 1989), Arg may play a similar role as the most basic amino acid residue. Such a C-terminal rearrangement could provide the information of the C-terminal amino acid, and a new idea for enhanced PMF originated from this phenomenon, thus through introducing the confirmed C-terminal amino acid sequences of peptides into the conventional PMF thereby improving the reliability of PMF method.

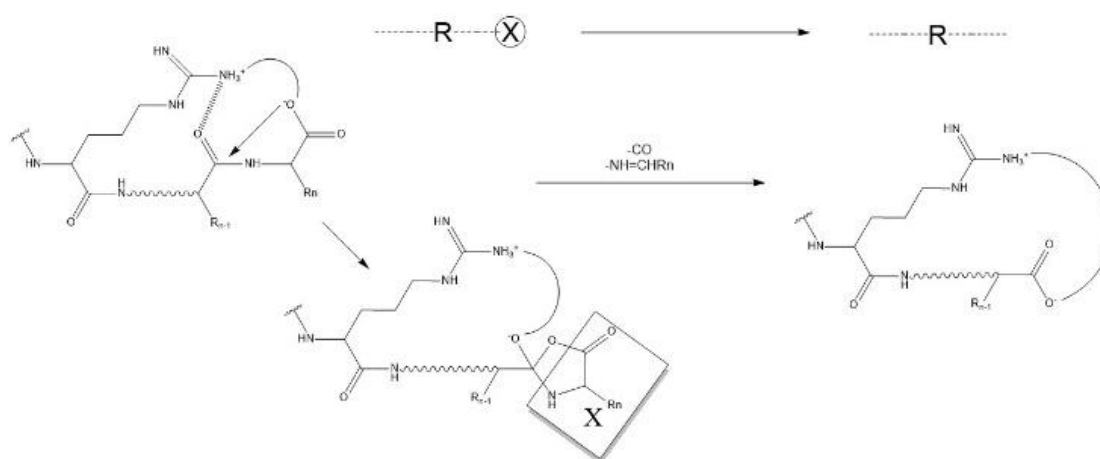


Figure. 13 Mechanism of C-terminal rearrangement of Arg-containing peptides.

2.2 Materials and Methods

2.2.1 Proteins and Chemicals

Bovine Serum Albumin (BSA), apo-Transferrin from bovine (TF), Cytochrome c (CYC) from equine heart, myoglobin from horse (MB), Myosin from rabbit (MYH), Phosphorylase b from rabbit (PGYM), Carbonic anhydrase from bovine (CA), ammonium bicarbonate, glycine, trifluoroacetic acid (TFA), LC/MS grade distilled water, and acetonitrile were purchased from Sigma-Aldrich (St. Louis, MO, USA). Synthetic peptides were purchased from GL Biochem (Shanghai, China). SDS-PAGE Molecular Weight Standards was purchased from Bio-Rad (Hercules, CA, USA). Sodium lauryl sulfate (SDS), sucrose and bromophenol blue were purchased from Nacalai Tesque (Kyoto, Japan). Tris base, dithiothreitol (DTT) and iodoacetic acid (IAA) were purchased from Wako (Osaka, Japan). LysN protease was purchased from Thermo Scientific (Rockford, IL, USA). Ultrapure water was supplied by a PURIC-MX II system (Organo, Tokyo, Japan).

2.2.2 Protein in Solution/Gel Digestion

10 mg protein was dissolved in 1mL 50mM NH₄HCO₃, 0.1% SDS solution (pH 8.0). Reduction of disulfide bonds was carried out by adding 20.41μL of 1M DTT

into protein solution to a final conc. of 20mM (1:50 dilution) and incubated at 37°C for 45min. Alkylation was carried out by adding 42.52µL of 1M IAA into reduced protein solution to a final conc. of 40mM (1:25 dilute) and incubated at R.T. for 15min in dark. The alkylated protein solution has been quenched by adding 10.74µL of 1M DTT to a final conc. of 10mM (1:100 dilution). 2µL of 0.5µg/µL LysN protease was applied to 8.5µL quenched protein solution (80µg) which diluted 10 times to conc. of 1µg/µL by adding 76.5µL 50mM NH₄HCO₃, 0.1% SDS solution, and incubated at 50 °C for 2h for digestion. The digests were stored in -20 °C to stop reaction, and desalted by Bond Elut-C18 (Agilent, Santa Clara, CA, USA). Purified peptides were dried by rotary vacuum micro-concentrator RMC-24 (KPI, Itami, Hyogo, Japan), and dissolved in 5% acetonitrile.

Gel bands were excised from the Coomassie blue-stained gel carefully, and prepared for in gel digestion. Gel pieces were washed three times with 50% MeOH/50 mM NH₄HCO₃ for 1h to overnight shanking at room temperature, removing the supernatant after each wash. Reduction of disulfide bonds was carried out by adding 0.5 mL of 10 mM DTT/100 mM NH₄HCO₃ into protein solution and incubated at 60°C for 1h. Alkylation was carried out by adding 100 µL of 50 mM IAA/100 mM NH₄HCO₃ into reduced protein and incubated at R.T. for 30min in dark. Reduction and alkylation solution were removed after reaction. Alkylated gels were washed by water and ACN twice respectively. 30 µL of 1 µg LysN protease were added to a gel band, and incubated at 50 °C for 2h for digestion. 30 µL of ACN/0.1% TFA was added to the gel digestion to a final conc. of 50% ACN, following with a sonication for 10 min, then supernatant was collected. 100 µL of 50% ACN/0.1% TFA was added with a following 10 min sonication, supernatant was collected, this step was repeated twice.

2.2.3 nanoHPLC Separation

Analysis of the LysN digest was addressed by offline nanoHPLC/MALDI-TOF/TOF MS, a nanoHPLC system (Ultimate 3000; Thermo Scientific, Idstein, Germany) and an MALDI-TOF/TOF 4700 mass spectrometer (AB Sciex, Foster City, CA, USA) were utilized in the experiments. Chromatographic separation of the peptides was performed by loading 10 μ L sample onto a trapping column (μ -Precolumn holder, 5 mm, with connecting tubing, 30 μ m internal diameter (i.d.); Dionex, Sunnyvale, CA, USA), and washed with 0.1% TFA at a flow rate of 20 μ L/min for 25 min. The trapped peptides were then eluted into the analysis column (IntegraFrit C18, 3 μ m, 100 Å, 75 μ m i.d. \times 100 mm; New Objective, Woburn, MA, USA), which had been equilibrated with 95% solvent A (5% ACN/95% H₂O containing 0.05% TFA). A solvent system contained solvent A and solvent B (100% ACN containing 0.5% TFA) mixed according to the linear gradient of 5–85% solvent B in 60 min, maintenance at 85% solvent B for 20 min, and linear gradient of 100–5% solvent B in 2 min were used for separation of peptides. The flow rate of the column was 200 nL/min. UV absorption at 220 nm and 280 nm was used for signal detection. 156 fractions of the effluent (each of 30 s) were spotted onto an Opti-TOF™ MALDI Plate System (192 spots; AB Sciex, Foster City, CA, USA) using a Probot microfraction collector (Dionex, Sunnyvale, CA, USA) from 20 min to 90 min of the run,.

2.2.4 MS/MS Measurement (MALDI-TOF/TOF)

The MALDI-TOF MS analyses were carried out on a 4700 MALDI TOF/TOF analyzer (Applied Biosystems, Framingham, MA) with a pulsed laser. The MS/MS was set in the positive mode and reflectron mode. The average number of laser shots was set at 800 on each sample well. The accelerating voltage in ion source 1 was 8 keV, and 15 keV in ion source 2. Metastable suppressor was set at “OFF”, and CID was “OFF” as well. The 4000 series Explorer

Software V3.6 was used to control the MS/MS measurement, and Data Explorer Software version 4.8 (Applied Biosystems, Framingham, MA) was used to process data. The matrixes for MALDI-TOF-TOF MS/MS were 5 mg/ml α -CHCA dissolved in 50% CAN containing 0.1% (v/v) TFA.

2.3 Results

2.3.1 Data Acquisition

It was a manual labor subjected by W.Y. First, the MS/MS was carried out according to m/z of precursor between 500 and 4000 by the 4000 series Explorer Software. Second, spectra data was convert to show on Data Explorer Software. On the spectrum, the metastable ion can be shown as a broad peak with low resolution, which could be easily differentiated from other ions. The corresponding fragment in-source ion was usually accompanied with a metastable ion peak, the m/z of which was around 3~4 Da smaller than that of the metastable ion. There were two type of metastable ions related which the C-terminal fragmentation: $[b_{n-1}]$ and $[b_{n-1}+H_2O]$ ions. If there was a C-terminal amino acid rearrangement occurred truly on a peptide, the C-terminal amino acid could be inferred from the difference of m/z between a precursor ion and in-source fragment ion (Figure. 14).

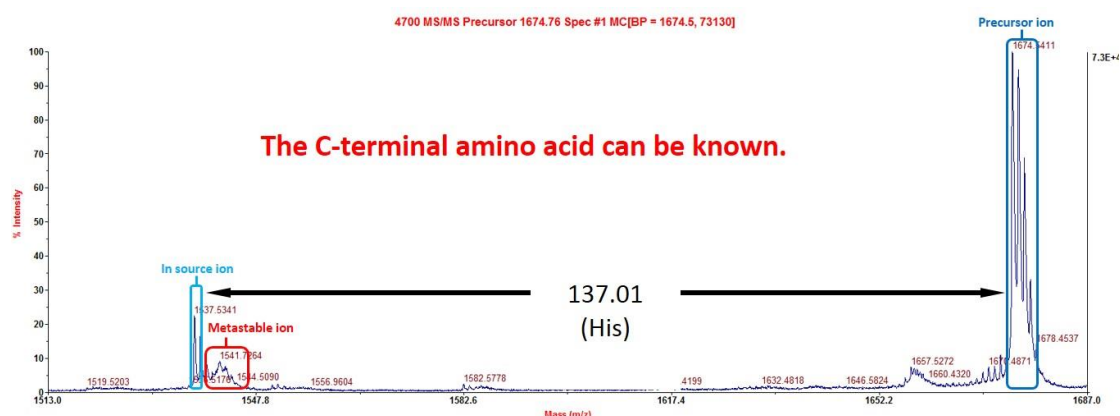


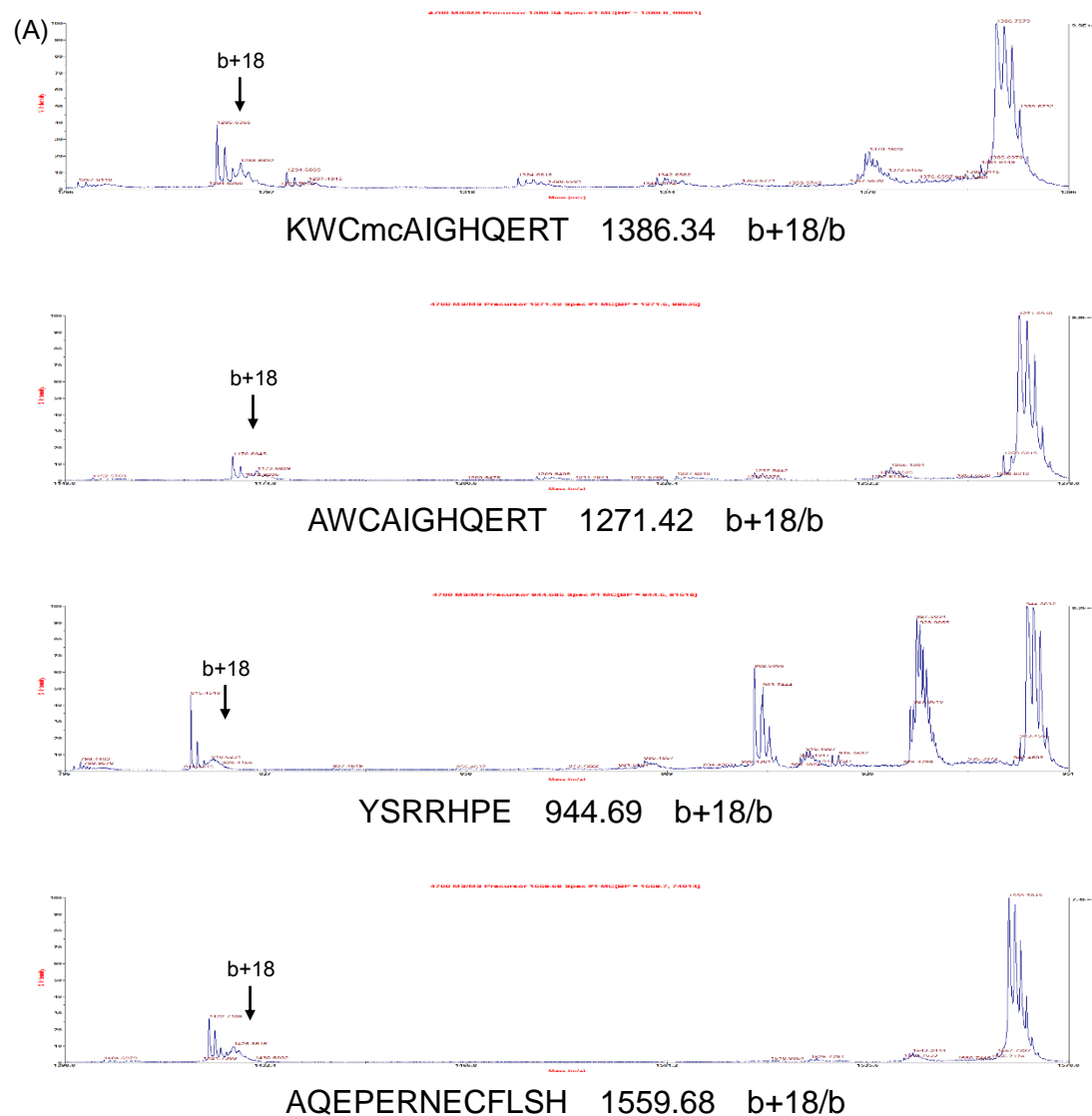
Figure. 14 C-terminal amino acid information of a peptide acquired with MS/MS.

2.3.2 Effect of a Basic Amino Acid on the C-terminal Fragmentation

As described above, a salt bridge forms between the guanidino group of Arg and the C-terminal carboxylate in one peptide, then the C-terminal rearrangement occurs and the remained sequence can be shown as a broad metastable ion $[b_{n-1}+H_2O]$ peak on the spectrum. Thereby it deduces the basic amino acid containing peptide to possess the capability to generate such C-terminal amino acid-truncated $[b_{n-1}+H_2O]$ ion in MS/MS measurement. In order to demonstrate the contribution of basic amino acid to the C-terminal rearrangement of peptides, we compared the spectra from several synthetic peptides and natural peptides from protein digests (Table 1). The spectra indicate the generation of $[b_{n-1}]$ (abbreviates to $[b]$) ions are general for all peptide sequences in the PSD spectra, except for $[b_{n-1}+H_2O]$ (abbreviates to $[b]$) ions which could only be generated by Arg-containing peptide (not at the C-terminus). The Arg-containing peptides can produce $[b+18]$ ions, as in the conclusion of the previous report, otherwise only $[b]$ ions can be observed. Moreover, through replacing the Lys to Ala, both of the spectra of one basic amino acid (Lys) contained peptide and no basic amino acid contained peptides show $[b]$ ion inferred to C-terminal fragmentation. These results indicate that the C-terminal fragmentation relative $[b]$ metastable ions occur generally in any peptide sequences, and the $[b+18]$ ions only occur in the Arg-containing peptides.

Table 1. Types of metastable ions relative to the truncation of C-terminal amino acid generated from different sequences of peptides.

basic amino acid	R (+)	R (-)
metastable ion	b+18	b
sequences	KWCmcAIGHQERT AWCAIGHQERT YSRRHPE AQEPERNECFLSH	KWCAIGHQEAT KQEPEANECFLSH AAEFVEVT



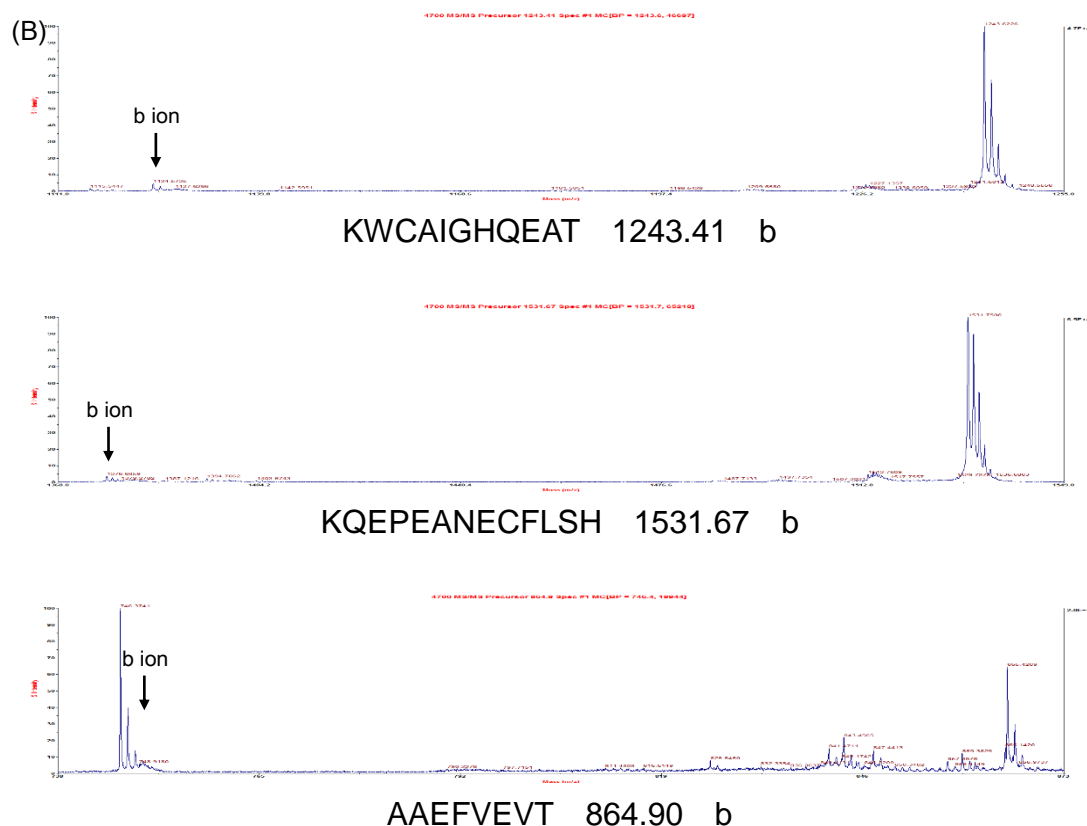


Figure. 15 (A) C-terminal amino acid sequences relative b+18 metastable ions in the spectra of peptides Containing internal Arg. (B) C-terminal amino acid sequences relative b metastable ions in the spectra of peptides containing non-internal Arg.

2.3.3 Effect of the C-terminal Carboxylate on the C-terminal Fragmentation

On the other hand, according to the previous report, the C-terminal carboxylate contributes to the rearrangement of C-terminus incorporation to Arg. Several peptides synthesized by replacing the C-terminal carboxyl group with an amide group were measured by MS/MS. Figure. 16 shows the spectra of peptides containing no internal Arg and peptide containing Arg with a C-terminal amide group, respectively. It indicates that the generation of [b] ions is not affected by C-terminal amide group, but the existence of Arg may suppress the generation of [b] ion under the condition without the existence of C-terminal amide group of a peptide.

applied to this analysis. According to the PSD spectra of those peptides (Figure. 15), [b] ions can be observed on most spectra except the peptides contain Arg (not at C-terminus), which show [b+18] ions on their spectra. It indicates that [b] ions occur generally among all the peptide sequences measured by MALDI-TOF/TOF MS, and only the Arg contained peptides (not at C-terminus) can generate [b+18] ions rather than b ions. In the spectra of peptides from trypsin and GluC digest, the known Lys, Arg or Glu can be observed. However, in the spectra of peptides from AspN and LysN digest, the C-terminal rearrangement can be measured and the amino acid at C-terminus can be inferred as well. On the other hand, the Lys or Asp at N-termini of the peptides from LysN or AspN digest are certain. Therefore, as to the peptides from proteins digested by LysN or AspN, three information of the sequences can be known after MALDI-TOF/TOF measurement: molecular mass, N-terminal amino acid and C-terminal amino acid. These findings can provide a new idea for protein identification by PMF, thus through introducing amino acids positioned at both N- and C-termini of peptides from LysN or ApsN digest, rather than the conventional utilizing of C-terminal Lys or Arg of peptides from trypsin digest only, can improve the reliability of PMF. Moreover, according to the characteristic of N-terminal rearrangement of AspN digested peptides can be observed on the PSD spectra (Figure. 15), tandem digestion by LysN and AspN are proposed to apply to this newly enhanced PMF method for increasing the reliability as well.

Table 2. Types of metastable ions generated from protein digested by different proteases.

protein	protease	miss	sequence	mass[M+H]	ion type
BSA	Trypsin	1	RHPYFYAPELLYYANK	2044.71	b+18
		1	QEPERNECmcFLSHK	1674.75	b+18
		1	LKECmcCmcDKPLLEK	1534.83	b
		0	HLVDEPQNLIK	1305.94	b
	AspN	0	DKPLLEKSHCmcIAEVEK	1896.95	b/D
		0	DESHAGCmcEKSLHTLFG	1788.72	b/D
		1	DKDVCmcKNYQEAk	1498.82	b/D
		0	DTHKSEIAHRFK	1468.88	b+18/ D
		0	DVCmcKNYQEAk	1255.83	b/D
		1	DFAEDK	724.86	b/D
	GluC	1	RALKAWSVARLSQKFPKAEF VE	2560.40	b+18
		0	KKFWGKLYE	1361.61	b
		1	IAHRFKDLGEE	1314.59	b+18
		0	KQIKKQTALVE	1285.76	b
		0	LCmcKVASLRE	1076.70	b+18
		0	YSRRHPE	944.69	b+18
	LysN	0	KVASLRETYGDMADCmcCmc E	2006.48	b+18
		1	KCmcCmcAADDKEACmcFAV EGP	1930.7	b

	1	KPDPNTLCmcDEFKADE	1779.63	b
	0	KQEPERNECmcFLSH	1764.61	b+18
	0	KTCmcVADESHAGCmcE	1465.52	b
	0	KYICmcDNQDTISS	1443.67	b
	1	KECmcCmcDKPLLE	1293.65	b
	0	KAWSVARLSQ	1145.67	b+18
	0	KLVVSTQTALA	1130.87	b
	0	KSHCmcIAEVE	1073.66	b
	0	KQNCmcDQFE	1069.64	b
	0	KAEFVEVT	922.75	b
	0	KATEEQL	818.78	b



KKFWGKYLYE 1361.61 b



KQEPERNECmcFLSH 1673.74 b+18

Figure. 16 MS/MS spectra of four specific peptides from proteins digested by trypsin, AspN, GluC and LysN.

2.4 Discussion

2.4.1 b Ion and b+18 Ion

Previous report elucidated the mechanism of the rearrangement on C-terminal of Arg-containing peptides described above, and also verified by us in this project, which act as the basic theoretical fundament of this research. Since the rearrangement can induce the generation of metastable ions, which can be observed as a broad peak in the TOF-MS spectra, derived from the truncated peptide missing the C-terminal amino acid, this observation could be used as a new condition for protein identification by PMF. As we know, for the conventional PMF, trypsin is used commonly for protein digestion, and peptides with a C-terminal Lys or Arg can be generated. According to the mechanism previously reported, only peptides with internal Arg can rearrange at C-termini, trypsin digested peptides cannot. If there is a kind of protease which can cleave the N-terminus of Arg in proteins, the C-terminal amino acids of all peptides digested by such protease could be revealed via the rearrangement of the C-termini. Unfortunately, there is not such proteases at present, but another protease named LysN exists, which can create N-terminal Lys-containing

peptides by protein digestion. According to the previously published report, we proposed the basic amino acid-containing peptide could produce the similar phenomenon, thus Lys may work as well as Arg for the C-terminal rearrangement of peptides. However, by our experiments, not all N-terminal Lys-containing peptides can produce $[b+18]$ metastable ion on the TOF-MS spectra derived from C-terminal amino acid truncated peptides, except the internal Arg-containing ones. After a series of MS measurements of several synthetic peptides, I found that beside the $[b+18]$ metastable ion generated by internal Arg-containing peptide, another kind of ion relative to C-terminal amino acid truncated peptide named $[b]$ metastable ion can be observed from non-internal Arg-containing peptides, even in the peptides without any basic amino acid. On the other hand, we also synthesized peptides by replacing the carboxylate to amide group on the C-terminal amino acid of peptides. The MS spectra show that under the condition of there is not Arg in the peptide, $[b]$ ion can be generated; but under the condition of there is Arg in the peptide, either $[b]$ or $[b+18]$ ion cannot be generated. Those results indicate Arg is not the necessary condition for the generation of b ion, as well as carboxylate; but Arg seems to suppress the generation of b ion if there is not a carboxylate.

2.4.2 Formation of a b ion adjacent to the C terminus

The most common PSD/CID fragment ion types are b and y ions (Spengler 1997). According to the mobile proton model, the proton(s) is usually localized at the most basic site in the peptide before activation, meanwhile it could be adducted to any carbonyl oxygen when there is no basic amino acid. (Wu, Lebrilla 1995, Paizs, Suhai 2004). The fragmentation mechanism involves carbonyl oxygen attack by its nucleophilicity to the neighboring amide carbonyl from the N- or C-terminal site; the carbonyl oxygen attack from the N-terminal site eventually cleaves the amide bond, leading to the proton transfer to the nitrogen atom (Fig. 18a), while the carbonyl oxygen attack from the C-terminal

site does not (Fig. 18b) (Freitas, Hendrickson & Marshall 1999, Wyttenbach, Bowers 1999). Through the former pathway, the b ion, apart from the C-terminal peptide portion, could be formed as an N-protonated oxazolone (Chen, Turecek 2005). In case of a singly protonated molecule, the site of such fragmentation is highly dependent on the location of a proton over the amino acid sequence, which could be, most probably, N -amino group or any carbonyl oxygen of amide bond in the absence of basic amino acids. (Figure. 18).

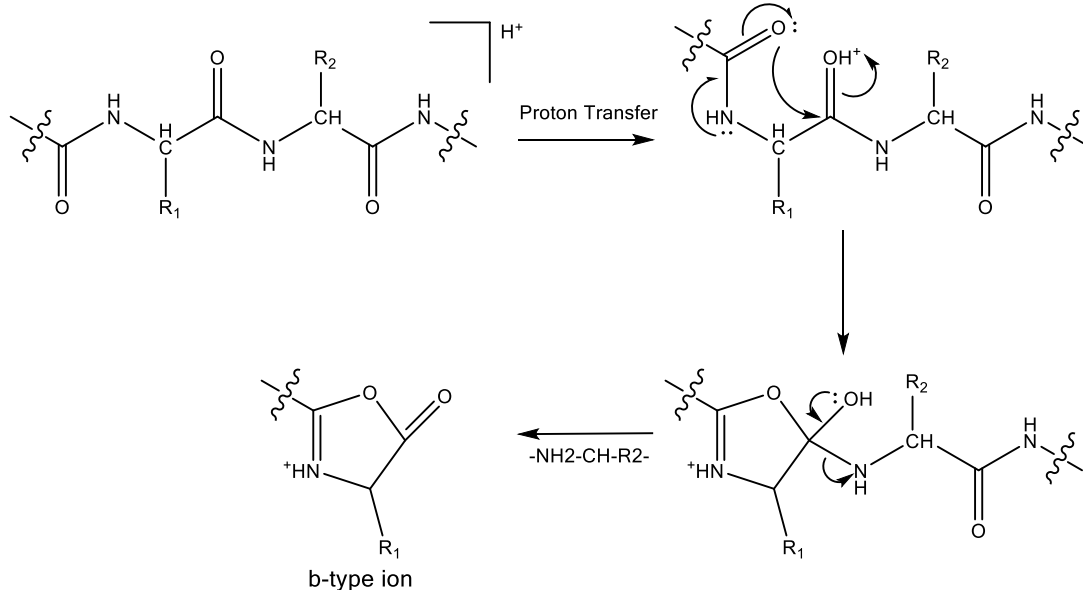


Figure. 18a Generation of b ion by common PSD/CID fragmentation.

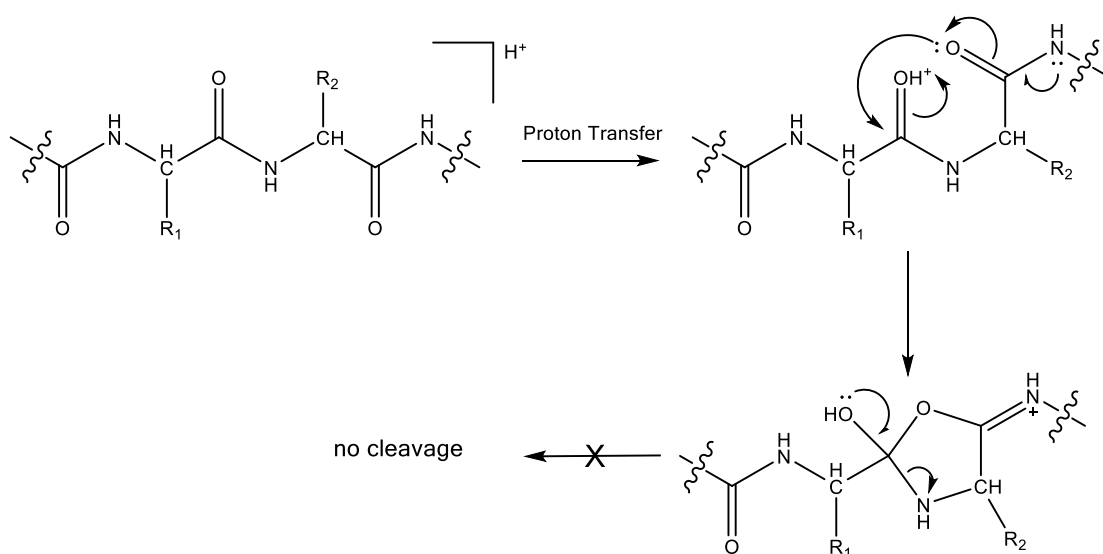


Figure. 18b No generation of b ion by proton transfer.

According to the PSD spectra obtained from MALDI-TOF/TOF MS/MS in the experiments described in this Chapter, the peptides without Arg in the sequence, but for the C terminus, gave the b-type metastable ions, which corresponded to the C-terminally-truncated peptides and were predominant among the metastable ions. The fragmentation at the last amide bond in gaseous phase could be accounted for by the two steps: the first step is decarboxylation at the C terminus; the second step is elimination of the terminal alkyl amine, followed by the formation of the b ion similar to the above fragmentation (Figure. 19). Unlike the formation of b ion at the internal amide bond in Fig. 18, there is a single pathway where the adjacent carbonyl oxygen anion attacks the carbonyl carbon, followed by elimination of the terminal $\text{-NHCH}_2(\text{R}_n)$ to form b_{n-1} ion. Thus, the b_{n-1} ion (C-terminally truncated peptide) could be preferentially generated than ordinary b ions in Fig. 18 during the flight in gaseous phase.

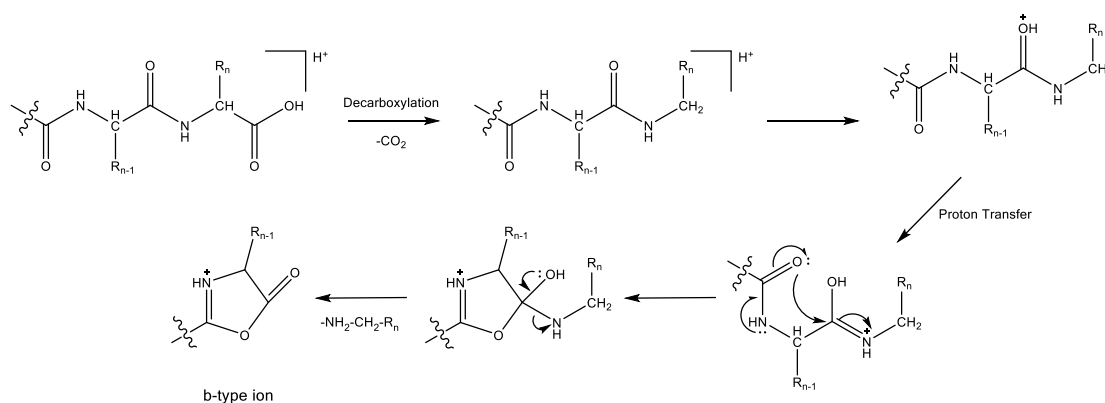


Figure. 19 Generation of C-terminally truncated b_{n-1} ion by PSD fragmentation.

3 Chapter III: Probability-Based Protein Identification by Searching Sequence Database Using Mass Spectrometry Data.

3.1 Introduction

Protein identification is a necessary part in proteomics. A wide range of accurate, effective and efficient algorithms and computer programs for protein identification by searching a sequence database using MS data are developed in the last two decades. There are two main methods for computational identification: Mass-based approaches and Tag-based approaches. The former one uses molecular masses of peptides from a protein digestion by an enzyme, which is represented by PMF; on the other hand, MS/MS data from one or more peptides from the digestion of a protein are used by the latter approaches, just like *de novo* searching; moreover, still other approaches combine the data of mass and amino acid sequence (sequence query). Among all protein identification methods, the scoring system is the key. Experimental mass data obtained from the MS measurement of unknown protein is compared with theoretical mass data of known proteins in the database, and the score is used to evaluate how well the experimental and theoretical data match to each other. A threshold significance is set in the scoring system. A score above the threshold can be counted as a "hit", and the highest hit usually represents the identification result of the unknown protein. Moreover, "no hits" means there are no scores above the threshold and the protein cannot be identified. Shared-peak count is a basic scoring system for comparison, which the number of MS peaks shared by the experimental and theoretical spectra is counted. The experimental spectrum with the highest shared-peak number can be treated as the closest match to the theoretical one. Another basic scoring function is termed "coverage". The coverage is the proportion of the unknown protein

covered by matched peptides, which represent peaks in the MS spectrum. In addition, several general statistic methods such as cross correlation (Eng, McCormack & Yates 1994), Bayesian probability (Zhang, Chait 2000), expectation maximization (Nesvizhskii et al. 2003) and machine learning (Gay et al. 2002, Arnold et al. 2006) are applied to the scoring systems. One of the common computer programs named “Mascot” for protein identification will be introduced and applied as follow.

3.1.1 Mascot: a commercially available searching engine

Mascot is a search engine for protein identification involves probability-based scoring, which issued by Matrix Science Ltd., in 1999. It contains three types of search, such as peptide mass fingerprinting, sequence query, and MS/MS ion search. Mascot calculates the distribution of the lengths of tryptic peptide through the whole sequence database by using a scoring system based on the MOWSE algorithm, and the probability for every peak on the spectrum can be calculated. The probability-based scoring system was described to explain how Mascot interpret data generated by itself (Perkins et al. 1999): *“The fundamental approach is to calculate the probability that the observed match between the experimental data set and each sequence database entry is a chance event. The match with the lowest probability is reported as the best match. Whether this match is also a significant match depends on the size of the database. To take a simple example, the calculated probability of matching six out of ten peptide masses to a particular sequence might be 10^{-5} . This may sound like a promising result but, if the real database contains 10^6 sequences, several scores of this magnitude may be expected by chance. A widely used significance threshold is that the probability of the observed event occurring by chance is less than one in twenty ($p < 0.05$). For a database of 10^6 entries, this would mean that significant matches were those with probabilities of less than 5×10^{-8} . The probability for a good match is usually a very small number, which*

must be expressed in scientific notation. This can be inconvenient, so we have adopted a convention often used in sequence similarity searches, and report a score which is $-10\log_{10}(P)$, where P is the probability. This means that the best match is the one with the highest score, and a significant match is typically a score of the order of 70. It indicates the smaller a protein database is, the lower scores for confidential level. This engine is available for users of the Matrix Science website.

3.2 Methods

Peptide masses data and C-terminal amino acid sequence data are acquired from the spectra according to Chapter II. Examples of the input window and output window are shown as Figure. 20 and Figure. 21.

MASCOT Sequence Query

Your name	<input type="text" value="kahn20002"/>	Email	<input type="text" value="kahn20003@gmail.com"/>
Search title	<input type="text" value="4P 0.5 1miss"/>		
Database(s)	<div> <div>Fungi_EST</div> <div>Environmental_EST</div> <div>SwissProt</div> <div>NCBIInr</div> <div>contaminants</div> </div>	Enzyme	<input type="text" value="Lys-N"/>
Taxonomy	<input type="text" value="All entries"/>		
Fixed modifications	<div>Carboxymethyl (C)</div> <div> <input type="checkbox"/> Display all modifications </div>	<div>></div> <div><</div>	<div> <div>Acetyl (K)</div> <div>Acetyl (N-term)</div> <div>Acetyl (Protein N-term)</div> <div>Amidated (C-term)</div> <div>Amidated (Protein C-term)</div> <div>Ammonia-loss (N-term C)</div> <div>Biotin (K)</div> <div>Biotin (N-term)</div> <div>Carbamidomethyl (C)</div> <div>Carbamyl (K)</div> <div>Carbamyl (N-term)</div> </div>
Variable modifications	<div>--- none selected ---</div> <div> <div>></div> <div><</div> </div>		
Peptide tol. ±	<input type="text" value="0.5"/> Da	# ¹³C	<input type="text" value="0"/>
Peptide charge	<input type="text" value="1+"/>	MS/MS tol. ±	<input type="text" value="0.6"/> Da
Query	<div> <div>2858.830078</div> <div>2755.893311</div> <div>2441.174561</div> <div>2429.008057 seq (C-R)</div> <div>2428.169189</div> <div>2335.285889 seq (C-S)</div> </div>		
Instrument	<input type="text" value="Default"/>		
Decoy	<input type="checkbox"/>		
Report top	<input type="text" value="50"/> hits		
<input type="button" value="Start Search ..."/>		<input type="button" value="Reset Form"/>	

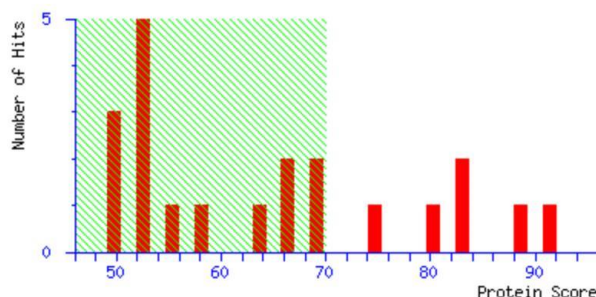
Figure. 20 Mascot input window.

MATRIX SCIENCE Mascot Search Results

User : kahn20002
 Email : kahn20003@gmail.com
 Search title : 4P 0.5 lmiss
 Database : SwissProt 2016_04 (550960 sequences; 196692942 residues)
 Timestamp : 17 Apr 2016 at 06:31:44 GMT
 Top Score : 91 for **MYG_GORBE**, Myoglobin OS=Gorilla gorilla beringei GN=MB PE=1 SV=2

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As	Concise Protein Summary	Help
Significance threshold p<	0.05	Max. number of hits 50
Preferred taxonomy	All entries	

1. [MYG_GORBE](#) **Mass:** 17221 **Score:** 91 **Expect:** 0.0004 **Matches:** 21
 Myoglobin OS=Gorilla gorilla beringei GN=MB PE=1 SV=2
[MYG_HUMAN](#) **Mass:** 17231 **Score:** 85 **Expect:** 0.0016 **Matches:** 20
 Myoglobin OS=Homo sapiens GN=MB PE=1 SV=2
[MYG_HYLAG](#) **Mass:** 17261 **Score:** 85 **Expect:** 0.0016 **Matches:** 20

Figure. 21 Mascot output window.

3.3 Results

3.3.1 Protein identification (Mascot) based on masses (PMF).

Table. 3 shows the Mascot protein identification by peptide masses obtained for seven single proteins. According to the output, the scores of BSA is 46, CYC is 43, MB is 29, CA is 48, and there are no scores of TF, MYH and PYGM. Input data and output data refer to the supplement.

Table. 3 Results of Mascot single protein identification by masses data of all peptides.

	BSA	TF	CYC	MB	MYH	PYGM	CA
Score	46	/	43	29	/	/	48
Number of false matched proteins	22	45	43	40	40	37	35

Table. 4 shows the Mascot protein identification by peptide masses obtained for a mixture of four proteins. According to the output, the scores of MB is 27 and there are no scores of BSA, TF and CYC. Input data and output data refer to the supplement.

Table. 4 Results of Mascot protein mixture identification by masses data of all peptides.

	BSA	TF	CYC	MB
Score	/	/	/	27
Number of false matched proteins	42			

3.3.2 Protein identification (Mascot) based on masses and C-terminal amino acid sequences of partial detected peptides.

Table. 5 shows the Mascot protein identification by masses of all detected peptides, which are the same as those used in 3.3.1 and C-terminal amino acid sequences of partial peptides derived from seven single proteins. According to the output, the scores of BSA is 293, TF is 138, CYC is 137, MB is 133, MYH is 134, PYGM is 124 and CA is 126. Input data and output data refer to the supplement.

Table. 5 Results of Mascot single protein identification by masses data of all peptides and C-terminal amino acid sequences of partial peptides.

	BSA	TF	CYC	MB	MYH	PYGM	CA
Score	293	138	137	133	134	124	126
Number of false matched proteins	45	28	31	15	46	37	44

Table. 6 shows the Mascot protein identification by masses data of all peptides and C-terminal amino acid sequences of partial peptides derived from a mixture of four proteins. According to the output, the scores of BSA is 64, TF is 48, CYC is 55, MB is 65 Input data and output data refer to the supplement.

Table. 6 Results of Mascot protein mixture identification by masses data of all peptides and C-terminal amino acid sequences of partial peptides.

	BSA	TF	CYC	MB
Score	64	48	55	65
Number of false matched proteins	16			

3.3.3 Protein identification (Mascot) by masses and C-terminal amino acid sequences of partial detected peptides (excluding the peptides with mass values only).

Table. 7 shows the Mascot protein identification by masses and C-terminal amino acids of partial detected peptides (excluding the peptides with mass values only) derived from seven single proteins. According to the output, the scores of BSA is 364, TF is 175, CYC is 176, MB is 201, MYH is 142, PYGM is 157 and CA is 142. Input data and output data refer to the supplement.

Table. 7 Results of Mascot single protein identification by masses data and C-terminal amino acids of partial detected peptides (excluding the peptides with mass values only)

	BSA	TF	CYC	MB	MYH	PYGM	CA
Score	364	175	176	201	142	157	142
Number of false matched proteins	36	31	11	2	26	38	37

Table. 8 shows the Mascot protein identification by masses data and C-terminal amino acids of partial detected peptides (excluding the peptides with mass values only) derived from a mixture of four proteins. According to the output, the scores of BSA is 61, CYC is 66 and MB is 84, but no score of TF. Input data and output data refer to the supplement.

Table. 8 Results of Mascot protein mixture identification by masses data and C-terminal amino acids of partial detected peptides (excluding the peptides with mass values only).

	BSA	TF	CYC	MB
Score	61	/	66	84
Number of false matched proteins	1			

3.4 Discussion

According to the above results of single protein identification, the conventional PMF by searching peptide masses could hardly be in use for protein identification. As to the single protein identification, only four proteins can be identified with scores lower than confidential threshold (for example at 70 when the size of a database is 10^6 sequences) of seven proteins, and other three ones cannot be identified. However, after inputting the additional C-terminal amino acid sequences of the peptides partially observed together with masses, all of the seven proteins can be identified with significant scores above 70, which indicates the additional C-terminal amino acid sequence can increase

the overall probability for a correct match. Moreover, after removing the peptides with masses data only from the input data, the scores of all seven identified protein increase higher than the second searches, it means that reducing the size of input data can decrease the opportunity of random matches to the theoretical data in the database. As well as the single protein identification, the experiments for protein mixture case also demonstrated the effectiveness of additional C-terminal amino acid sequences information in improving the conventional PMF: all of the four proteins in a mixture could be identified by peptides with masses and C-terminal amino acid sequences, meanwhile almost no protein could be identified by conventional PMF. Especially, after adding the C-terminal amino acid sequences of partially observed peptides into the input data, three proteins in a mixture contained four proteins except TF. However, TF could be identified by searching the masses and C-terminal amino acid sequences of partial observed peptides only. It is a significant improvement than the above mentioned case for the single protein digestion, not only reducing the random match by decreasing the amount of input data, but also the unknown protein can be identified. According to the comparison of the number of matches between the search of protein mixture by masses of all detected peptides and C-terminal amino acid sequences of partially detected peptides, and the search of protein mixture by masses and C-terminal amino acid sequences of partially detected peptides (shown in Supplement “4P mass/mass+c” and “4P mass +c”), the number of matches for MYG_HORSE, ALBU_BOVIN and CYC_HORSE decreases from 23 to 7, 31 to 8 and 20 to 5, respectively. Meanwhile, the kinds of protein identified also decreases from 21 to 7. Such a reduction of matched peptides to each protein and the species of identified protein offers a possibility of reducing the interference by noisy random matches, and increasing the accuracy of identification. It indicates an advantage of dealing with a mixture of proteins by introducing C-terminal amino acid sequences in conventional PMF.

4 Chapter IV: Non-Probability-Based Protein Identification by Searching Sequence Database Using Mass Spectrometry Data I: Computer Simulation.

4.1 Introduction of the algorithm for computer simulation of iD plus.

A non-probability-based sequence database searching software named “iD plus” was developed by our lab. There are two parts in the computational simulation: peptides from “Same Protein” (SP) and “Different Proteins” (DP) (Figure. 22). In the workflow of “SP” (Figure. 23 (A)), a protein database of LysN digested peptides was established. 1000 proteins were selected from the database randomly, and then four peptides were selected from each protein randomly in the 1000 proteins. The mass of a peptide, and both of the N-terminal (K) and C-terminal amino acids in the sequence of peptide were defined as a “set”, and every four sets from a same protein were arranged as a “combination”, 1000 combinations among all combinations were selected randomly and input into the database searching. In the results of database searching, if there was only one hit corresponded to a combination (4 peptides set), the result was denoted as “true”; if there was more than one hit corresponded to a combination, the result was denoted as “false”. All of the results were merged then output as a form with protein IDs for analysis. Figure 23. (B) shows the workflow of “DP”. 1000 proteins were generated randomly selected from the protein database and the LysN digested peptides were randomly generated, and then one peptide was selected from each of 1000 proteins in a random manner. $1000!/4!(1000-4)!$ combinations were subjected to the database searching, if there was no hit corresponding to any of the combinations, the result was denoted as “true”; if there were hits corresponding to any of the combinations, the result was denoted as “false”. All of the results were merged then output as a form with protein IDs for analysis.

database更新

Search Engine for Protein ID Search-study Freq

Key_MS error ± 0.3

====Q8IZX4====
 KDDKEPQAV_1029.521
 KHREEMRKERRRIQQLRRL_2747.555
 KPAVIDAYVRIRTTKDE_1975.098
 KDGHGK_641.337
 ====Q6UXU4====
 KRKVFEGGYREEPTFIDPEAI_2552.315
 KVFEQGYREEPTFIDPEAI_2268.119
 KYFRERME_1158.573
 KVFEQGYREEPTFIDPEAIKYFRERME_3407.67
 ====Q8NGZ2====
 KAFSNCVPHLVTVFLVTGAVAYL_2719.489
 KVLWNVRRSSGVMKR_1659.948
 KNKDI_617.3622
 KSALSKVLWNVRRSSGVM_1862.032
 ====Q5VYV0====
 KSSYSDDQPPYSYISLTAMAIQHSAE_2902.393
 KPPYSYISLTAMAIQHSAEKMLPLSDIY_3167.61
 KGSFWALHPDCGDMFENGSSFLRRRKRF_3315.605

OS= Homo sapiens

C_system Cmc

1 set 4 peptides

Random 1000 sets

Target Protein AA number >= 100

☐ Digest C-term of KX ☐ don't cut N-term of Pro

☒ Digest N-term of KX 特定のデータベースを作った

allow up to 1 miss cleavage

peptide_len 5 - 30

☒ peptide from the same Protein

☐ peptide from different Protein

① ランダムで取る

② 書き直す

③ サーチ

database更新

Search Engine for Protein ID Search-study Freq

Key_MS error ± 0.3

====Q8IZX4====
 C-V_1029.521
 C-L_2747.555
 C-E_1975.098
 C-K_641.337
 ====Q6UXU4====
 C-I_2552.315
 C-I_2268.119
 C-E_1158.573
 C-E_3407.673
 ====Q8NGZ2====
 C-L_2719.489
 C-R_1659.948
 C-I_617.3622
 C-M_1862.032
 ====Q5VYV0====
 C-E_2902.393
 C-Y_3167.616
 C-F_3315.605

OS= Homo sapiens

C_system Cmc

1 set 4 peptides

Random 1000 sets

Target Protein AA number >= 100

☐ Digest C-term of KX ☐ don't cut N-term of Pro

☒ Digest N-term of KX 特定のデータベースを作った

allow up to 1 miss cleavage

peptide_len 5 - 30

☒ peptide from the same Protein

☐ peptide from different Protein

① ランダムで取る

② 書き直す

③ サーチ

Figure. 22 Windows of iD plus for comuplational simulation. Above: random selection. Bottom: format change.

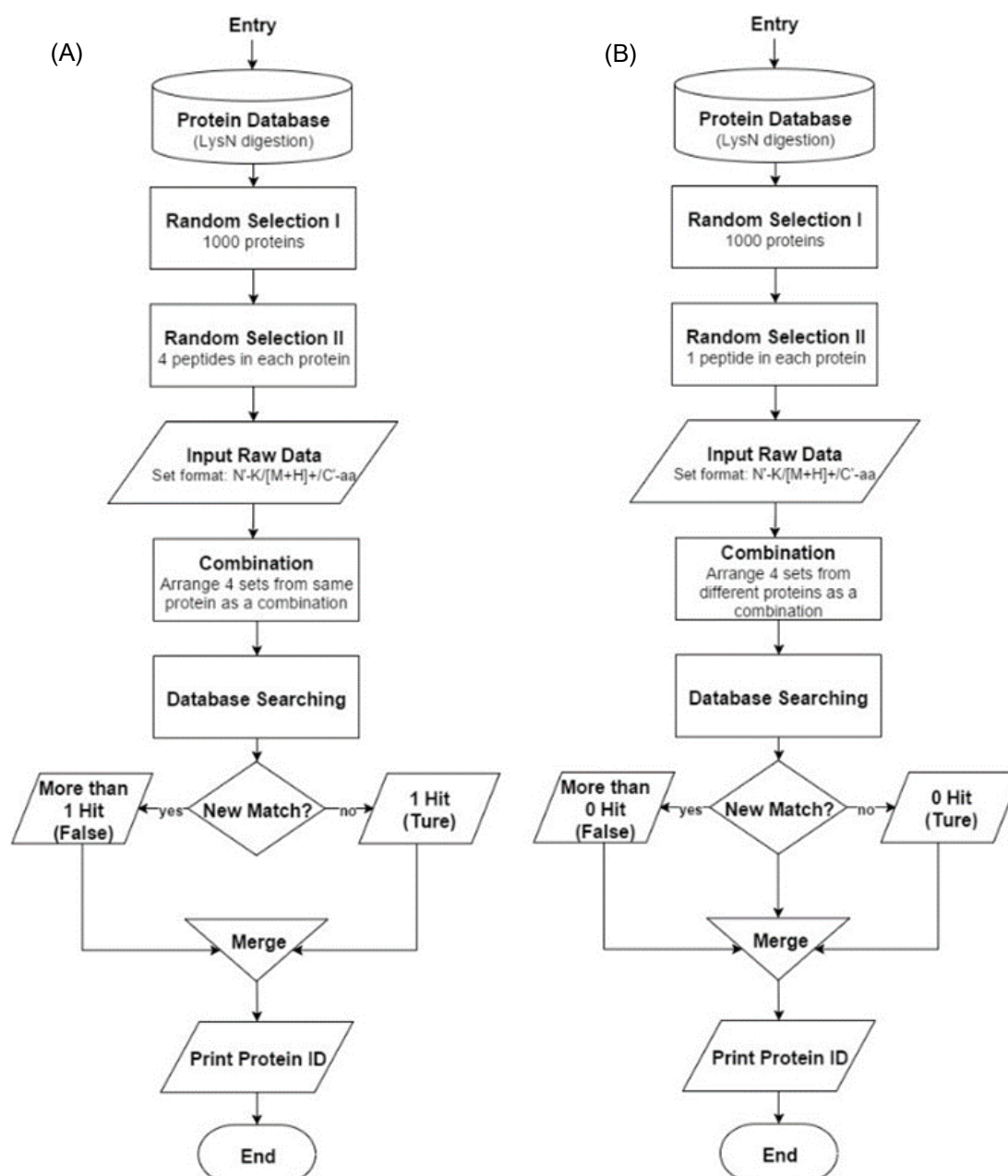


Figure. 23 Workflows of virtual searching of 1000 combinations of four sets of peptide masses and C-terminal amino acid sequences. (A) module for searching based on four sets from “Same Protein”. (B) module for searching based on four sets, each from “Different Proteins”.

4.2 Methods

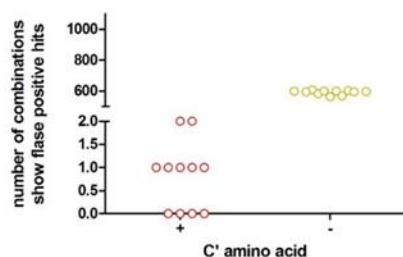
Peptide masses data and C-terminal amino acid sequence data are acquired from the spectra according to Chapter II. Examples of the input data format and

results format are shown in the part of supplement.

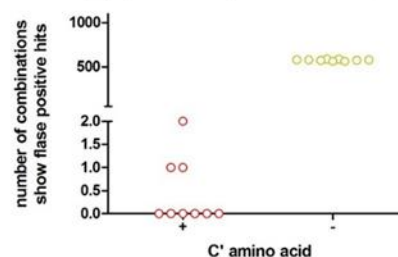
4.3 Results

Figure. 24 (A-1 & A-2) shows the comparison of searching reliability of peptides with or without C-terminal amino acid in both of “SP” and “DP” digested by LysN *in silico*. In the “SP”, there is around 60% of 11,000 combinations (three peptides) show false positive hits without C-terminal amino acid, whereas, only 0.09% of 11,000 combinations (three peptides) show false positive hits with C-terminal amino acid. “DP” shows a similar result as well. There is around 50% of 10,000 combinations (three peptides) show false positive hits, whereas only 0.04% of 10,000 combinations (three peptides). Figure. 24 (B-1 & B-2) shows the comparison of searching reliability by a combination contains different numbers of peptides in both of “SP” and “DP” digested by LysN *in silico*. In the “SP”, the rates of false positive hits resulted from searching by over 10,000 combinations contain one, two, three and four peptides are around 100%, 17-20%, 0.09% and 0%, respectively. In the “DP”, the rates of false positive hits resulted from searching by over 10,000 combinations contain one, two, three and four peptides are around 100%, 3-6%, 0.04% and 0%, respectively. These results clearly indicate the introduction of an additional C-terminal amino acid sequence is critically useful for increasing the reliability of PMF than using only one terminal amino acid information, which is deduced by the enzyme used. The reliability increases over around 100% by setting double-termini for searching than single-terminus for searching.

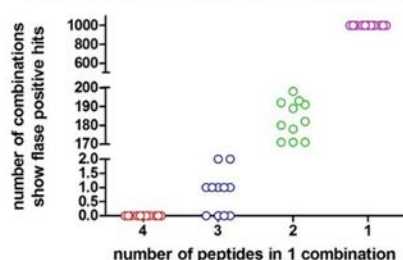
A-1 False protein identification by Lys-N digestion peptides combinations from same proteins (3 peptides compose 1 combination)



A-2 False protein identification by Lys-N digestion peptides combinations from different proteins (3 peptides compose 1 combination)



B-1 False protein identification by Lys-N digestion peptides combinations from same proteins (C'+)



B-2 False protein identification by Lys-N digestion peptides combinations from different proteins (C'+)

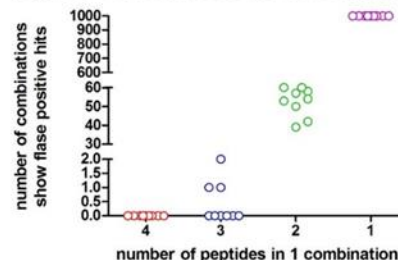


Figure. 24 Results of database searching using virtual LysN peptides. A-1: The number of false hits by LysN peptides derived from same proteins under the conditions with or without C-terminal amino acid; A-2: The number of false hits by LysN peptides derived from different proteins under the conditions with or without C-terminal amino acid; B-1: The number of false hits by different numbers of LysN peptides derived from same proteins with C-terminal amino acid sequences; B-2: The number of false hits by peptides derived from different proteins with C-terminal amino acid sequence. Each circle represents the result of 1000 combinations of database searching of peptide sets of which are generated in a random selection.

4.4 Discussion

Almost all of the protein identification performed by MS are based on computational database search software, for example the Mascot I described in Chapter III above. Mascot is a probability-based protein identification computer program by searching sequence database using MS data. The

probability-based algorithm involves calculating the theoretical fragments for all the peptides in the database. The disadvantages of probability-based identification are relative low reliability and it is difficult to identify proteins mixture. Different with Mascot, the in-house computer program “iD plus” developed in our lab is not a probability based database search software. According to the results of computational simulation, we believe that if four C-terminal truncated peptides from a protein digested by LysN protease, the confident level is at about almost 100%. Such a high confident level can be shown in both of identification for single protein and protein mixture. Moreover, even one peptide is enough to use for protein identification by MS/MS sequencing, while PMF usually requires a dozen of peptide masses for using. The number of observed peptides in mass spectra relative to the amount of protein sample, the larger amount of unknown protein, the more number of peptides derived from the digest can be obtained. So the ability to use fewer peptides for protein identification is important for the sensitivity. The simulation verify at least four peptides are enough for a positive identification, the number is much less than conventional PMF. The examples of experimental practice by iD plus searching would be described in the next chapter and be discussed further.

5 Chapter V: Non-Probability-Based Protein Identification by Searching Sequence Database Using Mass Spectrometry Data II: Experimental Practice.

5.1 Introduction of the algorithm for experimental practice of iD plus.

Fig. 25 shows the workflow of protein identification based on the peptide masses and C-terminal amino acid sequences of the observed peptides as well as the N-terminal Lys, which was set as the default from the enzyme specificity. The analysis process as divided into four parts: “Combination I” (C1), “Database Searching I” (DS1), “Combination II” (C2) and “Database Searching II” (DS2). In the progress of “C1”, based on the total number n of peptides, the combinations of four sets of peptide masses and their C-terminal amino acid sequences were generated $n!/4!(n-4)!$ combinations. Proteins matched to any combinations of four sets were searched in the progress of “DS1”. If any combination could match to one protein, the result was denoted as “true”, then saved in a tile. If any combination could not match to any protein, the sets in these combinations, m (where m refers to the number of remaining peptides after “DS1”) sets were arranged to generate $m!/3!(m-3)!$ Combinations (“C2”), which comprised of three sets of peptide masses and C-terminal amino acid sequences. Proteins matched to any combinations were searched in the progress of “DS2”. If any combination could match to one protein, the result was denoted as “semi-true”, then added into the “true” results of “DS1”; the remaining combinations of three sets that could not match with any proteins were discarded. Regarding to the merged “true” and “semi-true” results, sequence coverages, which are the percentage of the number of amino acids of the peptides occupied the total number of amino acids of the identified protein were calculated, and used for judgement of the reliability of merged results, in

case of multiple hits being obtained for a combination. Finally, protein IDs were output as identification result with the matched peptide masses and C-terminal amino acid sequences.

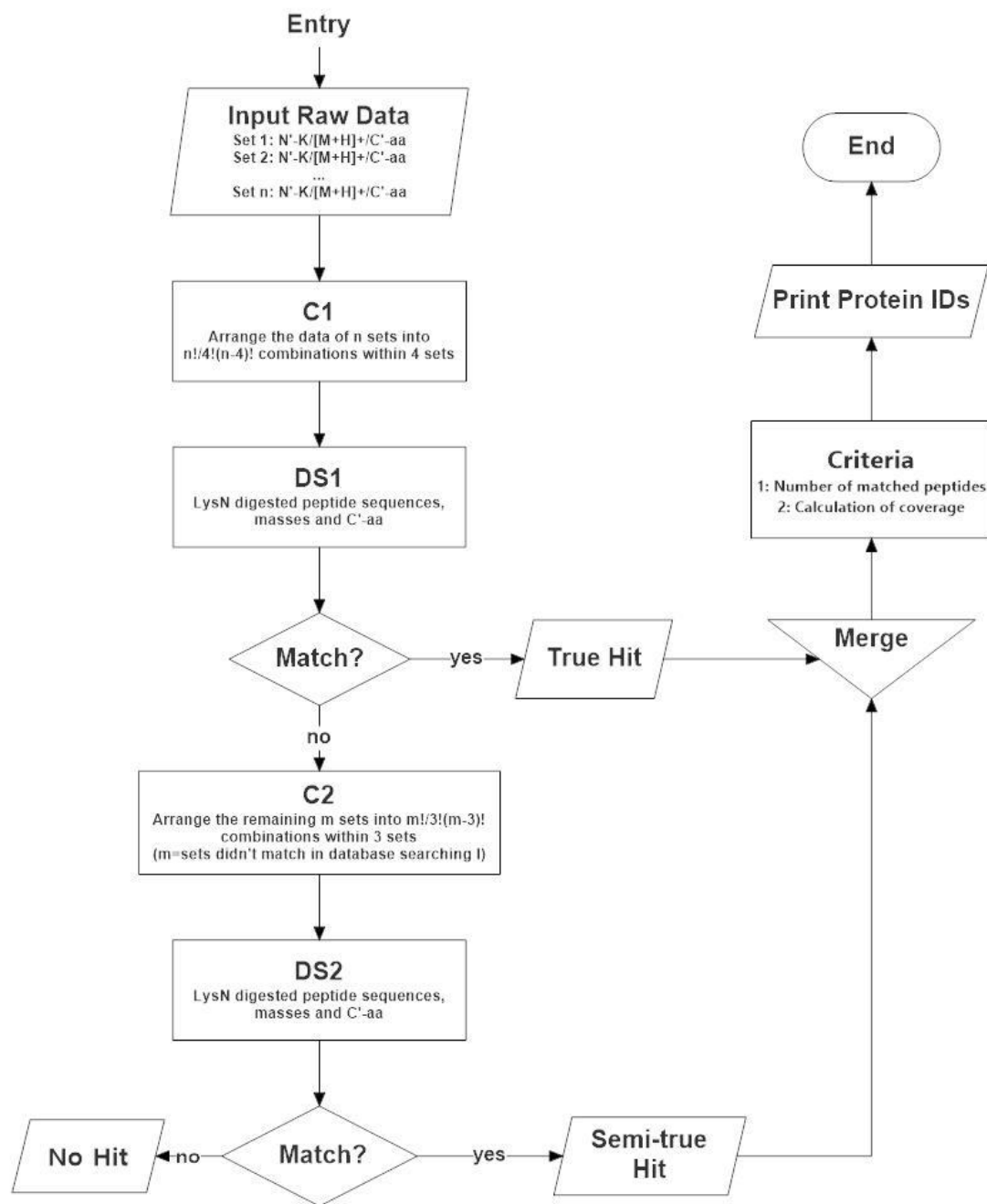


Fig. 25 Database searching workflow for protein identification by using in-house software "iD plus".

5.2 Methods

Peptide masses data (above Da) and C-terminal amino acid sequence data are acquired from the spectra according to Chapter II. Fig. 26 show the input window of iD plus. Examples of the input data format and results format are shown in the part of supplement. The database searching by iD plus was under the condition of allowing 0.5 Da error and 1 missed cleavage in the matched peptide sequences, and removing the noisy proteins titin (protein IDs of A2ASS6 and Q8WZ42).

Search Engine for Protein ID(ms,c-term) | Search Engine for Protein ID(1-n any ms) | Search Engine for Protein ID(ms) | Search-study | Freq

Query
(m/z, C-term AA)

error ± 0.3

2429.008057,R
2335.285889,S
1929.247437,H
1916.212646,H
1687.285645,H
1674.283813,H
1502.362671,T
1502.362671,B
1486.19397,E
1478.277832,E
1473.192627,E
1470.390625,N
1454.395996,T
1454.395996,B
1411.743286,B
1399.402344,T
1386.3927,T
1350.509644,J
1333.510986,H
1296.542358,R
1276.564087,R
1229.505371,S
1217.599976,H
1165.476563,Y

1/L=J
Q/K=B

Taxonomy All ☐ Titinを削除する

Cys(-SR) Cmc

Target Protein AA number >= 100

☐ Digest C-term of K ☐ don't cut N-term of Pro

☒ Digest N-term of K 特定のデータベースを作った

allow up to 2 miss cleavage

peptide_len 5 ~ 30

run

Figure. 26 Window of iD plus for experimental protein identification (searching engine). The range of allowing mass error is multiple, the tolerance for the number of missed cleavages is optional from 0 to 2, and the titin (A2ASS6 and Q8WZ42) can be chosen to keep or remove.

5.3 Results

5.3.1 Verification of algorithm

Before applying the experimental data to iD plus, the verification of algorithm is necessary. The theoretical mass values $[M+H^+]$ and the C-terminal of the peptides derived from BSA, TF, CYC and MB were input into the iD plus. According to Figure. 23, only the peptides with amino acid length between five and 30 in a database would be picked up by iD plus for database search. Table. 9 summarizes the results of algorithm verification by peptides from digest of four single proteins. All the peptide lengths between 5-30 amino acids could match to the derived proteins entirely, no additional proteins were identified.

Table. 9 Results of algorithm verification by theoretical digestion data.

Identified protein(s)	number of peptides from digest	number of peptides matched (5-30 aa)	sequence coverage
BSA	58	46	93.90%
TF	58	46	84.80%
CYC	17	11	86.70%
MB	18	11	87.70%

5.3.2 Single protein identification

Based on such a database searching workflow, various authentic proteins were measured and analyzed. BSA, TF, CYC, MB, MYH, PYGM and CA were addressed as the methodology part described in Chapter II, and the masses and C-terminal amino acid sequences of detected peptides were acquired from MALDI-TOF/TOF MS spectra. All the data was input into iD plus for sequence database searching. Table. 9-15 show the identification results by iD plus for BSA, TF, CYC, MB, MYH, PYGM and CA, respectively. For BSA identification, 73 peptide sets were input into iD plus, and 57 sets could assign to 17 proteins.

The protein with the most hits (21) and top coverage (35.10%) is BSA (P02769) (Table. 10). For TF identification, 47 peptide sets were input into iD plus, and 24 sets could assign to 5 proteins. The protein with the most hits (11) and top coverage (16.20%) is TF (Q29443) (Table.11). For CYC identification, 34 peptide sets were input into iD plus, and 27 sets could assign to 5 proteins. The protein with the most hits (8) and top coverage (89.50%) is CYC (P00004) (Table.12). For MB identification, 30 peptide sets were input into iD plus, and 17 sets could assign to 6 proteins. The protein with the most hits (8) and top coverage (61.00%) is MB (P68082/P68083) (Table.13). For MYH identification, 75 peptide sets were input into iD plus, and 59 sets could assign to 22 proteins. The protein with the most hits (14) and top coverage (7.40%) is MYH (Q28641) (Table.14). For PYGM identification, 53 peptide sets were input into iD plus, and 36 sets could assign to 9 proteins. The protein with the most hits (9) and top coverage (12.50%) is PYGM (P00489) (Table.15). For CA identification, 29 peptide sets were input into iD plus, and 18 sets could assign to 6 proteins. The protein with the most hits (6) and top coverage (28.10%) is CA (P00921) (Table.16). It indicates for single protein identification, the candidate with the most number of matched peptides and/or highest coverage can be confirmed as target protein.

Table. 10 Identification Results for BSA by iD plus.

BSA		
Number of sets	73	
Number of matched sets	57	
Number of matched proteins by more than three sets	17	
Coverage	Number of matched peptides	ID
35.10%	21	P02769
2.20%	5	Q6A078
0.20%	4	Q9I7U4
1.00%	4	Q8IDX6
0.80%	4	Q69Z23
0.80%	4	Q9UFH2
0.70%	4	Q555C6
1.70%	4	Q96RL7
1.40%	3	Q6YXP5
2.60%	3	Q9PQ74
0.80%	3	Q71LX6
2.70%	3	P21421
1.60%	3	P23466
1.50%	3	P0C568
3.30%	3	Q88VX7
0.90%	3	Q4U4S6
5.60%	3	Q46LV3

Table. 11 Identification Results for TF by iD plus.

TF		
Number of sets	47	
Number of matched sets	24	
Number of matched proteins by more than three sets	5	
Coverage	Number of matched peptides	ID
16.20%	11	Q29443
0.80%	4	Q9QYX7
1.00%	3	P09814
1.80%	3	P22082
7.60%	3	Q042P8

Table. 12 Identification Results for CYC by iD plus.

CYC		
Number of sets	34	
Number of matched sets	27	
Number of matched proteins by more than three sets	5	
Coverage	Number of matched peptides	ID
89.50%	8	P00004
0.40%	4	Q8I3Z1
0.40%	3	P0C6Y0
0.40%	3	C6KTB7
1.40%	3	Q6ZQQ6

Table. 13 Identification Results for MB by iD plus.

MB		
Number of sets	30	
Number of matched sets	17	
Number of matched proteins by more than three sets	6	
Coverage	Number of matched peptides	ID
61.00%	8	P68082
61.00%	8	P68083
3.70%	3	P14606
4.50%	3	Q6FKT1
0.50%	3	O68008
0.70%	3	Q4G0P3

Table. 14 Identification Results for MYH by iD plus.

MYH		
Number of sets	75	
Number of matched sets	59	
Number of matched proteins by more than three sets	22	
Coverage	Number of matched peptides	ID
7.40%	14	Q28641
7.40%	14	homology
7.60%	14	
7.60%	14	
7.60%	14	

7.80%	14	
1.30%	5	P62286
1.00%	5	P0C6U9
0.60%	5	P0C6X8
2.00%	4	A4QKG5
3.90%	4	P02562
1.80%	4	Q6EVK6
3.00%	3	Q54YD8
1.30%	3	Q68RU8
6.10%	3	A4XPN6
1.10%	3	Q8I4R2
6.20%	3	Q3YT49
0.20%	3	Q9I7U4
4.50%	3	P23316
4.90%	3	Q9LS42
3.70%	3	Q8ILT5
1.50%	3	Q00963

Table. 15 Identification Results for PYGM by iD plus.

PYGM		
Number of sets	53	
Number of matched sets	36	
Number of matched proteins by more than three sets	9	
Coverage	Number of matched peptides	ID
12.50%	9	P00489
0.40%	4	Q8I3Z1

3.80%	4	Q553B1
4.30%	3	Q5UR75
1.70%	3	Q6FSD2
2.50%	3	P37609
0.90%	3	Q8TDW7
2.30%	3	P49466
7.20%	3	Q5UPN0

Table. 16 Identification Results for CA by iD plus.

CA		
Number of sets	29	
Number of matched sets	18	
Number of matched proteins by more than three sets	6	
Coverage	Number of matched peptides	ID
28.10%	6	P00921
6.80%	4	P17480
6.80%	4	P25976
6.80%	4	P25977
0.50%	3	Q8IID4
0.50%	3	Q09666

5.3.3 Protein mixture identification

As to the protein identification from protein mixture by MS/MS based enhanced PMF, an artificial protein mixture of BSA, CYC and MB is measured by MALDI-TOF/TOF MS. Table.16 shows the identification results by iD plus for Table. 16 shows the searching result of the protein mixture digested LysN, proteins of a

protein mixture of BSA, TF, CYC and MB. For the mixture of four proteins identification, 59 peptide sets were input into iD plus, and 39 sets could assign to 10 proteins. The protein with the 6 hits and 8.1% of coverage can be identified as BSA (P02769), the protein with the 5 hits and 33.8% of coverage can be identified as MB (P68082), the protein with the 4 hits and 6.7% of coverage can be identified as TF (Q29443), and the protein with the 4 hits and 31.40% of coverage can be identified as CYC (P00004) (Table.16).

Table. 16 Identification Results for Protein Mixture by iD plus.

Protien Mixture		
Number of sets	59	
Number of matched sets	39	
Number of matched proteins by more than three sets	4	
Coverage	Number of matched peptides	ID
0.081	6	P02769
0.338	5	P68082
0.067	4	Q29443
>0.314	4	P00004

5.4 Discussion

The algorithm of iD plus is a non-probability based sequence database search, which is different with Mascot, a probability based sequence database search. The results of Mascot search in Chapter II already demonstrate the significance of C-terminal amino acid sequences deduced from metastable ions in the spectra of peptides derived from LysN digested proteins for protein identification. In this session, the algorithm of iD plus has been verified firstly by

theoretical peptide masses from the protein digest list. The result indicates the validity of the algorithm of iD plus. The tolerance conditions of iD plus search allow error of ± 0.5 Da, up to 1 missed cleavage in a peptide sequence and removing the sequence of titin (A2ASS6 and Q8WZ42) from the sequence database. The first two conditions of allowing error of ± 0.5 Da and up to 1 missed cleavage correspond with the conditions of Mascot search described in Chapter III, and the reason of removing A2ASS6 and Q8WZ42 from the sequence database is that the length of the sequence of these two proteins are very long (35,213 aa and 34,350 aa). As we know, the random matches would increase with the increasing of the length of protein. In the single protein identification by iD plus using an entire sequence database, A2ASS6 and Q8WZ42 were always identified as false proteins, and a few of peptide sequence derived from protein digest could be matched to titin because in the LysN digest of titin, many sequences contain the similar masses and C-terminal amino acid sequences to other peptides derived from LysN digest of BSA/TF/CYC/MB. Therefore, A2ASS6 and Q8WZ42 were removed from sequence database to improve the algorithm of iD plus. On another hand, only the peptides with masses above 800 kDa were used for protein identification due to in the mass range below 800 kDa, matrix and other background could be measured by MS and such false input data may increase the false identification by iD plus. Under these conditions, iD plus was run for protein identification by experimental peptides data acquired from MS spectra. For the single protein identification, all the seven proteins can be matched with the most number of peptides input than the number of peptides matched to other false proteins. In addition, the coverage of the identified proteins which the most number of peptides matched to are the highest among all proteins output by iD plus. Those results are similar as Mascot search for single protein using the same input data, but iD plus does not adopt the probability-based algorithm. Whereas, the iD plus can identify protein mixture with fewer number of peptides

better than Mascot does. Chapter III described that Mascot cannot identify all of the four proteins by partial peptides with masses and C-terminal amino acid sequences, though the four proteins can be identified in a mixture by adding more peptide masses without deduced C-terminal amino acid sequence. It indicates that the probability-based algorithm of Mascot cannot address the identification in the situation of fewer number of peptides can be used. However, iD plus can identify all the four proteins using the same data of peptides masses and C-terminal amino acid sequences as Mascot used and a non-probability based algorithm. Only the four proteins of BSA/MB/TF/CYC can be identified by 6, 5, 4, 4 peptides, other few number of false proteins can only match to less than 3 peptides. As to the simulation result described in Chapter IV, the reliability of protein identified by more than 4 peptides is the highest. It means the identification of protein mixture by iD plus is better than Mascot.

Conclusion

In this study, I have investigated the generation of [b] ions and [b+18] ions relative to C-terminal truncated of peptides measured by MALDI-TOF/TOF MS and proposed a new strategy of applying those metastable ions on conventional PMF to increase the reliability for protein identification. We experimentally demonstrated that the [b] ions can be generated by any peptide sequence, besides Arg-contained peptides which can produce [b+18] ions. A scheme of enhanced PMF based on the protein digest by LysN was established and the effect of C-terminal amino acid sequences were verified by Mascot. Furthermore, a non-probability based database searching algorithm “iD plus” was developed in-house. The performance of the experimental workflow and computational database searching was validated using single protein digest and protein mixture digest. The application of iD plus on addressing the identification of protein mixture was better and more reliable than the algorithm of PMF or query search of Mascot. We foresee more promising applications of the iD plus for protein identification.

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Supplement

Mascot input data format and iD plus input data (mass+c)

BSA
mass

2816.559814	1930.019165	1709.743408	1534.556763	1428.553345
2757.61377	1928.910522	1701.800903	1530.647583	1423.299072
2402.151123	1916.98645	1697.773682	1526.865356	1415.714722
2348.163574	1913.897705	1695.796753	1521.573975	1415.546875
2335.06958	1908.93457	1688.775146	1517.621826	1409.759277
2291.082031	1900.386353	1688.636475	1510.609009	1408.634766
2290.119385	1897.131348	1687.77771	1508.575317	1407.602539
2277.043213	1897.12793	1686.717285	1505.53772	1399.751709
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2261.196777	1876.000244	1674.760864	1499.684937	1394.594238
2248.214111	1872.000977	1673.685425	1497.787476	1386.591187
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2011.620117	1759.820557	1559.727173	1463.697754	1294.662964
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BSA
mass/mass+c

2816.559814	1897.131348 seq(C-G)	1651.729858
2757.61377	1897.12793	1640.772827
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2049.024658	1759.820557	1536.624512
2035.952393	1750.812256	1536.591919
2032.958496	1749.715088 seq(C-D)	1534.581177 seq(C-E)
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1966.901123	1695.796753	1497.787476
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1463.697754 seq(C-I)	1258.775879	1055.644409
1463.697754 seq(C-L)	1247.759521	1055.637329
1457.703735	1244.603882	1055.631592
1448.838013	1244.578613	1054.526489
1445.566528	1239.652344	1047.638672 seq(C-K)
1444.638428 seq(C-S)	1222.046753	1047.638672 seq(C-Q)
1439.839355	1221.66687	1045.564941 seq(C-F)
1439.827393	1221.564819	1044.11438
1433.767212	1216.69043	1043.588135
1433.609863	1214.560059	1042.328613
1430.494385	1203.718994	1038.425171
1428.553345	1203.681274	1035.466553
1423.299072	1199.574951	1033.495605
1415.714722	1177.654907	1032.499268
1415.546875	1163.658813 seq(C-A)	1029.55835
1409.759277	1162.638062 seq(C-F)	1028.548828
1408.634766	1157.663452	1028.474609
1407.602539	1149.611816	1027.588257
1399.751709	1145.716797	1025.549927
1399.734863 seq(C-D)	1145.670044 seq(C-K)	1021.55481
1394.594238	1145.670044 seq(C-Q)	1019.492432
1386.591187	1144.590088	1017.62323
1381.533325	1140.523682	1015.083008
1364.618042	1138.581299	1014.657776 seq(C-I)
1363.728271 seq(C-M)	1135.473633	1014.657776 seq(C-L)
1352.668579	1127.492432	1009.5578 seq(C-T)
1351.731201	1126.598022 seq(C-A)	1006.456116
1350.632935 seq(C-F)	1125.565918	1004.593506
1349.602295	1114.63208	1002.522644
1347.531006	1113.623169	1001.476868
1341.718994	1092.52832	1001.116943
1336.573486 seq(C-F)	1086.586182 seq(C-F)	998.5465088
1335.641724	1082.520142 seq(C-F)	996.526123 seq(C-T)
1321.675903	1077.621826 seq(C-R)	994.5374756
1305.719971 seq(C-M)	1077.498413	993.5001831
1305.719971 seq(C-I)	1075.625732	991.6455688 seq(C-R)
1305.719971 seq(C-L)	1075.51001	991.4567261
1294.662964	1069.486206 seq(C-E)	989.6400757 seq(C-K)
1293.702759	1067.554565 seq(C-T)	989.6400757 seq(C-Q)
1283.698242 seq(C-I)	1064.524536	988.5450439

988.444458	925.5374146	869.5291748
987.5665283 seq(C-F)	924.543335	861.5379028
985.5232544	922.5431519	860.6416626
983.4944458 seq(C-T)	922.5410767 seq(C-T)	860.322876
980.5427246	920.621582 seq(C-R)	858.5506592 seq(C-E)
977.4946899	920.5342407	857.5164185 seq(C-Y)
975.138916	918.4827881	854.3765259
974.5033569 seq(C-F)	916.5518188	844.4613647
973.5120239	915.5038452 seq(C-Y)	841.586731 seq(C-D)
970.6124878	912.6148071	841.3504639
964.5478516	908.4659424 seq(C-P)	840.994873 seq(C-I)
964.53302	907.208374	840.994873 seq(C-L)
962.5443115	906.5491943 seq(C-E)	840.5909424
959.6359863	906.5374146	840.5871582
959.4957275	904.5445557	840.5560913
956.5006104	891.5142212	836.3427734
956.4837646	886.4848022 seq(C-P)	835.5682373
950.5360107	881.5235596 seq(C-I)	835.550354
944.5249634	881.5235596 seq(C-L)	835.5477905
940.5581055 seq(C-E)	878.5324707 seq(C-I)	832.5363159
938.5315552	878.5324707 seq(C-L)	820.5339966 seq(C-I)
930.5982666 seq(C-I)	877.1182251	820.5339966 seq(C-L)
930.5982666 seq(C-L)	877.1004028	818.4763184 seq(C-I)
929.5328979	876.506897	818.4763184 seq(C-L)
928.5023193	872.56073	816.6785889
927.5256958 seq(C-E)	871.5302734	815.7810059

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2032.930298 seq(C-E)	1283.698242 seq(C-L)	940.5581055 seq(C-E)
2028.16687 seq(C-R)	1263.674927 seq(C-W)	930.5982666 seq(C-I)
1975.004639 seq(C-K)	1163.658813 seq(C-A)	930.5982666 seq(C-L)
1975.004639 seq(C-Q)	1162.638062 seq(C-F)	927.5256958 seq(C-E)
1916.98645 seq(C-N)	1145.670044 seq(C-K)	922.5410767 seq(C-T)
1897.131348 seq(C-G)	1145.670044 seq(C-Q)	920.621582 seq(C-R)
1872.000977 seq(C-T)	1126.598022 seq(C-A)	915.5038452 seq(C-Y)
1792.851929 seq(C-F)	1086.586182 seq(C-F)	908.4659424 seq(C-P)
1749.715088 seq(C-D)	1082.520142 seq(C-F)	906.5491943 seq(C-E)
1687.77771 seq(C-H)	1077.621826 seq(C-R)	886.4848022 seq(C-P)
1674.760864 seq(C-H)	1069.486206 seq(C-E)	881.5235596 seq(C-I)
1582.740112 seq(C-H)	1067.554565 seq(C-T)	881.5235596 seq(C-L)
1534.581177 seq(C-E)	1047.638672 seq(C-K)	878.5324707 seq(C-I)
1526.865356 seq(C-S)	1047.638672 seq(C-Q)	878.5324707 seq(C-L)
1463.697754 seq(C-I)	1045.564941 seq(C-F)	858.5506592 seq(C-E)
1463.697754 seq(C-L)	1014.657776 seq(C-I)	857.5164185 seq(C-Y)
1444.638428 seq(C-S)	1014.657776 seq(C-L)	841.586731 seq(C-D)
1399.734863 seq(C-D)	1009.5578 seq(C-T)	840.994873 seq(C-I)
1363.728271 seq(C-M)	996.526123 seq(C-T)	840.994873 seq(C-L)
1350.632935 seq(C-F)	991.6455688 seq(C-R)	820.5339966 seq(C-I)
1336.573486 seq(C-F)	989.6400757 seq(C-K)	820.5339966 seq(C-L)
1305.719971 seq(C-M)	989.6400757 seq(C-Q)	818.4763184 seq(C-I)
1305.719971 seq(C-I)	987.5665283 seq(C-F)	818.4763184 seq(C-L)
1305.719971 seq(C-L)	983.4944458 seq(C-T)	
1283.698242 seq(C-I)	974.5033569 seq(C-F)	

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2787.893799	1768.255737	1421.370361	1216.51355	1022.460693
2756.018311	1768.227783	1420.278809	1208.533569	1021.49884
2600.849121	1757.267212	1418.359375	1200.519531	1016.566467
2499.160156	1757.263672	1416.320679	1200.517334	1015.646545
2442.123047	1750.207764	1411.354248	1184.458252	1015.493042
2441.175781	1630.24939	1403.467896	1174.503052	1011.573364
2429.053955	1629.220947	1401.382568	1165.481934	1007.589966
2428.179932	1601.392212	1400.309204	1165.445068	1005.510681
2424.589355	1594.345825	1399.338257	1163.586548	1002.558838
2289.401855	1581.384033	1396.356323	1152.56189	1002.492737
2225.970947	1572.28064	1394.668945	1150.567993	1001.531067
2181.977295	1559.270142	1393.489502	1148.008057	999.5855103
2169.23999	1554.287964	1391.36853	1147.477661	994.5588989
2154.973877	1530.366577	1389.368774	1147.092041	986.6143188
2115.066895	1515.317261	1386.34314	1142.501831	982.5477905
2085.210449	1514.29541	1377.420166	1134.080078	973.6696777
2080.073486	1510.292969	1376.465942	1123.83313	969.5861206
2072.190918	1503.25061	1368.440674	1121.507446	966.0836182
2063.027344	1502.285278	1364.448608	1116.545044	965.5883179
2022.076416	1497.366333	1362.408081	1114.526245	964.5358887
2009.052124	1497.27124	1352.380737	1111.507324	959.5706177
1994.150269	1496.312866	1340.298706	1109.882813	957.5469971
1988.324219	1492.364502	1334.513916	1104.490967	955.5853271
1987.167236	1483.255127	1328.362915	1098.495728	951.5214233
1974.17749	1479.314209	1302.488647	1097.452637	944.5355225
1958.199341	1475.289673	1297.440796	1092.613525	939.5337524
1942.103516	1474.312256	1294.499512	1088.494263	936.6418457
1935.133301	1470.358765	1294.427979	1088.491577	933.6541748
1929.204956	1467.336914	1287.42688	1087.553345	931.5875854
1917.074707	1457.342529	1279.507935	1084.540283	931.5586548
1916.20874	1453.421021	1276.558228	1076.119385	919.6888428
1915.169434	1444.310303	1272.509888	1072.495972	915.6105347
1894.182007	1439.447144	1260.054932	1072.473511	911.6262207
1881.158447	1435.375	1250.996216	1070.520874	901.6019897
1830.206421	1434.39502	1248.535522	1063.520996	895.5405884
1827.675049	1433.367554	1242.417236	1060.516968	890.5458984
1826.240112	1433.30896	1235.790649	1057.526733	887.6663208
1824.234375	1432.318481	1229.467041	1052.512695	877.2188721
1815.24585	1431.378052	1223.437256	1049.502686	869.6452637
1792.08606	1429.404175	1221.55127	1040.535522	861.2653809
1782.233398	1422.404419	1221.514648	1029.587769	861.2609253

861.2212524	852.609314	846.6148682	829.7114868
857.6543579	851.6665649	837.5820923	825.6693726
857.6361084	849.5739136	832.5866699	

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2787.893799	1768.255737	1421.370361
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2600.849121	1757.267212 seq(C-G)	1418.359375
2499.160156	1757.263672	1416.320679
2442.123047	1750.207764	1411.354248
2441.175781	1630.24939	1403.467896
2429.053955 seq(C-R)	1629.220947	1401.382568
2428.179932	1601.392212	1400.309204
2424.589355	1594.345825	1399.338257 seq(C-T)
2289.401855	1581.384033	1396.356323 seq(C-V)
2225.970947	1572.28064	1394.668945
2181.977295	1559.270142	1393.489502
2169.23999	1554.287964	1391.36853
2154.973877	1530.366577	1389.368774 seq(C-I)
2115.066895	1515.317261	1389.368774 seq(C-L)
2085.210449	1514.29541	1386.34314 seq(C-T)
2080.073486	1510.292969	1377.420166 seq(C-V)
2072.190918 seq(C-N)	1503.25061	1376.465942
2063.027344	1502.285278	1368.440674
2022.076416	1497.366333	1364.448608 seq(C-V)
2009.052124	1497.27124	1362.408081
1994.150269	1496.312866	1352.380737
1988.324219	1492.364502	1340.298706
1987.167236 seq(C-H)	1483.255127	1334.513916 seq(C-R)
1974.17749 seq(C-H)	1479.314209	1328.362915 seq(C-V)
1958.199341	1475.289673	1302.488647
1942.103516	1474.312256	1297.440796
1935.133301	1470.358765	1294.499512
1929.204956	1467.336914	1294.427979 seq(C-V)
1917.074707	1457.342529	1287.42688
1916.20874 seq(C-H)	1453.421021	1279.507935 seq(C-R)
1915.169434	1444.310303 seq(C-T)	1276.558228 seq(C-R)
1894.182007	1439.447144	1272.509888
1881.158447	1435.375 seq(C-G)	1260.054932
1830.206421 seq(C-G)	1434.39502	1250.996216
1827.675049	1433.367554	1248.535522
1826.240112	1433.30896 seq(C-M)	1242.417236
1824.234375 seq(C-H)	1432.318481	1235.790649
1815.24585	1431.378052	1229.467041
1792.08606 seq(C-H)	1429.404175	1223.437256
1782.233398	1422.404419	1221.55127 seq(C-R)

1221.514648	1072.473511	951.5214233 seq(C-G)
1216.51355	1070.520874	944.5355225
1208.533569	1063.520996	939.5337524
1200.519531	1060.516968	936.6418457
1200.517334	1057.526733	933.6541748
1184.458252	1052.512695	931.5875854
1174.503052	1049.502686 seq(C-H)	931.5586548
1165.481934	1040.535522	919.6888428 seq(C-V)
1165.445068	1029.587769	915.6105347
1163.586548 seq(C-R)	1022.460693 seq(C-D)	911.6262207 seq(C-V)
1152.56189	1021.49884	901.6019897
1150.567993 seq(C-R)	1016.566467	895.5405884
1148.008057	1015.646545	890.5458984
1147.477661	1015.493042	887.6663208 seq(C-G)
1147.092041	1011.573364	877.2188721
1142.501831	1007.589966	869.6452637
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1123.83313	1002.558838 seq(C-S)	861.2609253
1121.507446	1002.492737	861.2212524
1116.545044 seq(C-S)	1001.531067	857.6543579
1114.526245	999.5855103	857.6361084
1111.507324	994.5588989	852.609314 seq(C-I)
1109.882813	986.6143188	852.609314 seq(C-L)
1104.490967	982.5477905	851.6665649
1098.495728	973.6696777	849.5739136
1097.452637 seq(C-F)	969.5861206	846.6148682
1092.613525 seq(C-R)	966.0836182	837.5820923 seq(C-G)
1088.494263	965.5883179	832.5866699
1088.491577	964.5358887	829.7114868 seq(C-G)
1087.553345	959.5706177	825.6693726
1084.540283 seq(C-T)	957.5469971 seq(C-K)	
1076.119385 seq(C-R)	957.5469971 seq(C-Q)	
1072.495972 seq(C-D)	955.5853271	

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2429.053955 seq(C-R)	1386.34314 seq(C-T)	1049.502686 seq(C-H)
2072.190918 seq(C-N)	1377.420166 seq(C-V)	1022.460693 seq(C-D)
1987.167236 seq(C-H)	1364.448608 seq(C-V)	1002.558838 seq(C-S)
1974.17749 seq(C-H)	1334.513916 seq(C-R)	957.5469971 seq(C-K)
1916.20874 seq(C-H)	1328.362915 seq(C-V)	957.5469971 seq(C-Q)
1830.206421 seq(C-G)	1294.427979 seq(C-V)	951.5214233 seq(C-G)
1824.234375 seq(C-H)	1279.507935 seq(C-R)	919.6888428 seq(C-V)
1792.08606 seq(C-H)	1276.558228 seq(C-R)	911.6262207 seq(C-V)
1768.227783 seq(C-R)	1221.55127 seq(C-R)	887.6663208 seq(C-G)
1757.267212 seq(C-G)	1163.586548 seq(C-R)	852.609314 seq(C-I)
1444.310303 seq(C-T)	1150.567993 seq(C-R)	852.609314 seq(C-L)
1435.375 seq(C-G)	1116.545044 seq(C-S)	837.5820923 seq(C-G)
1433.30896 seq(C-M)	1097.452637 seq(C-F)	829.7114868 seq(C-G)
1399.338257 seq(C-T)	1092.613525 seq(C-R)	
1396.356323 seq(C-V)	1084.540283 seq(C-T)	
1389.368774 seq(C-I)	1076.119385 seq(C-R)	
1389.368774 seq(C-L)	1072.495972 seq(C-D)	

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2818.575928	1511.766357	1338.278076	1237.787842	1032.715454
2805.641846	1511.67334	1332.779053	1219.820923	1016.734375
2788.53125	1505.717163	1332.6073	1205.61853	999.270813
2756.63501	1495.694824	1331.176514	1198.774536	992.8366089
1828.680054	1492.697144	1330.782471	1192.643311	985.7077637
1770.707153	1486.702881	1328.766479	1192.592896	981.8184204
1735.76355	1478.821289	1328.743042	1171.952148	942.6929932
1712.708618	1470.755127	1327.240845	1166.619995	923.8566895
1697.674194	1466.724609	1326.118896	1160.673706	917.8746338
1684.708618	1456.72583	1312.817749	1152.776123	907.8817749
1677.781494	1454.194702	1312.760376	1151.663208	907.8779907
1664.830811	1452.641235	1312.084229	1147.643799	879.7843018
1639.707764	1449.660156	1310.785645	1140.814941	877.4345093
1633.736938	1447.764038	1308.773193	1134.692505	877.3891602
1626.693726	1425.623291	1306.801392	1132.673462	872.6737671
1623.753296	1424.84436	1296.846191	1096.666138	864.8381958
1619.796265	1422.750244	1286.69812	1083.80835	861.6489868
1598.723145	1412.785522	1286.640381	1076.676025	861.4703369
1594.791016	1412.733032	1280.296265	1076.658936	859.9046021
1594.724121	1408.764526	1278.798096	1074.698242	856.7492065
1577.62085	1399.841431	1277.773193	1070.636597	832.8203735
1575.772339	1383.79187	1274.756714	1067.861084	828.838562
1569.707886	1366.76709	1274.643799	1063.769653	828.7350464
1553.657227	1364.785034	1273.191895	1057.733521	820.9054565
1536.810547	1354.822266	1256.74707	1051.725586	
1533.718262	1354.776733	1255.626709	1048.658936	
1528.708374	1350.802979	1240.681763	1042.687866	
1524.693237	1344.671631	1239.635132	1038.696411	

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2818.575928	1466.724609 seq(C-L)	1280.296265
2805.641846	1456.72583	1278.798096
2788.53125	1454.194702	1277.773193
2756.63501	1452.641235	1274.756714
1828.680054	1449.660156	1274.643799 seq(C-F)
1770.707153	1447.764038 seq(C-D)	1273.191895
1735.76355	1425.623291	1256.74707
1712.708618 seq(C-N)	1424.84436 seq(C-K)	1255.626709
1697.674194	1424.84436 seq(C-Q)	1240.681763
1684.708618	1422.750244	1239.635132
1677.781494 seq(C-W)	1412.785522	1237.787842
1664.830811	1412.733032	1219.820923
1639.707764	1408.764526 seq(C-I)	1205.61853
1633.736938	1408.764526 seq(C-L)	1198.774536
1626.693726	1399.841431	1192.643311
1623.753296	1383.79187	1192.592896
1619.796265	1366.76709	1171.952148
1598.723145	1364.785034	1166.619995
1594.791016 seq(C-I)	1354.822266	1160.673706
1594.791016 seq(C-L)	1354.776733 seq(C-N)	1152.776123
1594.724121	1350.802979 seq(C-I)	1151.663208
1577.62085	1350.802979 seq(C-L)	1147.643799
1575.772339 seq(C-K)	1344.671631	1140.814941
1575.772339 seq(C-Q)	1338.278076	1134.692505 seq(C-E)
1569.707886	1332.779053	1132.673462
1553.657227	1332.6073	1096.666138
1536.810547 seq(C-I)	1331.176514	1083.80835
1536.810547 seq(C-L)	1330.782471	1076.676025
1533.718262 seq(C-D)	1328.766479	1076.658936
1528.708374	1328.743042	1074.698242
1524.693237	1327.240845	1070.636597
1511.766357	1326.118896	1067.861084
1511.67334	1312.817749	1063.769653
1505.717163	1312.760376	1057.733521
1495.694824 seq(C-P)	1312.084229	1051.725586
1492.697144	1310.785645	1048.658936
1486.702881	1308.773193	1042.687866
1478.821289 seq(C-I)	1306.801392	1038.696411 seq(C-F)
1478.821289 seq(C-L)	1296.846191 seq(C-R)	1032.715454
1470.755127 seq(C-N)	1286.69812 seq(C-F)	1016.734375 seq(C-F)
1466.724609 seq(C-I)	1286.640381	999.270813

992.8366089 seq(C-I)	907.8817749 seq(C-Q)	861.4703369
992.8366089 seq(C-L)	907.8779907	859.9046021
985.7077637	879.7843018	856.7492065
981.8184204	877.4345093	832.8203735
942.6929932	877.3891602	828.838562 seq(C-T)
923.8566895	872.6737671	828.7350464
917.8746338	864.8381958	820.9054565
907.8817749 seq(C-K)	861.6489868	

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1712.708618 seq(C-N)	1470.755127 seq(C-N)	1286.69812 seq(C-F)
1677.781494 seq(C-W)	1466.724609 seq(C-I)	1274.643799 seq(C-F)
1594.791016 seq(C-I)	1466.724609 seq(C-L)	1134.692505 seq(C-E)
1594.791016 seq(C-L)	1447.764038 seq(C-D)	1038.696411 seq(C-F)
1575.772339 seq(C-K)	1424.84436 seq(C-K)	1016.734375 seq(C-F)
1575.772339 seq(C-Q)	1424.84436 seq(C-Q)	992.8366089 seq(C-I)
1536.810547 seq(C-I)	1408.764526 seq(C-I)	992.8366089 seq(C-L)
1536.810547 seq(C-L)	1408.764526 seq(C-L)	907.8817749 seq(C-K)
1533.718262 seq(C-D)	1354.776733 seq(C-N)	907.8817749 seq(C-Q)
1495.694824 seq(C-P)	1350.802979 seq(C-I)	828.838562 seq(C-T)
1478.821289 seq(C-I)	1350.802979 seq(C-L)	
1478.821289 seq(C-L)	1296.846191 seq(C-R)	

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2916.69043	1641.531128	1467.598267	1275.761841	978.7528076
2858.678467	1636.68457	1456.561157	1256.923218	978.7514648
2788.373535	1636.676514	1456.535767	1251.69812	978.7258911
2762.398682	1636.657715	1454.654541	1251.163696	976.7574463
2756.530762	1633.609375	1452.119263	1245.790649	964.8300781
2747.404297	1632.714722	1451.142578	1240.594849	962.8031006
2421.462402	1629.546631	1451.081055	1233.71875	962.7414551
2401.42334	1623.609131	1447.753906	1231.742188	960.7418213
2384.718262	1618.713257	1436.875244	1222.660156	955.8084717
2353.448242	1618.571899	1436.633545	1217.793213	954.7598877
2277.583008	1592.699463	1430.403076	1214.737305	952.8307495
2213.567871	1578.761108	1418.736206	1198.736572	952.8256836
2108.438965	1578.747437	1416.824951	1185.718628	950.8102417
2052.675781	1576.605347	1415.710815	1180.6604	942.7434082
1994.717407	1564.815063	1411.994019	1173.678955	937.8259277
1969.622192	1561.240234	1391.685791	1164.705444	935.3672485
1942.774902	1560.745605	1379.168701	1153.681152	934.8109131
1912.630371	1560.599243	1378.891479	1127.751099	934.7915039
1911.655884	1560.5979	1371.657471	1122.013062	930.7698364
1884.789185	1546.580688	1363.709839	1106.76123	920.7705688
1805.586426	1534.590942	1361.768188	1106.735107	906.8527832
1797.713745	1534.532227	1360.771606	1094.672852	895.6907349
1760.618408	1524.575439	1357.722656	1092.68811	894.7489624
1747.600952	1518.633667	1357.715454	1068.754761	887.3797607
1741.528931	1515.556274	1350.720337	1066.747925	885.3963013
1734.714966	1514.577759	1342.750488	1063.733276	883.7411499
1725.566284	1512.626709	1333.732056	1057.718018	877.3989868
1722.532837	1502.618042	1333.724609	1048.805786	876.8439331
1717.632324	1500.602905	1331.707153	1048.795166	874.8886108
1710.699707	1499.566528	1330.166138	1048.781982	873.697937
1709.578003	1497.587524	1315.708984	1043.764526	861.4491577
1699.660645	1494.805664	1313.681641	1036.694214	854.8812256
1694.656128	1484.573608	1303.760498	1014.725037	854.8062744
1689.696655	1483.578491	1299.754272	1010.798523	848.8024292
1687.662109	1479.588379	1297.696289	1008.778748	836.8319092
1670.630249	1479.58728	1297.65625	1006.725952	836.7806396
1661.505859	1470.617432	1296.722412	1001.666443	832.7191772
1659.592407	1469.967163	1293.691528	993.7507935	
1647.577148	1467.651245	1283.180298	992.7733154	

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2916.69043	1636.676514	1454.654541 seq(C-K)
2858.678467 seq(C-E)	1636.657715	1454.654541 seq(C-Q)
2788.373535	1633.609375	1452.119263
2762.398682	1632.714722	1451.142578
2756.530762	1629.546631	1451.081055
2747.404297	1623.609131	1447.753906
2421.462402	1618.713257	1436.875244 seq(C-M)
2401.42334	1618.571899	1436.633545
2384.718262	1592.699463	1430.403076
2353.448242	1578.761108	1418.736206
2277.583008	1578.747437 seq(C-M)	1416.824951
2213.567871	1576.605347 seq(C-M)	1415.710815
2108.438965	1564.815063 seq(C-M)	1411.994019
2052.675781	1561.240234	1391.685791
1994.717407	1560.745605 seq(C-I)	1379.168701
1969.622192	1560.745605 seq(C-L)	1378.891479 seq(C-I)
1942.774902	1560.599243	1378.891479 seq(C-L)
1912.630371	1560.5979	1371.657471
1911.655884	1546.580688	1363.709839
1884.789185 seq(C-S)	1534.590942	1361.768188
1805.586426	1534.532227	1360.771606 seq(C-A)
1797.713745	1524.575439	1357.722656
1760.618408	1518.633667	1357.715454
1747.600952 seq(C-D)	1515.556274	1350.720337
1741.528931	1514.577759	1342.750488
1734.714966	1512.626709	1333.732056
1725.566284	1502.618042 seq(C-T)	1333.724609
1722.532837	1500.602905	1331.707153
1717.632324	1499.566528	1330.166138
1710.699707	1497.587524	1315.708984
1709.578003	1494.805664	1313.681641
1699.660645	1484.573608	1303.760498
1694.656128 seq(C-M)	1483.578491	1299.754272 seq(C-E)
1689.696655	1479.588379	1297.696289
1687.662109 seq(C-G)	1479.58728	1297.65625
1670.630249	1470.617432	1296.722412
1661.505859	1469.967163	1293.691528
1659.592407	1467.651245	1283.180298
1647.577148	1467.598267 seq(C-S)	1275.761841
1641.531128	1456.561157	1256.923218
1636.68457 seq(C-M)	1456.535767	1251.69812

1251.163696	1048.781982 seq(C-I)	937.8259277
1245.790649	1048.781982 seq(C-L)	935.3672485
1240.594849	1043.764526	934.8109131
1233.71875	1036.694214	934.7915039
1231.742188 seq(C-M)	1014.725037	930.7698364
1222.660156	1010.798523	920.7705688 seq(C-I)
1217.793213 seq(C-H)	1008.778748 seq(C-Y)	920.7705688 seq(C-L)
1214.737305	1006.725952	906.8527832
1198.736572	1001.666443	895.6907349
1185.718628	993.7507935	894.7489624
1180.6604	992.7733154	887.3797607
1173.678955	978.7528076 seq(C-I)	885.3963013
1164.705444	978.7528076 seq(C-L)	883.7411499
1153.681152	978.7514648	877.3989868
1127.751099	978.7258911	876.8439331
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1106.76123	964.8300781	873.697937
1106.735107	962.8031006	861.4491577
1094.672852	962.7414551	854.8812256
1092.68811	960.7418213	854.8062744
1068.754761	955.8084717	848.8024292
1066.747925	954.7598877	836.8319092
1063.733276	952.8307495 seq(C-T)	836.7806396
1057.718018	952.8256836	832.7191772
1048.805786	950.8102417	
1048.795166	942.7434082	

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2858.678467 seq(C-E)	1502.618042 seq(C-T)	1048.781982 seq(C-I)
1884.789185 seq(C-S)	1467.598267 seq(C-S)	1048.781982 seq(C-L)
1747.600952 seq(C-D)	1454.654541 seq(C-K)	1008.778748 seq(C-Y)
1694.656128 seq(C-M)	1454.654541 seq(C-Q)	978.7528076 seq(C-I)
1687.662109 seq(C-G)	1436.875244 seq(C-M)	978.7528076 seq(C-L)
1636.68457 seq(C-M)	1378.891479 seq(C-I)	952.8307495 seq(C-T)
1578.747437 seq(C-M)	1378.891479 seq(C-L)	920.7705688 seq(C-I)
1576.605347 seq(C-M)	1360.771606 seq(C-A)	920.7705688 seq(C-L)
1564.815063 seq(C-M)	1299.754272 seq(C-E)	
1560.745605 seq(C-I)	1231.742188 seq(C-M)	
1560.745605 seq(C-L)	1217.793213 seq(C-H)	

MYH
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2790.51123	1575.621704	1311.596191	1080.829224	956.9020996
2788.46582	1574.722168	1310.604614	1064.777832	955.8689575
2772.569092	1535.662231	1306.693848	1063.768555	953.9066772
2757.561035	1534.679077	1305.783325	1057.768066	952.8338623
2757.535889	1526.692871	1304.68042	1055.848022	949.8082275
2746.507813	1525.699707	1296.753174	1054.777954	946.774292
2442.633545	1515.696655	1282.782349	1053.846802	942.7722778
2421.503174	1510.748657	1276.85791	1049.829346	939.8803101
2417.520752	1499.701782	1271.822754	1049.764282	938.8510132
2402.516846	1497.699585	1256.834229	1048.834351	930.7926025
2401.548828	1483.715576	1250.779053	1044.807007	927.8724976
2384.778076	1479.701294	1243.868774	1043.847046	924.8688965
2295.589355	1475.755615	1230.706543	1033.786987	922.8248291
2108.483887	1467.731201	1229.761841	1033.765625	916.7764282
1925.617798	1460.733643	1229.7052	1032.853027	908.8015137
1924.614136	1452.672485	1228.72644	1032.839844	907.7966309
1912.693359	1451.196411	1222.817871	1008.787537	906.8320923
1857.61499	1428.637817	1216.752319	1001.770447	905.8363037
1845.682983	1425.72876	1210.797974	998.8146362	900.8047485
1832.632935	1418.744873	1207.752319	995.791687	897.8425293
1831.647095	1413.814941	1203.717529	992.7546387	889.8115234
1818.594482	1412.699829	1190.754028	988.8284302	883.7246704
1816.581299	1411.705811	1189.788574	987.8497925	877.4474487
1802.557007	1398.643799	1180.750244	987.8343506	877.4467163
1801.559082	1381.729492	1162.77124	987.8249512	876.8532715
1783.564087	1380.731079	1158.769775	985.7678833	867.8869019
1760.662842	1379.693237	1157.838013	984.8272705	865.8723755
1737.797852	1379.209473	1153.76355	981.7717285	865.7950439
1722.606079	1364.224976	1148.714111	980.8398438	861.4850464
1712.726196	1361.765503	1147.851807	980.8132935	857.8754272
1693.668335	1359.730225	1145.614624	979.7949219	857.8071289
1692.659302	1347.75415	1124.693359	978.9077759	856.8398438
1661.636719	1346.75769	1119.796753	976.7911987	836.8388062
1659.651245	1335.748047	1113.836914	969.8065796	829.8153687
1630.573975	1334.753296	1105.820923	965.8393555	825.8765869
1629.667236	1332.739258	1092.724609	963.8600464	825.8381958
1596.695557	1324.639526	1085.702881	962.760437	822.8399048
1580.723999	1312.836914	1084.789917	960.7718506	

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2790.51123	1580.723999	1310.604614 seq(C-A)
2788.46582	1575.621704	1306.693848 seq(C-T)
2772.569092	1574.722168	1305.783325 seq(C-T)
2757.561035	1535.662231	1304.68042
2757.535889	1534.679077 seq(C-K)	1296.753174 seq(C-F)
2746.507813	1534.679077 seq(C-Q)	1282.782349 seq(C-F)
2442.633545	1526.692871	1276.85791
2421.503174 seq(C-K)	1525.699707	1271.822754 seq(C-F)
2421.503174 seq(C-Q)	1515.696655	1256.834229
2417.520752	1510.748657	1250.779053
2402.516846	1499.701782 seq(C-S)	1243.868774 seq(C-G)
2401.548828	1497.699585	1230.706543
2384.778076	1483.715576	1229.761841
2295.589355	1479.701294	1229.7052 seq(C-D)
2108.483887	1475.755615	1228.72644
1925.617798 seq(C-A)	1467.731201 seq(C-S)	1222.817871 seq(C-F)
1924.614136 seq(C-A)	1460.733643	1216.752319
1912.693359	1452.672485	1210.797974
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1845.682983 seq(C-S)	1428.637817 seq(C-T)	1203.717529
1832.632935 seq(C-G)	1425.72876	1190.754028 seq(C-R)
1831.647095 seq(C-M)	1418.744873 seq(C-V)	1189.788574 seq(C-V)
1831.647095 seq(C-I)	1413.814941 seq(C-F)	1180.750244 seq(C-Y)
1831.647095 seq(C-L)	1412.699829	1162.77124
1831.647095 seq(C-S)	1411.705811 seq(C-R)	1158.769775
1818.594482	1398.643799	1157.838013
1816.581299	1381.729492	1153.76355
1802.557007 seq(C-D)	1380.731079	1148.714111
1801.559082 seq(C-D)	1379.693237	1147.851807
1783.564087	1379.209473	1145.614624
1760.662842	1364.224976	1124.693359
1737.797852	1361.765503 seq(C-S)	1119.796753
1722.606079 seq(C-S)	1359.730225	1113.836914
1712.726196	1347.75415 seq(C-R)	1105.820923 seq(C-R)
1693.668335	1346.75769 seq(C-R)	1092.724609
1692.659302	1335.748047	1085.702881
1661.636719	1334.753296	1084.789917
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1596.695557 seq(C-S)	1311.596191	1057.768066 seq(C-A)

1055.848022	980.8132935	907.7966309 seq(C-Q)
1054.777954 seq(C-D)	979.7949219	906.8320923
1053.846802	978.9077759 seq(C-I)	905.8363037
1049.829346	978.9077759 seq(C-L)	900.8047485
1049.764282	976.7911987 seq(C-T)	897.8425293 seq(C-F)
1048.834351	969.8065796	889.8115234
1044.807007 seq(C-I)	965.8393555	883.7246704
1044.807007 seq(C-L)	963.8600464	877.4474487
1043.847046 seq(C-K)	962.760437	877.4467163
1043.847046 seq(C-Q)	960.7718506	876.8532715
1033.786987	956.9020996	867.8869019
1033.765625	955.8689575	865.8723755 seq(C-K)
1032.853027	953.9066772 seq(C-F)	865.8723755 seq(C-Q)
1032.839844 seq(C-T)	953.9066772 seq(C-E)	865.7950439
1008.787537	952.8338623	861.4850464
1001.770447	949.8082275 seq(C-S)	857.8754272 seq(C-I)
998.8146362	946.774292	857.8754272 seq(C-L)
995.791687	942.7722778	857.8071289 seq(C-Y)
992.7546387 seq(C-T)	939.8803101	856.8398438 seq(C-T)
988.8284302 seq(C-N)	938.8510132	836.8388062 seq(C-Y)
987.8497925 seq(C-G)	930.7926025	829.8153687
987.8343506 seq(C-N)	927.8724976	825.8765869 seq(C-V)
987.8249512 seq(C-T)	924.8688965 seq(C-E)	825.8381958
985.7678833	922.8248291	822.8399048 seq(C-F)
984.8272705 seq(C-F)	916.7764282 seq(C-V)	
981.7717285	908.8015137 seq(C-E)	
980.8398438 seq(C-V)	907.7966309 seq(C-K)	

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2421.503174 seq(C-K)
2421.503174 seq(C-Q)
1925.617798 seq(C-A)
1924.614136 seq(C-A)
1845.682983 seq(C-S)
1832.632935 seq(C-G)
1831.647095 seq(C-M)
1831.647095 seq(C-I)
1831.647095 seq(C-L)
1831.647095 seq(C-S)
1802.557007 seq(C-D)
1801.559082 seq(C-D)
1722.606079 seq(C-S)
1629.667236 seq(C-S)
1596.695557 seq(C-S)
1534.679077 seq(C-K)
1534.679077 seq(C-Q)
1499.701782 seq(C-S)
1467.731201 seq(C-S)
1428.637817 seq(C-T)
1418.744873 seq(C-V)
1413.814941 seq(C-F)
1411.705811 seq(C-R)
1361.765503 seq(C-S)
1347.75415 seq(C-R)
1346.75769 seq(C-R)
1312.836914 seq(C-D)
1310.604614 seq(C-A)
1306.693848 seq(C-T)
1305.783325 seq(C-T)
1296.753174 seq(C-F)
1282.782349 seq(C-F)
1271.822754 seq(C-F)
1243.868774 seq(C-G)
1229.7052 seq(C-D)
1222.817871 seq(C-F)
1190.754028 seq(C-R)
1189.788574 seq(C-V)
1180.750244 seq(C-Y)
1105.820923 seq(C-R)
1057.768066 seq(C-A)

1054.777954 seq(C-D)
1044.807007 seq(C-I)
1044.807007 seq(C-L)
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1043.847046 seq(C-Q)
1032.839844 seq(C-T)
992.7546387 seq(C-T)
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984.8272705 seq(C-F)
980.8398438 seq(C-V)
978.9077759 seq(C-I)
978.9077759 seq(C-L)
976.7911987 seq(C-T)
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953.9066772 seq(C-E)
949.8082275 seq(C-S)
924.8688965 seq(C-E)
916.7764282 seq(C-V)
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907.7966309 seq(C-K)
907.7966309 seq(C-Q)
897.8425293 seq(C-F)
865.8723755 seq(C-K)
865.8723755 seq(C-Q)
857.8754272 seq(C-I)
857.8754272 seq(C-L)
857.8071289 seq(C-Y)
856.8398438 seq(C-T)
836.8388062 seq(C-Y)
825.8765869 seq(C-V)
822.8399048 seq(C-F)

PYGM
mass

3254.551514	1625.582397	1411.229248	1106.755615	930.772644
2790.556396	1609.710449	1396.674316	1104.834106	925.829834
2788.436279	1608.716431	1388.757568	1104.754517	923.8497314
2772.476563	1604.789063	1386.75769	1092.72876	918.8183594
2757.483643	1579.653809	1386.71936	1063.765503	916.8471069
2756.526123	1576.773071	1377.737915	1059.798706	912.8253784
2747.481689	1542.800171	1373.69519	1057.757446	910.7963867
2746.456787	1538.670288	1364.695801	1053.843018	903.8121338
2442.572021	1533.79248	1357.651733	1041.756592	901.8586426
2422.481689	1525.763916	1356.740723	1037.329102	901.6080322
2421.506836	1517.736084	1332.778931	1033.839722	900.8648071
2402.529785	1515.691895	1319.871826	1022.854004	899.6054077
2401.530029	1511.691284	1316.708496	1001.762817	895.7163086
2295.573486	1510.671021	1315.7146	993.8158569	894.7789307
2271.54248	1500.721924	1305.766357	993.7835693	887.8449707
2233.507568	1499.689087	1303.81958	989.8299561	877.4468384
2056.559814	1499.662231	1289.781006	985.7603149	877.4179077
2042.551514	1497.697388	1289.755737	984.819519	872.8095703
1954.059692	1483.689209	1279.67981	977.7871704	867.8820801
1912.723755	1479.689087	1278.754761	976.7912598	867.8735962
1853.691162	1471.683716	1278.671265	974.7440186	864.8464355
1828.713745	1471.650513	1262.715576	973.751709	861.4810791
1812.779419	1470.679077	1257.748047	968.3094482	861.460144
1784.696899	1467.719849	1244.779663	963.8005371	859.8748169
1735.706177	1459.748779	1237.746094	962.8030396	857.8131104
1722.591919	1459.728271	1233.775146	962.7404785	855.9136963
1712.69519	1457.737061	1216.79248	961.7963257	854.3198242
1706.738525	1452.658569	1212.810913	960.762207	845.8710938
1706.071411	1451.179688	1204.757202	956.8988037	845.8451538
1690.195801	1444.685181	1203.707886	954.8301392	837.8336792
1687.694092	1443.699951	1181.774048	953.8131104	832.8786011
1677.738281	1428.739014	1180.733521	952.7982788	831.8587036
1677.70166	1428.659302	1177.73584	947.8063354	831.8585815
1665.794434	1428.646362	1158.766602	943.7611694	829.8762817
1661.758423	1427.758789	1145.799438	942.7630005	825.8621216
1656.794312	1427.745972	1136.817505	934.9040527	822.859375
1644.741577	1423.701294	1128.335327	932.7985229	
1640.310669	1423.686035	1122.76123	931.8108521	
1629.668823	1423.649536	1118.743408	930.833252	
1628.236572	1418.81897	1106.798096	930.7840576	

PYGM

mass/mass+c

3254.551514	1628.236572	1411.229248
2790.556396	1625.582397	1396.674316 seq(C-I)
2788.436279	1609.710449 seq(C-P)	1396.674316 seq(C-L)
2772.476563	1608.716431 seq(C-P)	1388.757568
2757.483643	1604.789063 seq(C-Y)	1386.75769
2756.526123	1579.653809 seq(C-E)	1386.71936
2747.481689	1576.773071	1377.737915
2746.456787	1542.800171 seq(C-R)	1373.69519
2442.572021	1538.670288	1364.695801
2422.481689 seq(C-K)	1533.79248	1357.651733
2422.481689 seq(C-Q)	1525.763916 seq(C-V)	1356.740723 seq(C-K)
2421.506836	1517.736084	1356.740723 seq(C-Q)
2402.529785	1515.691895	1332.778931
2401.530029	1511.691284	1319.871826
2295.573486	1510.671021	1316.708496
2271.54248	1500.721924	1315.7146 seq(C-Y)
2233.507568	1499.689087	1305.766357 seq(C-Y)
2056.559814	1499.662231 seq(C-A)	1303.81958
2042.551514 seq(C-D)	1497.697388	1289.781006 seq(C-Y)
1954.059692	1483.689209	1289.755737
1912.723755	1479.689087	1279.67981 seq(C-D)
1853.691162 seq(C-A)	1471.683716	1278.754761 seq(C-D)
1828.713745	1471.650513	1278.671265
1812.779419 seq(C-I)	1470.679077	1262.715576 seq(C-V)
1812.779419 seq(C-L)	1467.719849 seq(C-S)	1257.748047
1784.696899	1459.748779	1244.779663
1735.706177	1459.728271	1237.746094
1722.591919	1457.737061	1233.775146
1712.69519	1452.658569	1216.79248 seq(C-R)
1706.738525 seq(C-R)	1451.179688	1212.810913
1706.071411	1444.685181	1204.757202
1690.195801	1443.699951	1203.707886
1687.694092	1428.739014 seq(C-E)	1181.774048
1677.738281	1428.659302	1180.733521
1677.70166	1428.646362	1177.73584 seq(C-H)
1665.794434	1427.758789	1158.766602
1661.758423	1427.745972	1145.799438 seq(C-R)
1656.794312 seq(C-R)	1423.701294	1136.817505 seq(C-V)
1644.741577	1423.686035	1128.335327
1640.310669	1423.649536	1122.76123
1629.668823	1418.81897 seq(C-V)	1118.743408

1106.798096	960.762207	895.7163086
1106.755615	956.8988037	894.7789307
1104.834106	954.8301392	887.8449707
1104.754517	953.8131104	877.4468384
1092.72876	952.7982788	877.4179077
1063.765503 seq(C-T)	947.8063354 seq(C-I)	872.8095703 seq(C-Y)
1059.798706	947.8063354 seq(C-L)	867.8820801
1057.757446 seq(C-A)	943.7611694 seq(C-Y)	867.8735962 seq(C-I)
1053.843018 seq(C-Y)	942.7630005	867.8735962 seq(C-L)
1041.756592	934.9040527	864.8464355
1037.329102	932.7985229	861.4810791
1033.839722	931.8108521	861.460144
1022.854004 seq(C-V)	930.833252	859.8748169
1001.762817	930.7840576	857.8131104
993.8158569	930.772644	855.9136963 seq(C-I)
993.7835693	925.829834	855.9136963 seq(C-L)
989.8299561	923.8497314 seq(C-I)	854.3198242
985.7603149	923.8497314 seq(C-L)	845.8710938
984.819519 seq(C-A)	918.8183594 seq(C-I)	845.8451538 seq(C-Y)
977.7871704	918.8183594 seq(C-L)	837.8336792
976.7912598	916.8471069	832.8786011
974.7440186 seq(C-E)	912.8253784	831.8587036
973.751709	910.7963867	831.8585815
968.3094482	903.8121338	829.8762817
963.8005371	901.8586426	825.8621216
962.8030396	901.6080322	822.859375 seq(C-A)
962.7404785	900.8648071 seq(C-P)	
961.7963257	899.6054077	

PYGM
mass+c

2422.481689 seq(C-K)	1396.674316 seq(C-I)	984.819519 seq(C-A)
2422.481689 seq(C-Q)	1396.674316 seq(C-L)	974.7440186 seq(C-E)
2042.551514 seq(C-D)	1356.740723 seq(C-K)	947.8063354 seq(C-I)
1853.691162 seq(C-A)	1356.740723 seq(C-Q)	947.8063354 seq(C-L)
1812.779419 seq(C-I)	1315.7146 seq(C-Y)	943.7611694 seq(C-Y)
1812.779419 seq(C-L)	1305.766357 seq(C-Y)	923.8497314 seq(C-I)
1706.738525 seq(C-R)	1289.781006 seq(C-Y)	923.8497314 seq(C-L)
1656.794312 seq(C-R)	1279.67981 seq(C-D)	918.8183594 seq(C-I)
1609.710449 seq(C-P)	1278.754761 seq(C-D)	918.8183594 seq(C-L)
1608.716431 seq(C-P)	1262.715576 seq(C-V)	900.8648071 seq(C-P)
1604.789063 seq(C-Y)	1216.79248 seq(C-R)	872.8095703 seq(C-Y)
1579.653809 seq(C-E)	1177.73584 seq(C-H)	867.8735962 seq(C-I)
1542.800171 seq(C-R)	1145.799438 seq(C-R)	867.8735962 seq(C-L)
1525.763916 seq(C-V)	1136.817505 seq(C-V)	855.9136963 seq(C-I)
1499.662231 seq(C-A)	1063.765503 seq(C-T)	855.9136963 seq(C-L)
1467.719849 seq(C-S)	1057.757446 seq(C-A)	845.8451538 seq(C-Y)
1428.739014 seq(C-E)	1053.843018 seq(C-Y)	822.859375 seq(C-A)
1418.81897 seq(C-V)	1022.854004 seq(C-V)	

CA
mass

2790.38623	1497.610229	1145.641846	1029.670166	939.774231
2788.311035	1490.501587	1144.641724	1027.764038	938.7394409
2786.393555	1483.614746	1143.629761	1014.737976	930.7400513
2758.630371	1479.605591	1142.670166	1013.782654	925.7869263
2756.45752	1467.635986	1141.669189	1012.766052	917.6460571
2739.391846	1428.558228	1139.686035	1011.693848	917.6258545
2421.411865	1404.716797	1123.793823	1004.822876	914.2317505
2401.35791	1397.625977	1107.766602	1001.731628	901.6860962
2384.532715	1371.089966	1106.581299	998.737854	900.7536621
2237.273926	1346.555054	1102.817749	995.767334	900.7512207
2142.331299	1251.643799	1102.80896	995.7175903	900.732666
2126.29126	1248.750122	1102.740845	993.7227783	898.1929321
2096.271484	1234.687012	1101.816406	982.7697144	885.6591187
2081.077148	1224.656616	1101.798706	976.7338257	884.765625
2080.059326	1219.67981	1086.229492	973.742981	882.7706299
2002.52356	1203.645874	1085.727905	973.7310181	881.6503906
2001.523193	1201.5979	1085.310913	971.75	877.3825073
1912.55127	1199.655518	1078.668701	971.7416382	873.7632446
1759.567749	1180.671265	1077.678589	969.7683105	872.772644
1758.575195	1180.606567	1070.671753	962.7674561	868.7807617
1722.485474	1173.65332	1069.715332	962.7055054	867.8433228
1709.589111	1173.633545	1066.763184	960.7127686	859.7891235
1661.527466	1172.564575	1063.707764	955.7654419	859.6968384
1629.558472	1171.596924	1061.032837	952.7410278	858.8569946
1613.535156	1169.677002	1057.702759	951.7171021	857.8775635
1597.574707	1158.666382	1053.758423	946.8077393	843.7684937
1581.577515	1157.677856	1052.710571	943.7659912	825.8242798
1499.604004	1154.204468	1049.640625	942.7114258	

CA

mass/mass+c

2790.38623	1234.687012	1053.758423 seq(C-I)
2788.311035	1224.656616	1053.758423 seq(C-L)
2786.393555	1219.67981	1052.710571
2758.630371	1203.645874	1049.640625
2756.45752	1201.5979	1029.670166
2739.391846	1199.655518	1027.764038
2421.411865 seq(C-K)	1180.671265	1014.737976
2421.411865 seq(C-Q)	1180.606567	1013.782654
2401.35791 seq(C-Y)	1173.65332	1012.766052 seq(C-K)
2384.532715	1173.633545	1012.766052 seq(C-Q)
2237.273926	1172.564575	1011.693848
2142.331299	1171.596924	1004.822876
2126.29126	1169.677002	1001.731628
2096.271484 seq(C-R)	1158.666382	998.737854
2081.077148	1157.677856 seq(C-H)	995.767334
2080.059326	1154.204468	995.7175903
2002.52356 seq(C-T)	1145.641846	993.7227783
2001.523193 seq(C-T)	1144.641724	982.7697144
1912.55127	1143.629761	976.7338257
1759.567749 seq(C-T)	1142.670166	973.742981
1758.575195	1141.669189 seq(C-H)	973.7310181 seq(C-P)
1722.485474	1139.686035	971.75
1709.589111 seq(C-T)	1123.793823	971.7416382
1661.527466	1107.766602	969.7683105
1629.558472	1106.581299	962.7674561
1613.535156	1102.817749	962.7055054
1597.574707	1102.80896	960.7127686
1581.577515 seq(C-T)	1102.740845	955.7654419 seq(C-P)
1499.604004 seq(C-S)	1101.816406 seq(C-P)	952.7410278
1497.610229	1101.798706	951.7171021 seq(C-Y)
1490.501587	1086.229492	946.8077393
1483.614746	1085.727905	943.7659912
1479.605591	1085.310913	942.7114258
1467.635986 seq(C-S)	1078.668701	939.774231 seq(C-P)
1428.558228	1077.678589	938.7394409 seq(C-P)
1404.716797	1070.671753	930.7400513
1397.625977	1069.715332	925.7869263
1371.089966	1066.763184	917.6460571
1346.555054	1063.707764 seq(C-T)	917.6258545
1251.643799	1061.032837	914.2317505
1248.750122	1057.702759 seq(C-A)	901.6860962

900.7536621	881.6503906	859.6968384
900.7512207	877.3825073	858.8569946
900.732666	873.7632446	857.8775635
898.1929321	872.772644 seq(C-P)	843.7684937
885.6591187 seq(C-E)	868.7807617 seq(C-P)	825.8242798
884.765625	867.8433228	
882.7706299	859.7891235 seq(C-P)	

CA
mass+c

2421.411865 seq(C-K)	1467.635986 seq(C-S)	973.7310181 seq(C-P)
2421.411865 seq(C-Q)	1157.677856 seq(C-H)	955.7654419 seq(C-P)
2401.35791 seq(C-Y)	1141.669189 seq(C-H)	951.7171021 seq(C-Y)
2096.271484 seq(C-R)	1101.816406 seq(C-P)	939.774231 seq(C-P)
2002.52356 seq(C-T)	1063.707764 seq(C-T)	938.7394409 seq(C-P)
2001.523193 seq(C-T)	1057.702759 seq(C-A)	885.6591187 seq(C-E)
1759.567749 seq(C-T)	1053.758423 seq(C-I)	872.772644 seq(C-P)
1709.589111 seq(C-T)	1053.758423 seq(C-L)	868.7807617 seq(C-P)
1581.577515 seq(C-T)	1012.766052 seq(C-K)	859.7891235 seq(C-P)
1499.604004 seq(C-S)	1012.766052 seq(C-Q)	

4 Protein Mixture (BSA/TF/CYC/MB)

mass

2858.830078	1842.182739	1439.434082	1069.440918	920.7224121
2755.893311	1829.182007	1436.360718	1067.547485	920.6032104
2441.174561	1802.217285	1434.442993	1063.619629	920.5969238
2429.008057	1768.286133	1433.317261	1057.524048	911.6362915
2428.169189	1768.237671	1411.743286	1057.38562	906.6486206
2335.285889	1757.30188	1408.452393	1057.364502	906.6211548
2275.971924	1721.274048	1399.402344	1055.629395	904.640625
2262.945801	1709.266968	1386.3927	1055.601685	894.6185303
2260.138428	1688.268799	1362.428711	1048.594604	887.5177612
2168.071777	1687.378052	1360.533203	1048.594482	879.6194458
2155.034912	1687.285645	1360.528687	1035.459351	877.2085571
2085.22998	1687.281494	1354.498169	1019.489746	862.5372925
2085.106934	1674.283813	1350.509644	1017.631958	861.6519775
2072.093018	1670.793945	1350.489502	1016.501648	861.2481689
2064.188232	1578.452515	1349.36084	1010.564697	859.7211914
2035.098389	1578.427124	1333.510986	1009.585449	858.6847534
2032.00647	1578.411499	1299.461182	1008.587769	857.6600952
2028.285889	1578.343506	1296.551514	1006.469543	857.6257324
2028.250488	1575.335938	1296.542358	1002.55072	848.4562988
2027.303833	1553.853027	1294.450317	1001.13623	840.675293
2027.286133	1534.167114	1280.014648	996.5701294	837.5790405
2018.996338	1534.164185	1276.564087	993.0845947	832.6393433
2010.745605	1502.362671	1275.550903	989.6818237	829.7223511
1988.251343	1502.351074	1229.505371	987.6402588	829.7144165
1986.092285	1502.310181	1222.025391	987.6281738	828.6903076
1984.153931	1496.365967	1217.599976	987.6243896	825.3522949
1975.24585	1491.300293	1214.55127	983.5397949	820.7094727
1971.144409	1486.19397	1165.476563	974.5701294	820.7059937
1942.275024	1483.284302	1163.590332	967.5471191	820.7037964
1929.247437	1478.454102	1145.653076	957.555481	818.651062
1916.263916	1478.277832	1145.602905	952.6633301	815.9371338
1916.225464	1473.192627	1145.593628	952.6484985	806.7282715
1916.212646	1470.390625	1145.570923	943.1465454	805.5353394
1906.255615	1470.383057	1106.55188	942.5209961	804.5267944
1896.402222	1470.3479	1092.625244	940.6450806	790.697998
1896.335327	1467.356445	1087.371582	938.6039429	778.6956177
1884.322876	1465.216064	1086.538086	936.6383667	778.6812134
1875.428223	1456.381958	1084.595703	935.2019043	778.6808472
1871.318115	1454.395996	1082.475098	927.6098633	777.5285645
1868.191406	1447.391968	1079.485352	927.5964355	774.6795654
1855.1875	1439.477173	1076.133179	922.6243896	772.6639404

764.7042236	693.5146484	635.6629639	593.5908203	543.6234131
762.7720337	691.6974487	634.7706909	591.614624	543.6165771
760.713562	690.7011719	634.6541748	591.6079102	543.6021118
752.6557007	689.727356	630.7432251	591.5903931	543.5968018
749.6796875	684.5674438	626.6011353	591.5834961	534.6274414
749.6495972	684.5653687	626.5933228	589.5926514	534.6171875
748.6766968	676.7047729	626.5783691	589.5844116	534.6018677
736.6586304	672.3896484	626.5765381	589.5794678	534.5982056
735.6555786	672.3764648	626.5748901	587.5913086	531.7810669
733.6660767	668.6647339	625.6652222	587.5877686	526.6208496
732.5480957	667.5982666	624.6031494	587.5831299	524.6251221
730.5621338	666.3869629	624.5754395	587.5632935	524.6210327
725.6123657	665.7178955	622.5947266	585.7533569	524.6184082
724.5513916	661.6223145	622.5750732	585.6912231	524.6057739
721.6623535	660.7211304	620.6148682	583.6907349	522.6140137
720.7516479	659.7144165	620.6102295	580.6774292	522.598999
720.7410889	656.4310913	620.6001587	572.786499	520.6282959
720.7365112	656.428772	620.5884399	568.5828857	520.6279907
718.5739136	656.4207153	612.6273193	568.578064	520.6220093
718.5714722	655.6417236	612.6194458	568.5750732	520.6114502
712.6657104	651.7087402	612.6015625	568.56427	518.6223145
708.6532593	650.4429932	612.598938	561.6227417	517.7458496
706.5772705	649.585083	610.5945435	561.6199951	517.6523438
706.569519	649.5685425	609.6723633	561.6160889	517.6411743
706.545105	648.6061401	607.6520386	561.598999	517.6312866
706.5449829	646.6802368	604.7440796	550.5879517	516.6307983
706.5339355	642.5888672	603.6010132	550.5861206	516.6146851
697.586731	642.5884399	603.5826416	550.5775146	516.6135864
697.5727539	642.5767822	602.6186523	550.5664673	516.6091309
697.5658569	642.5634766	602.6038208	547.2503662	515.670166
693.5597534	640.6028442	601.6777344	546.5980835	514.6893921
693.5458984	639.6082764	599.7808838	545.6574097	514.6833496
693.5427856	636.7107544	593.7172241	544.5971069	
693.52771	636.6674194	593.6969604	544.5949707	

4 Protein Mixture (BSA/TF/CYC/MB)

mass/mass+c

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2275.971924	1721.274048	1434.442993
2262.945801	1709.266968	1433.317261
2260.138428	1688.268799	1411.743286 seq(C-K)
2168.071777	1687.378052	1411.743286 seq(C-Q)
2155.034912	1687.285645 seq(C-H)	1408.452393
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2072.093018	1670.793945	1362.428711
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1986.092285	1502.362671 seq(C-Q)	1296.542358 seq(C-R)
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1929.247437 seq(C-H)	1486.19397 seq(C-T)	1229.505371 seq(C-S)
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1916.212646 seq(C-H)	1478.277832 seq(C-E)	1214.55127
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1055.601685	906.6211548 seq(C-E)	760.713562 seq(C-Q)
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1048.594482 seq(C-I)	894.6185303	749.6796875
1048.594482 seq(C-L)	887.5177612	749.6495972
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514.6833496

4 Protein Mixture (BSA/TF/CYC/MB)

mass+c

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2335.285889 seq(C-S)	1009.585449 seq(C-T)	690.7011719 seq(C-E)
1929.247437 seq(C-H)	1006.469543 seq(C-Y)	689.727356 seq(C-S)
1916.212646 seq(C-H)	1002.55072 seq(C-S)	668.6647339 seq(C-F)
1687.285645 seq(C-H)	996.5701294 seq(C-T)	661.6223145 seq(C-P)
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1502.362671 seq(C-T)	989.6818237 seq(C-Q)	660.7211304 seq(C-Q)
1502.362671 seq(C-K)	987.6281738 seq(C-F)	659.7144165 seq(C-A)
1502.362671 seq(C-Q)	952.6633301 seq(C-T)	648.6061401 seq(C-P)
1486.19397 seq(C-E)	936.6383667 seq(C-S)	630.7432251 seq(C-I)
1478.277832 seq(C-E)	920.7224121 seq(C-R)	630.7432251 seq(C-L)
1473.192627 seq(C-E)	920.5969238 seq(C-I)	625.6652222 seq(C-F)
1470.390625 seq(C-N)	920.5969238 seq(C-L)	609.6723633 seq(C-E)
1454.395996 seq(C-T)	911.6362915 seq(C-T)	593.7172241 seq(C-H)
1454.395996 seq(C-K)	906.6486206 seq(C-E)	585.7533569 seq(C-I)
1454.395996 seq(C-Q)	906.6211548 seq(C-E)	585.7533569 seq(C-L)
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1106.55188 seq(C-E)	790.697998 seq(C-Q)	
1092.625244 seq(C-R)	774.6795654 seq(C-K)	
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1069.440918 seq(C-L)	760.713562 seq(C-K)	
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1019.489746 seq(C-Y)	748.6766968 seq(C-K)	
1017.631958 seq(C-S)	748.6766968 seq(C-Q)	
1017.631958 seq(C-K)	730.5621338 seq(C-M)	
1017.631958 seq(C-Q)	721.6623535 seq(C-Y)	

Mascot Output Format

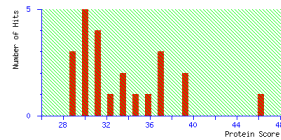
BSA mass

MASCOT SEARCH RESULTS

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 05:17:39 GMT
Top Score : 46 for **ALBU_BOVIN**, Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As	Concise Protein Summary	Help
Significance threshold p<	0.05	Max. number of hits 200
Preferred taxonomy	All entries	
Re-Search All	Search Unmatched	
1.	ALBU_BOVIN Mass: 71279 Score: 46 Expect: 13 Matches: 41 Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	
2.	SPJ1_SCHPO Mass: 42821 Score: 40 Expect: 62 Matches: 15 DnaJ-related protein spj1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=spj1 PE=2 SV=2	
3.	ROL2_LINMU Mass: 21025 Score: 39 Expect: 71 Matches: 10 Cytokinin-beta-glucosidase 2 OS=Linaria vulgaris GN=ROL2 PE=3 SV=1	
4.	ORR3_PEA Mass: 16795 Score: 38 Expect: 98 Matches: 14 Disease resistance response protein Pi49 OS=Pisum sativum GN=ORR49A PE=2 SV=1	
5.	PSMA4_ARATH Mass: 27574 Score: 37 Expect: 1.2e+002 Matches: 11 Proteasome subunit alpha type-4-A OS=Arabidopsis thaliana GN=PACT1 PE=1 SV=1	
6.	KAD_PSEPG Mass: 23308 Score: 37 Expect: 1.2e+002 Matches: 10 Adenylate kinase OS=Pseudomonas putida (strain Q8-1) GN=adk PE=3 SV=1 KAD_PSEPM Mass: 23308 Score: 37 Expect: 1.2e+002 Matches: 10 Adenylate kinase OS=Pseudomonas putida (strain W619) GN=adk PE=3 SV=1	
7.	RS16_FRAP2 Mass: 9104 Score: 36 Expect: 1.4e+002 Matches: 10 30S ribosomal protein S16 OS=Francisella philomiragia subsp. philomiragia (strain ATCC 25017) GN=rsps PE=3 SV=1 RS16_FRAT1 Mass: 9076 Score: 36 Expect: 1.4e+002 Matches: 10 30S ribosomal protein S16 OS=Francisella tularensis subsp. tularensis (strain FSC 198) GN=rsps PE=3 SV=1 RS16_FRATM Mass: 9076 Score: 36 Expect: 1.4e+002 Matches: 10 30S ribosomal protein S16 OS=Francisella tularensis subsp. mediasiatica (strain FSC147) GN=rsps PE=3 SV=1 RS16_FRATN Mass: 9076 Score: 36 Expect: 1.4e+002 Matches: 10 30S ribosomal protein S16 OS=Francisella tularensis subsp. novicida (strain UT112) GN=rsps PE=3 SV=1 RS16_FRATI Mass: 9076 Score: 36 Expect: 1.4e+002 Matches: 10 30S ribosomal protein S16 OS=Francisella tularensis subsp. tularensis (strain SCHU S4 / Schu 4) GN=rsps PE=3 SV=1 RS16_FRATW Mass: 9076 Score: 36 Expect: 1.4e+002 Matches: 10 30S ribosomal protein S16 OS=Francisella tularensis subsp. tularensis (strain WY96-3418) GN=rsps PE=3 SV=1	
8.	RL23_AERS4 Mass: 11156 Score: 34 Expect: 2e+002 Matches: 12 50S ribosomal protein L23 OS=Aeromonas salmonicida (strain A449) GN=rpL23 PE=3 SV=1	
9.	RL1_LACLA Mass: 24035 Score: 34 Expect: 2.5e+002 Matches: 14 50S ribosomal protein L1 OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=rpL1A PE=3 SV=1	
10.	CLPB_WOLSU Mass: 96049 Score: 33 Expect: 2.6e+002 Matches: 31 Chaperone protein ClpB OS=Mollinella succinoferens (strain ATCC 29543 / DSM 1740 / LMG 7466 / NCTC 11488 / FDC 602W) GN=clpB PE=3 SV=1	
11.	SUCC_GRAFK Mass: 43448 Score: 33 Expect: 2.9e+002 Matches: 18 SUCC_GRAFK Mass: 43448 Score: 33 Expect: 2.9e+002 Matches: 18 Succinyl-CoA lyase [ADP-forming] subunit beta OS=Gramella forsetii (strain KT0803) GN=succ PE=3 SV=1	
12.	KAD_PSEFS Mass: 23309 Score: 32 Expect: 3.8e+002 Matches: 8 Adenylate kinase OS=Pseudomonas fluorescens (strain SBIW25) GN=adk PE=3 SV=1	
13.	Y144_RICPR Mass: 18582 Score: 31 Expect: 4.4e+002 Matches: 14 Uncharacterized protein RP144 OS=Rickettsia prowazekii (strain Madrid E) GN=RP144 PE=4 SV=1	
14.	RS9_RHIME Mass: 16746 Score: 31 Expect: 4.5e+002 Matches: 10 30S ribosomal protein S9 OS=Rhizobium meliloti (strain 1021) GN=rsL1 PE=3 SV=1	
15.	FIB37_BPM1 Mass: 28266 Score: 31 Expect: 4.5e+002 Matches: 10 Long tail fiber protein p37 (Fragment) OS=Enterobacteria phage M1 GN=p37 PE=3 SV=1 FIB37_BPM2 Mass: 28176 Score: 31 Expect: 4.5e+002 Matches: 10 Long tail fiber protein p37 (Fragment) OS=Enterobacteria phage Oxy2 GN=p37 PE=3 SV=1	
16.	ENO_PECAS Mass: 45288 Score: 30 Expect: 5e+002 Matches: 16 Enolase OS=Pectobacterium atrosepticum (strain SORI 1043 / ATCC BAA-672) GN=eno PE=3 SV=1	
17.	RBS_MUSAC Mass: 20845 Score: 30 Expect: 5.1e+002 Matches: 13 Ribulose biphosphatase carboxylase small chain, chloroplastic OS=Musa acuminata GN=RBDS1 PE=2 SV=1	
18.	KAD_PSEPI Mass: 23324 Score: 30 Expect: 5.4e+002 Matches: 8 Adenylate kinase OS=Pseudomonas putida (strain F1 / ATCC 700007) GN=adk PE=3 SV=1 KAD_PSEPI Mass: 23324 Score: 30 Expect: 5.4e+002 Matches: 8 Adenylate kinase OS=Pseudomonas putida (strain KT2440) GN=adk PE=3 SV=1 KAD_PSEPU Mass: 23324 Score: 30 Expect: 5.4e+002 Matches: 8 Adenylate kinase OS=Pseudomonas putida GN=adk PE=3 SV=1	
19.	HBE_CA1MD Mass: 16852 Score: 30 Expect: 5.5e+002 Matches: 8 Hemoglobin subunit epsilon OS=Cairina moschata GN=HBE PE=2 SV=2	
20.	Y335_METJA Mass: 27921 Score: 30 Expect: 5.8e+002 Matches: 13 Uncharacterized protein MJ0335 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NERC 100440) GN=MJ0335 PE=4 SV=1	
21.	PF6B_CAUMD Mass: 13880 Score: 29 Expect: 6.5e+002 Matches: 9 Prefoldin subunit beta OS=Caldivirga maquilinensis (strain ATCC 700844 / DSM 13496 / JCM 10307 / IC-167) GN=pf6B PE=3 SV=1	
22.	KAD_BURM7 Mass: 24213 Score: 29 Expect: 6.6e+002 Matches: 11	

22.	KAD_BURW	Mass: 24213	Score: 29	Expect: 6.6e+002	Matches: 11
	Adenylate kinase OS=Burkholderia mallei (strain NCTC 10247) GN=adk PE=3 SV=1				
	KAD_BURM	Mass: 24213	Score: 29	Expect: 6.6e+002	Matches: 11
	Adenylate kinase OS=Burkholderia mallei (strain NCTC 10229) GN=adk PE=3 SV=1				
	KAD_BURWA	Mass: 24213	Score: 29	Expect: 6.6e+002	Matches: 11
	Adenylate kinase OS=Burkholderia mallei (strain ATCC 23344) GN=adk PE=3 SV=1				
	KAD_BURMS	Mass: 24213	Score: 29	Expect: 6.6e+002	Matches: 11
	Adenylate kinase OS=Burkholderia mallei (strain 34W11) GN=adk PE=3 SV=1				
	KAD_BURFO	Mass: 24213	Score: 29	Expect: 6.6e+002	Matches: 11
	Adenylate kinase OS=Burkholderia pseudomallei (strain 1106a) GN=adk PE=3 SV=1				
	KAD_BURP1	Mass: 24213	Score: 29	Expect: 6.6e+002	Matches: 11
	Adenylate kinase OS=Burkholderia pseudomallei (strain 1710b) GN=adk PE=1 SV=1				
	KAD_BURFS	Mass: 24213	Score: 29	Expect: 6.6e+002	Matches: 11
	Adenylate kinase OS=Burkholderia pseudomallei (strain 868) GN=adk PE=3 SV=1				
	KAD_BURFS	Mass: 24213	Score: 29	Expect: 6.6e+002	Matches: 11
	Adenylate kinase OS=Burkholderia pseudomallei (strain K96243) GN=adk PE=3 SV=1				
23.	HSLV_STA41	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain Mu3 / ATCC 700698) GN=hslV PE=3 SV=1				
	HSLV_STA42	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain JH1) GN=hslV PE=3 SV=1				
	HSLV_STA43	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain USA300) GN=hslV PE=3 SV=1				
	HSLV_STA48	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain NCTC 8325) GN=hslV PE=3 SV=1				
	HSLV_STA49	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain JH9) GN=hslV PE=3 SV=1				
	HSLV_STAAB	Mass: 19599	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain bovine RF122 / ET3-1) GN=hslV PE=3 SV=1				
	HSLV_STAAC	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain COL) GN=hslV PE=3 SV=1				
	HSLV_STA4E	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain Newman) GN=hslV PE=3 SV=1				
	HSLV_STAAM	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain Mu50 / ATCC 700699) GN=hslV PE=3 SV=1				
	HSLV_STAAN	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain N315) GN=hslV PE=1 SV=1				
	HSLV_STAAR	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain MRS4252) GN=hslV PE=3 SV=1				
	HSLV_STAAC	Mass: 19610	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain MRS4252) GN=hslV PE=3 SV=1				
	HSLV_STAAS	Mass: 19618	Score: 29	Expect: 7.1e+002	Matches: 8
	ATP-dependent protease subunit HslV OS=Staphylococcus aureus (strain MSSA476) GN=hslV PE=3 SV=1				

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.5 Da
 Fragment Mass Tolerance : ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument Type : Default
 Query1 (815.7810,1+): <no title>
 Query2 (818.6788,1+): <no title>
 Query3 (818.4763,1+): <no title>
 Query4 (820.5340,1+): <no title>
 Query5 (832.5363,1+): <no title>
 Query6 (835.5478,1+): <no title>
 Query7 (835.5504,1+): <no title>
 Query8 (835.5682,1+): <no title>
 Query9 (836.3428,1+): <no title>
 Query10 (840.5561,1+): <no title>
 Query11 (840.5872,1+): <no title>
 Query12 (840.5909,1+): <no title>
 Query13 (840.9949,1+): <no title>
 Query14 (841.3505,1+): <no title>
 Query15 (841.5867,1+): <no title>
 Query16 (844.4614,1+): <no title>
 Query17 (854.3765,1+): <no title>
 Query18 (857.5164,1+): <no title>
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 Query20 (860.3229,1+): <no title>
 Query21 (860.6417,1+): <no title>
 Query22 (861.5378,1+): <no title>
 Query23 (869.5292,1+): <no title>
 Query24 (871.5303,1+): <no title>
 Query25 (872.5607,1+): <no title>
 Query26 (876.5069,1+): <no title>
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 Query28 (877.1182,1+): <no title>
 Query29 (877.1182,1+): <no title>

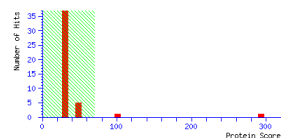
BSA mass/mass+c

MASCOT Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 06:45:07 GMT
Top Score : 293 for **ALBU_BOVIN**, Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary Help
Significance threshold p: 0.05 Max. number of hits: 200
Preferred taxonomy: All entries

Re-Search All Search Unmatched

1.	ALBU_BOVIN	Mass: 71279	Score: 293	Expect: 2.8e-024	Matches: 40
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4					
2.	ALBU_SHEEP	Mass: 71174	Score: 103	Expect: 2.8e-005	Matches: 28
2.	ALBU_SHEEP	Mass: 71174	Score: 103	Expect: 2.8e-005	Matches: 28
Serum albumin OS=Ovis aries GN=ALB PE=1 SV=1					
3.	MPAP1_PHLPR	Mass: 28845	Score: 53	Expect: 2.6	Matches: 11
Pollen allergen Phl p 1 OS=Phleum pratense GN=PHLP1 PE=1 SV=1					
4.	S2541_BOVIN	Mass: 38953	Score: 51	Expect: 4.8	Matches: 7
Solute carrier family 25 member 41 OS=Bos taurus GN=SLC25A41 PE=2 SV=1					
5.	ALBU_FELCA	Mass: 70645	Score: 47	Expect: 12	Matches: 17
Serum albumin OS=Felis catus GN=ALB PE=1 SV=1					
6.	SYT_PROMT	Mass: 74347	Score: 43	Expect: 29	Matches: 20
Threonine--tRNA ligase OS=Prochlorococcus marinus (strain NATL2A) GN=thrS PE=3 SV=1					
7.	CES7L_VENTR	Mass: 55003	Score: 42	Expect: 31	Matches: 17
Centrosomal protein cesp711 OS=Xenopus tropicalis GN=ces711 PE=2 SV=1					
8.	CAPSD_CLVX	Mass: 30401	Score: 39	Expect: 68	Matches: 7
Capsid protein OS=African cassava mosaic virus (isolate West Kenyan 844) GN=ARI PE=3 SV=1					
9.	EXPB1_ORYSJ	Mass: 29130	Score: 37	Expect: 1e+002	Matches: 9
Expansin-B1 OS=Oryza sativa subsp. japonica GN=EXPB1a PE=1 SV=2					
10.	ACP_GMAT	Mass: 6745	Score: 37	Expect: 1.2e+002	Matches: 7
Acyl carrier protein OS=Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505) GN=accP PE=3 SV=1					
11.	RHO24_HUMAN	Mass: 84843	Score: 36	Expect: 1.5e+002	Matches: 17
Rho GTPase-activating protein 24 OS=Homo sapiens GN=ARHGAP24 PE=1 SV=2					
12.	Y208_RICTY	Mass: 34149	Score: 36	Expect: 1.6e+002	Matches: 9
Uncharacterized glycosyltransferase RTO209 OS=Rickettsia typhi (strain ATCC VR-144 / Wilmington) GN=RTO209 PE=3 SV=1					
13.	YXIS_BPAPS	Mass: 14636	Score: 35	Expect: 1.6e+002	Matches: 8
Probable excisionase OS=Acyrthosiphon pisum secondary endosymbiont phase 1 GN=40 PE=3 SV=1					
14.	DNAI1_MYCPN	Mass: 37109	Score: 35	Expect: 1.7e+002	Matches: 12
DNAI-like protein MD002 homolog OS=Mycoplasma pneumoniae (strain ATCC 29342 / M129) GN=MPN_002 PE=3 SV=1					
15.	PSD_DINSH	Mass: 24440	Score: 35	Expect: 1.8e+002	Matches: 5
15.	PSD_DINSH	Mass: 24440	Score: 35	Expect: 1.8e+002	Matches: 5
Phosphatidylserine decarboxylase proenzyme OS=Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12) GN=psd PE=3 SV=1					
16.	RL3_BLOPP	Mass: 23822	Score: 35	Expect: 1.8e+002	Matches: 7
50S ribosomal protein L3 OS=Blotriehmannia pennsylvanicus (strain BPEN) GN=rpL3C PE=3 SV=1					
17.	AROR_CAMHC	Mass: 38914	Score: 35	Expect: 1.9e+002	Matches: 16
3-dehydroquinate synthase OS=Campylobacter hominis (strain ATCC BAA-381 / LMG 19568 / NCTC 13146 / CH001A) GN=aroB PE=3 SV=1					
18.	HBB_LEIXA	Mass: 16342	Score: 35	Expect: 1.9e+002	Matches: 4
Hemoglobin subunit beta OS=Leiosomus xanthurus GN=hbb PE=1 SV=1					
19.	CACB2_BABIT	Mass: 71249	Score: 34	Expect: 2.1e+002	Matches: 19
Voltage-dependent L-type calcium channel subunit beta-2 OS=Ornitholagus cuniculus GN=CACB2 PE=1 SV=1					
20.	ADD_CLOEK	Mass: 38130	Score: 34	Expect: 2.2e+002	Matches: 9
Adenosine deaminase OS=Clostridium botulinum (strain Okra / Type B1) GN=add PE=3 SV=1					
	ADD_CLOEK	Mass: 38154	Score: 32	Expect: 3.6e+002	Matches: 8
Adenosine deaminase OS=Clostridium botulinum (strain Loch Maree / Type A3) GN=add PE=3 SV=1					
21.	PSAH2_ARATH	Mass: 15264	Score: 34	Expect: 2.5e+002	Matches: 5
Photosystem I reaction center subunit VI-2, chloroplastic OS=Arabidopsis thaliana GN=PSAH2 PE=2 SV=1					
22.	KAD_BURMI	Mass: 24270	Score: 33	Expect: 2.6e+002	Matches: 8
Adenylate kinase OS=Burkholderia multivorans (strain ATCC 17616 / 249) GN=adk PE=3 SV=1					
23.	SYFA_BACFN	Mass: 38882	Score: 33	Expect: 2.6e+002	Matches: 7
Phenylalanine--tRNA ligase alpha subunit OS=Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) GN=pheS PE=3 SV=1					
	SYFA_BACFN	Mass: 38882	Score: 33	Expect: 2.6e+002	Matches: 7
Phenylalanine--tRNA ligase alpha subunit OS=Bacteroides fragilis (strain Y0446) GN=pheS PE=3 SV=1					
24.	CHD3_BRASE	Mass: 57447	Score: 33	Expect: 2.6e+002	Matches: 8
60 kDa chaperonin 3 OS=Bradyrhizobium sp. (strain BTA11 / ATCC BAA-1182) GN=chd3 PE=3 SV=1					
25.	YBEY_EXIS2	Mass: 18423	Score: 33	Expect: 2.6e+002	Matches: 7
Endoribonuclease YbeY OS=Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15) GN=ybeY PE=3 SV=1					
26.	KAD_BURPP	Mass: 24612	Score: 33	Expect: 2.7e+002	Matches: 8
Adenylate kinase OS=Burkholderia phytofirmans (strain DSM 17436 / PsJN) GN=adk PE=3 SV=1					

adenylate kinase OS=Burkholderia phytofirmans (strain DSM 11430 / FSJN) GN=Bak PE=3 SV=1					
27.	ATPE_CLONN	Mass: 14963	Score: 32	Expect: 3.1e+002	Matches: 7 ATP synthase epsilon chain OS=Clostridium novyi (strain NT) GN=atpC PE=3 SV=1
28.	RHG24_MOUSE	Mass: 84885	Score: 32	Expect: 3.2e+002	Matches: 14 Rho GTPase-activating protein 24 OS=Mus musculus GN=Arhaa24 PE=1 SV=2
29.	Y218_RICPR	Mass: 34113	Score: 32	Expect: 3.2e+002	Matches: 8 Uncharacterized glycosyltransferase RP128 OS=Rickettsia prowazekii (strain Madrid E) GN=RP218 PE=3 SV=1
30.	RS17_BACOR	Mass: 10198	Score: 32	Expect: 3.3e+002	Matches: 6 30S ribosomal protein S17 OS=Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711) GN=rps0 PE=3 SV=1
31.	TIG_MOLTR	Mass: 51462	Score: 32	Expect: 3.4e+002	Matches: 9 Trigger factor OS=Wolbachia sp. subsp. Brugia malayi (strain TRS) GN=tig PE=3 SV=1
32.	KAD_BURM	Mass: 24200	Score: 32	Expect: 3.4e+002	Matches: 8 Adenylate kinase OS=Burkholderia ambifaria (strain MC40-6) GN=adk PE=3 SV=1
	KAD_BURM	Mass: 24200	Score: 32	Expect: 3.7e+002	Matches: 8 Adenylate kinase OS=Burkholderia ambifaria (strain ATCC BAA-244 / AMMD) GN=adk PE=3 SV=1
33.	NADN_METJA	Mass: 19597	Score: 32	Expect: 3.4e+002	Matches: 5 Nicotinamide nucleotide adenyllyltransferase OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) GN=MJ0541 PE=1 SV=3
34.	RS14_EKXS2	Mass: 10114	Score: 32	Expect: 3.6e+002	Matches: 2 30S ribosomal protein S14 OS=Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15) GN=rpsN PE=3 SV=1
35.	NS5_LDCPR	Mass: 36011	Score: 32	Expect: 3.7e+002	Matches: 8 Non-structural protein 5 OS=Lymnaea dispar cynovirus 1 (isolate Rao) GN=NS9 PE=4 SV=1
36.	CRL_EC027	Mass: 15763	Score: 32	Expect: 3.7e+002	Matches: 4 Sigma factor-binding protein Crl OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=crl PE=3 SV=1
	CRL_EC071	Mass: 15763	Score: 32	Expect: 3.7e+002	Matches: 4 Sigma factor-binding protein Crl OS=Escherichia coli O7:H1 (strain 1A139 / ExPEC) GN=crl PE=3 SV=1
	CRL_EC016	Mass: 15806	Score: 32	Expect: 3.7e+002	Matches: 4 Sigma factor-binding protein Crl OS=Escherichia coli O6:H1 (strain CF1073 / ATCC 700928 / UPEC) GN=crl PE=3 SV=3
	CRL_EC011	Mass: 15778	Score: 32	Expect: 3.7e+002	Matches: 4 Sigma factor-binding protein Crl OS=Escherichia coli O17:H52:H18 (strain UMN026 / ExPEC) GN=crl PE=3 SV=1
37.	UL24_ELHWK	Mass: 26729	Score: 31	Expect: 4e+002	Matches: 11 Protein UL24 homolog OS=Elephantid herpesvirus 1 (isolate Asian elephant/Berlin/Kiba/1998) PE=2 SV=1
37.	UL24_ELHWK	Mass: 26729	Score: 31	Expect: 4e+002	Matches: 11 Protein UL24 homolog OS=Elephantid herpesvirus 1 (isolate Asian elephant/Berlin/Kiba/1998) PE=2 SV=1
38.	RAN_DROME	Mass: 24939	Score: 31	Expect: 4e+002	Matches: 11 GTP-binding nuclear protein Ran-like OS=Drosophila melanogaster GN=Ran-like PE=1 SV=1
39.	Msh3_MOUSE	Mass: 124331	Score: 31	Expect: 4.2e+002	Matches: 17 DNA mismatch repair protein Msh3 OS=Mus musculus GN=Msh3 PE=2 SV=3
40.	BRE5_YEAST	Mass: 57813	Score: 31	Expect: 4.2e+002	Matches: 15 UBP3-associated protein BRE5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=BRE5 PE=1 SV=1
41.	SFS3A_PROM5	Mass: 28564	Score: 31	Expect: 4.3e+002	Matches: 12 Sugar fermentation stimulation protein homolog OS=Prochlorococcus marinus (strain MIT 9515) GN=sfsA PE=3 SV=1
42.	RL26_BRACM	Mass: 16885	Score: 31	Expect: 4.5e+002	Matches: 6 60S ribosomal protein L26 OS=Brassica campestris GN=RPL26 PE=2 SV=1
43.	MURC_BACON	Mass: 49574	Score: 31	Expect: 4.6e+002	Matches: 8 UDP-N-acetyluramate-L-alanine ligase OS=Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NH 391-98) GN=murC PE=3 SV=1
44.	RS17_BACSU	Mass: 10193	Score: 31	Expect: 4.7e+002	Matches: 4 30S ribosomal protein S17 OS=Bacillus subtilis (strain 168) GN=rps0 PE=1 SV=3

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance: ± 0.5 Da
 Fragment Mass Tolerance: ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Query1 (815.7810,1+): <no title>
 Query2 (816.6786,1+): <no title>
 Query3 (818.4763,1+): <no title>
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 : seq(C-L)

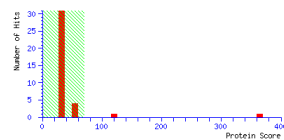
BSA mass+c

MASCOT Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 06:45:13 GMT
Top Score : 364 for **ALBU_BOVIN**, Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary [Help](#)
Significance threshold $p < 0.05$ Max. number of hits 200
Preferred taxonomy All entries

Re-Search All Search Unmatched

1.	ALBU_BOVIN	Mass: 71279	Score: 364	Expect: 2.2e-031	Matches: 21
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4					
2.	ALBU_SHEEP	Mass: 71174	Score: 111	Expect: 4.4e-006	Matches: 9
2.	ALBU_SHEEP	Mass: 71174	Score: 111	Expect: 4.4e-006	Matches: 9
Serum albumin OS=Ovis aries GN=ALB PE=1 SV=1					
3.	MPAP1_PHLPR	Mass: 28845	Score: 57	Expect: 1.2	Matches: 4
Pollen allergen Phl p 1 OS=Phleum pratense GN=PHLP1 PE=1 SV=1					
4.	S2541_BOVIN	Mass: 38953	Score: 49	Expect: 7.4	Matches: 3
Solute carrier family 25 member 41 OS=Bos taurus GN=S2541 PE=2 SV=1					
5.	ALBU_FELCA	Mass: 70645	Score: 48	Expect: 7.8	Matches: 4
Serum albumin OS=Felis catus GN=ALB PE=1 SV=1					
6.	ULAI_SCHPO	Mass: 60053	Score: 44	Expect: 22	Matches: 3
NEED8-activating enzyme E1 regulatory subunit OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=uba5 PE=3 SV=2					
7.	SYR_BUOCO	Mass: 67906	Score: 42	Expect: 37	Matches: 4
Arginine--tRNA ligase OS=Buchnera aphidicola subsp. Cinara cedri (strain Cc) GN=ParS PE=3 SV=1					
8.	ATPE_GLOMN	Mass: 14963	Score: 41	Expect: 48	Matches: 3
ATP synthase epsilon chain OS=Clostridium novyi (strain NT) GN=PatC PE=3 SV=1					
9.	HBB_LEIXA	Mass: 16342	Score: 37	Expect: 1.1e+002	Matches: 2
Hemoglobin subunit beta OS=Leleostomus xanthurus GN=Hbb PE=1 SV=1					
10.	RS14_EXIS2	Mass: 10114	Score: 36	Expect: 1.2e+002	Matches: 2
30S ribosomal protein S14 OS=Escherichia coli (strain ATCC 8739 / JCM 13430 / 255-15) GN=rsdN PE=3 SV=1					
11.	GTSE1_HUMAN	Mass: 77120	Score: 36	Expect: 1.3e+002	Matches: 3
G2 and S phase-expressed protein 1 OS=Homo sapiens GN=GTSE1 PE=1 SV=3					
12.	CAPSD_CLVK	Mass: 30401	Score: 36	Expect: 1.4e+002	Matches: 2
Capsid protein OS=African cassava mosaic virus (isolate West Kenyan 844) GN=ARI PE=3 SV=1					
13.	TRPD_DICTD	Mass: 37085	Score: 36	Expect: 1.4e+002	Matches: 3
Anthranilate phosphoribosyltransferase OS=Dictyostelium discoideum (strain Z-1310 / DSM 6724) GN=trpD PE=3 SV=1					
14.	SYA_BACME	Mass: 97031	Score: 36	Expect: 1.5e+002	Matches: 3
Alanine--tRNA ligase OS=Bacillus methylotrophicus (strain DSM 23117 / B50C 1046 / FZB42) GN=alaS PE=3 SV=1					
15.	OUT_EHRCJ	Mass: 16662	Score: 36	Expect: 1.5e+002	Matches: 2
15.	OUT_EHRCJ	Mass: 16662	Score: 36	Expect: 1.5e+002	Matches: 2
Deoxyuridine 5'-triphosphate nucleotidylhydrolase OS=Ehrlichia canis (strain Jake) GN=dut PE=3 SV=1					
16.	CITD_ENTFA	Mass: 11426	Score: 35	Expect: 1.6e+002	Matches: 2
Citrate lyase acyl carrier protein OS=Enterococcus faecalis (strain ATCC 700802 / V583) GN=citD PE=3 SV=1					
17.	MSH3_MOUSE	Mass: 124331	Score: 35	Expect: 1.7e+002	Matches: 3
DNA mismatch repair protein Msh3 OS=Mus musculus GN=Msh3 PE=2 SV=3					
18.	MED9_DICTDI	Mass: 22221	Score: 35	Expect: 1.7e+002	Matches: 3
Putative mediator of RNA polymerase II transcription subunit 9 OS=Dictyostelium discoideum GN=med9 PE=3 SV=1					
19.	RS14_BABEK	Mass: 11762	Score: 35	Expect: 1.8e+002	Matches: 2
30S ribosomal protein S14 OS=Bartonella bacilliformis (strain ATCC 35685 / K5583) GN=rrsN PE=3 SV=1					
20.	ACP_GEMAT	Mass: 8745	Score: 35	Expect: 1.8e+002	Matches: 2
Acyl carrier protein OS=Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505) GN=acpP PE=3 SV=1					
21.	EIF2B2_BOVIN	Mass: 39202	Score: 35	Expect: 1.9e+002	Matches: 2
Translation initiation factor eIF-2B subunit beta OS=Bos taurus GN=EIF2B2 PE=2 SV=1					
21.	EIF2B2_HUMAN	Mass: 39197	Score: 35	Expect: 1.9e+002	Matches: 2
Translation initiation factor eIF-2B subunit beta OS=Homo sapiens GN=EIF2B2 PE=1 SV=3					
22.	SYL_PROMI	Mass: 74347	Score: 35	Expect: 1.9e+002	Matches: 3
Threonine--tRNA ligase OS=Prochlorococcus marinus (strain NATL2A) GN=thrS PE=3 SV=1					
23.	RL3_MYOPE	Mass: 34151	Score: 34	Expect: 2e+002	Matches: 3
50S ribosomal protein L3 OS=Mycobacterium penetrans (strain HF-2) GN=rlpC PE=3 SV=2					
24.	CES7L_XENTR	Mass: 55003	Score: 34	Expect: 2.1e+002	Matches: 3
Centrosomal protein cep5711 OS=Xenopus tropicalis GN=cep5711 PE=2 SV=1					
25.	PSD_DINSH	Mass: 24440	Score: 34	Expect: 2.1e+002	Matches: 2
Phosphatidylserine decarboxylase proenzyme OS=Dictyostelium discoideum (strain DSM 16493 / NCIMB 14021 / DFL 12) GN=psd PE=3 SV=1					
26.	RS2_ACICJ	Mass: 28151	Score: 34	Expect: 2.4e+002	Matches: 2
30S ribosomal protein S2 OS=Acidiphilium cryptum (strain JF-5) GN=rsbB PE=3 SV=1					
27.	PSAH2_ARATH	Mass: 15264	Score: 33	Expect: 2.5e+002	Matches: 2
Photosystem I reaction center subunit VI-2, chloroplastic OS=Arabidopsis thaliana GN=PSAH2 PE=2 SV=1					

```
Type of search           : Sequence Query
Enzyme                   : Lys-N
Fixed modifications       : Carbamidomethyl (C)
Mass values              : Monoisotopic
Protein Mass             : Unrestricted
Peptide Mass Tolerance   : ± 0.5 Da
Fragment Mass Tolerance  : ± 0.6 Da
Max Missed Cleavages      : 1
Instrument type           : Default
Query1 (818.4763,1+)     : seq(C-I-)
Query2 (818.4763,1+)     : seq(C-I-)
Query3 (820.5340,1+)     : seq(C-I-)
Query4 (820.5340,1+)     : seq(C-I-)
Query5 (840.9949,1+)     : seq(C-L-)
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Query7 (841.5887,1+)     : seq(C-I-)
                          : seq(L-m)
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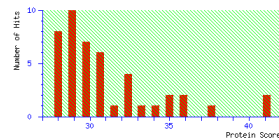
TF mass

MASCOT Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 198582750 residues)
Timestamp : 14 Apr 2016 at 05:29:40 GMT
Top Score : 41 for **ATPF_CANGA**, ATP synthase subunit 4, mitochondrial OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=ATP4 PE=3 SV=1

Mascot Score Histogram

Protein score is $-10 \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As	Concise Protein Summary	Help
Significance threshold p<	0.05	Max. number of hits 200
Preferred taxonomy	All entries	

Re-Search All Search Unmatched

1.	ATPF_CANGA	Mass: 26612	Score: 41	Expect: 43	Matches: 10	ATP synthase subunit 4, mitochondrial OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=ATP4 PE=3 SV=1
	ATP synthase subunit 4, mitochondrial OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=ATP4 PE=3 SV=1					
2.	PSE2_THEGJ	Mass: 22006	Score: 41	Expect: 43	Matches: 8	Proteasome subunit beta 2 OS=Thermococcus gammatolerans (strain DSM 15229 / JCM 11827 / EJS) GN=psmB2 PE=3 SV=1
3.	RUB6_PROMP	Mass: 39939	Score: 37	Expect: 1e+002	Matches: 12	Holliday junction ATP-dependent DNA helicase Rub6 OS=Prochlorococcus marinus subsp. pastoris (strain COM1886 / MED4) GN=rubB PE=3 SV=1
4.	RIMM_BACME	Mass: 19855	Score: 36	Expect: 1.3e+002	Matches: 10	Ribosome maturation factor RimM OS=Bacillus methylophilus (strain DSM 23117 / BGSC 10A6 / FZB42) GN=rmm PE=3 SV=1
5.	SERB_STR72	Mass: 23593	Score: 36	Expect: 1.5e+002	Matches: 10	Phosphoserine phosphatase OS=Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311) GN=srb PE=1 SV=1
6.	COR13_ARATH	Mass: 47415	Score: 35	Expect: 1.6e+002	Matches: 15	Cystine lyase COR13 OS=Arabidopsis thaliana GN=COR13 PE=1 SV=1
7.	GSH_BUR44	Mass: 13263	Score: 35	Expect: 1.9e+002	Matches: 6	Glycine cleavage system H protein OS=Burkholderia ambifaria (strain M40-6) GN=gcvH PE=3 SV=1
8.	RS9_THEAC	Mass: 14518	Score: 34	Expect: 2e+002	Matches: 9	30S ribosomal protein S8 OS=Thermoplasma acidophilum (strain ATCC 25905 / DSM 1728 / JCM 9062 / NBRC 15155 / AMRC-C165) GN=rps8 PE=3 SV=1
9.	Y1512_SULAC	Mass: 25392	Score: 34	Expect: 2.4e+002	Matches: 10	UPF0173 metal-dependent hydrolase Saci_1512 OS=Sulfolobus acidocaldarius (strain ATCC 33909 / DSM 639 / JCM 8929 / NBRC 15157 / NCIMB 11770) GN=Saci_1512 PE=3 SV=2
10.	RL7_STA60	Mass: 12643	Score: 33	Expect: 3e+002	Matches: 11	50S ribosomal protein L7/L12 OS=Staphylococcus epidermidis (strain ATCC 35984 / RP62A) GN=rpL PE=3 SV=1
	RL7_STA63	Mass: 12643	Score: 33	Expect: 3e+002	Matches: 11	50S ribosomal protein L7/L12 OS=Staphylococcus epidermidis (strain ATCC 12228) GN=rpL PE=3 SV=1
11.	Y275_METSB	Mass: 11924	Score: 33	Expect: 3e+002	Matches: 7	Nucleoid-associated protein Msi1_0275 OS=Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906) GN=Msi1_0275 PE=3 SV=1
12.	JPYR_HMEDU	Mass: 19470	Score: 33	Expect: 3e+002	Matches: 7	Inorganic pyrophosphatase OS=Haemophilus ducreyi (strain 35000HP / ATCC 700724) GN=ppa PE=3 SV=1
13.	RL20_AZ0V0	Mass: 13385	Score: 32	Expect: 3.1e+002	Matches: 8	50S ribosomal protein L20 OS=Azotobacter vinelandii (strain DJ / ATCC BAA-1303) GN=rpL PE=3 SV=1
	RL20_AZ0V1	Mass: 13429	Score: 32	Expect: 3.1e+002	Matches: 8	50S ribosomal protein L20 OS=Azotobacter vinelandii (strain DJ / ATCC BAA-1303) GN=rpL PE=3 SV=1
14.	CKKD1_ORYSJ	Mass: 47715	Score: 32	Expect: 3.9e+002	Matches: 12	Cyclin-dependent kinase D-1 OS=Oryza sativa subsp. indica GN=CKKD-1 PE=2 SV=1
	CKKD1_ORYSJ	Mass: 47699	Score: 32	Expect: 3.9e+002	Matches: 12	Cyclin-dependent kinase D-1 OS=Oryza sativa subsp. japonica GN=CKKD-1 PE=1 SV=1
15.	AMP_ONYFE	Mass: 24843	Score: 31	Expect: 4.4e+002	Matches: 11	Antigenic membrane protein OS=Onion yellows phytoplasma (strain OY-M) GN=amp PE=1 SV=3
16.	RL28_AZ0V0	Mass: 9075	Score: 31	Expect: 4.5e+002	Matches: 5	50S ribosomal protein L28 OS=Azotobacter vinelandii (strain DJ / ATCC BAA-1303) GN=rpsB PE=3 SV=1
17.	EFP_HALHL	Mass: 21088	Score: 31	Expect: 4.6e+002	Matches: 9	Elongation factor P OS=Halorhodospira halohila (strain DSM 244 / SL1) GN=efp PE=3 SV=1
18.	DHAJ_LACRO	Mass: 42068	Score: 31	Expect: 4.8e+002	Matches: 11	Chaperone protein DnaJ OS=Lactobacillus reuteri (strain DSM 20016) GN=dnaJ PE=3 SV=1
	DHAJ_LACRO	Mass: 42068	Score: 31	Expect: 4.8e+002	Matches: 11	Chaperone protein DnaJ OS=Lactobacillus reuteri (strain JCM 1112) GN=dnaJ PE=3 SV=1
19.	TRH10_ARATH	Mass: 17882	Score: 30	Expect: 4.9e+002	Matches: 7	Putative thioredoxin H10 OS=Arabidopsis thaliana GN=At3g56420 PE=3 SV=2
20.	ATPD_PSEAB	Mass: 19396	Score: 30	Expect: 4.9e+002	Matches: 8	ATP synthase subunit delta OS=Pseudalteromonas atlantica (strain T6c / ATCC BAA-1087) GN=atpH PE=3 SV=1
21.	SYR_HELHP	Mass: 62505	Score: 30	Expect: 5.6e+002	Matches: 14	Arginine--tRNA ligase OS=Helicobacter hepaticus (strain ATCC 51449 / 381) GN=Paras PE=3 SV=1
22.	Y717_DESDM	Mass: 10302	Score: 30	Expect: 5.6e+002	Matches: 8	UPF0295 protein Dred_0717 OS=Desulfotomaculum reducens (strain MI-1) GN=Dred_0717 PE=3 SV=1
23.	DOK_RAT	Mass: 30735	Score: 30	Expect: 5.6e+002	Matches: 10	Deoxycytidine kinase OS=Rattus norvegicus GN=Dok PE=1 SV=1
24.	BOH2_ARATH	Mass: 33871	Score: 30	Expect: 5.9e+002	Matches: 9	Beta-carotene 3-hydroxylase 2, chloroplastic OS=Arabidopsis thaliana GN=BETA-OHASE 2 PE=2 SV=1

24.	BETA-CAROTENE	Mass: 9004	Score: 30	Expect: 6e+002	Matches: 7	Beta-carotene 3-hydroxylase 2, chloroplastic OS=Arabidopsis thaliana GN=BETA-CHASE 2 PE=2 SV=1
25.	RL14E_THESM	Mass: 9004	Score: 30	Expect: 6e+002	Matches: 7	50S ribosomal protein L14e OS=Thermococcus sibiricus (strain IM 739 / DSM 12597) GN=rl14e PE=3 SV=1
26.	ZN727_HUMAN	Mass: 60196	Score: 30	Expect: 6.2e+002	Matches: 19	Putative zinc finger protein 727 OS=Homo sapiens GN=ZN727 PE=5 SV=3
27.	PSAH_BRAO	Mass: 15400	Score: 29	Expect: 6.3e+002	Matches: 7	Photosystem I reaction center subunit VI, chloroplastic OS=Brassica campestris GN=PSAH PE=2 SV=1
28.	URE3_CHSD	Mass: 11020	Score: 29	Expect: 6.5e+002	Matches: 7	Urease subunit gamma OS=Chronohalobacter salexigen (strain DSM 3043 / ATCC BAA-138 / NCIM 13768) GN=ureA PE=3 SV=1
29.	RL6_MANSN	Mass: 19027	Score: 29	Expect: 6.6e+002	Matches: 7	50S ribosomal protein L6 OS=Mannheimia succiniciproducens (strain MDEL55E) GN=rl6F PE=3 SV=1
30.	WINE_NITEU	Mass: 11560	Score: 29	Expect: 6.9e+002	Matches: 6	Cell division topological specificity factor OS=Nitrosomonas europaea (strain ATCC 19718 / NERC 14298) GN=winE PE=3 SV=1
31.	HIS6_BACLD	Mass: 27423	Score: 29	Expect: 6.9e+002	Matches: 8	Imidazole glycerol phosphate synthase subunit HisF OS=Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NERC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46) GN=hisF PE=3 SV=1
32.	Y2210_ARCFU	Mass: 8957	Score: 29	Expect: 6.9e+002	Matches: 6	Uncharacterized protein AF_2210 OS=Archaeoglobus fulgidus (strain ATCC 49558 / VC-16 / DSM 4304 / JCM 9628 / NERC 100126) GN=AF_2210 PE=4 SV=1
33.	ADH3_GEOSE	Mass: 36837	Score: 29	Expect: 7.3e+002	Matches: 11	Alcohol dehydrogenase OS=Geobacillus stearothermophilus PE=1 SV=1
34.	URE3_TOLAT	Mass: 11055	Score: 29	Expect: 7.6e+002	Matches: 8	Urease subunit gamma OS=Tolunosa avensis (strain DSM 9187 / T44) GN=ureA PE=3 SV=1
35.	ATPD_HYFNA	Mass: 19615	Score: 28	Expect: 7.8e+002	Matches: 8	ATP synthase subunit delta OS=Hyphomonas neptunium (strain ATCC 15444) GN=atpH PE=3 SV=1
36.	AURKB_DANRE	Mass: 37213	Score: 28	Expect: 7.8e+002	Matches: 8	Aurora kinase B OS=Danio rerio GN=aurkb PE=2 SV=1
37.	IHFA_PSYIN	Mass: 11032	Score: 28	Expect: 7.8e+002	Matches: 8	Integration host factor subunit alpha OS=Psychromonas ingrahamii (strain 37) GN=ihfA PE=3 SV=1
37.	IHFA_PSYIN	Mass: 11032	Score: 28	Expect: 7.8e+002	Matches: 8	Integration host factor subunit alpha OS=Psychromonas ingrahamii (strain 37) GN=ihfA PE=3 SV=1
38.	KAR_YEAST	Mass: 35596	Score: 28	Expect: 8.1e+002	Matches: 11	NADPH-dependent alpha-keto amide reductase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YDL124W PE=1 SV=1
39.	RAS4_MOUSE	Mass: 37201	Score: 28	Expect: 8.1e+002	Matches: 10	Ras association domain-containing protein 4 OS=Mus musculus GN=Rasf4 PE=1 SV=1
40.	MSM_MOUSE	Mass: 41279	Score: 28	Expect: 8.1e+002	Matches: 11	Mb/SANT-like DNA-binding domain-containing protein 4 OS=Mus musculus GN=Msantd4 PE=2 SV=1
	MSM_RAT	Mass: 41265	Score: 28	Expect: 8.1e+002	Matches: 11	Mb/SANT-like DNA-binding domain-containing protein 4 OS=Rattus norvegicus GN=Msantd4 PE=1 SV=1
41.	EMCN_RAT	Mass: 26616	Score: 28	Expect: 8.1e+002	Matches: 8	Endomucin OS=Rattus norvegicus GN=Emcn PE=2 SV=1
42.	GOST_CLOBU	Mass: 41806	Score: 28	Expect: 8.3e+002	Matches: 13	Aminomethyltransferase OS=Clostridium botulinum (strain Kyoto / Type A2) GN=gcvT PE=3 SV=1
43.	CMC26_KULLA	Mass: 30726	Score: 28	Expect: 8.7e+002	Matches: 14	PremRNA-splicing factor CMC26 OS=Kluyveromyces fragilis (strain ATCC 9595 / CBS 2359 / DSM 70799 / NERC 1267 / NRRL Y-1140 / RM37) GN=CMC26 PE=3 SV=1
44.	RRP1_DICDI	Mass: 57004	Score: 28	Expect: 8.7e+002	Matches: 17	Ribosomal RNA processing protein 1 homolog OS=Dictyostelium discoideum GN=rrp1 PE=3 SV=1
45.	TEX30_MOUSE	Mass: 25595	Score: 28	Expect: 8.7e+002	Matches: 10	Testis-expressed sequence 30 protein OS=Mus musculus GN=Tex30 PE=1 SV=1

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.5 Da
 Fragment Mass Tolerance : ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default

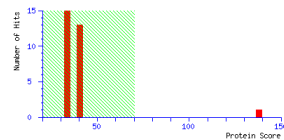
TF mass/mass+c

MASCOT Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 07:11:56 GMT
Top Score : 138 for **TRFE_BOVIN**, Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary Help
Significance threshold p: 0.05 Max. number of hits: 200
Preferred taxonomy: All entries

Re-Search All Search Unmatched

1.	TRFE_BOVIN	Mass: 79907	Score: 138	Expect: 8.7e-009	Matches: 15
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1					
2.	PGK_CORDI	Mass: 42755	Score: 42	Expect: 35	Matches: 7
Phosphoglycerate kinase OS=Corynebacterium diphtheriae (strain ATCC 700971 / NCTC 13129 / Biotype gravis) GN=pgk PE=3 SV=1					
3.	PURA_CLOBR	Mass: 47525	Score: 41	Expect: 40	Matches: 9
Adenylosuccinate synthetase OS=Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) GN=purA PE=3 SV=1					
4.	HPT_FERPA	Mass: 20256	Score: 40	Expect: 51	Matches: 8
Hypoxanthine/guanine phosphoribosyltransferase OS=Ferroplasma acidophilum (strain DSM 10642 / AED111200) GN=hpt PE=3 SV=1					
5.	HISF_BACDI	Mass: 27423	Score: 40	Expect: 55	Matches: 6
Imidazole glycerol phosphate synthase subunit HisF OS=Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NERC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46) GN=hisF PE=3 SV=1					
6.	MATK_DIOEL	Mass: 62416	Score: 40	Expect: 59	Matches: 11
Maturase K OS=Dioscorea elephantipes GN=matK PE=3 SV=1					
7.	IF2A_PYRAB	Mass: 31892	Score: 39	Expect: 63	Matches: 10
Translation initiation factor 2 subunit alpha OS=Pyrococcus abyssi (strain GE5 / Orsay) GN=if2a PE=1 SV=1					
8.	PSB2_THESJ	Mass: 22006	Score: 39	Expect: 73	Matches: 8
Proteasome subunit beta 2 OS=Thermococcus gammatolerans (strain DSM 15229 / JCM 11827 / EJJ) GN=psb2 PE=3 SV=1					
9.	ATP4_CANDJ	Mass: 26612	Score: 38	Expect: 81	Matches: 9
ATP synthase subunit 4, mitochondrial OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NERC 0622 / NRRL Y-65) GN=atp4 PE=3 SV=1					
10.	AF4_HUMAN	Mass: 127788	Score: 38	Expect: 81	Matches: 18
AF4/AFR2 family member 4 OS=Homo sapiens (strain AF4) PE=1 SV=1					
11.	TRNA_DDEBA	Mass: 30079	Score: 37	Expect: 1e+002	Matches: 5
tRNA pseudouridine synthase A OS=Deinvalvibrio bacteriovorus (strain ATCC 15356 / DSM 50701 / NCIB 9529 / HD100) GN=trnA PE=3 SV=1					
12.	NDK_PARP	Mass: 15273	Score: 37	Expect: 1e+002	Matches: 7
Nucleoside diphosphate kinase OS=Paracoccus denitrificans (strain Pd 1222) GN=ndk PE=3 SV=1					
13.	AURKB_DANRE	Mass: 37213	Score: 37	Expect: 1e+002	Matches: 8
Aurora kinase B OS=Danio rerio GN=aurkb PE=2 SV=1					
14.	PPYR_HMETU	Mass: 19470	Score: 37	Expect: 1.1e+002	Matches: 6
Inorganic pyrophosphatase OS=Haemophilus ducreyi (strain 35000HP / ATCC 700724) GN=ppa PE=3 SV=1					
15.	PUR9_CLOTE	Mass: 56689	Score: 37	Expect: 1.2e+002	Matches: 15
Bifunctional purine biosynthesis protein PurH OS=Clostridium tetani (strain Massachusetts / E88) GN=purH PE=3 SV=1					
16.	RUC1_BOVIN	Mass: 17555	Score: 36	Expect: 1.3e+002	Matches: 4
UT small nuclear ribonucleoprotein C OS=Bos taurus GN=SNRPC PE=2 SV=2					
16.	RUC1_CANLF	Mass: 17555	Score: 36	Expect: 1.3e+002	Matches: 4
UT small nuclear ribonucleoprotein C OS=Canis lupus familiaris GN=SNRPC PE=3 SV=1					
16.	RUC1_CHICK	Mass: 17557	Score: 36	Expect: 1.3e+002	Matches: 4
UT small nuclear ribonucleoprotein C OS=Gallus gallus GN=SNRPC PE=3 SV=1					
16.	RUC1_DANRE	Mass: 17448	Score: 36	Expect: 1.3e+002	Matches: 4
UT small nuclear ribonucleoprotein C OS=Danio rerio GN=snrpc PE=2 SV=1					
16.	RUC1_HUMAN	Mass: 17555	Score: 36	Expect: 1.3e+002	Matches: 4
UT small nuclear ribonucleoprotein C OS=Homo sapiens GN=SNRPC PE=1 SV=1					
16.	RUC1_MACMU	Mass: 17555	Score: 36	Expect: 1.3e+002	Matches: 4
UT small nuclear ribonucleoprotein C OS=Macaca mulatta GN=SNRPC PE=3 SV=1					
16.	RUC1_MOUSE	Mass: 17525	Score: 36	Expect: 1.3e+002	Matches: 4
UT small nuclear ribonucleoprotein C OS=Mus musculus GN=snrpc PE=1 SV=1					
16.	RUC1_RAT	Mass: 17525	Score: 36	Expect: 1.3e+002	Matches: 4
UT small nuclear ribonucleoprotein C OS=Rattus norvegicus GN=snrpc PE=3 SV=1					
16.	RUC1_XENLA	Mass: 17534	Score: 36	Expect: 1.3e+002	Matches: 4
UT small nuclear ribonucleoprotein C OS=Xenopus laevis GN=snrpc PE=2 SV=1					
16.	RUC1_XENTR	Mass: 17552	Score: 36	Expect: 1.3e+002	Matches: 4
UT small nuclear ribonucleoprotein C OS=Xenopus tropicalis GN=snrpc PE=2 SV=1					
17.	RR19_MALZE	Mass: 10750	Score: 36	Expect: 1.4e+002	Matches: 9
30S ribosomal protein S19, chloroplastic OS=Zea mays GN=rrs19-A PE=3 SV=4					
17.	RR19_SACHY	Mass: 10750	Score: 36	Expect: 1.4e+002	Matches: 9
30S ribosomal protein S19, chloroplastic OS=Saccharum hybrid GN=rrs19-A PE=3 SV=1					
17.	RR19_SACOF	Mass: 10750	Score: 36	Expect: 1.4e+002	Matches: 9
30S ribosomal protein S19, chloroplastic OS=Saccharum officinarum GN=rrs19 PE=3 SV=1					
17.	RR19_SORBI	Mass: 10750	Score: 36	Expect: 1.4e+002	Matches: 9
30S ribosomal protein S19, chloroplastic OS=Sorghum bicolor GN=rrs19 PE=3 SV=1					
18.	RL27_PEPOR	Mass: 10421	Score: 36	Expect: 1.4e+002	Matches: 5
50S ribosomal protein L27 OS=Peptoclostridium difficile (strain 630) GN=rplA PE=3 SV=1					
19.	EFG_BACCE	Mass: 1332	Score: 35	Expect: 1.6e+002	Matches: 3
Elongation factor G (Fragment) OS=Bacillus cereus GN=fusA PE=1 SV=2					
20.	ATPF_RALPJ	Mass: 17223	Score: 35	Expect: 1.7e+002	Matches: 6

20.	ATPF_RALPJ	Mass: 17223	Score: 35	Expect: 1.7e+002	Matches: 6
ATP synthase subunit b OS=Raistonia pickettii (strain 12J) GN=atpF PE=3 SV=1					
21.	Y010_OSHMF	Mass: 39543	Score: 35	Expect: 1.9e+002	Matches: 8
Uncharacterized protein ORF10 OS=Ostreid herpesvirus 1 (isolate France) GN=ORF10 PE=4 SV=1					
22.	RS18_CLOB1	Mass: 9513	Score: 35	Expect: 1.9e+002	Matches: 6
30S ribosomal protein S18 OS=Clostridium botulinum (strain ATCC 13037 / Type A) GN=rpsR PE=3 SV=1					
	RS18_CLOB6	Mass: 9513	Score: 35	Expect: 1.9e+002	Matches: 6
30S ribosomal protein S18 OS=Clostridium botulinum (strain 857 / Type Ba4) GN=rpsR PE=3 SV=1					
	RS18_CLOBH	Mass: 9513	Score: 35	Expect: 1.9e+002	Matches: 6
30S ribosomal protein S18 OS=Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A) GN=rpsR PE=3 SV=1					
	RS18_CLOBJ	Mass: 9513	Score: 35	Expect: 1.9e+002	Matches: 6
30S ribosomal protein S18 OS=Clostridium botulinum (strain Kyoto / Type A2) GN=rpsR PE=3 SV=1					
	RS18_CLOBK	Mass: 9513	Score: 35	Expect: 1.9e+002	Matches: 6
30S ribosomal protein S18 OS=Clostridium botulinum (strain Ukra / Type B1) GN=rpsR PE=3 SV=1					
	RS18_CLOBL	Mass: 9513	Score: 35	Expect: 1.9e+002	Matches: 6
30S ribosomal protein S18 OS=Clostridium botulinum (strain Langeland / NCTC 10281 / Type F) GN=rpsR PE=3 SV=1					
	RS18_CLOBM	Mass: 9513	Score: 35	Expect: 1.9e+002	Matches: 6
30S ribosomal protein S18 OS=Clostridium botulinum (strain Loch Maree / Type A3) GN=rpsR PE=3 SV=1					
23.	Y570_MYQSA	Mass: 8303	Score: 34	Expect: 2e+002	Matches: 3
UPF0154 protein MYQ5700 OS=Mycoplasma gallisepticum (strain R(low / passage 15 / clone 2)) GN=MYQ5700 PE=3 SV=1					
24.	RS20_MDOTA	Mass: 11763	Score: 34	Expect: 2e+002	Matches: 6
30S ribosomal protein S20 OS=Morella thermoacetica (strain ATCC 39073) GN=rpsT PE=3 SV=1					
25.	RL9_BUCAS	Mass: 18648	Score: 34	Expect: 2e+002	Matches: 8
50S ribosomal protein L9 OS=Buchnera aphidicola subsp. Acyrthosiphon pisum (strain 5A) GN=rplI PE=3 SV=1					
	RL9_BUCAL	Mass: 18648	Score: 34	Expect: 2e+002	Matches: 8
50S ribosomal protein L9 OS=Buchnera aphidicola subsp. Acyrthosiphon pisum (strain APS) GN=rplI PE=3 SV=1					
	RL9_BUCAT	Mass: 18648	Score: 34	Expect: 2e+002	Matches: 8
50S ribosomal protein L9 OS=Buchnera aphidicola subsp. Acyrthosiphon pisum (strain Tuc7) GN=rplI PE=3 SV=1					
26.	PRO0_HMETU	Mass: 20342	Score: 34	Expect: 2.1e+002	Matches: 7
RNA chaperone Pro0 OS=Haemophilus ducreyi (strain 35000HP / ATCC 700724) GN=pro0 PE=3 SV=1					
27.	R27A2_ARATH	Mass: 16340	Score: 34	Expect: 2.4e+002	Matches: 4
60S ribosomal protein L27a-2 OS=Arabidopsis thaliana GN=RPL27AB PE=2 SV=1					
	R27A3_ARATH	Mass: 16503	Score: 34	Expect: 2.4e+002	Matches: 4
60S ribosomal protein L27a-3 OS=Arabidopsis thaliana GN=RPL27AC PE=2 SV=2					
28.	HIS6_GEOSW	Mass: 27361	Score: 34	Expect: 2.4e+002	Matches: 5
Imidazole glycerol phosphate synthase subunit HisF OS=Geobacillus sp. (strain WCH70) GN=hisF PE=3 SV=1					
29.	BTS_ARATH	Mass: 43098	Score: 34	Expect: 2.5e+002	Matches: 7
BTS/POZ and TAZ domain-containing protein 5 OS=Arabidopsis thaliana GN=BTS PE=1 SV=1					

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.5 Da
 Fragment Mass Tolerance : ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Query1 (825.8694,1+): <no title>
 Query2 (829.7115,1+): <no title>
 : seq(C-6)
 Query3 (832.5867,1+): <no title>
 Query4 (837.5821,1+): <no title>
 : seq(C-6)
 Query5 (846.6149,1+): <no title>
 Query6 (849.5739,1+): <no title>
 Query7 (851.8666,1+): <no title>
 Query8 (852.8093,1+): <no title>
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 Query9 (852.8093,1+): <no title>
 : seq(C-1)
 Query10 (857.6361,1+): <no title>
 Query11 (857.6544,1+): <no title>
 Query12 (861.2213,1+): <no title>
 Query13 (861.2609,1+): <no title>
 Query14 (861.2654,1+): <no title>
 Query15 (869.6453,1+): <no title>
 Query16 (877.2189,1+): <no title>
 Query17 (887.6663,1+): <no title>
 : seq(C-6)

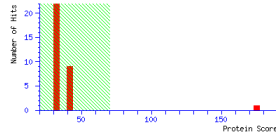
TF mass+c

MASCOT Search Results

User : Y. Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 07:12:05 GMT
Top Score : 175 for **TRFE_BOVIN**, Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary [Help](#)
Significance threshold p: 0.05 Max. number of hits: 200
Preferred taxonomy: All entries

Re-Search All Search Unmatched

1.	TRFE_BOVIN	Mass: 79907	Score: 175	Expect: 1.7e-012	Matches: 11
Serotransferrin OS=Bos taurus GN=TF PE=2 SV=1					
2.	EFG_BACCE	Mass: 1332	Score: 45	Expect: 18	Matches: 3
Elongation factor G (Fragment) OS=Bacillus cereus GN=fusA PE=1 SV=2					
2.	EFG_BACCE	Mass: 1332	Score: 45	Expect: 18	Matches: 3
Elongation factor G (Fragment) OS=Bacillus cereus GN=fusA PE=1 SV=2					
3.	MURD_LACGA	Mass: 51710	Score: 41	Expect: 47	Matches: 3
UDP-N-acetylmuramoylalanine-D-glutamate ligase OS=Lactobacillus casei (strain ATCC 33923 / DSM 20243 / JCM 1131 / NCIMB 11718 / AM63) GN=murD PE=3 SV=1					
4.	RUIC_BOVIN	Mass: 17555	Score: 39	Expect: 66	Matches: 2
UI small nuclear ribonucleoprotein C OS=Bos taurus GN=SNRPC PE=2 SV=2					
RUIC_CANLE Mass: 17555 Score: 39 Expect: 66 Matches: 2					
UI small nuclear ribonucleoprotein C OS=Canis lupus familiaris GN=SNRPC PE=3 SV=1					
RUIC_CHICK Mass: 17557 Score: 39 Expect: 66 Matches: 2					
UI small nuclear ribonucleoprotein C OS=Gallus gallus GN=SNRPC PE=3 SV=1					
RUIC_DANRE Mass: 17448 Score: 39 Expect: 66 Matches: 2					
UI small nuclear ribonucleoprotein C OS=Danio rerio GN=snrpc PE=2 SV=1					
RUIC_HUMAN Mass: 17555 Score: 39 Expect: 66 Matches: 2					
UI small nuclear ribonucleoprotein C OS=Homo sapiens GN=SNRPC PE=1 SV=1					
RUIC_MACMU Mass: 17555 Score: 39 Expect: 66 Matches: 2					
UI small nuclear ribonucleoprotein C OS=Macaca mulatta GN=SNRPC PE=3 SV=1					
RUIC_MOUSE Mass: 17525 Score: 39 Expect: 66 Matches: 2					
UI small nuclear ribonucleoprotein C OS=Mus musculus GN=snrpc PE=1 SV=1					
RUIC_RAT Mass: 17525 Score: 39 Expect: 66 Matches: 2					
UI small nuclear ribonucleoprotein C OS=Rattus norvegicus GN=snrpc PE=3 SV=1					
RUIC_XENLA Mass: 17534 Score: 39 Expect: 66 Matches: 2					
UI small nuclear ribonucleoprotein C OS=Xenopus laevis GN=snrpc PE=2 SV=1					
RUIC_XENTR Mass: 17552 Score: 39 Expect: 66 Matches: 2					
UI small nuclear ribonucleoprotein C OS=Xenopus tropicalis GN=snrpc PE=2 SV=1					
5.	Y570_MYOGA	Mass: 8303	Score: 39	Expect: 69	Matches: 2
UPF0154 protein MYOGA5700 OS=Mycoplasma gallisepticum (strain R(low / passage 15 / clone 2)) GN=MYOGA5700 PE=3 SV=1					
6.	TRUA_FDEBA	Mass: 30079	Score: 38	Expect: 78	Matches: 2
tRNA pseudouridine synthase A OS=Belleville bacteriophage (strain ATCC 15356 / DSM 50701 / NCIB 9529 / HD100) GN=trnA PE=3 SV=1					
7.	RSS_NEIGI	Mass: 14371	Score: 38	Expect: 91	Matches: 2
30S ribosomal protein S9 OS=Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090) GN=rpsI PE=3 SV=1					
RSS_NEIGQ Mass: 14371 Score: 38 Expect: 91 Matches: 2					
30S ribosomal protein S9 OS=Neisseria gonorrhoeae (strain NCCP11945) GN=rpsI PE=3 SV=1					
RSS_NEIMI Mass: 14417 Score: 38 Expect: 91 Matches: 2					
30S ribosomal protein S9 OS=Neisseria meningitidis serogroup C (strain 053442) GN=rpsI PE=3 SV=1					
RSS_NEIMA Mass: 14417 Score: 38 Expect: 91 Matches: 2					
30S ribosomal protein S9 OS=Neisseria meningitidis serogroup C (strain 053442) GN=rpsI PE=3 SV=1					
RSS_NEIME Mass: 14417 Score: 38 Expect: 91 Matches: 2					
30S ribosomal protein S9 OS=Neisseria meningitidis serogroup A / serotype 4A (strain Z2491) GN=rpsI PE=3 SV=1					
RSS_NEIME Mass: 14417 Score: 38 Expect: 91 Matches: 2					
30S ribosomal protein S9 OS=Neisseria meningitidis serogroup B (strain M058) GN=rpsI PE=3 SV=1					
RSS_NEIME Mass: 14417 Score: 38 Expect: 91 Matches: 2					
30S ribosomal protein S9 OS=Neisseria meningitidis serogroup C / serotype 2a (strain ATCC 700532 / DSM 15464 / FAM18) GN=rpsI PE=3 SV=1					
RSS_CHRYO Mass: 14357 Score: 36 Expect: 1.2e+002 Matches: 2					
30S ribosomal protein S9 OS=Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) GN=rpsI PE=3 SV=1					
8.	MRAZ_MARMS	Mass: 17461	Score: 38	Expect: 96	Matches: 2
Transcriptional regulator MraZ OS=Marinomonas sp. (strain MMYL1) GN=mraZ PE=3 SV=1					
9.	RSS_MOOTA	Mass: 11783	Score: 37	Expect: 1e+002	Matches: 2
30S ribosomal protein S20 OS=Morella thermoacetica (strain ATCC 39073) GN=rpsT PE=3 SV=1					
10.	TFPI_TREPA	Mass: 19485	Score: 37	Expect: 1e+002	Matches: 2
Antigen TpF1 OS=Treponema pallidum (strain Nichols) GN=tfp1 PE=1 SV=2					
TFPI_TREPE Mass: 19493 Score: 37 Expect: 1e+002 Matches: 2					
Antigen TpF1 OS=Treponema pallidum subsp. pertenue PE=3 SV=2					
11.	YOGF_SHEON	Mass: 15475	Score: 36	Expect: 1.4e+002	Matches: 2
Putative pre-16S rRNA nuclease OS=Shewanella oneidensis (strain MR-1) GN=SO_3347 PE=3 SV=1					
12.	R27A2_ARATH	Mass: 16340	Score: 36	Expect: 1.4e+002	Matches: 2
60S ribosomal protein L27a-2 OS=Arabidopsis thaliana GN=RPL27AB PE=2 SV=1					
R27A3_ARATH Mass: 16503 Score: 36 Expect: 1.4e+002 Matches: 2					
60S ribosomal protein L27a-3 OS=Arabidopsis thaliana GN=RPL27AC PE=2 SV=2					
13.	R5MA_MANSM	Mass: 33164	Score: 36	Expect: 1.5e+002	Matches: 2
Ribosomal RNA small subunit methyltransferase A OS=Mannheimia succiniciproducens (strain MBEL55E) GN=rsmA PE=3 SV=1					
14.	RSS_PSYME	Mass: 17279	Score: 35	Expect: 1.6e+002	Matches: 2
30S ribosomal protein S5 OS=Psychrobacter sp. (strain PFW-1) GN=rpsE PE=3 SV=1					
15.	T5AD_HAEIU	Mass: 37901	Score: 35	Expect: 1.7e+002	Matches: 2
tRNA N6-adenosine threonylcarbamoyltransferase OS=Haemophilus ducreyi (strain 35000HP / ATCC 700724) GN=tsaD PE=3 SV=1					
16.	MED26_XENLA	Mass: 66196	Score: 35	Expect: 1.8e+002	Matches: 2
Mediator of RNA polymerase II transcription subunit 26 OS=Xenopus laevis GN=med26 PE=2 SV=1					

Search Parameters

126

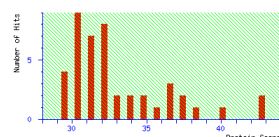
CYC mass

MASCOT Search Results

User : Y Wang
Email : kahnz0003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 05:21:29 GMT
Top Score : 43 for [HLP_RICCN](#), Histone-like DNA-binding protein OS=Rickettsia conorii (strain ATCC VR-613 / Malish 7) GN=RC1088 PE=3 SV=1

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: [Concise Protein Summary](#) [Help](#)
Significance threshold $p < 0.05$ Max. number of hits 200
Preferred taxonomy All entries

[Re-Search All](#) [Search Unmatched](#)

1.	HLP_RICCN	Mass: 10732	Score: 43	Expect: 30	Matches: 9	Histone-like DNA-binding protein OS=Rickettsia conorii (strain ATCC VR-613 / Malish 7) GN=RC1088 PE=3 SV=1
2.	CYC_HORSE	Mass: 11941	Score: 42	Expect: 31	Matches: 10	Cytochrome c OS=Equus caballus GN=CYC5 PE=1 SV=2
2.	CYC_HORSE	Mass: 11941	Score: 42	Expect: 31	Matches: 10	Cytochrome c OS=Equus caballus GN=CYC5 PE=1 SV=2
3.	RR4_CUSEP	Mass: 23499	Score: 40	Expect: 58	Matches: 8	Plastid 30S ribosomal protein S4 OS=Daucus reflexa GN=rrs4 PE=3 SV=1
4.	KATG_KORVE	Mass: 83080	Score: 38	Expect: 85	Matches: 12	Catalase-peroxidase OS=Koribacter versatilis (strain E11n345) GN=katG PE=3 SV=1
5.	ARPP_YARLI	Mass: 44375	Score: 38	Expect: 94	Matches: 10	Actin-like protein ARPP OS=Yarrowia lipolytica (strain CLIB 122 / E 150) GN=ARPP6 PE=3 SV=1
6.	RR4_CUSEX	Mass: 23490	Score: 37	Expect: 1e+002	Matches: 7	Plastid 30S ribosomal protein S4 OS=Daucus exaltata GN=rrs4 PE=3 SV=1
7.	SSB_BPHZ2	Mass: 13335	Score: 37	Expect: 1.1e+002	Matches: 7	Single-strand-binding protein OS=Bacillus phage phi29 GN=5 PE=1 SV=1
	SSB_BPHZ2	Mass: 13322	Score: 37	Expect: 1.1e+002	Matches: 7	Single-strand-binding protein OS=Bacillus phage P2A GN=5 PE=3 SV=1
8.	HLP_RICRI	Mass: 10713	Score: 36	Expect: 1.3e+002	Matches: 8	Histone-like DNA-binding protein OS=Rickettsia rickettsii PE=3 SV=1
9.	RL23_STREA	Mass: 10861	Score: 36	Expect: 1.3e+002	Matches: 8	50S ribosomal protein L23 OS=Streptococcus equi subsp. equi (strain 4047) GN=rlpW PE=3 SV=1
10.	RS9_RHOP2	Mass: 17423	Score: 35	Expect: 1.6e+002	Matches: 8	30S ribosomal protein S9 OS=Rhodospirillum rubrum (strain Ha2) GN=rs9 PE=3 SV=1
11.	MSCL_PROMH	Mass: 14918	Score: 35	Expect: 1.7e+002	Matches: 5	Large-conductance mechanosensitive channel OS=Proteus mirabilis (strain HI4320) GN=mscL PE=3 SV=1
12.	ORF14_SPVVC	Mass: 4266	Score: 35	Expect: 1.8e+002	Matches: 6	Uncharacterized protein ORF14 OS=Spirillum volutans SV=1 GN=ORF14 PE=4 SV=1
13.	RL28_PSEFS	Mass: 8903	Score: 34	Expect: 2.2e+002	Matches: 6	50S ribosomal protein L28 OS=Pseudomonas fluorescens (strain DSM25) GN=rlpB PE=3 SV=1
14.	YAT_CAMVP	Mass: 17833	Score: 34	Expect: 2.4e+002	Matches: 10	Aphid transmission protein OS=Cauliflower mosaic virus (strain PV147) GN=ORF II PE=3 SV=1
14.	YAT_CAMVP	Mass: 17833	Score: 34	Expect: 2.4e+002	Matches: 10	Aphid transmission protein OS=Cauliflower mosaic virus (strain PV147) GN=ORF II PE=3 SV=1
15.	ORP7_ASPCL	Mass: 83800	Score: 33	Expect: 2.5e+002	Matches: 12	ATP-dependent RNA helicase dhp7 OS=Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) GN=dhp7 PE=3 SV=1
16.	RL18_PSEMY	Mass: 12637	Score: 33	Expect: 2.8e+002	Matches: 6	50S ribosomal protein L18 OS=Pseudomonas mendocina (strain ynp) GN=rlpR PE=3 SV=1
17.	CYC_EQUAS	Mass: 11927	Score: 32	Expect: 3.1e+002	Matches: 9	Cytochrome c OS=Equus asinus GN=CYC5 PE=1 SV=2
	CYC_EQUBU	Mass: 11927	Score: 32	Expect: 3.1e+002	Matches: 9	Cytochrome c OS=Equus burchellii GN=CYC5 PE=1 SV=2
18.	DnaK_RENSM	Mass: 68526	Score: 32	Expect: 3.1e+002	Matches: 11	Chaperone protein DnaK OS=Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NERC 15589 / NCIMB 2235) GN=dnaK PE=3 SV=1
19.	PYRH_PELCD	Mass: 25884	Score: 32	Expect: 3.1e+002	Matches: 7	Uridylate kinase OS=Pelobacter carbinolicus (strain DSM 2380 / Gra Bd 1) GN=pyrH PE=3 SV=1
20.	ATPA_BUMMI	Mass: 55394	Score: 32	Expect: 3.2e+002	Matches: 9	ATP synthase subunit alpha, chloroplastic OS=Brassica microphylla GN=atpA PE=3 SV=1
21.	RR4_LACSA	Mass: 23324	Score: 32	Expect: 3.2e+002	Matches: 7	30S ribosomal protein S4, chloroplastic OS=Lactuca sativa GN=rrs4 PE=3 SV=1
	RR4_HELAN	Mass: 23284	Score: 32	Expect: 3.3e+002	Matches: 7	30S ribosomal protein S4, chloroplastic OS=Helianthus annuus GN=rrs4 PE=3 SV=1
22.	ICE2_DROME	Mass: 79889	Score: 32	Expect: 3.4e+002	Matches: 10	Little elongation complex subunit 2 OS=Drosophila melanogaster GN=ice2 PE=1 SV=1
23.	RR4_DAUCA	Mass: 23398	Score: 32	Expect: 3.4e+002	Matches: 8	30S ribosomal protein S4, chloroplastic OS=Daucus carota GN=rrs4 PE=3 SV=1
24.	EFIS_GEOLS	Mass: 33619	Score: 32	Expect: 3.6e+002	Matches: 10	Elongation factor Ts OS=Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ) GN=tsf PE=3 SV=1
25.	MIAA_CALBD	Mass: 36265	Score: 32	Expect: 3.9e+002	Matches: 10	tRNA dimethylallyltransferase OS=Caldicellulosigranulatus (strain ATCC BAA-1888 / DSM 6725 / Z-1320) GN=miaA PE=3 SV=1
26.	UBIG_HHEPS	Mass: 27310	Score: 32	Expect: 3.9e+002	Matches: 7	Ubiquitin-conjugating enzyme E2 OS=Heliobacterium salinarum (strain ATCC 35061 / DSM 9790) GN=ubiG PE=3 SV=1

26.	UBIG_HKEPS	Mass: 27310	Score: 32	Expect: 3.9e+002	Matches: 7
Ubiquinone biosynthesis O-methyltransferase OS=Haemophilus parasuis serovar 5 (strain SH0185) GN=ubiG PE=3 SV=1					
27.	RS17_CHLPN	Mass: 9883	Score: 31	Expect: 4e+002	Matches: 9
30S ribosomal protein S17 OS=Chlamydia pneumoniae GN=rpsJ PE=3 SV=1					
28.	R64_OFOMI	Mass: 23729	Score: 31	Expect: 4e+002	Matches: 8
Plastid 30S ribosomal protein S4 OS=Oronanche minor GN=rps4 PE=3 SV=1					
29.	TMB_WOLPM	Mass: 26351	Score: 31	Expect: 4.1e+002	Matches: 8
tRNA (guanine-N(7)-)-methyltransferase OS=Molbachia pipientis vMel GN=trnB PE=3 SV=1					
30.	RL14_STRMU	Mass: 13013	Score: 31	Expect: 4.2e+002	Matches: 8
50S ribosomal protein L14 OS=Streptococcus mutans serotype c (strain ATCC 700610 / UA159) GN=rp14 PE=3 SV=1					
31.	RL28_HAHCH	Mass: 8972	Score: 31	Expect: 4.3e+002	Matches: 7
50S ribosomal protein L28 OS=Halella chejuensis (strain KCTC 2396) GN=rplB PE=3 SV=1					
32.	YAPC4_PYRHO	Mass: 17179	Score: 31	Expect: 4.6e+002	Matches: 7
Ribonuclease VapC4 OS=Pyrococcus horikoshii (strain ATCC 700860 / DSM 12428 / JCM 9974 / NBRC 100139 / OT-3) GN=vapC4 PE=1 SV=1					
33.	EFP_SODGM	Mass: 20693	Score: 31	Expect: 4.8e+002	Matches: 6
Elongation factor P OS=Sodalis glossinidius (strain morsitans) GN=efp PE=3 SV=1					
34.	Y921_STAHI	Mass: 19235	Score: 31	Expect: 4.8e+002	Matches: 6
UFP0840 protein SH0921 OS=Staphylococcus haemolyticus (strain JCS1435) GN=SH0921 PE=3 SV=1					
35.	Y2358_BACLD	Mass: 11830	Score: 30	Expect: 4.9e+002	Matches: 6
Nucleoid-associated protein BLI00029/BL02358 OS=Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46) GN=BLI00029 PE=3 SV=1					
36.	FLIJ_SALTI	Mass: 17369	Score: 30	Expect: 4.9e+002	Matches: 5
Flagellar FljJ protein OS=Salmonella typhi GN=fljJ PE=3 SV=1					
	FLIJ_SALTY	Mass: 17369	Score: 30	Expect: 4.9e+002	Matches: 5
Flagellar FljJ protein OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=fljJ PE=1 SV=1					
37.	C06A5_HUMAN	Mass: 291832	Score: 30	Expect: 5e+002	Matches: 23
Collagen alpha-5(VI) chain OS=Homo sapiens GN=C06A5 PE=1 SV=1					
38.	LYS4_NEURC	Mass: 94375	Score: 30	Expect: 5.3e+002	Matches: 11
Homocitrate, mitochondrial OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) GN=lys-4 PE=3 SV=1					
39.	LYS4_NEURP	Mass: 94375	Score: 30	Expect: 5.3e+002	Matches: 11
Homocitrate, mitochondrial OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) GN=lys-4 PE=3 SV=1					
39.	ATPA_RHIL0	Mass: 55038	Score: 30	Expect: 5.4e+002	Matches: 8
ATP synthase subunit alpha OS=Rhizobium loti (strain MAFF303099) GN=atpA PE=3 SV=1					
40.	JSPF_CLOAB	Mass: 31458	Score: 30	Expect: 5.5e+002	Matches: 10
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / WM B-1787) GN=ispE PE=3 SV=1					
41.	R59_RHIL2	Mass: 16680	Score: 30	Expect: 5.6e+002	Matches: 6
30S ribosomal protein S9 OS=Rhizobium leguminosarum bv. viciae (strain 3841) GN=rpsI PE=3 SV=1					
42.	RL34_UREP2	Mass: 5701	Score: 30	Expect: 5.9e+002	Matches: 7
50S ribosomal protein L34 OS=Ureaplasma parvum serovar 3 (strain ATCC 27815 / 27 / NCTC 11736) GN=rplH PE=3 SV=1					
	RL34_UREPA	Mass: 5701	Score: 30	Expect: 5.9e+002	Matches: 7
50S ribosomal protein L34 OS=Ureaplasma parvum serovar 3 (strain ATCC 700970) GN=rplH PE=3 SV=1					
43.	RL28_SHEHH	Mass: 9224	Score: 30	Expect: 5.9e+002	Matches: 6
50S ribosomal protein L28 OS=Shewanella halifaxensis (strain HAM-EB4) GN=rplB PE=3 SV=1					
	RL28_SHEPA	Mass: 9240	Score: 30	Expect: 5.9e+002	Matches: 6
50S ribosomal protein L28 OS=Shewanella pealeana (strain ATCC 700345 / ANG-S01) GN=rplB PE=3 SV=1					
44.	RL28_PSEP1	Mass: 8975	Score: 30	Expect: 6.2e+002	Matches: 7
50S ribosomal protein L28 OS=Pseudomonas putida (strain F1 / ATCC 700007) GN=rplB PE=3 SV=1					

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance: \pm 0.5 Da
 Fragment Mass Tolerance: \pm 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Query1 (820.9055,1+): <no title>
 Query2 (828.7350,1+): <no title>
 Query3 (828.8386,1+): <no title>
 Query4 (832.8204,1+): <no title>
 Query5 (856.7492,1+): <no title>
 Query6 (859.9046,1+): <no title>

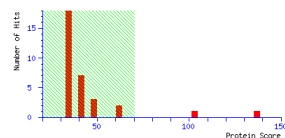
CYC mass/mass+c

MASCOT Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 07:29:14 GMT
Top Score : 137 for [CYC_HORSE](#), Cytochrome c OS=Equus caballus GN=CYCS PE=1 SV=2

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary [Help](#)
Significance threshold $p < 0.05$ Max. number of hits 200
Preferred taxonomy All entries

[Re-Search All](#) [Search Unmatched](#)

1.	CYC_HORSE	Mass: 11941	Score: 137	Expect: 1.1e-008	Matches: 10
	Cytochrome c OS=Equus caballus GN=CYCS PE=1 SV=2				
	CYC_MACG1	Mass: 11743	Score: 61	Expect: 0.41	Matches: 5
	Cytochrome c OS=Macropus eiaanteus GN=CYCS PE=1 SV=2				
	CYC_MACG1	Mass: 11743	Score: 61	Expect: 0.41	Matches: 5
	Cytochrome c OS=Macropus eiaanteus GN=CYCS PE=1 SV=2				
	CYC_HIPAM	Mass: 11770	Score: 40	Expect: 50	Matches: 4
	Cytochrome c OS=Hippopotamus amphibius GN=CYCS PE=1 SV=2				
	CYC_CAMEP	Mass: 11756	Score: 40	Expect: 55	Matches: 4
	Cytochrome c OS=Camelus dromedarius GN=CYCS PE=1 SV=2				
	CYC_ESORD	Mass: 11756	Score: 40	Expect: 55	Matches: 4
	Cytochrome c OS=Eschrichtius robustus GN=CYCS PE=1 SV=2				
	CYC_LAMGU	Mass: 11756	Score: 40	Expect: 55	Matches: 4
	Cytochrome c OS=Lama guanicoe GN=CYCS PE=1 SV=2				
	CYC_MOUSE	Mass: 11714	Score: 40	Expect: 55	Matches: 4
	Cytochrome c, somatic OS=Mus musculus GN=Cycs PE=1 SV=2				
	CYC_RAT	Mass: 11714	Score: 40	Expect: 55	Matches: 4
	Cytochrome c, somatic OS=Rattus norvegicus GN=Cycs PE=1 SV=2				
	CYC_TARBA	Mass: 11728	Score: 40	Expect: 55	Matches: 4
	Cytochrome c OS=Tarsius bancanus GN=CYCS PE=3 SV=3				
2.	CYC_EQUAS	Mass: 11927	Score: 100	Expect: 5.8e-005	Matches: 9
	Cytochrome c OS=Equus asinus GN=CYCS PE=1 SV=2				
	CYC_EQUBU	Mass: 11927	Score: 100	Expect: 5.8e-005	Matches: 9
	Cytochrome c OS=Equus burchelli GN=CYCS PE=1 SV=2				
	CYC_MIRLE	Mass: 11726	Score: 45	Expect: 17	Matches: 5
	Cytochrome c OS=Microtus lewisii GN=CYCS PE=1 SV=2				
	CYC_CANLE	Mass: 11741	Score: 45	Expect: 19	Matches: 5
	Cytochrome c OS=Canis lupus familiaris GN=CYCS PE=1 SV=2				
	CYC_MINSC	Mass: 11683	Score: 45	Expect: 19	Matches: 5
	Cytochrome c OS=Miniopterus schreibersii GN=CYCS PE=1 SV=2				
3.	CYC2_BOVIN	Mass: 11848	Score: 62	Expect: 0.35	Matches: 5
	Cytochrome c 2 OS=Bos taurus GN=CYCT PE=3 SV=3				
4.	CYC_ALLMI	Mass: 11733	Score: 62	Expect: 0.38	Matches: 5
	Cytochrome c OS>Alligator mississippiensis PE=1 SV=2				
5.	CYC_BOVIN	Mass: 11812	Score: 48	Expect: 8	Matches: 6
	Cytochrome c OS=Bos taurus GN=CYCS PE=1 SV=2				
	CYC_PIG	Mass: 11812	Score: 48	Expect: 8	Matches: 6
	Cytochrome c OS=Sus scrofa GN=CYCS PE=1 SV=2				
	CYC_SHEEP	Mass: 11812	Score: 48	Expect: 8	Matches: 6
	Cytochrome c OS>Ovis aries GN=CYCS PE=1 SV=2				
	Cytochrome c OS=Ovis aries GN=CYCS PE=1 SV=2				
6.	RL5_BORAI	Mass: 20185	Score: 46	Expect: 16	Matches: 7
	50S ribosomal protein L5 OS=Bordetella avium (strain 187N) GN=rpIE PE=3 SV=1				
7.	BAF_BOVIN	Mass: 10284	Score: 44	Expect: 20	Matches: 3
	Barrier-to-autointegration factor OS=Bos taurus GN=BANF1 PE=3 SV=1				
	BAF_HUMAN	Mass: 10284	Score: 44	Expect: 20	Matches: 3
	Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1 SV=1				
	BAF_PONAB	Mass: 10284	Score: 44	Expect: 20	Matches: 3
	Barrier-to-autointegration factor OS=Pongo abelii GN=BANF1 PE=3 SV=1				
8.	CYC_RABIT	Mass: 11800	Score: 43	Expect: 29	Matches: 5
	Cytochrome c OS=Oryctolagus cuniculus GN=CYCS PE=1 SV=2				
9.	Y989_METJA	Mass: 12743	Score: 41	Expect: 45	Matches: 4
	Uncharacterized protein MJ0989 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NERC 100440) GN=MJ0989 PE=4 SV=1				
10.	RL5_BORER	Mass: 20261	Score: 40	Expect: 51	Matches: 6
	50S ribosomal protein L5 OS=Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) GN=rpIE PE=3 SV=1				
	RL5_BORPA	Mass: 20261	Score: 40	Expect: 51	Matches: 6
	50S ribosomal protein L5 OS=Bordetella parapertussis (strain 12822 / ATCC BAA-587 / NCTC 13253) GN=rpIE PE=3 SV=1				
	RL5_BORPE	Mass: 20261	Score: 40	Expect: 51	Matches: 6
	50S ribosomal protein L5 OS=Bordetella pertussis (strain Tohama 1 / ATCC BAA-589 / NCTC 13251) GN=rpIE PE=3 SV=1				
11.	RL5_RHOFT	Mass: 20185	Score: 39	Expect: 69	Matches: 4
	50S ribosomal protein L5 OS=Rhodospirillum rubrum (strain ATCC BAA-621 / DSM 15236 / T118) GN=rpIE PE=3 SV=1				
12.	ATPA_RUONI	Mass: 55394	Score: 39	Expect: 74	Matches: 8
	ATP synthase subunit alpha, chloroplastic OS=Brassica microphylla GN=atpA PE=3 SV=1				
13.	HIS5_LIS96	Mass: 23241	Score: 38	Expect: 78	Matches: 5
	Imidazole glycerol phosphate synthase subunit HisH OS=Listeria welshimeri serovar 6b (strain ATCC 35897 / DSM 20650 / SLO05334) GN=HisH PE=3 SV=1				
14.	MURA_THEYD	Mass: 45440	Score: 38	Expect: 83	Matches: 8
	UDP-N-acetylglucosamine 1-carboxyvinyltransferase OS=Thermodesulfobrevibacterium yellowstonii (strain ATCC 51303 / DSM 11347 / YP87) GN=murA PE=3 SV=1				
15.	RL5_POLSJ	Mass: 20219	Score: 38	Expect: 96	Matches: 4
	50S ribosomal protein L5 OS=Polaronomonas sp. (strain JS668 / ATCC BAA-500) GN=rpIE PE=3 SV=1				
16.	RLM1_STIIF	Mass: 51977	Score: 37	Expect: 1.1e+002	Matches: 6

Search Parameters

130

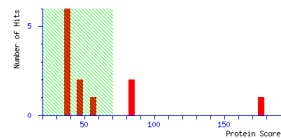
CYC mass+c

MASCOT Search Results

User : Y Wang
Email : kahz20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 07:29:21 GMT
Top Score : 176 for [CYC_HORSE](#), Cytochrome c OS=Equus caballus GN=CYCS PE=1 SV=2

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary [Help](#)
Significance threshold p: 0.05 Max. number of hits: 200
Preferred taxonomy: All entries

Re-Search All Search Unmatched

1.	CYC_HORSE	Mass: 11941	Score: 176	Expect: 1.4e-012	Matches: 8
	Cytochrome c OS=Equus caballus GN=CYCS PE=1 SV=2				
	CYC_EQUUS	Mass: 11927	Score: 118	Expect: 8.7e-007	Matches: 6
	Cytochrome c OS=Equus asinus GN=CYCS PE=1 SV=2				
	CYC_EQUUS	Mass: 11927	Score: 118	Expect: 8.7e-007	Matches: 6
	Cytochrome c OS=Equus asinus GN=CYCS PE=1 SV=2				
	CYC_EQUUS	Mass: 11927	Score: 118	Expect: 8.7e-007	Matches: 6
	Cytochrome c OS=Equus caballus GN=CYCS PE=1 SV=2				
	CYC_MUS	Mass: 11743	Score: 81	Expect: 0.0048	Matches: 4
	Cytochrome c OS=Macropus giganteus GN=CYCS PE=1 SV=2				
	CYC_HIPAM	Mass: 11770	Score: 53	Expect: 2.6	Matches: 3
	Cytochrome c OS=Hippopotamus amphibius GN=CYCS PE=1 SV=2				
	CYC_MIRLE	Mass: 11726	Score: 53	Expect: 2.6	Matches: 3
	Cytochrome c OS=Mirounga leonina GN=CYCS PE=1 SV=2				
	CYC_BOVIN	Mass: 11812	Score: 53	Expect: 3	Matches: 3
	Cytochrome c OS=Bos taurus GN=CYCS PE=1 SV=2				
	CYC_CAMEL	Mass: 11756	Score: 53	Expect: 3	Matches: 3
	Cytochrome c OS=Camelus dromedarius GN=CYCS PE=1 SV=2				
	CYC_CANLF	Mass: 11741	Score: 53	Expect: 3	Matches: 3
	Cytochrome c OS=Canis lupus familiaris GN=CYCS PE=1 SV=2				
	CYC_ESCHR	Mass: 11756	Score: 53	Expect: 3	Matches: 3
	Cytochrome c OS=Eschscholus robustus GN=CYCS PE=1 SV=2				
	CYC_LAMGU	Mass: 11756	Score: 53	Expect: 3	Matches: 3
	Cytochrome c OS=Lama guanicoe GN=CYCS PE=1 SV=2				
	CYC_MUSC	Mass: 11683	Score: 53	Expect: 3	Matches: 3
	Cytochrome c OS=Miniopterus schreibersii GN=CYCS PE=1 SV=2				
	CYC_MOUSE	Mass: 11714	Score: 53	Expect: 3	Matches: 3
	Cytochrome c, somatic OS=Mus musculus GN=CYCS PE=1 SV=2				
	CYC_PIG	Mass: 11812	Score: 53	Expect: 3	Matches: 3
	Cytochrome c OS=Sus scrofa GN=CYCS PE=1 SV=2				
	CYC_RABIT	Mass: 11800	Score: 53	Expect: 3	Matches: 3
	Cytochrome c OS=Caprolaus cuniculus GN=CYCS PE=1 SV=2				
	CYC_RAT	Mass: 11714	Score: 53	Expect: 3	Matches: 3
	Cytochrome c, somatic OS=Rattus norvegicus GN=CYCS PE=1 SV=2				
	CYC_SHEEP	Mass: 11812	Score: 53	Expect: 3	Matches: 3
	Cytochrome c OS=Ovis aries GN=CYCS PE=1 SV=2				
	CYC_TARBA	Mass: 11728	Score: 53	Expect: 3	Matches: 3
	Cytochrome c OS=Tarsius bancanus GN=CYCS PE=3 SV=3				
2.	CYC2_BOVIN	Mass: 11848	Score: 82	Expect: 0.0036	Matches: 4
	Cytochrome c 2 OS=Bos taurus GN=CYC2 PE=3 SV=3				
3.	CYC_ALUMI	Mass: 11733	Score: 81	Expect: 0.0043	Matches: 4
	Cytochrome c OS>Alligator mississippiensis PE=1 SV=2				
..	CYC_ALUMI	Mass: 11733	Score: 81	Expect: 0.0043	Matches: 4
	Cytochrome c OS>Alligator mississippiensis PE=1 SV=2				
4.	BAF_BOVIN	Mass: 10284	Score: 60	Expect: 0.5	Matches: 3
	Barrier-to-autointegration factor OS=Bos taurus GN=BAF1 PE=3 SV=1				
	BAF_HUMAN	Mass: 10284	Score: 60	Expect: 0.5	Matches: 3
	Barrier-to-autointegration factor OS=Homo sapiens GN=BAF1 PE=1 SV=1				
	BAF_PONAB	Mass: 10284	Score: 60	Expect: 0.5	Matches: 3
	Barrier-to-autointegration factor OS=Ponab abelii GN=BAF1 PE=3 SV=1				
5.	OCL1L_CHICK	Mass: 56206	Score: 44	Expect: 23	Matches: 3
	Cytochrome c 1 light intermediate chain 1 OS=Galus gallus GN=OCL1L11 PE=1 SV=1				
6.	RS19_NITRK	Mass: 10248	Score: 43	Expect: 30	Matches: 2
	30S ribosomal protein S19 OS=Nitrobacter hamburgensis (strain X14 / DSM 10228) GN=rsps PE=3 SV=1				
	RS19_NITWN	Mass: 10255	Score: 43	Expect: 30	Matches: 2
	30S ribosomal protein S19 OS=Nitrobacter winogradskyi (strain N6-255 / ATCC 25391) GN=rsps PE=3 SV=1				
	RS19_OLTGO	Mass: 10110	Score: 42	Expect: 37	Matches: 2
	30S ribosomal protein S19 OS=Oligotrocha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5) GN=rsps PE=3 SV=1				
	RS19_BRADU	Mass: 10197	Score: 42	Expect: 37	Matches: 2
	30S ribosomal protein S19 OS=Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NERC 14792 / USDA 110) GN=rsps PE=3 SV=1				
	RS19_BRASR	Mass: 10211	Score: 42	Expect: 37	Matches: 2
	30S ribosomal protein S19 OS=Bradyrhizobium sp. (strain BTA11 / ATCC BAA-1182) GN=rsps PE=3 SV=1				
	RS19_BRASO	Mass: 10211	Score: 42	Expect: 37	Matches: 2
	30S ribosomal protein S19 OS=Bradyrhizobium sp. (strain ORS278) GN=rsps PE=3 SV=1				
	RS19_RHOP2	Mass: 10213	Score: 42	Expect: 37	Matches: 2
	30S ribosomal protein S19 OS=Rhodospirillum rubrum (strain HaK2) GN=rsps PE=3 SV=1				
	RS19_RHOP5	Mass: 10225	Score: 42	Expect: 37	Matches: 2
	30S ribosomal protein S19 OS=Rhodospirillum rubrum (strain B15453) GN=rsps PE=3 SV=1				
	RS19_RHOP4	Mass: 10213	Score: 42	Expect: 37	Matches: 2
	30S ribosomal protein S19 OS=Rhodospirillum rubrum (strain ATCC BAA-98 / CGA009) GN=rsps PE=1 SV=3				
	RS19_RHOP1	Mass: 10213	Score: 42	Expect: 37	Matches: 2
	30S ribosomal protein S19 OS=Rhodospirillum rubrum (strain TIE-1) GN=rsps PE=3 SV=1				
7.	MIC27_ZYORG	Mass: 26638	Score: 40	Expect: 49	Matches: 2
	MIC27 complex subunit MIC27 OS=Zygosaccharomyces rouxii (strain ATCC 26223 / CBS 732 / NRC 1130 / NCYC 568 / NRRL Y-229) GN=MIC27 PE=3 SV=1				
8.	SSL_DROME	Mass: 25580	Score: 40	Expect: 54	Matches: 2
	Suppressor-of-stellate-like protein OS=Drosophila melanogaster GN=SSL PE=2 SV=1				
9.	RLS_RHOET	Mass: 20165	Score: 39	Expect: 65	Matches: 2
	30S ribosomal protein S19 OS=Rhodospirillum rubrum (strain B15453) GN=rsps PE=3 SV=1				

Type of search	: Sequence Query
Enzyme	: Lys-N
Fixed modifications	: Carbamidomethyl (C)
Mass values	: Monoisotopic
Protein Mass	: Unrestricted
Peptide Mass Tolerance	: ± 0.5 Da
Protein Mass	: Unrestricted
Peptide Mass Tolerance	: ± 0.5 Da
Fragment Mass Tolerance	: ± 0.6 Da
Max Missed Cleavages	: 1
Instrument type	: Default
Query1 (828, 8386, 1+)	: cno (title) seq(C-T)
Query2 (907, 8818, 1+)	: cno (title) seq(C-K)
Query3 (907, 8818, 1+)	: cno (title) seq(C-T)
Query4 (992, 8366, 1+)	: cno (title) seq(C-L)
Query5 (992, 8366, 1+)	: cno (title) seq(C-L)
Query6 (1016, 7344, 1+)	: cno (title) seq(C-T)
Query7 (1038, 6964, 1+)	: cno (title) seq(C-F)
Query8 (1134, 6925, 1+)	: cno (title) seq(C-F)
Query9 (1274, 6438, 1+)	: cno (title) seq(C-F)
Query10 (1286, 6981, 1+)	: cno (title) seq(C-R)
Query11 (1296, 8462, 1+)	: cno (title) seq(C-R)
Query12 (1350, 8030, 1+)	: cno (title) seq(C-L)
Query13 (1350, 8030, 1+)	: cno (title) seq(C-L)
Query14 (1354, 7767, 1+)	: cno (title) seq(C-N)
Query15 (1408, 7645, 1+)	: cno (title) seq(C-L)
Query16 (1408, 7645, 1+)	: cno (title) seq(C-L)
Query17 (1424, 8444, 1+)	: cno (title) seq(C-K)
Query18 (1424, 8444, 1+)	: cno (title) seq(C-O)
Query19 (1447, 7640, 1+)	: cno (title) seq(C-I)
Query20 (1466, 7246, 1+)	: cno (title) seq(C-I)

MB mass

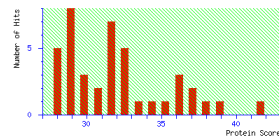


Mascot Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 09:55:30 GMT
Top Score : 42 for **TRUB_LISIN**, tRNA pseudouridine synthase B OS=Listeria innocua serovar 6a (strain CLIP 11262) GN=truD PE=3 SV=1

Mascot Score Histogram

Protein score is $-10 \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary [Help](#)
Significance threshold p: 0.05 Max. number of hits: 200
Preferred taxonomy: All entries

[Re-Search All](#) [Search Unmatched](#)

1.	TRUB_LISIN	Mass: 34120	Score: 42	Expect: 38	Matches: 15
tRNA pseudouridine synthase B OS=Listeria innocua serovar 6a (strain CLIP 11262) GN=truD PE=3 SV=1					
tRNA pseudouridine synthase B OS=Listeria innocua serovar 6a (strain CLIP 11262) GN=truD PE=3 SV=1					
2.	RPOC2_MAPPO	Mass: 160810	Score: 39	Expect: 65	Matches: 23
DNA-directed RNA polymerase subunit beta'' OS=Marchantia polymorpha GN=rpoC2 PE=3 SV=1					
3.	RL6_GEOUR	Mass: 19356	Score: 38	Expect: 91	Matches: 11
50S ribosomal protein L6 OS=Geobacter uranifedens (strain R14) GN=rplF PE=3 SV=1					
4.	PYRF_SACE1	Mass: 29255	Score: 37	Expect: 1e+002	Matches: 12
Orotidine 5'-phosphate decarboxylase OS=Saccharomyces fibulizera GN=rpoC2 PE=3 SV=1					
5.	IF1_BORAP	Mass: 8471	Score: 37	Expect: 1e+002	Matches: 7
Translation initiation factor IF-1 OS=Borrelia afzelii (strain P16) GN=infA PE=3 SV=1					
	IF1_BORBP	Mass: 8470	Score: 30	Expect: 6e+002	Matches: 6
Translation initiation factor IF-1 OS=Borrelia bavarivensis (strain ATCC BAA-2496 / DSM 23469 / PB1) GN=infA PE=3 SV=1					
	IF1_BORBU	Mass: 8470	Score: 30	Expect: 6e+002	Matches: 6
Translation initiation factor IF-1 OS=Borrelia burgdorferi (strain ATCC 35210 / B31 / CIP 102532 / DSM 4680) GN=infA PE=3 SV=3					
6.	RST_MAGSA	Mass: 17846	Score: 36	Expect: 1.3e+002	Matches: 10
30S ribosomal protein S7 OS=Magnetospirillum magnetum (strain AMB-1 / ATCC 700264) GN=rpsG PE=3 SV=1					
7.	PHYA_PEA	Mass: 125167	Score: 36	Expect: 1.3e+002	Matches: 17
Phytochrome A OS=Pisum sativum GN=PHYA PE=3 SV=1					
	PHYA_LATSA	Mass: 125390	Score: 30	Expect: 5e+002	Matches: 16
Phytochrome type A OS=Lathyrus sativus GN=PHYA PE=3 SV=1					
8.	RL18_RICPU	Mass: 13331	Score: 36	Expect: 1.4e+002	Matches: 12
50S ribosomal protein L18 OS=Rickettsia peacockii (strain Rustic) GN=rplR PE=3 SV=1					
9.	TEG7_ELMVK	Mass: 35757	Score: 35	Expect: 1.6e+002	Matches: 9
Teament protein UL51 homolog OS=Elephantid herpesvirus 1 (isolate Asian elephant/Berlin/Kiba/1998) PE=3 SV=1					
10.	PCP_STAHI	Mass: 22833	Score: 34	Expect: 2e+002	Matches: 9
Pyrolydine-carboxylate peptidase OS=Staphylococcus haemolyticus (strain JSC1435) GN=pcp PE=3 SV=1					
11.	CRO25_MOUSE	Mass: 26662	Score: 33	Expect: 2.7e+002	Matches: 8
Uncharacterized protein C18orf25 homolog OS=Mus musculus PE=1 SV=1					
12.	TOP1_CAEEL	Mass: 94435	Score: 33	Expect: 3e+002	Matches: 20
DNA topoisomerase 1 OS=Caenorhabditis elegans GN=top-1 PE=2 SV=1					
12.	LUF1_CAEEL	Mass: 89430	Score: 33	Expect: 3e+002	Matches: 20
DNA topoisomerase 1 OS=Caenorhabditis elegans GN=top-1 PE=2 SV=1					
13.	FABP4_RAT	Mass: 14815	Score: 32	Expect: 3.1e+002	Matches: 11
Fatty acid-binding protein, adipocyte OS=Rattus norvegicus GN=Fabp4 PE=1 SV=3					
14.	SSA1_NAJPA	Mass: 7286	Score: 32	Expect: 3.2e+002	Matches: 8
Orytoxin 1 OS=Naja pallida PE=1 SV=1					
15.	PEPAD_CLOAB	Mass: 50360	Score: 32	Expect: 3.2e+002	Matches: 15
Putative polysaccharide biosynthesis protein with aminopeptidase-like domain OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / UMG 5710 / WM B-1787) GN=PAP_C2195 PE=1 SV=					
16.	RL14_MYCP	Mass: 13398	Score: 32	Expect: 3.4e+002	Matches: 7
50S ribosomal protein L14 OS=Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1) GN=rplN PE=3 SV=1					
17.	RL31_PYRAB	Mass: 11019	Score: 32	Expect: 3.5e+002	Matches: 9
50S ribosomal protein L31e OS=Pyrococcus abyssi (strain GE5 / Orsay) GN=rpl31e PE=3 SV=1					
18.	ANK30A_HUMAN	Mass: 160476	Score: 32	Expect: 3.7e+002	Matches: 30
Ankyrin repeat domain-containing protein 30A OS=Homo sapiens GN=ANKRD30A PE=2 SV=3					
19.	SSA2_NAJMO	Mass: 7259	Score: 32	Expect: 3.8e+002	Matches: 10
Orytoxin 2 OS=Naja mossambica PE=1 SV=1					
20.	LXND_CHLCV	Mass: 39098	Score: 32	Expect: 3.9e+002	Matches: 10
UDP-3-O-acetylglucosamine N-acyltransferase OS=Chlamydomonas caviae (strain GPIC) GN=lxnd PE=3 SV=1					
21.	RL14_BEUC1	Mass: 13366	Score: 32	Expect: 3.9e+002	Matches: 6
50S ribosomal protein L14 OS=Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NRC 16432) GN=rplN PE=3 SV=1					
22.	RL28_HREDU	Mass: 9049	Score: 31	Expect: 4e+002	Matches: 5
50S ribosomal protein L28 OS=Haemophilus ducreyi (strain 35000HP / ATCC 700724) GN=rplB PE=3 SV=1					
23.	SUOD_STAAC	Mass: 31754	Score: 31	Expect: 4.1e+002	Matches: 10
Succinyl-CoA lyase [ADP-forming] subunit alpha OS=Staphylococcus aureus (strain COL) GN=sudC PE=3 SV=1					
	SUOD_STAAM	Mass: 31754	Score: 31	Expect: 4.1e+002	Matches: 10
Succinyl-CoA lyase [ADP-forming] subunit alpha OS=Staphylococcus aureus (strain MJE0 / ATCC 700699) GN=sudC PE=3 SV=1					
	SUOD_STAAN	Mass: 31754	Score: 31	Expect: 4.1e+002	Matches: 10
Succinyl-CoA lyase [ADP-forming] subunit alpha OS=Staphylococcus aureus (strain N315) GN=sudC PE=1 SV=1					

Type of search	: Sequence Query
Enzyme	: Lys-N
Fixed modifications	: Carboxymethyl (C)
Mass values	: Monoisotopic
Protein Mass	: Unrestricted
Peptide Mass Tolerance	: ± 0.5 Da
Fragment Mass Tolerance	: ± 0.6 Da
Max Missed Cleavages	: 1
Instrument type	: Default
Query1 (832.7192,1+)	: <no title>
Query2 (836.7806,1+)	: <no title>
Query3 (836.8319,1+)	: <no title>
Query4 (848.8024,1+)	: <no title>

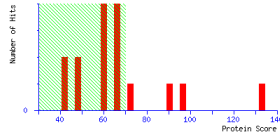
MB mass/mass+c

MASCOT Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 07:22:29 GMT
Top Score : 133 for **MYG_EQUBU**, Myoglobin OS=Equus burchelli GN=MB PE=1 SV=2

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary [Help](#)
Significance threshold $p < 0.05$ Max. number of hits 200
Preferred taxonomy All entries

Re-Search All Search Unmatched

- MYG_EQUBU** Mass: 17072 Score: 133 Expect: 2.8e-008 Matches: 13
Myoglobin OS=Equus burchelli GN=MB PE=1 SV=2
MYG_HORSE Mass: 17072 Score: 133 Expect: 2.8e-008 Matches: 13
Myoglobin OS=Equus caballus GN=MB PE=1 SV=2
MYG_HORSE Mass: 17072 Score: 133 Expect: 2.8e-008 Matches: 13
Myoglobin OS=Equus caballus GN=MB PE=1 SV=2
MYG_CANLF Mass: 17326 Score: 65 Expect: 0.19 Matches: 8
Myoglobin OS=Canis lupus familiaris GN=MB PE=1 SV=2
MYG_LVXP1 Mass: 17353 Score: 65 Expect: 0.19 Matches: 8
Myoglobin OS=Lycan pictus GN=MB PE=1 SV=2
MYG_OTOME Mass: 17326 Score: 65 Expect: 0.19 Matches: 8
Myoglobin OS=Otocyon megalotis GN=MB PE=1 SV=2
MYG_VULCH Mass: 17326 Score: 65 Expect: 0.19 Matches: 8
Myoglobin OS=Vulpes chama GN=MB PE=1 SV=2
MYG_MACRU Mass: 17258 Score: 51 Expect: 4 Matches: 7
Myoglobin OS=Macropus rufus GN=MB PE=1 SV=2
MYG_LEPMU Mass: 17063 Score: 43 Expect: 26 Matches: 4
Myoglobin OS=Lepilemur mustelinus GN=MB PE=1 SV=2
MYG_TUPGL Mass: 17088 Score: 43 Expect: 30 Matches: 4
Myoglobin OS=Tupaia glis GN=MB PE=1 SV=2
- MYG_PERPO** Mass: 17052 Score: 94 Expect: 0.00022 Matches: 12
Myoglobin OS=Perodicticus potto edwardsi GN=MB PE=1 SV=2
MYG_MACFA Mass: 17165 Score: 73 Expect: 0.027 Matches: 10
Myoglobin OS=Macaca fascicularis GN=MB PE=1 SV=2
MYG_NTCOO Mass: 16944 Score: 58 Expect: 0.87 Matches: 7
Myoglobin OS=Neoticebus coucang GN=MB PE=1 SV=2
MYG_RABIT Mass: 17210 Score: 56 Expect: 1.6 Matches: 7
Myoglobin OS>Oryctolagus cuniculus GN=MB PE=1 SV=2
MYG_ONDZI Mass: 17257 Score: 55 Expect: 1.7 Matches: 7
Myoglobin OS=Ondatra zibethicus GN=MB PE=1 SV=2
MYG_OTOLU Mass: 17091 Score: 55 Expect: 1.7 Matches: 6
Myoglobin OS=Otlemur crassicaudatus GN=MB PE=1 SV=2
- MYG_INDCP** Mass: 17270 Score: 89 Expect: 0.00065 Matches: 12
Myoglobin OS=Indopacetus pacificus GN=MB PE=2 SV=3
MYG_MESCU Mass: 17256 Score: 83 Expect: 0.0026 Matches: 11
Myoglobin OS=Mesolodon carlini GN=MB PE=1 SV=2
MYG_MESST Mass: 17256 Score: 83 Expect: 0.0026 Matches: 11
Myoglobin OS=Mesolodon stejnegeri GN=MB PE=2 SV=3
MYG_ZIPCA Mass: 17298 Score: 67 Expect: 0.12 Matches: 10
Myoglobin OS=Ziphius cavirostris GN=MB PE=1 SV=2
MYG_BALAD Mass: 17275 Score: 53 Expect: 2.9 Matches: 8
Myoglobin OS=Balaenoptera acutorostrata GN=MB PE=1 SV=2
MYG_BALON Mass: 17298 Score: 53 Expect: 2.9 Matches: 8
Myoglobin OS=Balaenoptera acutorostrata GN=MB PE=1 SV=2
MYG_BALBO Mass: 17238 Score: 53 Expect: 2.9 Matches: 8
Myoglobin OS=Balaenoptera borealis GN=MB PE=2 SV=3
MYG_BALEL Mass: 17238 Score: 53 Expect: 2.9 Matches: 8
Myoglobin OS=Balaenoptera edeni GN=MB PE=2 SV=3
MYG_DELEU Mass: 17195 Score: 53 Expect: 2.9 Matches: 8
Myoglobin OS=Delphinapterus leucas GN=MB PE=1 SV=2
MYG_ESORD Mass: 17238 Score: 53 Expect: 2.9 Matches: 8
Myoglobin OS=Eschrichtius robustus GN=MB PE=1 SV=2
MYG_INIQU Mass: 17191 Score: 53 Expect: 2.9 Matches: 8
Myoglobin OS=Inia geoffrensis GN=MB PE=1 SV=2
MYG_MESND Mass: 17252 Score: 53 Expect: 2.9 Matches: 8
Myoglobin OS=Megaptera novaeangliae GN=MB PE=1 SV=2
- MYG_HALGR** Mass: 17417 Score: 75 Expect: 0.018 Matches: 11
Myoglobin OS=Halichoerus grypus GN=MB PE=1 SV=2
MYG_PHOVI Mass: 17417 Score: 75 Expect: 0.018 Matches: 11
Myoglobin OS=Phoca vitulina GN=MB PE=1 SV=2
MYG_PUSSI Mass: 17472 Score: 70 Expect: 0.054 Matches: 9
Myoglobin OS=Pusa sibirica GN=MB PE=1 SV=2
- MYG_CASTI** Mass: 17140 Score: 67 Expect: 0.12 Matches: 10
Myoglobin OS=Castor fiber GN=MB PE=1 SV=2
- MYG_ERYPA** Mass: 17137 Score: 66 Expect: 0.13 Matches: 10
Myoglobin OS=Erythrocebus patas GN=MB PE=1 SV=2
MYG_PAPAN Mass: 17137 Score: 66 Expect: 0.13 Matches: 10
Myoglobin OS=Papio anubis GN=MB PE=1 SV=2
MYG_SENCH Mass: 17137 Score: 66 Expect: 0.13 Matches: 10
Myoglobin OS=Senopithecus entellus GN=MB PE=1 SV=2
- MYG_GORGE** Mass: 17221 Score: 65 Expect: 0.19 Matches: 10
Myoglobin OS=Gorilla gorilla berinsei GN=MB PE=1 SV=2
MYG_HUMAN Mass: 17221 Score: 65 Expect: 0.19 Matches: 10
Myoglobin OS=Homo sapiens GN=MB PE=1 SV=2
MYG_HYLAG Mass: 17261 Score: 65 Expect: 0.19 Matches: 10
Myoglobin OS=Hylobates agilis GN=MB PE=1 SV=2
MYG_PANTR Mass: 17240 Score: 65 Expect: 0.19 Matches: 10
Myoglobin OS=Pan troglodytes GN=MB PE=1 SV=2
MYG_PONPY Mass: 17187 Score: 65 Expect: 0.19 Matches: 10
Myoglobin OS=Pongo pygmaeus GN=MB PE=1 SV=2

	MYG_PONFY	Mass: 17187	Score: 65	Expect: 0.19	Matches: 10
	Myoglobin OS=Panor. pygmaeus GN=MB PE=1 SV=2				
	MYG_SYMSY	Mass: 17261	Score: 65	Expect: 0.19	Matches: 10
	Myoglobin OS=Symphalangus syndactylus GN=MB PE=1 SV=2				
8.	MYG_AOTTR	Mass: 17150	Score: 64	Expect: 0.22	Matches: 9
	Myoglobin OS=Aotus trivirgatus GN=MB PE=1 SV=2				
	MYG_CALJA	Mass: 17164	Score: 64	Expect: 0.22	Matches: 9
	Myoglobin OS=Callithrix jacchus GN=MB PE=1 SV=2				
9.	MYG_KOGER	Mass: 17357	Score: 60	Expect: 0.56	Matches: 9
	Myoglobin OS=Kogia brevipes GN=MB PE=2 SV=3				
	MYG_KOGLI	Mass: 17357	Score: 60	Expect: 0.56	Matches: 9
	Myoglobin OS=Kogia sima GN=MB PE=1 SV=2				
10.	MYG_GLONE	Mass: 17205	Score: 58	Expect: 0.78	Matches: 9
	Myoglobin OS=Globicephala melas GN=MB PE=1 SV=2				
11.	MYG_RALPH	Mass: 17206	Score: 58	Expect: 0.78	Matches: 9
	Myoglobin OS=Balaenoptera physalus GN=MB PE=1 SV=2				
12.	MYG_PHYCO	Mass: 17320	Score: 58	Expect: 0.87	Matches: 9
	Myoglobin OS=Physeter catodon GN=MB PE=1 SV=2				
13.	MYG_MELME	Mass: 17086	Score: 47	Expect: 12	Matches: 5
	Myoglobin OS=Meles meles GN=MB PE=1 SV=2				
14.	MYG_LAGLA	Mass: 17155	Score: 45	Expect: 16	Matches: 6
	Myoglobin OS=Lagothrix lagotricha GN=MB PE=1 SV=2				
15.	MYG_ROUAE	Mass: 17068	Score: 45	Expect: 19	Matches: 5
	Myoglobin OS=Rousettus aegyptiacus GN=MB PE=1 SV=2				
16.	CEIA_SULTO	Mass: 49305	Score: 42	Expect: 35	Matches: 14
	Cobyrinate a,c-diamide synthase OS=Suifuobolus tokodai (strain DSM 16993 / JCM 10545 / NBRC 100140 / 7) GN=dbiA PE=3 SV=1				

Type of search	Sequence Query
Enzyme	Lys-N
Type of search	Sequence Query
Enzyme	Lys-N
Fixed modifications	Carboxymethyl (C)
Mass values	Monoisotopic
Protein Mass Tolerance	Mass filtered
Peptide Mass Tolerance	± 0.5 Da
Fragment Mass Tolerance	± 0.6 Da
Max Missed Cleavages	Default
Query1 (832,719.21+)	(no title)
Query2 (836,780.61+)	(no title)
Query3 (838,831.91+)	(no title)
Query4 (848,902.41+)	(no title)
Query5 (854,806.31+)	(no title)
Query6 (854,881.21+)	(no title)
Query7 (861,449.2+)	(no title)
Query8 (873,937.91+)	(no title)
Query9 (874,888.61+)	(no title)
Query10 (876,843.39+)	(no title)
Query11 (877,399.01+)	(no title)
Query12 (882,931.91+)	(no title)
Query13 (885,396.31+)	(no title)
Query14 (887,379.81+)	(no title)
Query15 (894,749.01+)	(no title)
Query16 (895,830.71+)	(no title)
Query17 (906,852.81+)	(no title)
Query18 (920,770.61+)	seq(C-1)
Query19 (920,770.61+)	(no title)
Query20 (930,769.81+)	seq(C-1)
Query21 (934,791.51+)	(no title)
Query22 (934,837.01+)	(no title)
Query23 (935,367.21+)	(no title)
Query24 (937,825.91+)	(no title)
Query25 (942,743.41+)	(no title)
Query26 (950,810.01+)	(no title)
Query27 (952,825.71+)	(no title)
Query28 (952,830.71+)	(no title)
Query29 (954,759.81+)	seq(C-1)
Query30 (955,808.51+)	(no title)
Query31 (960,741.81+)	(no title)
Query32 (962,741.51+)	(no title)
Query33 (962,803.11+)	(no title)

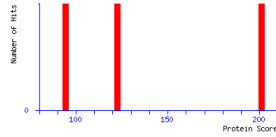
MB mass+c

MASCOT Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 07:22:38 GMT
Top Score : 201 for **MYG_EQUBU**, Myoglobin OS=Equus burchelli GN=MB PE=1 SV=2

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary [Help](#)
Significance threshold p: 0.05 Max. number of hits: 200
Preferred taxonomy: All entries

Re-Search All Search Unmatched

1.	MYG_EQUBU	Mass: 17072	Score: 201	Expect: 4.4e-015	Matches: 9
	Myoglobin OS=Equus burchelli GN=MB PE=1 SV=2				
	MYG_HORSE	Mass: 17072	Score: 201	Expect: 4.4e-015	Matches: 9
	Myoglobin OS=Equus caballus GN=MB PE=1 SV=2				
	MYG_HORSE	Mass: 17072	Score: 201	Expect: 4.4e-015	Matches: 9
	Myoglobin OS=Equus caballus GN=MB PE=1 SV=2				
	MYG_HALGR	Mass: 17417	Score: 99	Expect: 7.3e-005	Matches: 5
	Myoglobin OS=Halichoerus erythropus GN=MB PE=1 SV=2				
	MYG_PHOVI	Mass: 17417	Score: 99	Expect: 7.3e-005	Matches: 5
	Myoglobin OS=Phoca vitulina GN=MB PE=1 SV=2				
	MYG_PUSSI	Mass: 17472	Score: 99	Expect: 7.3e-005	Matches: 5
	Myoglobin OS=Pusa sibirica GN=MB PE=1 SV=2				
	MYG_INDCP	Mass: 17270	Score: 98	Expect: 9.6e-005	Matches: 5
	Myoglobin OS=Indracetus pacificus GN=MB PE=2 SV=3				
	MYG_MESCA	Mass: 17256	Score: 98	Expect: 9.6e-005	Matches: 5
	Myoglobin OS=Mesolodon carlhubbsi GN=MB PE=1 SV=2				
	MYG_MESSI	Mass: 17256	Score: 98	Expect: 9.6e-005	Matches: 5
	Myoglobin OS=Mesolodon stejnegeri GN=MB PE=2 SV=3				
	MYG_CANLF	Mass: 17326	Score: 98	Expect: 0.00016	Matches: 5
	Myoglobin OS=Canis lupus familiaris GN=MB PE=1 SV=2				
	MYG_LYXPI	Mass: 17353	Score: 98	Expect: 0.00016	Matches: 5
	Myoglobin OS=Lycan pictus GN=MB PE=1 SV=2				
	MYG_OTOME	Mass: 17326	Score: 96	Expect: 0.00016	Matches: 5
	Myoglobin OS=Otocyon megalotis GN=MB PE=1 SV=2				
	MYG_VULCH	Mass: 17326	Score: 96	Expect: 0.00016	Matches: 5
	Myoglobin OS=Vulpes chama GN=MB PE=1 SV=2				
	MYG_KOGBR	Mass: 17357	Score: 76	Expect: 0.013	Matches: 4
	Myoglobin OS=Kogia breviceps GN=MB PE=2 SV=3				
	MYG_KOCSI	Mass: 17357	Score: 76	Expect: 0.013	Matches: 4
	Myoglobin OS=Kogia sima GN=MB PE=1 SV=2				
	MYG_PHYOD	Mass: 17320	Score: 76	Expect: 0.013	Matches: 4
	Myoglobin OS=Physeter catodon GN=MB PE=1 SV=2				
	MYG_BALAL	Mass: 17275	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Balaenoptera acutorostrata GN=MB PE=1 SV=2				
	MYG_BALBO	Mass: 17238	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Balaenoptera borealis GN=MB PE=2 SV=3				
	MYG_BALED	Mass: 17238	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Balaenoptera edeni GN=MB PE=2 SV=3				
	MYG_BALPH	Mass: 17206	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Balaenoptera physalus GN=MB PE=1 SV=2				
	MYG_DELLE	Mass: 17165	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Delphinapterus leucas GN=MB PE=1 SV=2				
	MYG_ESORO	Mass: 17238	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Eschrichtius robustus GN=MB PE=1 SV=2				
	MYG_ESORO	Mass: 17205	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Eschrichtius robustus GN=MB PE=1 SV=2				
	MYG_GLOME	Mass: 17205	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Globicephala melas GN=MB PE=1 SV=2				
	MYG_INIGE	Mass: 17191	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Inia geoffrensis GN=MB PE=1 SV=2				
	MYG_MEGND	Mass: 17252	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Megaptera novaeangliae GN=MB PE=1 SV=2				
	MYG_ZIPCA	Mass: 17298	Score: 75	Expect: 0.018	Matches: 4
	Myoglobin OS=Ziphius cavirostris GN=MB PE=1 SV=2				
	MYG_MADRU	Mass: 17258	Score: 74	Expect: 0.025	Matches: 4
	Myoglobin OS=Macropus rufus GN=MB PE=1 SV=2				
	MYG_LEPMU	Mass: 17063	Score: 57	Expect: 1	Matches: 3
	Myoglobin OS=Leptemur mustelinus GN=MB PE=1 SV=2				
	MYG_ROUAE	Mass: 17068	Score: 57	Expect: 1.2	Matches: 3
	Myoglobin OS=Rousettus aegyptiacus GN=MB PE=1 SV=2				
	MYG_TUPGL	Mass: 17088	Score: 57	Expect: 1.2	Matches: 3
	Myoglobin OS=Tupaia glis GN=MB PE=1 SV=2				
	MYG_MELME	Mass: 17066	Score: 57	Expect: 1.2	Matches: 3
	Myoglobin OS=Meles meles GN=MB PE=1 SV=2				
	MYG_ZALCA	Mass: 17369	Score: 56	Expect: 1.4	Matches: 3
	Myoglobin OS=Zalophus californianus GN=MB PE=1 SV=2				
2.	MYG_PERRD	Mass: 17052	Score: 125	Expect: 1.7e-007	Matches: 6
	Myoglobin OS=Perodicticus potto edwardsi GN=MB PE=1 SV=2				
	MYG_MACEA	Mass: 17165	Score: 100	Expect: 5.5e-005	Matches: 5
	Myoglobin OS=Macaca fascicularis GN=MB PE=1 SV=2				
	MYG_RABIT	Mass: 17210	Score: 79	Expect: 0.0065	Matches: 4
	Myoglobin OS=Unctolagus cuniculus GN=MB PE=1 SV=2				
	MYG_WTODD	Mass: 16944	Score: 79	Expect: 0.0073	Matches: 4
	Myoglobin OS=Neoticebus coucang GN=MB PE=1 SV=2				
	MYG_CASEL	Mass: 17140	Score: 78	Expect: 0.0089	Matches: 4
	Myoglobin OS=Castor fiber GN=MB PE=1 SV=2				
	MYG_ERYPY	Mass: 17137	Score: 78	Expect: 0.0089	Matches: 4
	Myoglobin OS=Erythrocebus patas GN=MB PE=1 SV=2				
	MYG_GORGE	Mass: 17221	Score: 78	Expect: 0.0089	Matches: 4
	Myoglobin OS=Gorilla gorilla berinsei GN=MB PE=1 SV=2				
	MYG_HUMAN	Mass: 17231	Score: 78	Expect: 0.0089	Matches: 4
	Myoglobin OS=Homo sapiens GN=MB PE=1 SV=2				
	MYG_HYLAG	Mass: 17261	Score: 78	Expect: 0.0089	Matches: 4
	Myoglobin OS=Hylobates agilis GN=MB PE=1 SV=2				

Search Parameters

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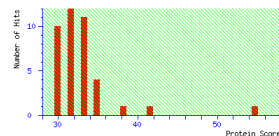
MYH mass

Mascot Search Results

User : Y. Wang
Email : kahz20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 08:37:08 GMT
Top Score : 55 for [PP11_STAHI](#), Putative peptidyl-prolyl cis-trans isomerase OS=Staphylococcus haemolyticus (strain JCSC1435) GN=SH1997 PE=3 SV=1

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As	Concise Protein Summary	Help
Significance threshold p<	0.05	Max. number of hits 200
Preferred taxonomy	All entries	
Re-Search All	Search Unmatched	
1.	PP11_STAHI Mass: 21712 Score: 55 Expect: 1.9 Matches: 10 Putative peptidyl-prolyl cis-trans isomerase OS=Staphylococcus haemolyticus (strain JCSC1435) GN=SH1997 PE=3 SV=1	
2.	NCAP_INBAD Mass: 61831 Score: 41 Expect: 45 Matches: 17 Nucleoprotein OS=Influenza B virus (strain B/Ann Arbor/1/1968 [wild-type]) GN=NP PE=3 SV=1	
3.	MTCO_TETTH Mass: 19529 Score: 37 Expect: 1e+002 Matches: 11 Cadmium metallothionein OS=Tetrahymena thermophila GN=MTT1 PE=1 SV=1	
4.	Y1071_STAAR Mass: 10769 Score: 35 Expect: 1.7e+002 Matches: 7 UFFO223 protein SAR1071 OS=Staphylococcus aureus (strain MRSA292) GN=SAR1071 PE=3 SV=1	
5.	SECA_BACSK Mass: 95717 Score: 35 Expect: 1.8e+002 Matches: 18 Protein translocase subunit SecA OS=Bacillus clausii (strain KSM-K16) GN=secA PE=3 SV=1	
6.	TIF2_DROME Mass: 118766 Score: 34 Expect: 2e+002 Matches: 20 Transcription termination factor 2 OS=Drosophila melanogaster GN=Tifs PE=1 SV=2	
7.	Y1094_THEMA Mass: 50515 Score: 34 Expect: 2e+002 Matches: 14 Uncharacterized RNA methyltransferase TM_1094 OS=Thermotoga maritima (strain ATCC 43589 / MS88 / DSM 3109 / JCM 10099) GN=TM_1094 PE=3 SV=1	
8.	YK112_DENAN Mass: 6982 Score: 34 Expect: 2.3e+002 Matches: 6 Kunitz-type serine protease inhibitor dendrotoxin DdC1 OS=Dendroaspis angusticeps PE=1 SV=1 YK116_DENAN Mass: 6982 Score: 34 Expect: 2.3e+002 Matches: 6 Kunitz-type serine protease inhibitor long epsilon-dendrotoxin Arg55 OS=Dendroaspis angusticeps PE=1 SV=1	
9.	AKT2_MOUSE Mass: 56112 Score: 33 Expect: 2.6e+002 Matches: 10 RAC-beta serine/threonine-protein kinase OS=Mus musculus GN=Akt2 PE=1 SV=1	
10.	Y2215_THIDA Mass: 26161 Score: 33 Expect: 2.7e+002 Matches: 9 Probable transcriptional regulatory protein Tbd_2215 OS=Thiobacillus denitrificans (strain ATCC 25259) GN=Tbd_2215 PE=3 SV=1	
11.	GLB4_GLYDI Mass: 15227 Score: 33 Expect: 2.7e+002 Matches: 7 Globin, monomeric component M-IV OS=Glycera dibranchiata PE=1 SV=2	
12.	RL15_CHLCH Mass: 19963 Score: 33 Expect: 3e+002 Matches: 8 50S ribosomal protein L15 OS=Chlorobium chlorochromatii (strain CaD3) GN=rp10 PE=3 SV=1	
13.	GPX4_PIG Mass: 22845 Score: 33 Expect: 3e+002 Matches: 7 Phospholipid hydroperoxide glutathione peroxidase, mitochondrial OS=Sus scrofa GN=GPX4 PE=1 SV=3	
14.	JLVE_SYNY3 Mass: 34104 Score: 33 Expect: 3e+002 Matches: 10 Probable branched-chain-amino-acid aminotransferase OS=Symechocystis sp. (strain PCC 6803 / Kazusa) GN=ilve PE=3 SV=1	
14.	JLVE_SYNY3 Mass: 34104 Score: 33 Expect: 3e+002 Matches: 10 Probable branched-chain-amino-acid aminotransferase OS=Symechocystis sp. (strain PCC 6803 / Kazusa) GN=ilve PE=3 SV=1	
15.	ANKR1_CHICK Mass: 36598 Score: 33 Expect: 3e+002 Matches: 10 Ankyrin repeat domain-containing protein 1 OS=Gallus gallus GN=ANKRD1 PE=2 SV=1	
16.	EIF2A_DICDI Mass: 68455 Score: 32 Expect: 3.1e+002 Matches: 12 Eukaryotic translation initiation factor 2A OS=Dictyostelium discoideum GN=elf2a PE=3 SV=1	
17.	CLPB_AQUAE Mass: 114467 Score: 32 Expect: 3.2e+002 Matches: 26 Chaperone protein ClpB OS=Aquifex aeolicus (strain VF5) GN=clpB PE=3 SV=1	
18.	RL12_EUGGR Mass: 14420 Score: 32 Expect: 3.2e+002 Matches: 7 50S ribosomal protein L12, chloroplastic OS=Euglena gracilis GN=rl12 PE=3 SV=1	
19.	KAD_MOLPM Mass: 24177 Score: 32 Expect: 3.2e+002 Matches: 8 Adenylate kinase OS=Molbachia pipiensis wMel GN=ack PE=3 SV=1	
20.	RSP_PSEAE Mass: 27176 Score: 32 Expect: 3.4e+002 Matches: 12 30S ribosomal protein S2 OS=Pseudomonas atlantica (strain T6c / ATCC BAA-1087) GN=rpsB PE=3 SV=1	
21.	PXRI_CHAGB Mass: 40710 Score: 32 Expect: 3.5e+002 Matches: 9 Protein PXRI OS=Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NRC 6347 / NRRL 1970) GN=PXRI PE=3 SV=2	
22.	RL23_STREX Mass: 10829 Score: 32 Expect: 3.6e+002 Matches: 8 50S ribosomal protein L23 OS=Streptococcus sanguinis (strain SK36) GN=rl19 PE=3 SV=1	
23.	SIGA_BACSP Mass: 43429 Score: 32 Expect: 3.9e+002 Matches: 10 RNA polymerase sigma factor SigA OS=Bacillus sp. GN=sigA PE=3 SV=1	
24.	RL30_METME Mass: 17342 Score: 32 Expect: 3.9e+002 Matches: 12 50S ribosomal protein L30P OS=Methanococcus maripaludis (strain CS / ATCC BAA-1333) GN=rp130b PE=3 SV=1 RL30_METM7 Mass: 17342 Score: 32 Expect: 3.9e+002 Matches: 12 50S ribosomal protein L30P OS=Methanococcus maripaludis (strain C7 / ATCC BAA-1331) GN=rp130b PE=3 SV=1	
25.	Y115_METJA Mass: 18237 Score: 31 Expect: 4e+002 Matches: 12 Uncharacterized protein MJ0115 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NRC 100440) GN=MJ0115 PE=4 SV=1	
26.	AMPA_CYP47 Mass: 52233 Score: 31 Expect: 4.3e+002 Matches: 10 Probable cytosol aminopeptidase OS=Cyanospora sp. (strain PCC 7424) GN=PepA PE=3 SV=1	

Probable cytosolic aminopeptidase OS=Vannotheca sp. (strain RU, 1424) GN=pepA PE=3 SV=1					
27.	NUP1_YEAS	Mass: 113629	Score: 31	Expect: 4.3e+002	Matches: 15 Nucleoporin NUP1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=NUP1 PE=1 SV=1
28.	RS18_SYNJR	Mass: 8252	Score: 31	Expect: 4.4e+002	Matches: 6 S0S ribosomal protein S18 OS=Synecoccus sp. (strain JA-2-38'a(2-13)) GN=rpsR PE=3 SV=1
29.	PHNC2_BACH	Mass: 27145	Score: 31	Expect: 4.4e+002	Matches: 11 Phosphates import ATP-binding protein PhnC 2 OS=Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) GN=phnC2 PE=3 SV=2
30.	ARP7_ARATH	Mass: 40285	Score: 31	Expect: 4.6e+002	Matches: 8 Actin-related protein 7 OS=Arabidopsis thaliana GN=ARP7 PE=1 SV=1
31.	RLK1_CXB1	Mass: 33345	Score: 31	Expect: 4.7e+002	Matches: 9 Probable alpha-L-glutamate liase OS=Coxiella burnetii (strain CbkJ_0154) GN=rnkK PE=3 SV=1
	RLK1_CXB2	Mass: 33345	Score: 31	Expect: 4.7e+002	Matches: 9 Probable alpha-L-glutamate liase OS=Coxiella burnetii (strain CbkJ_0212) GN=rnkK PE=3 SV=1
	RLK1_CXB3	Mass: 33345	Score: 31	Expect: 4.7e+002	Matches: 9 Probable alpha-L-glutamate liase OS=Coxiella burnetii (strain Duway_5J108-111) GN=rnkK PE=3 SV=1
	RLK1_CXB4	Mass: 33345	Score: 31	Expect: 4.7e+002	Matches: 9 Probable alpha-L-glutamate liase OS=Coxiella burnetii (strain RSA_331 / Henzerling 11) GN=rnkK PE=3 SV=1
	RLK1_CXB5	Mass: 33345	Score: 31	Expect: 4.7e+002	Matches: 9 Probable alpha-L-glutamate liase OS=Coxiella burnetii (strain RSA_493 / Nine Mile phase 1) GN=rnkK PE=3 SV=1
32.	HIS6_FLAJ1	Mass: 27212	Score: 30	Expect: 4.9e+002	Matches: 8 Imidazole glycerol phosphate synthase subunit HisF OS=Flavobacterium johnsoniae (strain ATCC 17061 / DSM 2064 / UMI01) GN=hisF PE=3 SV=1
33.	GRE4_PROA2	Mass: 18273	Score: 30	Expect: 5.1e+002	Matches: 7 Transcription elongation factor GreA OS=Prosthecochloris aestuarii (strain DSM 271 / SK 413) GN=greA PE=3 SV=1
34.	REC4_MYCP	Mass: 36963	Score: 30	Expect: 5.3e+002	Matches: 12 Protein RecA OS=Mycoplasma penetrans (strain HF-2) GN=rrecA PE=3 SV=1
35.	RL23_STRS2	Mass: 10857	Score: 30	Expect: 5.3e+002	Matches: 8 S0S ribosomal protein L23 OS=Streptococcus suis (strain 98HAH33) GN=rplW PE=3 SV=1
	RL23_STRS3	Mass: 10857	Score: 30	Expect: 5.3e+002	Matches: 8 S0S ribosomal protein L23 OS=Streptococcus suis (strain 05ZYH33) GN=rplW PE=3 SV=1
36.	G6P_DEPH	Mass: 36985	Score: 30	Expect: 5.3e+002	Matches: 8 GTPase G6p OS=Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513) GN=g6p PE=3 SV=2
36.	G6P_DEPH2	Mass: 36985	Score: 30	Expect: 5.3e+002	Matches: 8 GTPase G6p OS=Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513) GN=g6p PE=3 SV=2
37.	HEB_CICCI	Mass: 18370	Score: 30	Expect: 5.4e+002	Matches: 6 Hemoglobin subunit beta OS=Ciconia ciconia GN=HEB PE=1 SV=1
38.	3HAD1_ASPO	Mass: 21940	Score: 30	Expect: 5.5e+002	Matches: 7 3-hydroxyanthranilate 3,4-dioxygenase 1 OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=hna1-1 PE=3 SV=1
39.	MYB08_ANTMA	Mass: 26786	Score: 30	Expect: 5.5e+002	Matches: 8 Mb-related protein 308 OS=Antirrhinum majus GN=MYB08 PE=2 SV=1
40.	RL23_STRG2	Mass: 10785	Score: 30	Expect: 5.6e+002	Matches: 9 S0S ribosomal protein L23 OS=Streptococcus gordonii (strain Challis / ATCC 35105 / CHI / DLT / V288) GN=rplW PE=3 SV=1
	RL23_STRP2	Mass: 10779	Score: 30	Expect: 5.6e+002	Matches: 9 S0S ribosomal protein L23 OS=Streptococcus pneumoniae serotype 2 (strain D39 / NCTC 7466) GN=rplW PE=3 SV=1
	RL23_STRP4	Mass: 10779	Score: 30	Expect: 5.6e+002	Matches: 9 S0S ribosomal protein L23 OS=Streptococcus pneumoniae serotype 19F (strain G54) GN=rplW PE=3 SV=1
	RL23_STRP7	Mass: 10779	Score: 30	Expect: 5.6e+002	Matches: 9 S0S ribosomal protein L23 OS=Streptococcus pneumoniae (strain 70585) GN=rplW PE=3 SV=1

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.5 Da
 Fragment Mass Tolerance : ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Query1 (822.8399,1+): <no title>
 Query2 (825.8382,1+): <no title>
 Query3 (825.8766,1+): <no title>
 Query4 (829.8154,1+): <no title>
 Query5 (836.8398,1+): <no title>
 Query6 (856.8398,1+): <no title>
 Query7 (857.8071,1+): <no title>
 Query8 (857.8754,1+): <no title>
 Query9 (861.4850,1+): <no title>
 Query10 (865.7950,1+): <no title>

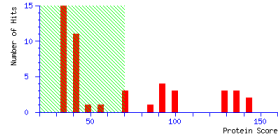
MYH mass/mass+c

MASCOT Search Results

User : Y. Wang
Email : kahz20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 08:36:17 GMT
Top Score : 143 for **MYH1_FIG**, Myosin-I OS=Sus scrofa GN=MYH1 PE=2 SV=1

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary [Help](#)
Significance threshold $p < 0.05$ Max. number of hits: 200
Preferred taxonomy: All entries

Re-Search All Search Unmatched

1.	MYH1_FIG	Mass: 223963	Score: 143	Expect: 2.8e-009	Matches: 32
Myosin-I OS=Sus scrofa GN=MYH1 PE=2 SV=1					
2.	MYH1_BOVIN	Mass: 223780	Score: 142	Expect: 3.5e-009	Matches: 31
2.	MYH1_BOVIN	Mass: 223780	Score: 142	Expect: 3.5e-009	Matches: 31
Myosin-I OS=Bos taurus GN=MYH1 PE=2 SV=2					
3.	MYH1_CANLF	Mass: 223938	Score: 138	Expect: 8.7e-009	Matches: 32
Myosin-I OS=Canis lupus familiaris GN=MYH1 PE=3 SV=2					
4.	MYH1_MOUSE	Mass: 224131	Score: 138	Expect: 8.7e-009	Matches: 33
Myosin-I OS=Mus musculus GN=Myh1 PE=1 SV=1					
5.	MYH1_RABIT	Mass: 223856	Score: 134	Expect: 2.2e-008	Matches: 30
Myosin-4 OS=Oryctolagus cuniculus GN=MYH4 PE=1 SV=1					
6.	MYH1_HORSE	Mass: 223788	Score: 132	Expect: 3.5e-008	Matches: 30
Myosin-I OS=Equus caballus GN=MYH1 PE=2 SV=1					
7.	MYH1_HUMAN	Mass: 223993	Score: 129	Expect: 6.9e-008	Matches: 35
Myosin-I OS=Homo sapiens GN=MYH1 PE=1 SV=3					
8.	MYH1_FIG	Mass: 224025	Score: 127	Expect: 1.1e-007	Matches: 32
Myosin-4 OS=Sus scrofa GN=MYH4 PE=2 SV=1					
9.	MYH2_CANLF	Mass: 224000	Score: 99	Expect: 7.3e-005	Matches: 23
Myosin-2 OS=Canis lupus familiaris GN=MYH2 PE=3 SV=1					
10.	MYH2_FIG	Mass: 223940	Score: 98	Expect: 8.3e-005	Matches: 22
Myosin-2 OS=Sus scrofa GN=MYH2 PE=2 SV=1					
11.	MYH2_HORSE	Mass: 223538	Score: 96	Expect: 0.00014	Matches: 25
Myosin-2 OS=Equus caballus GN=MYH2 PE=2 SV=1					
12.	MYH1_MOUSE	Mass: 223648	Score: 94	Expect: 0.0002	Matches: 29
Myosin-4 OS=Mus musculus GN=Myh4 PE=2 SV=1					
	MYH1_RAT	Mass: 223669	Score: 94	Expect: 0.00022	Matches: 29
Myosin-4 OS=Rattus norvegicus GN=Myh4 PE=1 SV=1					
13.	MYH1_HUMAN	Mass: 223918	Score: 94	Expect: 0.00021	Matches: 30
Myosin-4 OS=Homo sapiens GN=MYH4 PE=1 SV=2					
14.	MYH8_HUMAN	Mass: 223611	Score: 90	Expect: 0.00058	Matches: 19
Myosin-8 OS=Homo sapiens GN=MYH8 PE=1 SV=3					
14.	MYH8_HUMAN	Mass: 223611	Score: 90	Expect: 0.00058	Matches: 19
Myosin-8 OS=Homo sapiens GN=MYH8 PE=1 SV=3					
15.	MYH2_BOVIN	Mass: 224108	Score: 89	Expect: 0.00065	Matches: 23
Myosin-2 OS=Bos taurus GN=MYH2 PE=2 SV=1					
16.	MYH8_CANLF	Mass: 223657	Score: 84	Expect: 0.0024	Matches: 22
Myosin-8 OS=Canis lupus familiaris GN=MYH8 PE=3 SV=1					
17.	MYH1_CANLF	Mass: 223791	Score: 70	Expect: 0.05	Matches: 26
Myosin-4 OS=Canis lupus familiaris GN=MYH1 PE=3 SV=1					
18.	MYH8_MOUSE	Mass: 223672	Score: 70	Expect: 0.056	Matches: 22
Myosin-8 OS=Mus musculus GN=Myh8 PE=2 SV=2					
19.	MYH2_HUMAN	Mass: 223950	Score: 70	Expect: 0.06	Matches: 24
Myosin-2 OS=Homo sapiens GN=MYH2 PE=1 SV=1					
20.	MYSS_RABIT	Mass: 125760	Score: 55	Expect: 1.7	Matches: 21
Myosin heavy chain, skeletal muscle (Fragments) OS=Oryctolagus cuniculus PE=1 SV=2					
21.	MYH13_HUMAN	Mass: 224625	Score: 45	Expect: 17	Matches: 20
Myosin-13 OS=Homo sapiens GN=MYH13 PE=2 SV=2					
22.	MYH13_CANLF	Mass: 224304	Score: 44	Expect: 22	Matches: 20
Myosin-13 OS=Canis lupus familiaris GN=MYH13 PE=3 SV=1					
23.	RS96_METST	Mass: 14431	Score: 42	Expect: 32	Matches: 6
30S ribosomal protein S6e OS=Methanospaera stadtmanae (strain ATCC 43021 / DSM 3091 / JCM 11832 / MCB-3) GN=rs96 PE=3 SV=1					
24.	PP11_STAHL	Mass: 21712	Score: 42	Expect: 33	Matches: 8
Putative peptidylprolyl cis-trans isomerase OS=Staphylococcus haemolyticus (strain JCS1435) GN=SH1997 PE=3 SV=1					
25.	PTP14_STYPL	Mass: 13836	Score: 42	Expect: 38	Matches: 4
Tyrosine-protein phosphatase 14 (Fragment) OS=Styela plicata GN=STY-14 PE=2 SV=1					
26.	USE1_YEAST	Mass: 28089	Score: 41	Expect: 48	Matches: 5
Protein transport protein USE1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=USE1 PE=1 SV=1					
27.	GIR8_BORBU	Mass: 71522	Score: 40	Expect: 53	Matches: 7
DNA gyrase subunit B OS=Borrelia burgdorferi (strain ATCC 35210 / B31 / CIP 102532 / DSM 4680) GN=gyrB PE=3 SV=4					

27.	DND_EUCAL	Mass: 71922	Score: 40	Expect: 33	Matches: 7
DNA gyrase subunit B OS=Borrelia burgdorferi (strain ATCC 35210 / B31 / CIP 102532 / DSM 4680) GN=gyrB PE=3 SV=4					
28.	MND_YEAST	Mass: 21098	Score: 40	Expect: 54	Matches: 4
1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=ADI1 PE=1 SV=1					
29.	DHAJ_MANNM	Mass: 41675	Score: 39	Expect: 63	Matches: 7
Chaperone protein DnaJ OS=Mannheimia succiniciproducens (strain NBEL55E) GN=dnaJ PE=3 SV=2					
30.	EFP_FRASN	Mass: 20055	Score: 39	Expect: 68	Matches: 5
Elongation factor P OS=Frankia sp. (strain EAW15ec) GN=efp PE=3 SV=1					
31.	MYH_MOUSE	Mass: 224754	Score: 39	Expect: 74	Matches: 19
Myosin-3 OS=Mus musculus GN=Myh3 PE=2 SV=2					
32.	TYT_STRUO	Mass: 47196	Score: 38	Expect: 89	Matches: 8
Tyrosine--tRNA ligase OS=Streptococcus uberis (strain ATCC BAA-854 / 0140J) GN=tyrS PE=3 SV=1					
33.	YCR8_CYAPA	Mass: 20097	Score: 37	Expect: 1.1e+002	Matches: 5
Uncharacterized protein in petA-psaM intergenic region OS=Cyanophora paradoxa PE=1 SV=1					
34.	TAL_DESHO	Mass: 23021	Score: 37	Expect: 1.1e+002	Matches: 4
Probable transaldolase OS=Desulfitobacterium hafniense (strain DCS-2 / DSM 10864) GN=tal PE=3 SV=1					
	TAL_DESHI	Mass: 23021	Score: 37	Expect: 1.1e+002	Matches: 4
Probable transaldolase OS=Desulfitobacterium hafniense (strain Y51) GN=tal PE=3 SV=1					
35.	YLR27_YEAST	Mass: 41192	Score: 37	Expect: 1.2e+002	Matches: 10
Uncharacterized protein YLR27C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YLR27C PE=1 SV=1					
36.	CSE15_BACSU	Mass: 37704	Score: 36	Expect: 1.4e+002	Matches: 8
Sporulation protein cse15 OS=Bacillus subtilis (strain 168) GN=cse15 PE=2 SV=1					
37.	RAD50_SCHPO	Mass: 150212	Score: 36	Expect: 1.4e+002	Matches: 18
DNA repair protein rad50 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=rad50 PE=1 SV=3					
38.	BANF_BOVIN	Mass: 10757	Score: 36	Expect: 1.4e+002	Matches: 2
Barrier-to-autointegration factor-like protein OS=Bos taurus GN=BNF2 PE=3 SV=1					
39.	Y1071_STAAR	Mass: 10769	Score: 36	Expect: 1.5e+002	Matches: 6
UPF0223 protein SAR1071 OS=Staphylococcus aureus (strain MRSA252) GN=SAR1071 PE=3 SV=1					
40.	MUTS_LEPBJ	Mass: 97582	Score: 36	Expect: 1.6e+002	Matches: 16
DNA mismatch repair protein Muts OS=Leptospira borapetersenii serovar Hardjo-bovis (strain JB197) GN=mutS PE=3 SV=1					
	MUTS_LEPEL	Mass: 97582	Score: 36	Expect: 1.6e+002	Matches: 16
DNA mismatch repair protein Muts OS=Leptospira borapetersenii serovar Hardjo-bovis (strain L550) GN=mutS PE=3 SV=1					
41.	MYH3_CHICK	Mass: 223664	Score: 35	Expect: 1.6e+002	Matches: 24
Myosin-3 OS=Gallus gallus GN=MYH3 PE=2 SV=3					
42.	ROR6_ARATH	Mass: 138234	Score: 35	Expect: 1.7e+002	Matches: 8
RNA-dependent RNA polymerase 6 OS=Arabidopsis thaliana GN=ROR6 PE=1 SV=1					
43.	SLA1_DEJAC	Mass: 17712	Score: 35	Expect: 1.8e+002	Matches: 4
Snaclec agglutinin subunit alpha-1 OS=Deinagkistrodon acutus PE=1 SV=1					
44.	ATP5F1_HUMAN	Mass: 28948	Score: 35	Expect: 1.9e+002	Matches: 6
ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2					
45.	PINH_ECOLI	Mass: 9187	Score: 35	Expect: 1.9e+002	Matches: 3
Putative DNA-invertase from prophage CP4-44 (Fragment) OS=Escherichia coli (strain K12) GN=pinH PE=5 SV=2					
46.	RP23_PSEAK	Mass: 11021	Score: 34	Expect: 2e+002	Matches: 5
50S ribosomal protein L23, chloroplastic OS=Pseudomonas aeruginosa GN=rpL23 PE=3 SV=1					
47.	SPR2E_MOUSE	Mass: 9154	Score: 34	Expect: 2.1e+002	Matches: 3
Small proline-rich protein 2E OS=Mus musculus GN=Spr2e PE=2 SV=1					

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance: \pm 0.5 Da
 Fragment Mass Tolerance: \pm 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Query1 (822.8389,1+): <no title>
 Query2 (825.8382,1+): <no title>

MYH mass+c

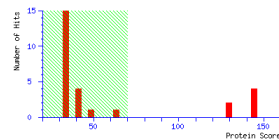


Mascot Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 08:36:32 GMT
Top Score : 144 for MYH_MOUSE, Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary Help
Significance threshold $p < 0.05$ Max. number of hits 200
Preferred taxonomy All entries

Re-Search All Search Unmatched

- MYH_MOUSE** Mass: 224131 Score: 144 Expect: 2.2e-009 Matches: 14
Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1
MYH_PIG Mass: 223940 Score: 102 Expect: 3.5e-005 Matches: 11
Myosin-2 OS=Sus scrofa GN=MYH2 PE=2 SV=1
MYH_PIG Mass: 223940 Score: 102 Expect: 3.5e-005 Matches: 11
Myosin-2 OS=Sus scrofa GN=MYH2 PE=2 SV=1
MYH_MOUSE Mass: 223648 Score: 101 Expect: 4.4e-005 Matches: 11
Myosin-4 OS=Mus musculus GN=Myh4 PE=2 SV=1
MYH_RAT Mass: 223659 Score: 101 Expect: 4.4e-005 Matches: 11
Myosin-4 OS=Rattus norvegicus GN=Myh4 PE=1 SV=1
MYH_CANLF Mass: 224000 Score: 100 Expect: 5.5e-005 Matches: 11
Myosin-2 OS=Canis lupus familiaris GN=MYH2 PE=3 SV=1
MYH_HORSE Mass: 223538 Score: 100 Expect: 5.5e-005 Matches: 11
Myosin-2 OS=Equus caballus GN=MYH2 PE=2 SV=1
MYH_BOVIN Mass: 224108 Score: 82 Expect: 0.0031 Matches: 9
Myosin-2 OS=Bos taurus GN=MYH2 PE=2 SV=1
MYH_HUMAN Mass: 223611 Score: 78 Expect: 0.0089 Matches: 9
Myosin-8 OS=Homo sapiens GN=MYH8 PE=1 SV=3
MYH_CANLF Mass: 223791 Score: 75 Expect: 0.016 Matches: 9
Myosin-4 OS=Canis lupus familiaris GN=MYH4 PE=3 SV=1
MYH_HUMAN Mass: 223950 Score: 66 Expect: 0.15 Matches: 8
Myosin-2 OS=Homo sapiens GN=MYH2 PE=1 SV=1
MYH_CHICK Mass: 223664 Score: 42 Expect: 31 Matches: 6
Myosin-3 OS=Gallus gallus GN=MYH3 PE=2 SV=3
MYH3_HUMAN Mass: 224625 Score: 42 Expect: 39 Matches: 5
Myosin-13 OS=Homo sapiens GN=MYH13 PE=2 SV=2
MYSS_CHICK Mass: 223692 Score: 39 Expect: 95 Matches: 5
Myosin heavy chain, skeletal muscle, adult OS=Gallus gallus PE=1 SV=4
MYH_MOUSE Mass: 224754 Score: 35 Expect: 1.6e+002 Matches: 5
Myosin-3 OS=Mus musculus GN=Myh3 PE=2 SV=2
MYH3_RAT Mass: 224764 Score: 35 Expect: 1.6e+002 Matches: 5
Myosin-3 OS=Rattus norvegicus GN=Myh3 PE=3 SV=1
MYH3_RAT Mass: 224628 Score: 35 Expect: 1.6e+002 Matches: 3
Myosin-8 (Fragment) OS=Rattus norvegicus GN=Myh8 PE=2 SV=1
- MYH_PIG** Mass: 223963 Score: 144 Expect: 2.2e-009 Matches: 14
Myosin-1 OS=Sus scrofa GN=MYH1 PE=2 SV=1
MYH_BOVIN Mass: 223780 Score: 143 Expect: 2.8e-009 Matches: 14
Myosin-1 OS=Bos taurus GN=MYH1 PE=2 SV=2
MYH_HORSE Mass: 223788 Score: 143 Expect: 2.8e-009 Matches: 14
Myosin-1 OS=Equus caballus GN=MYH1 PE=2 SV=1
- MYH_RABIT** Mass: 223856 Score: 142 Expect: 3.5e-009 Matches: 14
Myosin-4 OS=Onchotylagus cuniculus GN=MYH4 PE=1 SV=1
Myosin-4 OS=Onchotylagus cuniculus GN=MYH4 PE=1 SV=1
- MYH_CANLF** Mass: 223938 Score: 142 Expect: 3.5e-009 Matches: 14
Myosin-1 OS=Canis lupus familiaris GN=MYH1 PE=3 SV=2
- MYH_PIG** Mass: 224025 Score: 130 Expect: 5.5e-008 Matches: 13
Myosin-4 OS=Sus scrofa GN=MYH4 PE=2 SV=1
MYH_HUMAN Mass: 223918 Score: 103 Expect: 2.8e-005 Matches: 11
Myosin-4 OS=Homo sapiens GN=MYH4 PE=1 SV=2
MYH_CANLF Mass: 223957 Score: 78 Expect: 0.0085 Matches: 9
Myosin-8 OS=Canis lupus familiaris GN=MYH8 PE=3 SV=1
MYH_MOUSE Mass: 223672 Score: 66 Expect: 0.14 Matches: 8
Myosin-8 OS=Mus musculus GN=Myh8 PE=2 SV=2
MYH3_CANLF Mass: 224304 Score: 41 Expect: 48 Matches: 5
Myosin-13 OS=Canis lupus familiaris GN=MYH13 PE=3 SV=1
- MYH_HUMAN** Mass: 223993 Score: 129 Expect: 6.9e-008 Matches: 13
Myosin-1 OS=Homo sapiens GN=MYH1 PE=1 SV=3
- MYSS_RABIT** Mass: 125780 Score: 66 Expect: 0.14 Matches: 7
Myosin heavy chain, skeletal muscle (Fragments) OS=Onchotylagus cuniculus PE=1 SV=2
- MYH3_HUMAN** Mass: 224869 Score: 46 Expect: 14 Matches: 6
Myosin-3 OS=Homo sapiens GN=MYH3 PE=1 SV=3
- GYSB_BORBU** Mass: 71522 Score: 44 Expect: 22 Matches: 3
DNA gyrase subunit B OS=Borrelia burgdorferi (strain ATCC 35210 / B31 / CIP 102532 / DSM 4680) GN=gyrB PE=3 SV=4
- BAFL_BOVIN** Mass: 10757 Score: 42 Expect: 32 Matches: 2
Barrier-to-autointegration factor-like protein OS=Bos taurus GN=BAFL2 PE=3 SV=1
- DNAL_MANSU** Mass: 41675 Score: 40 Expect: 54 Matches: 3
Chaperone protein DnaJ OS=Mannheimia succiniciproducens (strain NEBEL55E) GN=dnaJ PE=3 SV=2
- CASP_ARATH** Mass: 79751 Score: 38 Expect: 96 Matches: 4
Protein CASP OS=Arabidopsis thaliana GN=CASP PE=1 SV=2
- SPR2E_MOUSE** Mass: 9154 Score: 37 Expect: 1.2e+002 Matches: 2
Small proline-rich protein 2E OS=Mus musculus GN=Spr2e PE=2 SV=1
SPR21_MOUSE Mass: 9104 Score: 37 Expect: 1.2e+002 Matches: 2
Small proline-rich protein 21 OS=Mus musculus GN=Spr21 PE=3 SV=1

Type of search	Sequence Query
Enzyme	Lys-N
Fixed modifications	None/oxymethyl
Mass values	Monoisotopic
Protein Mass	Unrestricted
Peptide Mass Tolerance	± 0.5 Da
Fragment Mass Tolerance	± 0.6 Da
Max Missed Cleavages	1
Instrument type	Default
Query1 (822.8399,1+)	(no title) seq(C-F)
Query2 (825.8768,1+)	(no title) seq(C-Y)
Query3 (836.8388,1+)	(no title) seq(C-Y)
Query4 (856.8398,1+)	(no title) seq(C-Y)
Query5 (857.8071,1+)	(no title) seq(C-Y)
Query6 (857.8754,1+)	(no title) seq(C-F)
Query7 (857.8754,1+)	(no title) seq(C-L)
Query8 (865.8724,1+)	(no title) seq(C-F)
Query9 (865.8724,1+)	(no title) seq(C-D)
Query10 (897.8425,1+)	(no title) seq(C-D)
Query11 (907.7966,1+)	(no title) seq(C-K)
Query12 (907.7966,1+)	(no title) seq(C-Q)

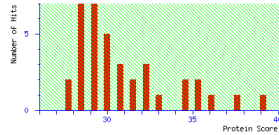
PYGM mass

Mascot Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 09:10:30 GMT
Top Score : 39 for [HIS2_METFK](#), Phosphoribosyl-ATP pyrophosphatase OS=Methylobacillus flagellatus (strain KT / ATCC 51484 / DSM 6875) GN=hisE PE=3 SV=1

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As	Concise Protein Summary	Help
Significance threshold p<	0.05	Max. number of hits 200
Preferred taxonomy	All entries	
Re-Search All	Search Unmatched	
1.	HIS2_METFK Mass: 11579 Score: 39 Expect: 68 Matches: 7 Phosphoribosyl-ATP pyrophosphatase OS=Methylobacillus flagellatus (strain KT / ATCC 51484 / DSM 6875) GN=hisE PE=3 SV=1	
2.	PSTB_SACO2 Mass: 32647 Score: 38 Expect: 94 Matches: 9 Phosphate import ATP-binding protein PstB OS=Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024) GN=pstB PE=3 SV=1	
2.	PSTB_SACO2 Mass: 32647 Score: 38 Expect: 94 Matches: 9 Phosphate import ATP-binding protein PstB OS=Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024) GN=pstB PE=3 SV=1	
3.	RHOJ_BOVIN Mass: 28502 Score: 36 Expect: 1.3e+002 Matches: 10 Rho-related GTP-binding protein RhoJ OS=Bos taurus GN=RHOJ PE=2 SV=1	
4.	ERA_LACLA Mass: 34773 Score: 35 Expect: 1.7e+002 Matches: 13 GTPase Era OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=era PE=3 SV=1	
4.	ERA_LACLM Mass: 34773 Score: 35 Expect: 1.7e+002 Matches: 13 GTPase Era OS=Lactococcus lactis subsp. cremoris (strain M3183) GN=era PE=3 SV=1	
4.	ERA_LACLS Mass: 34787 Score: 34 Expect: 2e+002 Matches: 13 GTPase Era OS=Lactococcus lactis subsp. cremoris (strain SK11) GN=era PE=3 SV=1	
5.	RAP1_PHYPO Mass: 21313 Score: 35 Expect: 1.7e+002 Matches: 8 Ras-related protein Rap-1 OS=Physarum polycephalum GN=RAP1 PE=2 SV=1	
6.	RXT3_YEAST Mass: 33907 Score: 34 Expect: 2e+002 Matches: 10 Transcriptional regulatory protein RXT3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=RXT3 PE=1 SV=1	
7.	RL1_CARYO Mass: 24778 Score: 34 Expect: 2e+002 Matches: 10 50S ribosomal protein L1 OS=Carboxydothermus hydrogenofomans (strain ATCC 204508 / Z-2901) GN=rlA PE=3 SV=1	
8.	NIR_EMENI Mass: 124019 Score: 33 Expect: 2.7e+002 Matches: 23 Nitrite reductase [NAD(P)H] OS=Emicella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 184 / M139) GN=nirA PE=3 SV=2	
9.	PGK2_METEV Mass: 35072 Score: 32 Expect: 3.2e+002 Matches: 9 2-phosphoglycerate kinase OS=Methanothermobacter fervidus (strain ATCC 43054 / DSM 2088 / JCM 10308 / V24 S) GN=pgk2 PE=1 SV=1	
10.	TRMD_FRATN Mass: 28391 Score: 32 Expect: 3.3e+002 Matches: 12 tRNA (guanine-N(1))-methyltransferase OS=Francisella tularensis subsp. novicida (strain U112) GN=trmD PE=3 SV=1	
11.	PYRH_METSS Mass: 24295 Score: 32 Expect: 3.4e+002 Matches: 7 Uridylate kinase OS=Metallosphaera sedula (strain ATCC 51363 / DSM 5348) GN=pyrH PE=3 SV=1	
12.	ARR8_ARATH Mass: 25629 Score: 32 Expect: 3.7e+002 Matches: 9 Two-component response regulator ARR8 OS=Arabidopsis thaliana GN=ARR8 PE=1 SV=1	
13.	ARG8_PACAH Mass: 27604 Score: 31 Expect: 4e+002 Matches: 12 Acetylglutamate kinase OS=Bacillus thuringiensis (strain AI Hakan) GN=argB PE=3 SV=2	
13.	ARG8_PACAH Mass: 27604 Score: 31 Expect: 4e+002 Matches: 12 Acetylglutamate kinase OS=Bacillus thuringiensis (strain AI Hakan) GN=argB PE=3 SV=2	
14.	ILVC_HELPY Mass: 36695 Score: 31 Expect: 4.9e+002 Matches: 13 Ketol-acid reductoisomerase OS=Helicobacter pylori (strain ATCC 700392 / 26695) GN=ilvC PE=3 SV=1	
15.	ALBA_METML Mass: 9922 Score: 31 Expect: 4.4e+002 Matches: 8 DNA/RNA-binding protein Alba OS=Methanococcus marisnigri (strain ATCC 35101 / DSM 1498 / JRI) GN=alba PE=3 SV=1	
16.	Y888_METJA Mass: 37757 Score: 31 Expect: 4.8e+002 Matches: 10 Uncharacterized protein MJ0988 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NERC 100440) GN=MJ0988 PE=4 SV=1	
17.	RL28_LACOC Mass: 6973 Score: 30 Expect: 5.1e+002 Matches: 7 50S ribosomal protein L28 OS=Lactobacillus casei (strain ATCC 334) GN=rlmB PE=3 SV=1	
17.	RL28_LACOC Mass: 6973 Score: 30 Expect: 5.1e+002 Matches: 7 50S ribosomal protein L28 OS=Lactobacillus casei (strain ATCC 334) GN=rlmB PE=3 SV=1	
18.	ALBU_PONAB Mass: 71465 Score: 30 Expect: 5.3e+002 Matches: 18 Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=2	
19.	APT_CHLEP Mass: 19180 Score: 30 Expect: 5.6e+002 Matches: 6 Adenine phosphoribosyltransferase OS=Chlorobium phaeovibrioides (strain DSM 285 / 1930) GN=apt PE=3 SV=1	
20.	MURB_RICBR Mass: 33322 Score: 30 Expect: 5.8e+002 Matches: 12 UDP-N-acetylenolpyruvylglucosamine reductase OS=Rickettsia bellii (strain RML389-C) GN=murB PE=3 SV=1	
21.	CHLB_PROMS Mass: 58218 Score: 30 Expect: 5.9e+002 Matches: 12 Light-independent protochlorophyllide reductase subunit B OS=Prochlorococcus marinus (strain AS9601) GN=chlB PE=3 SV=1	
22.	SURA_VIBPA Mass: 47464 Score: 29 Expect: 6.3e+002 Matches: 12 Chaperone SurA OS=Vibrio parahaemolyticus serotype O3:K8 (strain RIMD 2210633) GN=surA PE=3 SV=1	
23.	FABA_VIBOC Mass: 19146 Score: 29 Expect: 6.3e+002 Matches: 6 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Vibrio cholerae serotype O1 (strain ATCC 39541 / Classical Ogawa 395 / O395) GN=fabA PE=3 SV=1	
23.	FABA_VIBOC Mass: 19146 Score: 29 Expect: 6.3e+002 Matches: 6 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Vibrio cholerae serotype O1 (strain ATCC 39541 / El Tor Inaba N16961) GN=fabA PE=3 SV=1	
23.	FABA_VIBOM Mass: 19146 Score: 29 Expect: 6.3e+002 Matches: 6 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase OS=Vibrio cholerae serotype O1 (strain ATCC 39541 / El Tor Inaba N16961) GN=fabA PE=3 SV=1	
24.	MAM3_ARATH Mass: 55832 Score: 29 Expect: 6.3e+002 Matches: 15 Methylthioalkylmalate synthase 3, chloroplastic OS=Arabidopsis thaliana GN=MAM3 PE=1 SV=1	

Methylthioalkylmalate synthase 3, chloroplastic OS=Arabidopsis thaliana GN=MAM3 PE=1 SV=1					
25.	AEP2_YEAS1	Mass: 68173	Score: 29	Expect: 6.5e+002	Matches: 15
ATPase expression protein 2, mitochondrial OS=Saccharomyces cerevisiae (strain RM11-1a) GN=AEP2 PE=3 SV=1					
	AEP2_YEAS6	Mass: 68146	Score: 29	Expect: 6.5e+002	Matches: 15
ATPase expression protein 2, mitochondrial OS=Saccharomyces cerevisiae (strain AWRI1631) GN=AEP2 PE=3 SV=1					
	AEP2_YEAS8	Mass: 68173	Score: 29	Expect: 6.5e+002	Matches: 15
ATPase expression protein 2, mitochondrial OS=Saccharomyces cerevisiae (strain Lalvin EC1118 / Prise de mousse) GN=AEP2 PE=3 SV=1					
26.	KAD_PSEFS	Mass: 23309	Score: 29	Expect: 6.8e+002	Matches: 6
Adenylate kinase OS=Pseudomonas fluorescens (strain SBN25) GN=adk PE=3 SV=1					
27.	Y6387_DICD1	Mass: 4917	Score: 29	Expect: 7.1e+002	Matches: 7
Putative uncharacterized protein ODB_G0285187 OS=Dictyostelium discoideum GN=ODB_G0285187 PE=4 SV=1					
28.	AROD_STAA1	Mass: 27063	Score: 29	Expect: 7.1e+002	Matches: 10
3-dehydroquinate dehydratase OS=Staphylococcus aureus (strain M3 / ATCC 700698) GN=aroD PE=3 SV=1					
	AROD_STAA2	Mass: 27063	Score: 29	Expect: 7.1e+002	Matches: 10
3-dehydroquinate dehydratase OS=Staphylococcus aureus (strain JH1) GN=aroD PE=3 SV=1					
	AROD_STAA9	Mass: 27063	Score: 29	Expect: 7.1e+002	Matches: 10
3-dehydroquinate dehydratase OS=Staphylococcus aureus (strain JH9) GN=aroD PE=3 SV=1					
	AROD_STAA6	Mass: 27063	Score: 29	Expect: 7.1e+002	Matches: 10
3-dehydroquinate dehydratase OS=Staphylococcus aureus (strain M50 / ATCC 700699) GN=aroD PE=3 SV=1					
	AROD_STAA8	Mass: 27063	Score: 29	Expect: 7.1e+002	Matches: 10
3-dehydroquinate dehydratase OS=Staphylococcus aureus (strain N315) GN=aroD PE=3 SV=1					
29.	MH_ECO71	Mass: 32491	Score: 29	Expect: 7.3e+002	Matches: 10
Malate dehydrogenase OS=Escherichia coli 07:K1 (strain JAI39 / ExPEC) GN=mdh PE=3 SV=1					
	MH_ECO10	Mass: 32490	Score: 29	Expect: 7.3e+002	Matches: 10
Malate dehydrogenase OS=Escherichia coli 017:H52:H18 (strain UNW26 / ExPEC) GN=mdh PE=3 SV=1					
	MH_ECO39	Mass: 32491	Score: 29	Expect: 7.3e+002	Matches: 10
Malate dehydrogenase OS=Escherichia coli (strain SMS-3-5 / SEDEC) GN=mdh PE=3 SV=1					
30.	NIA2_ARATH	Mass: 103706	Score: 29	Expect: 7.4e+002	Matches: 15
Nitrate reductase [NADH] 2 OS=Arabidopsis thaliana GN=NIA2 PE=1 SV=1					
31.	SYC_LACAC	Mass: 55092	Score: 29	Expect: 7.4e+002	Matches: 11
Cysteine-tRNA ligase OS=Lactobacillus acidophilus (strain ATCC 700396 / NK956 / NZ / NORM) GN=CysS PE=3 SV=1					
32.	YGRW_YEAST	Mass: 44504	Score: 29	Expect: 7.4e+002	Matches: 13
Uncharacterized protein YGR168C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YGR168C PE=4 SV=1					
32.	YGRW_YEAST1	Mass: 44504	Score: 29	Expect: 7.4e+002	Matches: 13
Uncharacterized protein YGR168C OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YGR168C PE=4 SV=1					
33.	BUCC_APLCA	Mass: 53493	Score: 29	Expect: 7.6e+002	Matches: 9
Buccalin OS=Aplysia californica PE=1 SV=2					
34.	AEP2_YEAS7	Mass: 68231	Score: 28	Expect: 7.8e+002	Matches: 17
ATPase expression protein 2, mitochondrial OS=Saccharomyces cerevisiae (strain YJM789) GN=AEP2 PE=3 SV=1					
35.	RL17_MYOMO	Mass: 13613	Score: 28	Expect: 8.1e+002	Matches: 7
50S ribosomal protein L17 OS=Mycoplasma mobile (strain ATCC 43863 / 163K / NCTC 11711) GN=rpLQ PE=3 SV=1					
36.	ATPF_GUTH	Mass: 20228	Score: 28	Expect: 8.9e+002	Matches: 10
ATP synthase subunit b, chloroplastic OS=Guillardia theta GN=atpF PE=3 SV=1					
37.	RL35A_MOUSE	Mass: 12662	Score: 28	Expect: 9.4e+002	Matches: 7
60S ribosomal protein L35a OS=Mus musculus GN=Rpl35a PE=1 SV=2					

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.5 Da
 Fragment Mass Tolerance : ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Query1 (822.8594,1+) : <no title>
 Query2 (825.8621,1+) : <no title>
 Query3 (829.8763,1+) : <no title>
 Query4 (831.8586,1+) : <no title>
 Query5 (831.8587,1+) : <no title>
 Query6 (832.8786,1+) : <no title>
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 Query8 (845.8452,1+) : <no title>
 Query9 (845.8711,1+) : <no title>
 Query10 (854.3198,1+) : <no title>
 Query11 (855.9137,1+) : <no title>
 Query12 (857.8131,1+) : <no title>
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 Query14 (861.4601,1+) : <no title>

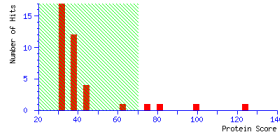
PYGM mass/mass+c

Mascot Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 09:24:26 GMT
Top Score : 124 for [PYGM_RABIT](#), Glycogen phosphorylase, muscle form OS=Oryctolagus cuniculus GN=PYGM PE=1 SV=3

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: Concise Protein Summary [Help](#)
Significance threshold $p < 0.05$ Max. number of hits 200
Preferred taxonomy All entries

Re-Search All Search Unmatched

1.	PYGM_RABIT	Mass: 97750	Score: 124	Expect: 2.2e-007	Matches: 14	Glycogen phosphorylase, muscle form OS=Oryctolagus cuniculus GN=PYGM PE=1 SV=3
2.	PYGM_HUMAN	Mass: 97495	Score: 101	Expect: 4.4e-005	Matches: 11	
2.	PYGM_HUMAN	Mass: 97495	Score: 101	Expect: 4.4e-005	Matches: 11	Glycogen phosphorylase, muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6
	PYGM_MACACA	Mass: 97553	Score: 101	Expect: 4.4e-005	Matches: 11	Glycogen phosphorylase, muscle form OS=Macaca fascicularis GN=PYGM PE=2 SV=3
3.	PYGM_MOUSE	Mass: 97689	Score: 81	Expect: 0.0048	Matches: 9	Glycogen phosphorylase, muscle form OS=Mus musculus GN=Pygm PE=1 SV=3
4.	PYGM_SHEEP	Mass: 97710	Score: 78	Expect: 0.0091	Matches: 9	Glycogen phosphorylase, muscle form OS=Ovis aries GN=PYGM PE=2 SV=3
	PYGM_BOVIN	Mass: 97696	Score: 62	Expect: 0.32	Matches: 8	Glycogen phosphorylase, muscle form OS=Bos taurus GN=PYGM PE=1 SV=3
5.	PYGM_RAT	Mass: 97734	Score: 60	Expect: 0.62	Matches: 8	Glycogen phosphorylase, muscle form OS=Rattus norvegicus GN=Pygm PE=1 SV=5
6.	DNAJ_MYCPU	Mass: 42383	Score: 46	Expect: 14	Matches: 11	Chaperone protein DnaJ OS=Mycoplasma pulmonis (strain UAB CTIP) GN=dnaJ PE=3 SV=2
7.	RL1_CARBQ	Mass: 24778	Score: 45	Expect: 19	Matches: 8	50S ribosomal protein L1 OS=Carboxydothermus hydrogenofomans (strain ATCC BAA-161 / DSM 6008 / Z-2901) GN=rp1A PE=3 SV=1
8.	FIM1_NEIMA	Mass: 18239	Score: 42	Expect: 32	Matches: 7	Fimbrial protein OS=Neisseria meningitidis serogroup A / serotype 4A (strain Z491) GN=piIE PE=1 SV=1
9.	HIS2_METBK	Mass: 11579	Score: 41	Expect: 40	Matches: 5	Phosphoribosyl-ATP pyrophosphatase OS=Methylobacillus flagellatus (strain KT / ATCC 51484 / DSM 6875) GN=hisE PE=3 SV=1
10.	SUR4_VIBPA	Mass: 47464	Score: 39	Expect: 68	Matches: 12	Chaperone SurA OS=Vibrio parahaemolyticus serotype O3:H6 (strain RIMD Z210633) GN=surA PE=3 SV=1
11.	RL22_CALS8	Mass: 13894	Score: 38	Expect: 91	Matches: 7	50S ribosomal protein L22 OS=Caldicellulosiruptor saccharolyticus (strain ATCC 43494 / DSM 8903 / Tc8T 6331) GN=rp1V PE=3 SV=1
12.	W_HENDH	Mass: 49553	Score: 37	Expect: 1e+002	Matches: 7	Protein W OS=Hendra virus (isolate Horse/Australia/Hendra/1994) GN=PPV/C PE=3 SV=1
13.	EFTS_THIDA	Mass: 31135	Score: 37	Expect: 1e+002	Matches: 9	Elongation factor Ts OS=Thiobacillus denitrificans (strain ATCC 25259) GN=tsf PE=3 SV=1
						Elongation factor Is OS=Thiobacillus denitrificans (strain ATCC 25259) GN=tsf PE=3 SV=1
14.	RLUC_PASBU	Mass: 37194	Score: 36	Expect: 1.9e+002	Matches: 8	Ribosomal large subunit pseudouridine synthase C OS=Pasteurella multocida (strain Pm70) GN=rpluC PE=3 SV=1
15.	YBEY_BORBP	Mass: 17829	Score: 36	Expect: 1.4e+002	Matches: 5	Endoribonuclease YbeY OS=Borrelia burgdorferi (strain ATCC BAA-2496 / DSM 23469 / PB1) GN=ybeY PE=3 SV=1
16.	IAA3_ARATH	Mass: 21913	Score: 36	Expect: 1.4e+002	Matches: 10	Auxin-responsive protein IAA3 OS=Arabidopsis thaliana GN=IAA3 PE=1 SV=1
17.	RL21_SHEM1	Mass: 11356	Score: 36	Expect: 1.5e+002	Matches: 5	50S ribosomal protein L21 OS=Shewanella sp. (strain MR-4) GN=rp1U PE=3 SV=1
	RL21_SHEM1	Mass: 11356	Score: 36	Expect: 1.5e+002	Matches: 5	50S ribosomal protein L21 OS=Shewanella sp. (strain MR-7) GN=rp1U PE=3 SV=1
18.	RL10E_METS5	Mass: 20052	Score: 35	Expect: 1.6e+002	Matches: 5	50S ribosomal protein L10e OS=Metallosphaera sedula (strain ATCC 51363 / DSM 5348) GN=rp10e PE=3 SV=1
19.	CIF1_SCHPO	Mass: 36053	Score: 35	Expect: 1.7e+002	Matches: 6	Calnexin-independent factor 1 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=cif1 PE=4 SV=1
20.	MSBA_HAETU	Mass: 64539	Score: 35	Expect: 1.7e+002	Matches: 7	Lipid A export ATP-binding/permease protein MsbA OS=Haemophilus ducreyi (strain 35000HP / ATCC 700724) GN=msbA PE=3 SV=1
21.	Y214_RICPE	Mass: 64599	Score: 35	Expect: 1.7e+002	Matches: 8	Putative export ATP-binding/permease protein RF_0214 OS=Rickettsia felis (strain ATCC VR-1525 / URRMXCa12) GN=RF_0214 PE=3 SV=2
22.	HMOH1_DICDI	Mass: 61161	Score: 35	Expect: 1.8e+002	Matches: 9	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 OS=Dictyostelium discoideum GN=hmgA PE=2 SV=1
23.	RPO4_BREBN	Mass: 34825	Score: 35	Expect: 1.9e+002	Matches: 8	DNA-directed RNA polymerase subunit alpha OS=Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599) GN=rpoA PE=3 SV=1
24.	ARO3_STA41	Mass: 27063	Score: 34	Expect: 2e+002	Matches: 9	3-dehydroquinate dehydratase OS=Staphylococcus aureus (strain N3 / ATCC 700698) GN=farD PE=3 SV=1
	ARO3_STA42	Mass: 27063	Score: 34	Expect: 2e+002	Matches: 9	3-dehydroquinate dehydratase OS=Staphylococcus aureus (strain JH1) GN=farD PE=3 SV=1
	ARO3_STA49	Mass: 27063	Score: 34	Expect: 2e+002	Matches: 9	3-dehydroquinate dehydratase OS=Staphylococcus aureus (strain JH9) GN=farD PE=3 SV=1
	ARO3_STA4M	Mass: 27063	Score: 34	Expect: 2e+002	Matches: 9	

Type of search	: Sequence Query
Enzyme	: Lys-N
Fixed modifications	: Carbamidomethyl (C)
Modifications	: Monoisotopic
Protein Mass	: Unrestricted
Peptide Mass Tolerance:	: ± 0.5 Da
Fragment Mass Tolerance:	: ± 0.8 Da
Mass Tolerances	: Missed Cleavages
Instrument type	: Default
Query1 (822.8584,1+)	: cno (title)
	: cno (seq)
Query2 (825.8862,1+)	: cno (title)
Query3 (829.8763,1+)	: cno (title)
Query4 (831.8858,1+)	: cno (title)
Query5 (831.8954,1+)	: cno (title)
Query6 (832.8786,1+)	: cno (title)
Query7 (837.8337,1+)	: cno (title)
Query8 (845.8452,1+)	: cno (title)
	: seq (C)
Query9 (845.8711,1+)	: cno (title)
Query10 (854.3198,1+)	: cno (title)
	: seq (C)

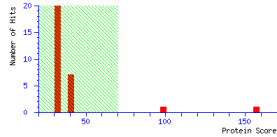
PYGM mass+

Mascot Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 09:24:40 GMT
Top Score : 157 for PYGM_RAB17, Glycogen phosphorylase, muscle form OS=Oryctolagus cuniculus GN=PYGM PE=1 SV=3

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As	Concise Protein Summary	Help
Significance threshold p<	0.05	Max. number of hits 200
Preferred taxonomy	All entries	
Re-Search All	Search Unmatched	
1.	<p>PYGM_RAB17 Mass: 97750 Score: 157 Expect: 1.1e-010 Matches: 9 Glycogen phosphorylase, muscle form OS=Oryctolagus cuniculus GN=PYGM PE=1 SV=3 PYGM_HUMAN Mass: 97495 Score: 121 Expect: 4.4e-007 Matches: 7 Glycogen phosphorylase, muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6 PYGM_HUMAN Mass: 97495 Score: 121 Expect: 4.4e-007 Matches: 7 Glycogen phosphorylase, muscle form OS=Homo sapiens GN=PYGM PE=1 SV=6 PYGM_MACFA Mass: 97553 Score: 121 Expect: 4.4e-007 Matches: 7 Glycogen phosphorylase, muscle form OS=Macaca fascicularis GN=PYGM PE=2 SV=3 PYGM_SHEEP Mass: 97710 Score: 97 Expect: 0.0001 Matches: 6 Glycogen phosphorylase, muscle form OS=Ovis aries GN=PYGM PE=2 SV=3 PYGM_BOVIN Mass: 97696 Score: 79 Expect: 0.0074 Matches: 5 Glycogen phosphorylase, muscle form OS=Bos taurus GN=PYGM PE=1 SV=3 PYGM_RAT Mass: 97734 Score: 63 Expect: 0.28 Matches: 4 Glycogen phosphorylase, muscle form OS=Rattus norvegicus GN=PYGM PE=1 SV=5</p>	
2.	<p>PYGM_MOUSE Mass: 97689 Score: 96 Expect: 0.00013 Matches: 6 Glycogen phosphorylase, muscle form OS=Mus musculus GN=PYGM PE=1 SV=3</p>	
3.	<p>YL170_MIMIV Mass: 51930 Score: 44 Expect: 25 Matches: 3 Putative FNIP repeat-containing protein L170 OS=Acanthamoeba polyphaga mimivirus GN=MIMI_L170 PE=4 SV=1</p>	
4.	<p>DNAJ_MYCPU Mass: 42383 Score: 42 Expect: 36 Matches: 3 Chaperone protein DnaJ OS=Mycobacterium tuberculosis (strain H37Rv) GN=dnaJ PE=3 SV=2</p>	
5.	<p>RL30_BACLD Mass: 6633 Score: 40 Expect: 55 Matches: 2 50S ribosomal protein L30 OS=Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NERC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46) GN=rpL PE=3 SV=1</p>	
6.	<p>YAGL_CANTS Mass: 18717 Score: 40 Expect: 62 Matches: 2 Uncharacterized 18.6 kDa protein in alpha-glucosidase 3' region OS=Candida tsukubaensis PE=4 SV=1</p>	
7.	<p>E8_VACCC Mass: 31973 Score: 36 Expect: 1.2e+002 Matches: 2 Protein E8 OS=Vaccinia virus (strain Copenhagen) GN=E8R PE=2 SV=1 E8_VACCV Mass: 31868 Score: 36 Expect: 1.2e+002 Matches: 2 Protein E8 OS=Vaccinia virus (strain Western Reserve) GN=VACV0064 PE=1 SV=1</p>	
8.	<p>DOF53_ARATH Mass: 29531 Score: 36 Expect: 1.3e+002 Matches: 2 Bif zinc finger protein DOF5.3 OS=Arabidopsis thaliana GN=DOF5.3 PE=2 SV=1</p>	
9.	<p>Y8776_DICD1 Mass: 14040 Score: 36 Expect: 1.3e+002 Matches: 2 Putative uncharacterized protein DOB_G0286001 OS=Dictyostelium discoideum GN=DOB_G0286001 PE=4 SV=1</p>	
10.	<p>RL22_CALS8 Mass: 13894 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L22 OS=Caldicellulosigranulatus saccharolyticus (strain ATCC 43494 / DSM 8903 / Tc8T 6331) GN=rpL PE=3 SV=1</p>	
11.	<p>RL21_SHER2 Mass: 11403 Score: 36 Expect: 1.3e+002 Matches: 2</p>	
11.	<p>RL21_SHER2 Mass: 11403 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella baltica (strain OS223) GN=rpL PE=3 SV=1 RL21_SHER3 Mass: 11403 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella baltica (strain OS195 / ATCC BAA-1091) GN=rpL PE=3 SV=1 RL21_SHER8 Mass: 11403 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella baltica (strain OS185) GN=rpL PE=3 SV=1 RL21_SHER9 Mass: 11403 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella baltica (strain OS195) GN=rpL PE=3 SV=1 RL21_SHERD Mass: 11329 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella denitrificans (strain OS217 / ATCC BAA-1090 / DSM 15013) GN=rpL PE=3 SV=1 RL21_SHERN Mass: 11360 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella frigidimarina (strain NCIMB 400) GN=rpL PE=3 SV=1 RL21_SHERH Mass: 11475 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella halifaxensis (strain HAM-EB4) GN=rpL PE=3 SV=1 RL21_SHERP Mass: 11475 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella loihica (strain ATCC BAA-1088 / PV-4) GN=rpL PE=3 SV=1 RL21_SHERA Mass: 11475 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella pealeana (strain ATCC 700345 / ANG-S01) GN=rpL PE=3 SV=1 RL21_SHERC Mass: 11361 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella putrefaciens (strain OS192 / ATCC BAA-453) GN=rpL PE=3 SV=1 RL21_SHERW Mass: 11448 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella piezotolerans (strain WP3 / JCM 13877) GN=rpL PE=3 SV=1 RL21_SHERS Mass: 11389 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella sediminis (strain HAM-EB3) GN=rpL PE=3 SV=1 RL21_SHERM Mass: 11361 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella sp. (strain MS-18-1) GN=rpL PE=3 SV=1 RL21_SHERN Mass: 11505 Score: 36 Expect: 1.3e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella woodii (strain ATCC 51908 / MS32) GN=rpL PE=3 SV=1 RL21_SHERM Mass: 11356 Score: 35 Expect: 1.8e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella sp. (strain MR-4) GN=rpL PE=3 SV=1 RL21_SHERS Mass: 11356 Score: 35 Expect: 1.8e+002 Matches: 2 50S ribosomal protein L21 OS=Shewanella sp. (strain MR-7) GN=rpL PE=3 SV=1</p>	
12.	<p>TEN1_YEAST Mass: 18882 Score: 36 Expect: 1.4e+002 Matches: 2 Telomere length regulation protein TEN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TEN1 PE=1 SV=1</p>	
13.	<p>RL22_CHLD Mass: 13257 Score: 36 Expect: 1.4e+002 Matches: 2 50S ribosomal protein L22 OS=Chlorobium phaeobacteroides (strain DSM 266) GN=rpL PE=3 SV=1</p>	
14.	<p>IDA_DADT1 Mass: 96470 Score: 36 Expect: 1.4e+002 Matches: 2</p>	

Type of search	: Sequence Query
Enzyme	: Lys-N
Fixed modifications	: Carboxymethyl (C)
Mass values	: Monoisotopic
Protein Mass	: Unrestricted
Peptide Mass Tolerance	: ± 0.5 Da
Fragment Mass Tolerance	: ± 0.6 Da
Max Missed Cleavages	: 1
Instrument type	: Default
Query1 (822.8594,1+)	: <no title> : seq(A)
Query2 (845.8452,1+)	: <no title> : seq(C-Y)
Query3 (855.9137,1+)	: <no title> : seq(C-L)
Query4 (855.9137,1+)	: <no title> : seq(C-L)
Query5 (867.8736,1+)	: <no title> : seq(C-L)
Query6 (867.8736,1+)	: <no title> : seq(C-L)
Query7 (872.8096,1+)	: <no title> : seq(C-L)
Query8 (900.8648,1+)	: <no title> : seq(C-P)
Query9 (918.8184,1+)	: <no title> : seq(C-L)
Query10 (918.8184,1+)	: <no title> : seq(C-L)
Query11 (923.8497,1+)	: <no title>

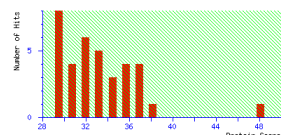
CA mass

MASCOT Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 09:50:30 GMT
Top Score : 48 for **CAN2_BOVIN**, Carbonic anhydrase 2 OS=Bos taurus GN=CA2 PE=1 SV=3

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As		Concise Protein Summary		Help	
Significance threshold p<		0.05		Max. number of hits 200	
Preferred taxonomy		All entries			
Re-Search All		Search Unmatched			
1.	CAN2_BOVIN	Mass: 29096	Score: 48	Expect: 8.5	Matches: 11
Carbonic anhydrase 2 OS=Bos taurus GN=CA2 PE=1 SV=3					
2.	RS16_SHEFN	Mass: 9318	Score: 38	Expect: 78	Matches: 5
30S ribosomal protein S16 OS=Shewanella frigidimarina (strain NCIMB 400) GN=rpsP PE=3 SV=1					
2.	RS16_SHEFN	Mass: 9318	Score: 38	Expect: 78	Matches: 5
30S ribosomal protein S16 OS=Shewanella frigidimarina (strain NCIMB 400) GN=rpsP PE=3 SV=1					
3.	METN2_STAB	Mass: 38372	Score: 38	Expect: 98	Matches: 9
Methionine import ATP-binding protein MetN 2 OS=Staphylococcus aureus (strain bovine RF122 / ET3-1) GN=metN2 PE=3 SV=1					
	METN2_STAAM	Mass: 38351	Score: 38	Expect: 98	Matches: 9
Methionine import ATP-binding protein MetN 2 OS=Staphylococcus aureus (strain M50 / ATCC 700699) GN=metN2 PE=1 SV=1					
	METN2_STAN	Mass: 38351	Score: 38	Expect: 98	Matches: 9
Methionine import ATP-binding protein MetN 2 OS=Staphylococcus aureus (strain N315) GN=metN2 PE=1 SV=1					
4.	AP4S1_HUMAN	Mass: 17168	Score: 37	Expect: 1.1e+002	Matches: 8
AP-4 complex subunit sigma-1 OS=Homo sapiens GN=AP4S1 PE=2 SV=1					
5.	AP4S1_MOUSE	Mass: 16981	Score: 37	Expect: 1.1e+002	Matches: 8
AP-4 complex subunit sigma-1 OS=Mus musculus GN=Ap4s1 PE=2 SV=1					
6.	COB0_PYSFU	Mass: 32432	Score: 37	Expect: 1.2e+002	Matches: 7
Probable cobalamin biosynthesis protein CobD OS=Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1) GN=cobD PE=3 SV=1					
7.	BLOD_CLOB	Mass: 25775	Score: 36	Expect: 1.4e+002	Matches: 8
ATP-dependent dethiobiotin synthetase BldD OS=Clostridium botulinum (strain BkIund 17B / Type B) GN=bldD PE=3 SV=1					
8.	LEUD_CYTH	Mass: 22298	Score: 36	Expect: 1.4e+002	Matches: 8
3-isocrotylate dehydratase small subunit OS=Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469) GN=leuD PE=3 SV=1					
9.	RAN_SALSA	Mass: 24532	Score: 36	Expect: 1.6e+002	Matches: 9
GTP-binding nuclear protein Ran OS=Salmo salar GN=ran PE=2 SV=1					
10.	SLP1_BACAN	Mass: 86568	Score: 35	Expect: 1.7e+002	Matches: 20
S-layer protein sap OS=Bacillus anthracis GN=sap PE=1 SV=1					
11.	RS17_STROD	Mass: 10714	Score: 35	Expect: 1.7e+002	Matches: 9
30S ribosomal protein S17 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) GN=rpsD PE=3 SV=1					
12.	DST2_DICDI	Mass: 131280	Score: 35	Expect: 1.8e+002	Matches: 19
Serine/threonine-protein kinase dst2 OS=Dictyostelium discoideum GN=dst2 PE=3 SV=1					
13.	Y723_THERF	Mass: 12245	Score: 34	Expect: 2e+002	Matches: 7
Nucleoid-associated protein tlr0723 OS=Thermosynechococcus elongatus (strain BP-1) GN=tlr0723 PE=3 SV=1					
Nucleoid-associated protein tlr0723 OS=Thermosynechococcus elongatus (strain BP-1) GN=tlr0723 PE=3 SV=1					
14.	PLSX_PEPD	Mass: 37029	Score: 34	Expect: 2.3e+002	Matches: 12
Phosphate acyltransferase OS=Peptoclostridium difficile (strain 630) GN=plsX PE=3 SV=1					
15.	ATPF_VIBCB	Mass: 17707	Score: 33	Expect: 2.6e+002	Matches: 9
ATP synthase subunit b OS=Vibrio cholerae serotype O1 (strain ATCC 39541 / Classical Osawa 395 / O395) GN=atpF PE=3 SV=1					
	ATPF_VIBCH	Mass: 17707	Score: 33	Expect: 2.6e+002	Matches: 9
ATP synthase subunit b OS=Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N18961) GN=atpF PE=3 SV=1					
16.	RL18_PYRIL	Mass: 23217	Score: 33	Expect: 2.6e+002	Matches: 10
50S ribosomal protein L18 OS=Pyrobaculum islandicum (strain DSM 4184 / JCM 9189 / GE03) GN=rlp18 PE=3 SV=1					
17.	CAN2_SHEEP	Mass: 29193	Score: 33	Expect: 2.6e+002	Matches: 7
Carbonic anhydrase 2 OS=Ovis aries GN=CA2 PE=1 SV=2					
18.	OCAD2_HUMAN	Mass: 17291	Score: 33	Expect: 2.9e+002	Matches: 7
OCA1A domain-containing protein 2 OS=Homo sapiens GN=OCAD2 PE=1 SV=1					
19.	RL15_RICAE	Mass: 16738	Score: 32	Expect: 3.5e+002	Matches: 10
50S ribosomal protein L15 OS=Rickettsia africae (strain ESF-5) GN=rlp10 PE=3 SV=1					
	RL15_RICCN	Mass: 16738	Score: 32	Expect: 3.5e+002	Matches: 10
50S ribosomal protein L15 OS=Rickettsia conorii (strain ATCC VR-613 / Malish 7) GN=rlp10 PE=3 SV=1					
	RL15_RICPU	Mass: 16742	Score: 32	Expect: 3.5e+002	Matches: 10
50S ribosomal protein L15 OS=Rickettsia peacockii (strain Rustic) GN=rlp10 PE=3 SV=1					
20.	RNA14_CANAL	Mass: 91733	Score: 32	Expect: 3.6e+002	Matches: 20
mRNA 3'-end-processing protein RNA14 OS=Candida albicans (strain SC5314 / ATCC MYA-2876) GN=RNA14 PE=3 SV=1					
21.	CDC42_BOVIN	Mass: 21593	Score: 32	Expect: 3.7e+002	Matches: 6
Cell division control protein 42 homolog OS=Bos taurus GN=CDC42 PE=1 SV=1					
	CDC42_CANLE	Mass: 21593	Score: 32	Expect: 3.7e+002	Matches: 6
Cell division control protein 42 homolog OS=Canis lupus familiaris GN=CDC42 PE=2 SV=2					
	CDC42_CHICK	Mass: 21807	Score: 32	Expect: 3.7e+002	Matches: 6
Cell division control protein 42 homolog OS=Gallus gallus GN=CDC42 PE=2 SV=1					
	CDC42_HUMAN	Mass: 21593	Score: 32	Expect: 3.7e+002	Matches: 6
Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2					
	CDC42_MACFA	Mass: 21592	Score: 32	Expect: 3.7e+002	Matches: 6
Cell division control protein 42 homolog OS=Macaca fascicularis GN=CDC42 PE=2 SV=1					
	CDC42_MOUSE	Mass: 21593	Score: 32	Expect: 3.7e+002	Matches: 6
Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2					

	CDC42_MOUSE	Mass: 21593	Score: 32	Expect: 3.7e+002	Matches: 6
	Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2				
	CDC42_PTC	Mass: 21593	Score: 32	Expect: 3.7e+002	Matches: 6
	Cell division control protein 42 homolog OS=Sus scrofa GN=CDC42 PE=2 SV=2				
	CDC42_RAT	Mass: 21593	Score: 32	Expect: 3.7e+002	Matches: 6
	Cell division control protein 42 homolog OS=Rattus norvegicus GN=Cdc42 PE=1 SV=2				
22.	ENB8_STRUD	Mass: 22675	Score: 32	Expect: 3.9e+002	Matches: 7
	Probable GTP-binding protein Enb8 OS=Streptococcus uberis (strain ATCC BAA-854 / 0140J) GN=enb8 PE=3 SV=1				
23.	YIDC_BUCAP	Mass: 62678	Score: 32	Expect: 3.9e+002	Matches: 12
	Membrane protein insertase YidC OS=Buchnera aphidicola subsp. Schizaphis eranimum (strain Sg) GN=yidC PE=3 SV=3				
24.	SSS1G_YEAST	Mass: 8996	Score: 31	Expect: 4e+002	Matches: 6
	Protein transport protein SSS1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=SSS1 PE=1 SV=2				
25.	ATP6_PHOL	Mass: 17396	Score: 31	Expect: 4.7e+002	Matches: 7
	ATP synthase subunit b OS=Photobacterium luminescens subsp. laumondii (strain DSM 15139 / CIP 105585 / TT01) GN=atp6 PE=3 SV=1				
26.	YBEY_ALQND	Mass: 17980	Score: 31	Expect: 4.7e+002	Matches: 6
	Endoribonuclease YbeY OS=Alkaliphilus metalliredigens (strain QMF) GN=ybeY PE=3 SV=1				
27.	RS20_RHOE	Mass: 9265	Score: 30	Expect: 5e+002	Matches: 6
	30S ribosomal protein S20 OS=Rhodococcus opacus (strain B4) GN=rpsT PE=3 SV=1				
28.	YHEB_SCHPO	Mass: 34075	Score: 30	Expect: 5.3e+002	Matches: 7
	Uncharacterized oxidoreductase C215.11c OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=SPBC215.11c PE=3 SV=1				
29.	IGVP_BP3K9	Mass: 26834	Score: 30	Expect: 5.4e+002	Matches: 7
	Ig-like virion protein OS=Serratia phase KSP90 PE=1 SV=2				
30.	F16P2_BRANA	Mass: 37597	Score: 30	Expect: 5.4e+002	Matches: 8
	Fructose-1,6-bisphosphatase, cytosolic OS=Brassica napus PE=2 SV=1				
31.	HIS1_GEONG	Mass: 24122	Score: 30	Expect: 5.4e+002	Matches: 6
	ATP phosphoribosyltransferase OS=Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) GN=hisG PE=3 SV=1				
32.	EF2_DEBHA	Mass: 93715	Score: 30	Expect: 5.8e+002	Matches: 14
	Elongation factor 2 OS=Debaromyces hansenii (strain ATCC 36239 / CBS 767 / JCM 1990 / NRC 0083 / ICG 2968) GN=EFT1 PE=3 SV=1				
33.	THI1_SULTO	Mass: 41325	Score: 30	Expect: 6e+002	Matches: 12
33.	THI1_SULTO	Mass: 41325	Score: 30	Expect: 6e+002	Matches: 12
	Probable tRNA sulfurtransferase OS=Sulfolobus tokodaii (strain DSM 16893 / JCM 10545 / NRC 100140 / 7) GN=thi1 PE=3 SV=1				
34.	PSAE_PROMO	Mass: 7617	Score: 30	Expect: 6e+002	Matches: 5
	Photosystem I reaction center subunit IV OS=Prochlorococcus marinus (strain MIT 9301) GN=psaE PE=3 SV=1				
	PSAE_PROMO	Mass: 7621	Score: 30	Expect: 6e+002	Matches: 5
	Photosystem I reaction center subunit IV OS=Prochlorococcus marinus (strain MIT 9312) GN=psaE PE=3 SV=1				
	PSAE_PROMS	Mass: 7617	Score: 30	Expect: 6e+002	Matches: 5
	Photosystem I reaction center subunit IV OS=Prochlorococcus marinus (strain AS9601) GN=psaE PE=3 SV=1				
35.	KAD_AROAE	Mass: 23629	Score: 30	Expect: 6.2e+002	Matches: 8
	Adenylyate kinase OS=Aromatoleum aromaticum (strain EBNT) GN=adk PE=3 SV=1				
36.	CVFB_STAS1	Mass: 34210	Score: 30	Expect: 6.2e+002	Matches: 11
	Conserved virulence factor B OS=Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229) GN=cvfb PE=3 SV=1				

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance: ± 0.5 Da
 Fragment Mass Tolerance: ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Query1 (825.8243.1+): <no title>
 Query2 (843.7685.1+): <no title>
 Query3 (857.8776.1+): <no title>
 Query4 (858.8570.1+): <no title>
 Query5 (859.6968.1+): <no title>
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 Query13 (882.7706.1+): <no title>
 Query14 (884.7656.1+): <no title>
 Query15 (886.8501.1+): <no title>

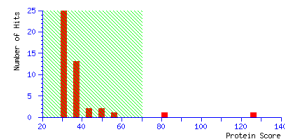
CA mass/mass+c

MASCOT Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 09:50:38 GMT
Top Score : 126 for [CAH2_BOVIN](#), Carbonic anhydrase 2 OS=Bos taurus GN=CA2 PE=1 SV=3

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: **Concise Protein Summary** [Help](#)
Significance threshold $p < 0.05$ Max. number of hits **200**
Preferred taxonomy **All entries**

[Re-Search All](#) [Search Unmatched](#)

1.	CAH2_BOVIN	Mass: 29096	Score: 126	Expect: 1.4e-007	Matches: 10
	Carbonic anhydrase 2 OS=Bos taurus GN=CA2 PE=1 SV=3				
	CAH2_HUMAN	Mass: 29286	Score: 50	Expect: 6.2	Matches: 4
	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2				
	CAH2_HUMAN	Mass: 29286	Score: 50	Expect: 6.2	Matches: 4
	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2				
2.	CAH2_SHEEP	Mass: 29193	Score: 82	Expect: 0.0032	Matches: 7
	Carbonic anhydrase 2 OS=Ovis aries GN=CA2 PE=1 SV=2				
3.	CAH2_RABIT	Mass: 29598	Score: 57	Expect: 1.1	Matches: 7
	Carbonic anhydrase 2 OS=Oryctolagus cuniculus GN=CA2 PE=1 SV=3				
4.	UBF1_HUMAN	Mass: 89698	Score: 52	Expect: 3.2	Matches: 16
	Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=1 SV=1				
	UBF1_RAT	Mass: 89729	Score: 52	Expect: 3.6	Matches: 11
	Nucleolar transcription factor 1 OS=Rattus norvegicus GN=Ubf1 PE=1 SV=1				
5.	UBF1_MOUSE	Mass: 89801	Score: 48	Expect: 8	Matches: 12
	Nucleolar transcription factor 1 OS=Mus musculus GN=Ubf1 PE=1 SV=1				
6.	CAH2_RAT	Mass: 29270	Score: 44	Expect: 22	Matches: 6
	Carbonic anhydrase 2 OS=Rattus norvegicus GN=Ca2 PE=1 SV=2				
	CAH2_MOUSE	Mass: 29131	Score: 40	Expect: 50	Matches: 5
	Carbonic anhydrase 2 OS=Mus musculus GN=Ca2 PE=1 SV=4				
7.	CHLB_CHAYU	Mass: 58116	Score: 40	Expect: 50	Matches: 8
	Light-independent protochlorophyllide reductase subunit B OS=Chara vulgaris GN=chlB PE=3 SV=1				
8.	ATPF_GEOL	Mass: 22811	Score: 39	Expect: 69	Matches: 5
	ATP synthase subunit b OS=Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) GN=atpF PE=3 SV=2				
9.	PT117_YEAST	Mass: 12331	Score: 39	Expect: 69	Matches: 6
	Protein PET117, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PET117 PE=3 SV=1				
10.	FEN1_METAS	Mass: 55587	Score: 37	Expect: 1.2e+002	Matches: 12
	Flap endonuclease 1 OS=Methanococcus aeolicus (strain Nankai-3 / ATCC BAA-1280) GN=fen PE=3 SV=1				
11.	Y1720_HAEIN	Mass: 21850	Score: 36	Expect: 1.4e+002	Matches: 8
	Uncharacterized protein HI_1720 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) GN=HI_1720 PE=3 SV=1				
12.	AP4S1_HUMAN	Mass: 17168	Score: 36	Expect: 1.4e+002	Matches: 8
	AP-4 complex subunit sigma-1 OS=Homo sapiens GN=AP4S1 PE=2 SV=1				
13.	AP4S1_MOUSE	Mass: 16981	Score: 36	Expect: 1.4e+002	Matches: 8
	AP-4 complex subunit sigma-1 OS=Mus musculus GN=Ap4s1 PE=2 SV=1				
13.	AP4S1_MOUSE	Mass: 16981	Score: 36	Expect: 1.4e+002	Matches: 8
	AP-4 complex subunit sigma-1 OS=Mus musculus GN=Ap4s1 PE=2 SV=1				
14.	ASB15_BOVIN	Mass: 66736	Score: 36	Expect: 1.5e+002	Matches: 4
	Ankyrin repeat and SOCS box protein 15 OS=Bos taurus GN=ASB15 PE=2 SV=2				
15.	LARP7_MOUSE	Mass: 65226	Score: 36	Expect: 1.5e+002	Matches: 9
	La-related protein 7 OS=Mus musculus GN=Larp7 PE=1 SV=2				
16.	SYGA_HELPIS	Mass: 34801	Score: 35	Expect: 1.8e+002	Matches: 5
	Glycine--tRNA ligase alpha subunit OS=Helicobacter pylori (strain Shi470) GN=GalYQ PE=3 SV=1				
17.	TIG_DESERV	Mass: 48727	Score: 35	Expect: 1.8e+002	Matches: 14
	Trigger factor OS=Desulfotomaculum reducens (strain ML-1) GN=Tig PE=3 SV=1				
18.	MSP2_ASCSU	Mass: 14355	Score: 35	Expect: 1.9e+002	Matches: 2
	Major sperm protein isoform beta OS=Ascaris suum PE=1 SV=3				
19.	CAMP1_XENLA	Mass: 177217	Score: 34	Expect: 2e+002	Matches: 12
	Calmodulin-regulated spectrin-associated protein 1 OS=Xenopus laevis GN=camsap1 PE=2 SV=1				
20.	RYEB8_DANFE	Mass: 28882	Score: 34	Expect: 2.1e+002	Matches: 6
	RING1 and YY1-binding protein 8 OS=Danio rerio GN=ryeb8 PE=2 SV=1				
21.	RS17_STROD	Mass: 10714	Score: 34	Expect: 2.4e+002	Matches: 9
	30S ribosomal protein S17 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) GN=rpsQ PE=3 SV=1				
22.	ASSY_DANFE	Mass: 47505	Score: 33	Expect: 2.5e+002	Matches: 8
	Argininosuccinate synthase OS=Danio rerio GN=ass1 PE=2 SV=1				
23.	Y723_THEEB	Mass: 12245	Score: 33	Expect: 2.6e+002	Matches: 7
	Nucleoid-associated protein tlr0723 OS=Thermosynechococcus elongatus (strain BP-1) GN=tlr0723 PE=3 SV=1				
24.	DNA2_GHLIN	Mass: 51729	Score: 33	Expect: 2.7e+002	Matches: 9
	Chromosomal replication initiator protein DnaA 2 OS=Chlamydia pneumoniae GN=dna2 PE=3 SV=1				
25.	GCHI_CAMCT	Mass: 21780	Score: 33	Expect: 3e+002	Matches: 4
	GTP cyclohydrolase 1 OS=Campylobacter concisus (strain 13826) GN=foIE PE=3 SV=1				
26.	URFE_BACHD	Mass: 17320	Score: 32	Expect: 3.3e+002	Matches: 4

26.	UREF_BACHD	Mass: 17320	Score: 32	Expect: 3.3e+002	Matches: 4	Urease accessory protein UreE OS=Bacillus halodurans (strain ATCC BAA-125 / DSM 18187 / FERM 7344 / JCM 9153 / C-125) GN=ureE PE=3 SV=1
27.	EXO1_RPT4	Mass: 39315	Score: 32	Expect: 3.3e+002	Matches: 5	Exonuclease subunit 1 OS=Enterobacteria phage T4 GN=47 PE=1 SV=1
28.	CSM6_DEBHA	Mass: 53267	Score: 32	Expect: 3.5e+002	Matches: 5	ODP9 signalosome complex subunit 5 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / JCM 1990 / NBRC 0083 / IGC 2968) GN=RR11 PE=3 SV=2
29.	MURA_RUCBP	Mass: 45326	Score: 32	Expect: 3.6e+002	Matches: 9	UDP-N-acetylglucosamine 1-carboxyvinyltransferase OS=Buchnera aphidicola subsp. Baizongia pistaciae (strain Bp) GN=murA PE=3 SV=1
30.	PIRA_SYNMV	Mass: 47713	Score: 32	Expect: 3.6e+002	Matches: 3	Adenylosuccinate synthetase OS=Syntrophobacter fumaroxidans (strain DSM 10017 / MFOB) GN=pirA PE=3 SV=1
31.	MINE_ALOCS	Mass: 9450	Score: 32	Expect: 3.6e+002	Matches: 3	Cell division topological specificity factor OS=Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2) GN=minE PE=3 SV=1
32.	SYGA_HELPG	Mass: 34711	Score: 32	Expect: 3.6e+002	Matches: 3	Glycine--tRNA ligase alpha subunit OS=Helicobacter pylori (strain G27) GN=glyQ PE=3 SV=1
33.	RPC1_DEBHA	Mass: 163618	Score: 32	Expect: 3.8e+002	Matches: 12	DNA-directed RNA polymerase III subunit RPC1 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / JCM 1990 / NBRC 0083 / IGC 2968) GN=RPC1 PE=3 SV=2
34.	RS15_THEAC	Mass: 18504	Score: 32	Expect: 3.9e+002	Matches: 6	30S ribosomal protein S15 OS=Thermoplasma acidophilum (strain ATCC 25905 / DSM 1728 / JCM 9062 / NBRC 15155 / AMRC-C185) GN=rps15 PE=3 SV=1
35.	RL21_BAUCH	Mass: 12172	Score: 31	Expect: 4e+002	Matches: 5	50S ribosomal protein L21 OS=Baumannia cicadellinicola subsp. Homalodisca coagulata GN=rpIU PE=3 SV=1
36.	UL24_ELHVK	Mass: 26729	Score: 31	Expect: 4.1e+002	Matches: 6	Protein UL24 homolog OS=Elephantid herpesvirus 1 (isolate Asian elephant/Berlin/Kiba/1998) PE=2 SV=1
37.	P2C76_ARATH	Mass: 46106	Score: 31	Expect: 4.2e+002	Matches: 7	Probable protein phosphatase 2C 76 OS=Arabidopsis thaliana GN=At5g53140 PE=2 SV=1
38.	LIPA_RHOPS	Mass: 35521	Score: 31	Expect: 4.2e+002	Matches: 3	Lipoyl synthase OS=Rhodospseudomonas palustris (strain Bis5) GN=lipA PE=3 SV=1
39.	PpdaD_METAB	Mass: 17860	Score: 31	Expect: 4.4e+002	Matches: 4	Pyruvoyl-dependent arginine decarboxylase OS=Methanococcus aeolicus (strain Nankai-3 / ATCC BAA-1280) GN=PpdaD PE=3 SV=1
39.	PpdaD_METAB	Mass: 17860	Score: 31	Expect: 4.4e+002	Matches: 4	Pyruvoyl-dependent arginine decarboxylase OS=Methanococcus aeolicus (strain Nankai-3 / ATCC BAA-1280) GN=PpdaD PE=3 SV=1
40.	ATP_FIBO3	Mass: 17707	Score: 31	Expect: 4.4e+002	Matches: 7	ATP synthase subunit b OS=Vibrio cholerae serotype 01 (strain ATCC 39541 / Classical Ogawa 395 / O395) GN=atpF PE=3 SV=1
	ATP_FIBO3H	Mass: 17707	Score: 31	Expect: 4.4e+002	Matches: 7	ATP synthase subunit b OS=Vibrio cholerae serotype 01 (strain ATCC 39315 / El Tor Inaba N16961) GN=atpF PE=3 SV=1
41.	RS7_EX1S2	Mass: 17976	Score: 31	Expect: 4.4e+002	Matches: 4	30S ribosomal protein S7 OS=Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15) GN=rpsG PE=3 SV=1
42.	NPH2_VADCC	Mass: 77899	Score: 31	Expect: 4.5e+002	Matches: 6	RNA helicase NPH-II OS=Vaccinia virus (strain Copenhagen) GN=NPH2 PE=2 SV=1
43.	ILV5_ORYZA	Mass: 62686	Score: 31	Expect: 4.6e+002	Matches: 5	Ketol-acid reductoisomerase, chloroplastic OS=Oryza sativa subsp. japonica GN=Os05g0573700 PE=1 SV=1
44.	KAD_PELPB	Mass: 24348	Score: 31	Expect: 4.7e+002	Matches: 4	Adenylyl kinase OS=Pelodictyon phaeoclathratiforme (strain DSM 5477 / BJ-1) GN=kadK PE=3 SV=1
45.	MFE_ASFE2	Mass: 100427	Score: 31	Expect: 4.7e+002	Matches: 10	Probable mRNA-capping enzyme OS=African swine fever virus (strain Badajoz 1971 Vero-adapted) GN=Ba71V-101 PE=3 SV=1
	MFE_ASFP4	Mass: 100439	Score: 31	Expect: 4.7e+002	Matches: 10	Probable mRNA-capping enzyme OS=African swine fever virus (isolate Tick/South Africa/Pretoriuskop Pr4/1996) GN=Pret-113 PE=3 SV=1

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.5 Da
 Fragment Mass Tolerance : ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Query1 (825.8243.1+): <no title>
 Query2 (843.7685.1+): <no title>
 Query3 (857.8776.1+): <no title>
 Query4 (856.8570.1+): <no title>
 Query5 (859.8968.1+): <no title>

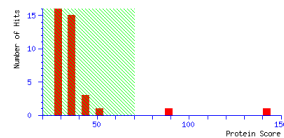
CA mass+c

Mascot Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 09:50:46 GMT
Top Score : 142 for [CAH2_BOVIN](#), Carbonic anhydrase 2 OS=Bos taurus GN=CA2 PE=1 SV=3

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As

Concise Protein Summary

Help

Significance threshold p<

0.05

Max. number of hits

200

Preferred taxonomy

All entries

Re-Search All

Search Unmatched

1.

CAH2_BOVIN

Mass: 29096

Score: 142

Expect: 3.5e-009

Matches: 6

Carbonic anhydrase 2 OS=Bos taurus GN=CA2 PE=1 SV=3

CAH2_RABIT

Mass: 29598

Score: 62

Expect: 0.35

Matches: 3

Carbonic anhydrase 2 OS=Oryctolagus cuniculus GN=CA2 PE=1 SV=3

CAH2_RABIT

Mass: 29598

Score: 62

Expect: 0.35

Matches: 3

Carbonic anhydrase 2 OS=Oryctolagus cuniculus GN=CA2 PE=1 SV=3

CAH2_HUMAN

Mass: 29286

Score: 60

Expect: 0.53

Matches: 3

Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2

CAH2_RAT

Mass: 29270

Score: 38

Expect: 85

Matches: 2

Carbonic anhydrase 2 OS=Rattus norvegicus GN=Ca2 PE=1 SV=2

CAH2_MOUSE

Mass: 29131

Score: 38

Expect: 85

Matches: 2

Carbonic anhydrase 2 OS=Mus musculus GN=Ca2 PE=1 SV=4

2.

CAH2_SHEEP

Mass: 29193

Score: 89

Expect: 0.00076

Matches: 4

Carbonic anhydrase 2 OS=Ovis aries GN=CA2 PE=1 SV=2

3.

UBTF_HUMAN

Mass: 89698

Score: 53

Expect: 3

Matches: 4

Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=1 SV=1

UBTF_RAT

Mass: 89729

Score: 52

Expect: 3.2

Matches: 4

Nucleolar transcription factor 1 OS=Rattus norvegicus GN=Ubtff PE=1 SV=1

UBTF_MOUSE

Mass: 89801

Score: 52

Expect: 3.2

Matches: 4

Nucleolar transcription factor 1 OS=Mus musculus GN=Ubtff PE=1 SV=1

4.

MSP2_ASCSU

Mass: 14355

Score: 46

Expect: 13

Matches: 2

Major sperm protein isoform beta OS=Ascaris suum PE=1 SV=3

5.

PT117_YEAST

Mass: 12331

Score: 40

Expect: 53

Matches: 2

Protein PET117, mitochondrial OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=PT117 PE=3 SV=1

6.

ARGB_LACLA

Mass: 30827

Score: 40

Expect: 54

Matches: 2

Acetylglutamate kinase OS=Lactococcus lactis subsp. lactis (strain IL1403) GN=argB PE=3 SV=1

7.

LIPA_PARL1

Mass: 36066

Score: 39

Expect: 69

Matches: 2

Lipoyl synthase OS=Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966) GN=lipA PE=3 SV=1

8.

PURA_SINFM

Mass: 47713

Score: 39

Expect: 74

Matches: 2

Adenylosuccinate synthetase OS=Synthrobacter fumaroxidans (strain DSM 10017 / MFOB) GN=purA PE=3 SV=1

9.

SPR11_MACMU

Mass: 10309

Score: 38

Expect: 78

Matches: 2

Cornifin OS=Macaca mulatta GN=SPR11 PE=2 SV=1

10.

SYGA_HELP2

Mass: 34768

Score: 37

Expect: 1e+002

Matches: 2

Glycine--tRNA ligase alpha subunit OS=Helicobacter pylori (strain P12) GN=hglyQ PE=3 SV=1

SYGA_HELP3

Mass: 34711

Score: 37

Expect: 1e+002

Matches: 2

Glycine--tRNA ligase alpha subunit OS=Helicobacter pylori (strain G27) GN=hglyQ PE=3 SV=1

SYGA_HELP4

Mass: 34711

Score: 37

Expect: 1e+002

Matches: 2

Glycine--tRNA ligase alpha subunit OS=Helicobacter pylori (strain G27) GN=hglyQ PE=3 SV=1

SYGA_HELP5

Mass: 34760

Score: 37

Expect: 1e+002

Matches: 2

Glycine--tRNA ligase alpha subunit OS=Helicobacter pylori (strain J99 / ATCC 700824) GN=hglyQ PE=3 SV=1

SYGA_HELP6

Mass: 35204

Score: 37

Expect: 1e+002

Matches: 2

Glycine--tRNA ligase alpha subunit OS=Helicobacter pylori (strain ATCC 700392 / 26695) GN=hglyQ PE=3 SV=1

SYGA_HELP7

Mass: 34801

Score: 37

Expect: 1.2e+002

Matches: 2

Glycine--tRNA ligase alpha subunit OS=Helicobacter pylori (strain Shi470) GN=hglyQ PE=3 SV=1

11.

ASB15_BOVIN

Mass: 66736

Score: 37

Expect: 1e+002

Matches: 2

Ankyrin repeat and SOCS box protein 15 OS=Bos taurus GN=ASB15 PE=2 SV=2

12.

LIPA_RHOPS

Mass: 35521

Score: 37

Expect: 1.1e+002

Matches: 2

Lipoyl synthase OS=Rhodospirillum rubrum (strain B185) GN=lipA PE=3 SV=1

13.

DSE3_CANGA

Mass: 49252

Score: 37

Expect: 1.2e+002

Matches: 2

Protein DSE3 OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NERC 0622 / NRRL Y-65) GN=DSE3 PE=3 SV=1

14.

ATPF_GEOSL

Mass: 22811

Score: 36

Expect: 1.3e+002

Matches: 2

ATP synthase subunit b OS=Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) GN=atpF PE=3 SV=2

15.

HSLU_CAUCN

Mass: 46672

Score: 36

Expect: 1.4e+002

Matches: 2

ATP-dependent protease ATPase subunit HslU OS=Caulobacter crescentus (strain NA1000 / CB15N) GN=hslU PE=3 SV=1

HSLU_CAUCR

Mass: 46672

Score: 36

Expect: 1.4e+002

Matches: 2

ATP-dependent protease ATPase subunit HslU OS=Caulobacter crescentus (strain ATCC 19089 / CB15) GN=hslU PE=3 SV=1

16.

YR773_MIMIV

Mass: 57161

Score: 35

Expect: 1.7e+002

Matches: 2

Putative BTB/POZ domain-containing protein R773 OS=Acanthamoeba polyphaga mimivirus GN=MIM1_R773 PE=3 SV=1

17.

BIOW_SULSY

Mass: 28542

Score: 35

Expect: 1.8e+002

Matches: 2

6-carboxyhexanoate--CoA ligase OS=Sulfurihydrogenibium sp. (strain Y03ADP1) GN=biow PE=3 SV=1

18.

CHLB_CHAYU

Mass: 58116

Score: 35

Expect: 1.9e+002

Matches: 2

Light-independent protochlorophyllide reductase subunit B OS=Chara vulgaris GN=chIB PE=3 SV=1

19.

ILV5_ORYSJ

Mass: 62686

Score: 35

Expect: 1.9e+002

Matches: 2

Ketolactol reductoisomerase, chloroplastic OS=Oryza sativa subsp. japonica GN=Os05g0573700 PE=1 SV=1

20.

RS15_THEAC

Mass: 16504

Score: 34

Expect: 2.2e+002

Matches: 2

30S ribosomal protein S15 OS=Thermoplasma acidophilum (strain ATCC 25805 / DSM 1728 / JCM 3062 / NERC 15155 / AMRC-C185) GN=rps15 PE=3 SV=1

Search Parameters

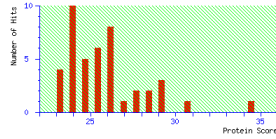
4P mass

MASCOT Search Results

User : Y Wang
Email : kahn20003@gmail.com
Search title :
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 14 Apr 2016 at 00:41:24 GMT
Top Score : 34 for [Y2104_STRP1](#), UF0246 protein SPY_2104/M5005_Spy1788 OS=Streptococcus pyogenes serotype M1 GN=SPY_2104 PE=3 SV=1

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As: [Help](#)
Significance threshold p< Max. number of hits
Preferred taxonomy:

1.	Y2104_STRP1	Mass: 29485	Score: 34	Expect: 2e+002	Matches: 14	UF0246 protein SPY_2104/M5005_Spy1788 OS=Streptococcus pyogenes serotype M1 GN=SPY_2104 PE=3 SV=1
2.	PF02_MOUSE	Mass: 18582	Score: 31	Expect: 4.6e+002	Matches: 14	Prefoldin subunit 2 OS=Mus musculus GN=Pfdr2 PE=1 SV=2
2.	PF02_MOUSE	Mass: 18582	Score: 31	Expect: 4.6e+002	Matches: 14	Prefoldin subunit 2 OS=Mus musculus GN=Pfdr2 PE=1 SV=2
3.	AGB8_CLOPS	Mass: 24414	Score: 30	Expect: 6.2e+002	Matches: 18	Putative AarB-like protein OS=Clostridium perfringens (strain SM101 / Type A) GN=OPR_1532 PE=3 SV=1
4.	RS20_MESPL	Mass: 8890	Score: 29	Expect: 6.9e+002	Matches: 12	30S ribosomal protein S20 OS=Mesoplasma florum (strain ATCC 33453 / NERC 100688 / NCTC 11704 / L1) GN=rpsT PE=3 SV=1
5.	ATPD_MYOMD	Mass: 21112	Score: 29	Expect: 6.9e+002	Matches: 31	ATP synthase subunit delta OS=Mycoplasma mobile (strain ATCC 43663 / 163K / NCTC 11711) GN=HtpH PE=3 SV=1
6.	Y1742_STRP2	Mass: 28499	Score: 29	Expect: 7.4e+002	Matches: 12	UF0246 protein SPY_49_1742 OS=Streptococcus pyogenes serotype M49 (strain NZ131) GN=Spy49_1742 PE=3 SV=1
6.	Y1772_STRPM	Mass: 28926	Score: 29	Expect: 7.4e+002	Matches: 12	UF0246 protein M28_Spy1772 OS=Streptococcus pyogenes serotype M28 (strain MGAS180) GN=M28_Spy1772 PE=3 SV=1
6.	Y1856_STRPD	Mass: 28499	Score: 29	Expect: 7.4e+002	Matches: 12	UF0246 protein MGAS10270_Spy1856 OS=Streptococcus pyogenes serotype M2 (strain MGAS10270) GN=MGAS10270_Spy1856 PE=3 SV=1
7.	RL6_FRAH1	Mass: 19064	Score: 28	Expect: 7.8e+002	Matches: 10	50S ribosomal protein L6 OS=Francisella tularensis subsp. novicida (strain U112) GN=rplF PE=3 SV=1
8.	MAK5_YANFO	Mass: 85852	Score: 28	Expect: 9.8e+002	Matches: 35	ATP-dependent RNA helicase MAK5 OS=Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294) GN=MAK5 PE=3 SV=1
9.	PDH_SHEH1	Mass: 24242	Score: 27	Expect: 1e+003	Matches: 15	Pyridoxine/pyridoxamine 5'-phosphate oxidase OS=Shewanella halifaxensis (strain HAM-EB4) GN=pdhH PE=3 SV=1
10.	MVG_EQUBU	Mass: 17072	Score: 27	Expect: 1e+003	Matches: 27	Myoglobin OS=Equus burchelli GN=MB PE=1 SV=2
10.	MVG_HORSE	Mass: 17072	Score: 27	Expect: 1e+003	Matches: 27	Myoglobin OS=Equus caballus GN=MB PE=1 SV=2
11.	Y1408_METJA	Mass: 40097	Score: 26	Expect: 1.3e+003	Matches: 28	Uncharacterized protein MJ1408 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NERC 100440) GN=MJ1408 PE=3 SV=2
12.	NFEA_SHEH1	Mass: 52860	Score: 26	Expect: 1.4e+003	Matches: 29	Cytochrome c-552 OS=Shewanella sediminis (strain HAM-EB3) GN=nrfA PE=3 SV=1
13.	MVG_GORBE	Mass: 17221	Score: 26	Expect: 1.4e+003	Matches: 23	Myoglobin OS=Gorilla gorilla beringei GN=MB PE=1 SV=2
13.	MVG_GORBE	Mass: 17221	Score: 26	Expect: 1.4e+003	Matches: 23	Myoglobin OS=Gorilla gorilla beringei GN=MB PE=1 SV=2
14.	CCYC_ANDGA	Mass: 31887	Score: 26	Expect: 1.4e+003	Matches: 14	Cyclin-C OS=Anopheles gambiae GN=CycC PE=3 SV=2
15.	RRF_SHEAM	Mass: 20893	Score: 26	Expect: 1.4e+003	Matches: 19	Ribosome-recycling factor OS=Shewanella amazonensis (strain ATCC BAA-1098 / SE2B) GN=rrf PE=3 SV=1
16.	RS15_EDWI9	Mass: 10203	Score: 26	Expect: 1.4e+003	Matches: 8	30S ribosomal protein S15 OS=Edwardsiella ictaluri (strain 93-146) GN=rpsO PE=3 SV=1
17.	RS15_PECAS	Mass: 10133	Score: 26	Expect: 1.4e+003	Matches: 8	30S ribosomal protein S15 OS=Pectobacterium atrosepticum (strain SORI 1043 / ATCC BAA-672) GN=rpsO PE=3 SV=1
18.	Y1712_CAMUR	Mass: 28428	Score: 26	Expect: 1.4e+003	Matches: 19	UF0271 protein CJE1712 OS=Campylobacter jejuni (strain RM1221) GN=CJE1712 PE=3 SV=1
19.	Y1526_CAMJU	Mass: 28414	Score: 26	Expect: 1.5e+003	Matches: 20	UF0271 protein CUJ81176_1526 OS=Campylobacter jejuni subsp. jejuni serotype O:23/36 (strain 81-176) GN=CUJ81176_1526 PE=3 SV=1
19.	Y1541_CAMJU	Mass: 28414	Score: 26	Expect: 1.5e+003	Matches: 20	UF0271 protein Cj1541 OS=Campylobacter jejuni subsp. jejuni serotype O:2 (strain ATCC 700819 / NCTC 11168) GN=Cj1541 PE=3 SV=1
20.	SYT_SULAC	Mass: 40880	Score: 25	Expect: 1.6e+003	Matches: 19	Tyrosine-tRNA ligase OS=Sulfolobus acidocaldarius (strain ATCC 33909 / DSM 639 / JCM 8929 / NERC 15157 / NCIMB 11770) GN=tyrS PE=3 SV=1
21.	EFTS_NOVAD	Mass: 32084	Score: 25	Expect: 1.6e+003	Matches: 19	Elongation factor Ts OS=Novosphingobium aromaticivorans (strain DSM 12444 / F199) GN=tsf PE=3 SV=1
22.	RSRC2_MOUSE	Mass: 43908	Score: 25	Expect: 1.6e+003	Matches: 20	Arginine/serine-rich coiled-coil protein 2 OS=Mus musculus GN=Rsrc2 PE=2 SV=1
23.	PDS_BACCI	Mass: 31581	Score: 25	Expect: 1.6e+003	Matches: 18	Pyridoxal 5'-phosphate synthase subunit Pds OS=Bacillus circulans GN=pds PE=3 SV=1
24.	ARR6_ARATH	Mass: 21341	Score: 25	Expect: 1.7e+003	Matches: 11	Two-component response regulator ARR6 OS=Arabidopsis thaliana GN=ARR6 PE=1 SV=2
25.	UREG_STAAS	Mass: 22403	Score: 25	Expect: 1.7e+003	Matches: 15	Urease accessory protein Ureg OS=Staphylococcus aureus (strain M334476) GN=ureG PE=3 SV=1

25.	UREG_STABG	Mass: 22403	Score: 20	Expect: 1.7e+003	Matches: 10
Urease accessory protein UreG OS=Staphylococcus aureus (strain MCS4476) GN=ureG PE=3 SV=1					
	UREG_STABM	Mass: 22403	Score: 25	Expect: 1.7e+003	Matches: 15
Urease accessory protein UreG OS=Staphylococcus aureus (strain MW2) GN=ureG PE=3 SV=1					
26.	PF02_RAT	Mass: 16628	Score: 25	Expect: 1.7e+003	Matches: 10
Prefoldin subunit 2 OS=Rattus norvegicus GN=Pfdn2 PE=2 SV=1					
27.	RIMM_THEM	Mass: 20580	Score: 25	Expect: 1.8e+003	Matches: 10
Ribosome maturation factor RimM OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=rmm PE=3 SV=1					
	RIMM_THEP1	Mass: 20580	Score: 25	Expect: 1.8e+003	Matches: 10
Ribosome maturation factor RimM OS=Thermotoga petrophila (strain RKU-1 / ATCC BAA-488 / DSM 13995) GN=rmm PE=3 SV=1					
28.	DAPL1_BOVIN	Mass: 11872	Score: 25	Expect: 1.8e+003	Matches: 8
Death-associated protein-like 1 OS=Bos taurus GN=DAPL1 PE=2 SV=1					
29.	RL6_FRAP2	Mass: 19192	Score: 24	Expect: 2e+003	Matches: 11
50S ribosomal protein L6 OS=Francisella philomiragia subsp. philomiragia (strain ATCC 25017) GN=rpLF PE=3 SV=1					
30.	RRE_METCA	Mass: 21129	Score: 24	Expect: 2.1e+003	Matches: 9
Ribosome-recycling factor OS=Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) GN=rrr PE=3 SV=1					
31.	GMR1_MOUSE	Mass: 37980	Score: 24	Expect: 2.1e+003	Matches: 14
GMP reductase 1 OS=Mus musculus GN=Gmr PE=1 SV=1					
32.	DAPD_RUCBP	Mass: 30924	Score: 24	Expect: 2.1e+003	Matches: 17
2,3,4,5-tetrahydroxyridine-2,6-dicarboxylate N-succinyltransferase OS=Buchnera aphidicola subsp. Baizonsia pistaciae (strain Bb) GN=dapD PE=3 SV=1					
33.	BBB2_SOYBN	Mass: 10007	Score: 24	Expect: 2.1e+003	Matches: 8
Bowman-Birk type proteinase inhibitor C-II OS=Glycine max PE=1 SV=2					
34.	RUVA_PROM1	Mass: 25712	Score: 24	Expect: 2.1e+003	Matches: 16
Holliday junction ATP-dependent DNA helicase RuvA OS=Prochlorococcus marinus (strain NATL1A) GN=ruvA PE=3 SV=1					
35.	Y1790_STRP3	Mass: 28453	Score: 24	Expect: 2.2e+003	Matches: 13
UPF0246 protein SpvM3_1790 OS=Streptococcus pyogenes serotype M3 (strain ATCC BAA-595 / MGAS315) GN=SpvM3_1790 PE=3 SV=1					
	Y1790_STRP0	Mass: 28453	Score: 24	Expect: 2.2e+003	Matches: 13
UPF0246 protein Spv1787 OS=Streptococcus pyogenes serotype M3 (strain SSI-1) GN=Spv1787 PE=3 SV=1					
36.	MYX_CRODR	Mass: 5234	Score: 24	Expect: 2.3e+003	Matches: 7
Crotamine 11e-19 OS=Crotalus durissus durissus GN=PE=1 SV=2					
36.	MYX_CRODR	Mass: 5234	Score: 24	Expect: 2.3e+003	Matches: 7
Crotamine 11e-19 OS=Crotalus durissus durissus GN=PE=1 SV=2					
37.	YDF_BACSU	Mass: 13109	Score: 24	Expect: 2.3e+003	Matches: 13
Uncharacterized protein YdF OS=Bacillus subtilis (strain 168) GN=ydF PE=4 SV=1					
38.	Y088_MYCPN	Mass: 11588	Score: 24	Expect: 2.4e+003	Matches: 8
Uncharacterized protein MPN_088 OS=Mycoplasma pneumoniae (strain ATCC 28342 / M129) GN=MPN_088 PE=4 SV=1					
39.	RSS_STAMP	Mass: 23668	Score: 24	Expect: 2.4e+003	Matches: 13
30S ribosomal protein S5 OS=Staphylothermus marinus (strain ATCC 43588 / DSM 3639 / JCM 9404 / F1) GN=rps5 PE=3 SV=1					
40.	UBIE_LARHH	Mass: 27238	Score: 24	Expect: 2.5e+003	Matches: 17
Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE OS=Laribacter hongkongensis (strain HLK9) GN=ubiE PE=3 SV=1					
41.	PAN_NETH	Mass: 46140	Score: 24	Expect: 2.5e+003	Matches: 15
Protease-activating nucleotidase OS=Methanothermobacter thermautotrophicus (strain ATCC 29096 / DSM 1053 / JCM 10044 / NERC 100330 / Delta H) GN=pan PE=3 SV=1					
42.	GLMJ_CARHZ	Mass: 48583	Score: 23	Expect: 2.6e+003	Matches: 19
Bifunctional protein GlnJ OS=Carboxydothermus hydrogenoformans (strain ATCC BAA-161 / DSM 6008 / Z-2901) GN=glnJ PE=3 SV=1					
43.	RL22_DINSH	Mass: 14224	Score: 23	Expect: 2.6e+003	Matches: 8
50S ribosomal protein L22 OS=Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12) GN=rpIV PE=3 SV=1					

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.5 Da
 Fragment Mass Tolerance : ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Query1 (514.6834,1+): <no title>
 Query2 (514.6894,1+): <no title>
 Query3 (515.6702,1+): <no title>
 Query4 (516.6091,1+): <no title>
 Query5 (516.6136,1+): <no title>
 Query6 (516.6147,1+): <no title>
 Query7 (516.6308,1+): <no title>

4P mass/mass+c

Mascot Search Results

User : kahn20002
Email : kahn20002@gmail.com
Search title : 4P 0.5 Iniss
Database : SwissProt 2016_04 (550960 sequences; 196692942 residues)
Timestamp : 17 Apr 2016 at 06:25:46 GMT
Top Score : 91 for MYG_GORBE, Myoglobin OS=Gorilla gorilla beringei GN=MB PE=1 SV=2

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).

Score Distribution

Concise Protein Summary Report

Format As	Concise Protein Summary	Help	
Significance threshold p<	0.05	Max. number of hits	50
Preferred taxonomy	All entries		

Re-Search All Search Unmatched

1.	MYG_GORBE	Mass: 17221	Score: 91	Expect: 0.0004	Matches: 21
	Myoglobin OS=Gorilla gorilla beringei GN=MB PE=1 SV=2				
	MYG_HUMAN	Mass: 17231	Score: 85	Expect: 0.0016	Matches: 20
	Myoglobin OS=Homo sapiens GN=MB PE=1 SV=2				
	MYG_HYLAG	Mass: 17261	Score: 85	Expect: 0.0016	Matches: 20
	Myoglobin OS=Hylobates agilis GN=MB PE=1 SV=2				
	MYG_SYMSY	Mass: 17261	Score: 85	Expect: 0.0016	Matches: 20
	Myoglobin OS=Symphalangus syndactylus GN=MB PE=1 SV=2				
	MYG_PANTR	Mass: 17240	Score: 81	Expect: 0.0048	Matches: 19
	Myoglobin OS=Pan troglodytes GN=MB PE=1 SV=2				
	MYG_PONPY	Mass: 17187	Score: 81	Expect: 0.0048	Matches: 19
	Myoglobin OS=Pongo pygmaeus GN=MB PE=1 SV=2				
	MYG_ERIYA	Mass: 17137	Score: 80	Expect: 0.0062	Matches: 18
	Myoglobin OS=Erythrocebus patas GN=MB PE=1 SV=2				
	MYG_ERIYA	Mass: 17137	Score: 80	Expect: 0.0062	Matches: 18
	Myoglobin OS=Erythrocebus patas GN=MB PE=1 SV=2				
	MYG_PAPAN	Mass: 17137	Score: 80	Expect: 0.0062	Matches: 18
	Myoglobin OS=Papio anubis GN=MB PE=1 SV=2				
	MYG_SEMEN	Mass: 17137	Score: 80	Expect: 0.0062	Matches: 18
	Myoglobin OS=Simnopithecus entellus GN=MB PE=1 SV=2				
	MYG_MACFA	Mass: 17185	Score: 63	Expect: 0.28	Matches: 15
	Myoglobin OS=Macaca fascicularis GN=MB PE=1 SV=2				
2.	MYG_EQUBU	Mass: 17072	Score: 90	Expect: 0.00062	Matches: 23
	Myoglobin OS=Equus burchelli GN=MB PE=1 SV=2				
	MYG_HORSE	Mass: 17072	Score: 90	Expect: 0.00062	Matches: 23
	Myoglobin OS=Equus caballus GN=MB PE=1 SV=2				
3.	MYG_BALBO	Mass: 17238	Score: 83	Expect: 0.0025	Matches: 22
	Myoglobin OS=Balaenoptera borealis GN=MB PE=2 SV=3				
	MYG_BALEI	Mass: 17238	Score: 83	Expect: 0.0025	Matches: 22
	Myoglobin OS=Balaenoptera edeni GN=MB PE=2 SV=3				
	MYG_ESORD	Mass: 17238	Score: 83	Expect: 0.0025	Matches: 22
	Myoglobin OS=Eschrichtius robustus GN=MB PE=1 SV=2				
	MYG_MEGND	Mass: 17252	Score: 83	Expect: 0.0025	Matches: 22
	Myoglobin OS=Megaptera novaeangliae GN=MB PE=1 SV=2				
	MYG_BALAL	Mass: 17275	Score: 79	Expect: 0.0071	Matches: 21
	Myoglobin OS=Balaenoptera acronotata GN=MB PE=1 SV=2				
	MYG_BALPH	Mass: 17208	Score: 79	Expect: 0.0071	Matches: 21
	Myoglobin OS=Balaenoptera physalus GN=MB PE=1 SV=2				
	MYG_DELLE	Mass: 17185	Score: 61	Expect: 0.46	Matches: 17
	Myoglobin OS=Delphinapterus leucas GN=MB PE=1 SV=2				
	MYG_GLOME	Mass: 17205	Score: 61	Expect: 0.46	Matches: 17
	Myoglobin OS=Globicephala melas GN=MB PE=1 SV=2				
	MYG_ZIPCA	Mass: 17238	Score: 61	Expect: 0.46	Matches: 17
	Myoglobin OS=Ziphius cavirostris GN=MB PE=1 SV=2				
	MYG_INDCP	Mass: 17270	Score: 59	Expect: 0.68	Matches: 17
	Myoglobin OS=Indopacetus pacificus GN=MB PE=2 SV=3				
	MYG_MESCU	Mass: 17256	Score: 59	Expect: 0.68	Matches: 17
	Myoglobin OS=Mesoplodon carlini GN=MB PE=1 SV=2				
	MYG_MESSI	Mass: 17256	Score: 59	Expect: 0.68	Matches: 17
	Myoglobin OS=Mesoplodon stejnegeri GN=MB PE=2 SV=3				
4.	MYG_INIGE	Mass: 17191	Score: 82	Expect: 0.0036	Matches: 19
4.	MYG_INIGE	Mass: 17191	Score: 82	Expect: 0.0036	Matches: 19
	Myoglobin OS=Inia geoffrensis GN=MB PE=1 SV=2				
5.	MYG_PHYCD	Mass: 17320	Score: 81	Expect: 0.0045	Matches: 16
	Myoglobin OS=Physeter catodon GN=MB PE=1 SV=2				
	MYG_KOGER	Mass: 17357	Score: 62	Expect: 0.31	Matches: 14
	Myoglobin OS=Kogia breviceps GN=MB PE=2 SV=3				
	MYG_KOGSI	Mass: 17357	Score: 62	Expect: 0.31	Matches: 14
	Myoglobin OS=Kogia sima GN=MB PE=1 SV=2				
6.	ALBU_BOVIN	Mass: 71279	Score: 74	Expect: 0.02	Matches: 31
	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4				
7.	MYG_RABIT	Mass: 17210	Score: 70	Expect: 0.056	Matches: 18
	Myoglobin OS=Oryctolagus cuniculus GN=MB PE=1 SV=2				
8.	MYG_CASTI	Mass: 17140	Score: 70	Expect: 0.059	Matches: 21
	Myoglobin OS=Castor fiber GN=MB PE=1 SV=2				
9.	MYG_PERPO	Mass: 17052	Score: 67	Expect: 0.11	Matches: 20
	Myoglobin OS=Perodicticus potto edwardsi GN=MB PE=1 SV=2				
10.	MYG_MACRU	Mass: 17258	Score: 68	Expect: 0.13	Matches: 17
	Myoglobin OS=Macropus rufus GN=MB PE=1 SV=2				
11.	CYC_HORSE	Mass: 11941	Score: 64	Expect: 0.21	Matches: 20
	Cytochrome c OS=Equus caballus GN=CYC PE=1 SV=2				
12.	MYG_PHODA	Mass: 17221	Score: 58	Expect: 0.87	Matches: 12
	Myoglobin OS=Phocoenoides dalli GN=MB PE=1 SV=2				
	MYG_PHOPH	Mass: 17221	Score: 58	Expect: 0.87	Matches: 12
	Myoglobin OS=Phocoena phocaena GN=MB PE=1 SV=2				
13.	MYG_ROUAE	Mass: 17068	Score: 55	Expect: 1.9	Matches: 16
	Myoglobin OS=Rousettus aegyptiacus GN=MB PE=1 SV=2				
14.	MYG_HALGR	Mass: 17417	Score: 53	Expect: 2.9	Matches: 15
	Myoglobin OS=Halichoerus erythropus GN=MB PE=1 SV=2				
	MYG_PHOVI	Mass: 17417	Score: 53	Expect: 2.9	Matches: 15
	Myoglobin OS=Phoca vitulina GN=MB PE=1 SV=2				

	MYG_PTU1	Mass: 17417	Score: 50	Expect: 2.9	Matches: 19
	Moglobin OS=Pica vitulina GN=MB PE=1 SV=2				
	MYG_PUS1	Mass: 17472	Score: 53	Expect: 2.9	Matches: 15
	Moglobin OS=Pusa sibirica GN=MB PE=1 SV=2				
15.	MYG_CAN1	Mass: 17326	Score: 52	Expect: 3.2	Matches: 17
	Moglobin OS=Canis lupus familiaris GN=MB PE=1 SV=2				
	MYG_LYC1	Mass: 17353	Score: 52	Expect: 3.2	Matches: 17
	Moglobin OS=Lycan pictus GN=MB PE=1 SV=2				
	MYG_OTOM	Mass: 17326	Score: 52	Expect: 3.2	Matches: 17
	Moglobin OS=Otocyon megalotis GN=MB PE=1 SV=2				
16.	MYG_VUL1	Mass: 17326	Score: 52	Expect: 3.2	Matches: 17
	Moglobin OS=Vulpes chama GN=MB PE=1 SV=2				
17.	CYC_SAISC	Mass: 11898	Score: 52	Expect: 3.5	Matches: 15
	Cytochrome c OS=Saaimiri sciureus GN=CYCS PE=3 SV=3				
18.	ING2_HUMAN	Mass: 33493	Score: 52	Expect: 3.9	Matches: 20
	Inhibitor of growth protein 2 OS=Homo sapiens GN=ING2 PE=1 SV=2				
19.	CYC_EQUAS	Mass: 11927	Score: 50	Expect: 4.9	Matches: 18
	Cytochrome c OS=Equus asinus GN=CYCS PE=1 SV=2				
	CYC_EQUEU	Mass: 11927	Score: 50	Expect: 4.9	Matches: 18
	Cytochrome c OS=Equus burchelli GN=CYCS PE=1 SV=2				
20.	MYG_OND1	Mass: 17257	Score: 50	Expect: 5.1	Matches: 15
	Moglobin OS=Ondatra zibethicus GN=MB PE=1 SV=2				
21.	MCE_MYXV	Mass: 39813	Score: 50	Expect: 5.9	Matches: 14
	Cap-specific mRNA (nucleoside-2''-O)-methyltransferase OS=Myxoma virus (strain Lausanne) GN=PAPS PE=3 SV=1				

Search Parameters

Type of search : Sequence Query
 Enzyme : Lys-N
 Fixed modifications : [Carboxymethyl \(C\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.5 Da
 Fragment Mass Tolerance : ± 0.6 Da
 Peptide Mass Tolerance : ± 0.5 Da
 Fragment Mass Tolerance : ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : Default
 Query1 (514.8834.1+): <no title>
 Query2 (514.8894.1+): <no title>
 Query3 (515.6702.1+): <no title>
 Query4 (516.8091.1+): <no title>
 Query5 (516.8136.1+): <no title>
 Query6 (516.8147.1+): <no title>
 Query7 (516.8308.1+): <no title>
 Query8 (517.8313.1+): <no title>
 Query9 (517.8412.1+): <no title>
 Query10 (517.8523.1+): <no title>
 Query11 (517.7459.1+): <no title>
 Query12 (518.6223.1+): <no title>
 Query13 (520.6114.1+): <no title>
 Query14 (520.6220.1+): <no title>
 Query15 (520.6280.1+): <no title>
 Query16 (520.6283.1+): <no title>
 Query17 (522.5890.1+): <no title>
 Query18 (522.6140.1+): <no title>
 Query19 (524.6058.1+): <no title>
 Query20 (524.6184.1+): <no title>
 Query21 (524.6210.1+): <no title>
 Query22 (524.6251.1+): <no title>
 Query23 (526.6209.1+): <no title>
 Query24 (531.7811.1+): <no title>
 Query25 (534.5882.1+): <no title>
 Query26 (534.6019.1+): <no title>
 Query27 (534.6172.1+): <no title>
 Query28 (534.6274.1+): <no title>
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 Query30 (543.6021.1+): <no title>
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 Query33 (544.5950.1+): <no title>
 Query34 (544.5971.1+): <no title>
 Query35 (545.8574.1+): <no title>
 Query36 (546.5981.1+): <no title>
 : seq(C-P)
 Query37 (547.2504.1+): <no title>
 Query38 (550.5665.1+): <no title>
 Query39 (550.5775.1+): <no title>
 Query40 (550.5861.1+): <no title>

4P mass+c

Mascot Search Results

User : kahn20002
Email : kahn20003@gmail.com
Search title : 4P 0.5 hits
Database : SwissProt 2016_03 (550740 sequences; 196582750 residues)
Timestamp : 17 Apr 2016 at 04:44:57 GMT
Top Score : 111 for **MYG_EQUBU**, Myoglobin OS=Equus burchelli GN=MB PE=1 SV=2

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant ($p < 0.05$).

Score Distribution

Concise Protein Summary Report

Format As	Concise Protein Summary	Help
Significance threshold p<	0.05	Max. number of hits 50
Preferred taxonomy	All entries	

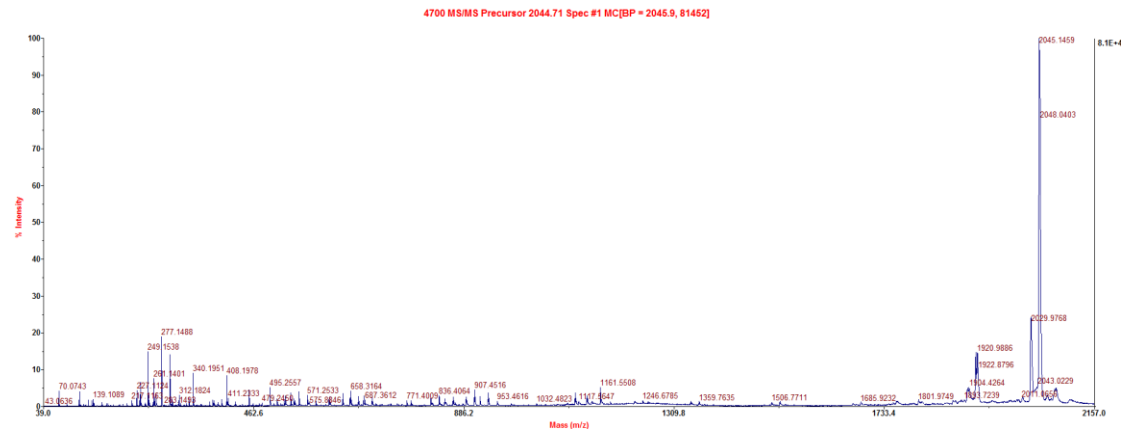
Re-Search All Search Unmatched

- | | | | | |
|---|-------------|------------|-----------------|------------|
| MYG_EQUBU | Mass: 17072 | Score: 111 | Expect: 4.4e-06 | Matches: 7 |
| Myoglobin OS=Equus burchelli GN=MB PE=1 SV=2 | | | | |
| MYG_HERSE | Mass: 17072 | Score: 111 | Expect: 4.4e-06 | Matches: 7 |
| Myoglobin OS=Equus caballus GN=MB PE=1 SV=2 | | | | |
| MYG_PHYCD | Mass: 17320 | Score: 93 | Expect: 0.00029 | Matches: 6 |
| Myoglobin OS=Phvseter catodon GN=MB PE=1 SV=2 | | | | |
| MYG_BALAC | Mass: 17275 | Score: 90 | Expect: 0.0005 | Matches: 6 |
| Myoglobin OS=Balaenoptera acutorostrata GN=MB PE=1 SV=2 | | | | |
| MYG_BALBO | Mass: 17238 | Score: 90 | Expect: 0.0005 | Matches: 6 |
| Myoglobin OS=Balaenoptera borealis GN=MB PE=2 SV=3 | | | | |
| MYG_BALED | Mass: 17238 | Score: 90 | Expect: 0.0005 | Matches: 6 |
| Myoglobin OS=Balaenoptera edeni GN=MB PE=2 SV=3 | | | | |
| MYG_BALPH | Mass: 17206 | Score: 90 | Expect: 0.0005 | Matches: 6 |
| Myoglobin OS=Balaenoptera physalus GN=MB PE=1 SV=2 | | | | |
| MYG_ESORD | Mass: 17238 | Score: 90 | Expect: 0.0005 | Matches: 6 |
| Myoglobin OS=Eschrichtius robustus GN=MB PE=1 SV=2 | | | | |
| MYG_INIGE | Mass: 17191 | Score: 90 | Expect: 0.0005 | Matches: 6 |
| Myoglobin OS>Inia geoffrensis GN=MB PE=1 SV=2 | | | | |
| MYG_MEQND | Mass: 17252 | Score: 90 | Expect: 0.0005 | Matches: 6 |
| Myoglobin OS=Megaptera novaeangliae GN=MB PE=1 SV=2 | | | | |
| MYG_KOGER | Mass: 17357 | Score: 72 | Expect: 0.038 | Matches: 5 |
| Myoglobin OS=Kogia breviceps GN=MB PE=2 SV=3 | | | | |
| MYG_KOGSI | Mass: 17357 | Score: 72 | Expect: 0.038 | Matches: 5 |
| Myoglobin OS=Kogia sima GN=MB PE=1 SV=2 | | | | |
| MYG_DELEL | Mass: 17195 | Score: 70 | Expect: 0.059 | Matches: 5 |
| Myoglobin OS=Delphinapterus leucas GN=MB PE=1 SV=2 | | | | |
| MYG_GLOME | Mass: 17205 | Score: 70 | Expect: 0.059 | Matches: 5 |
| Myoglobin OS=Globicephala melas GN=MB PE=1 SV=2 | | | | |
| MYG_ZIPCA | Mass: 17298 | Score: 70 | Expect: 0.059 | Matches: 5 |
| Myoglobin OS=Ziphius cavirostris GN=MB PE=1 SV=2 | | | | |
| MYG_INEPO | Mass: 17270 | Score: 68 | Expect: 0.089 | Matches: 5 |
| Myoglobin OS=Indopacetus pacificus GN=MB PE=2 SV=3 | | | | |
| MYG_MACRU | Mass: 17258 | Score: 68 | Expect: 0.089 | Matches: 5 |
| Myoglobin OS=Macropus rufus GN=MB PE=1 SV=2 | | | | |
| MYG_MESCU | Mass: 17256 | Score: 68 | Expect: 0.089 | Matches: 5 |
| Myoglobin OS=Mesolodon carlhubbsi GN=MB PE=1 SV=2 | | | | |
| MYG_MESSI | Mass: 17256 | Score: 68 | Expect: 0.089 | Matches: 5 |
| Myoglobin OS=Mesolodon steineyeri GN=MB PE=2 SV=3 | | | | |
| MYG_PHODA | Mass: 17221 | Score: 60 | Expect: 0.51 | Matches: 4 |
| Myoglobin OS=Phocoenoides dalli GN=MB PE=1 SV=2 | | | | |
| MYG_PHODH | Mass: 17221 | Score: 60 | Expect: 0.51 | Matches: 4 |
| Myoglobin OS=Phocoena phocoena GN=MB PE=1 SV=2 | | | | |
| MYG_HALOP | Mass: 17417 | Score: 55 | Expect: 1.7 | Matches: 4 |
| Myoglobin OS=Halichoerus grypus GN=MB PE=1 SV=2 | | | | |
| MYG_PHOVI | Mass: 17417 | Score: 55 | Expect: 1.7 | Matches: 4 |
| Myoglobin OS=Phoca vitulina GN=MB PE=1 SV=2 | | | | |
| MYG_PUSSI | Mass: 17472 | Score: 55 | Expect: 1.7 | Matches: 4 |
| Myoglobin OS=Phoca sibirica GN=MB PE=1 SV=2 | | | | |
| MYG_CANLE | Mass: 17326 | Score: 52 | Expect: 3.3 | Matches: 4 |
| Myoglobin OS=Canis lupus familiaris GN=MB PE=1 SV=2 | | | | |
| MYG_LYOPI | Mass: 17353 | Score: 52 | Expect: 3.3 | Matches: 4 |
| Myoglobin OS=Lycodon pictus GN=MB PE=1 SV=2 | | | | |
| MYG_LYOP1 | Mass: 17353 | Score: 52 | Expect: 3.3 | Matches: 4 |
| Myoglobin OS=Lycodon pictus GN=MB PE=1 SV=2 | | | | |
| MYG_OTOME | Mass: 17326 | Score: 52 | Expect: 3.3 | Matches: 4 |
| Myoglobin OS>Otocyon megalotis GN=MB PE=1 SV=2 | | | | |
| MYG_VULCH | Mass: 17326 | Score: 52 | Expect: 3.3 | Matches: 4 |
| Myoglobin OS=Vulpes chama GN=MB PE=1 SV=2 | | | | |
| MYG_AOTTR | Mass: 17150 | Score: 51 | Expect: 4.5 | Matches: 4 |
| Myoglobin OS=Artus triviratus GN=MB PE=1 SV=2 | | | | |
| MYG_CALJA | Mass: 17184 | Score: 51 | Expect: 4.5 | Matches: 4 |
| Myoglobin OS=Callithrix jacchus GN=MB PE=1 SV=2 | | | | |
- | | | | | |
|--|-------------|-----------|----------------|------------|
| MYG_ERYPA | Mass: 17137 | Score: 90 | Expect: 0.0006 | Matches: 6 |
| Myoglobin OS=Erythrocebus patas GN=MB PE=1 SV=2 | | | | |
| MYG_GORGE | Mass: 17221 | Score: 90 | Expect: 0.0006 | Matches: 6 |
| Myoglobin OS=Gorilla gorilla gorilla GN=MB PE=1 SV=2 | | | | |
| MYG_HUMAN | Mass: 17231 | Score: 90 | Expect: 0.0006 | Matches: 6 |
| Myoglobin OS=Homo sapiens GN=MB PE=1 SV=2 | | | | |
| MYG_HYLAG | Mass: 17261 | Score: 90 | Expect: 0.0006 | Matches: 6 |
| Myoglobin OS=Hylobates agilis GN=MB PE=1 SV=2 | | | | |
| MYG_PANTR | Mass: 17240 | Score: 90 | Expect: 0.0006 | Matches: 6 |
| Myoglobin OS=Pan troglodytes GN=MB PE=1 SV=2 | | | | |
| MYG_PAPAN | Mass: 17137 | Score: 90 | Expect: 0.0006 | Matches: 6 |
| Myoglobin OS=Papio anubis GN=MB PE=1 SV=2 | | | | |
| MYG_PONPY | Mass: 17187 | Score: 90 | Expect: 0.0006 | Matches: 6 |
| Myoglobin OS=Pongo pygmaeus GN=MB PE=1 SV=2 | | | | |
| MYG_SEMEN | Mass: 17137 | Score: 90 | Expect: 0.0006 | Matches: 6 |
| Myoglobin OS=Simulium entellus GN=MB PE=1 SV=2 | | | | |
| MYG_SYMSY | Mass: 17261 | Score: 90 | Expect: 0.0006 | Matches: 6 |
| Myoglobin OS=Symphalangus syndactylus GN=MB PE=1 SV=2 | | | | |
| MYG_PEPPO | Mass: 17052 | Score: 74 | Expect: 0.021 | Matches: 5 |
| Myoglobin OS=Perodicticus potto edwardsi GN=MB PE=1 SV=2 | | | | |
| MYG_RABIT | Mass: 17210 | Score: 74 | Expect: 0.021 | Matches: 5 |
| Myoglobin OS=Oryctolagus cuniculus GN=MB PE=1 SV=2 | | | | |
| MYG_CASE1 | Mass: 17140 | Score: 72 | Expect: 0.032 | Matches: 5 |
| Myoglobin OS=Castor fiber GN=MB PE=1 SV=2 | | | | |
| MYG_MACFA | Mass: 17165 | Score: 72 | Expect: 0.032 | Matches: 5 |
| Myoglobin OS=Macaca fascicularis GN=MB PE=1 SV=2 | | | | |
| MYG_ONOCE | Mass: 17257 | Score: 56 | Expect: 1.2 | Matches: 4 |
| Myoglobin OS=Ondatra zibethicus GN=MB PE=1 SV=2 | | | | |
| MYG_ROUWE | Mass: 17068 | Score: 56 | Expect: 1.5 | Matches: 4 |
| Myoglobin OS=Reutheria neotoma GN=MB PE=1 SV=2 | | | | |

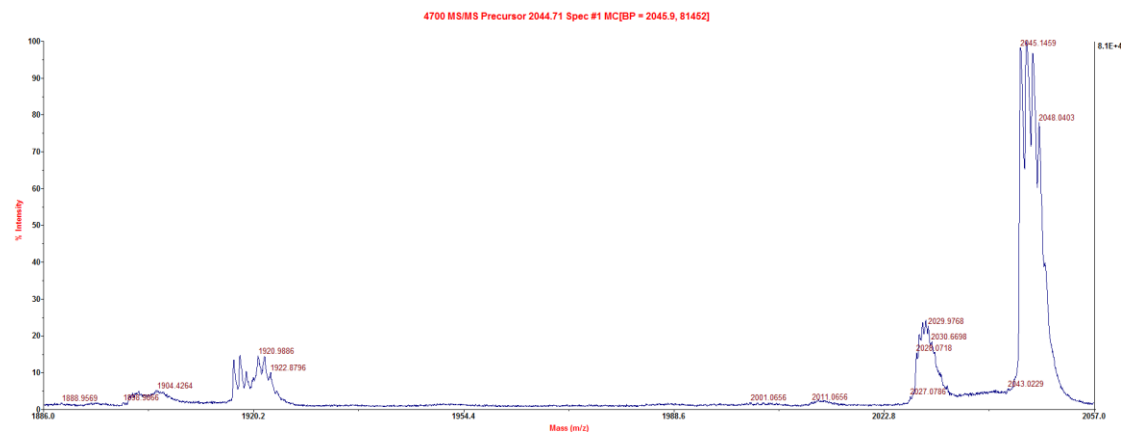
Spectra of peptides derived from BSA digested by different proteases

Trypsin digest

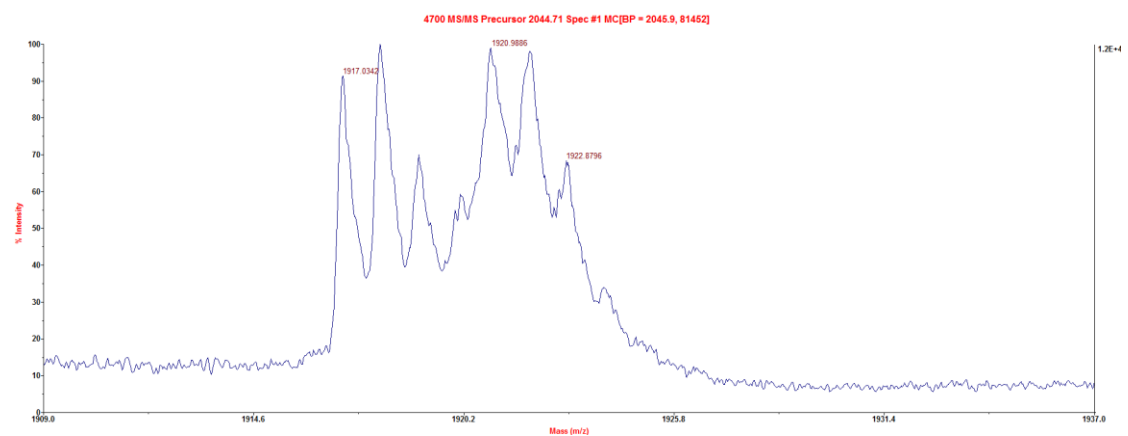
2044.71 RHPYFYAPELLYYANK



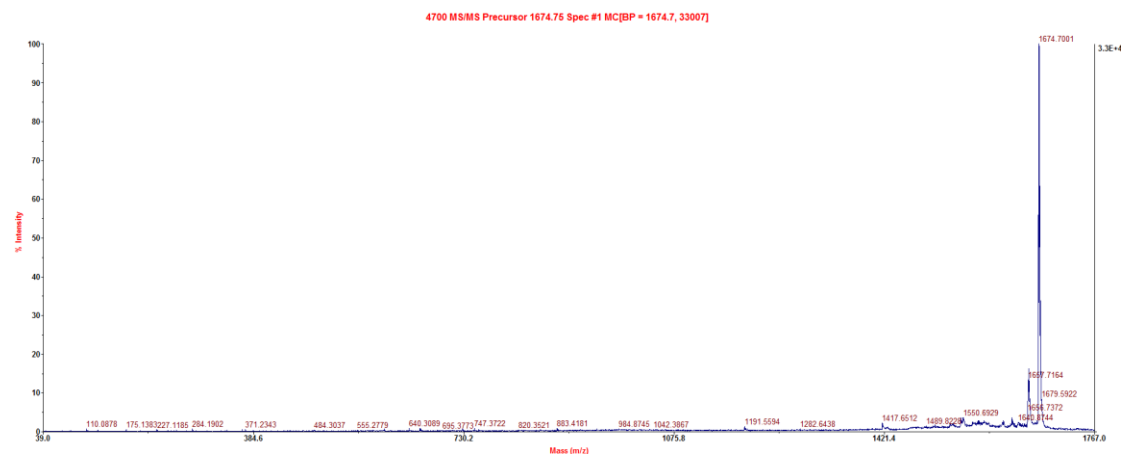
Precursor



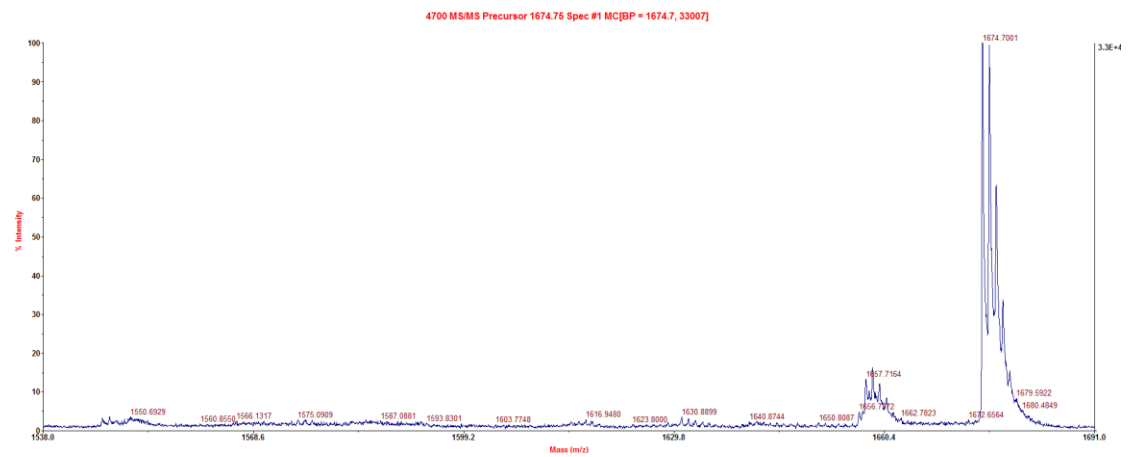
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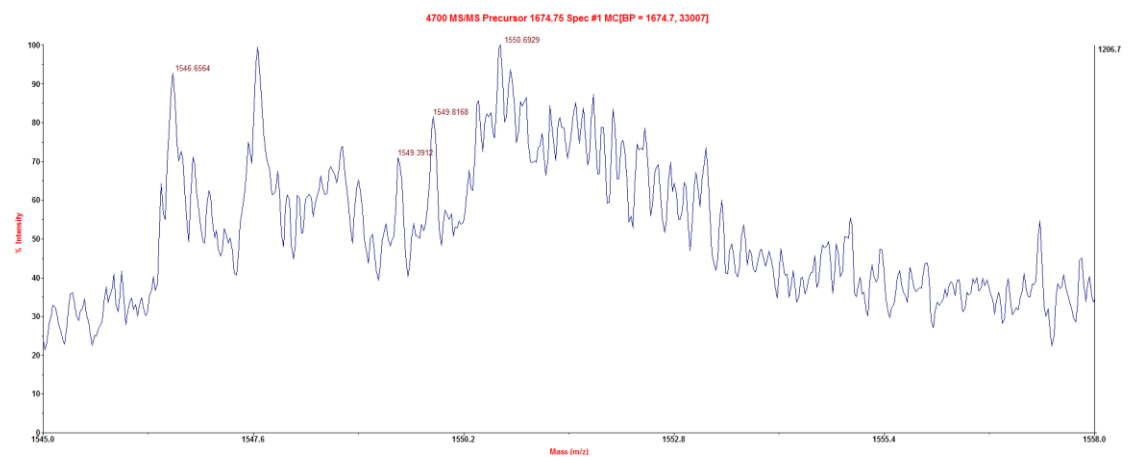
1674.75 RHPYFYAPELLYYAN



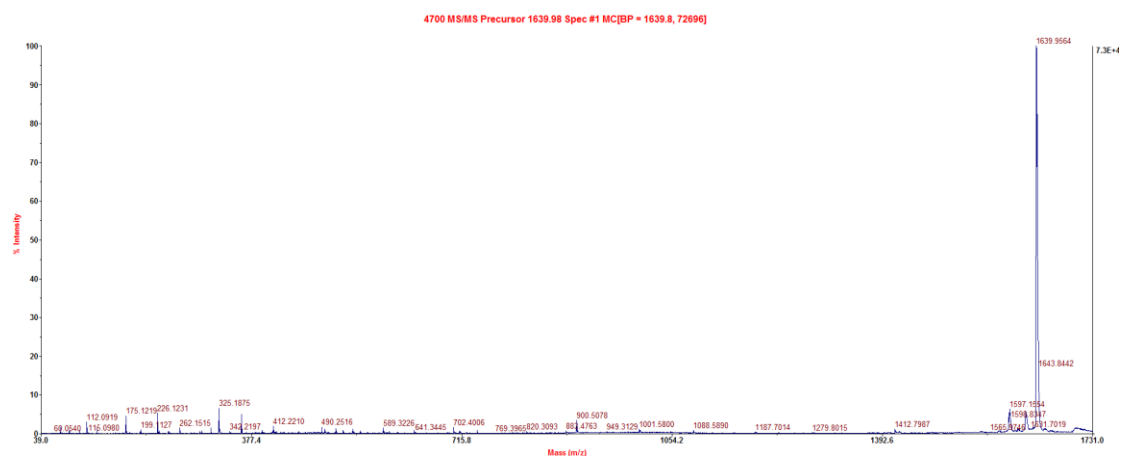
Precursor



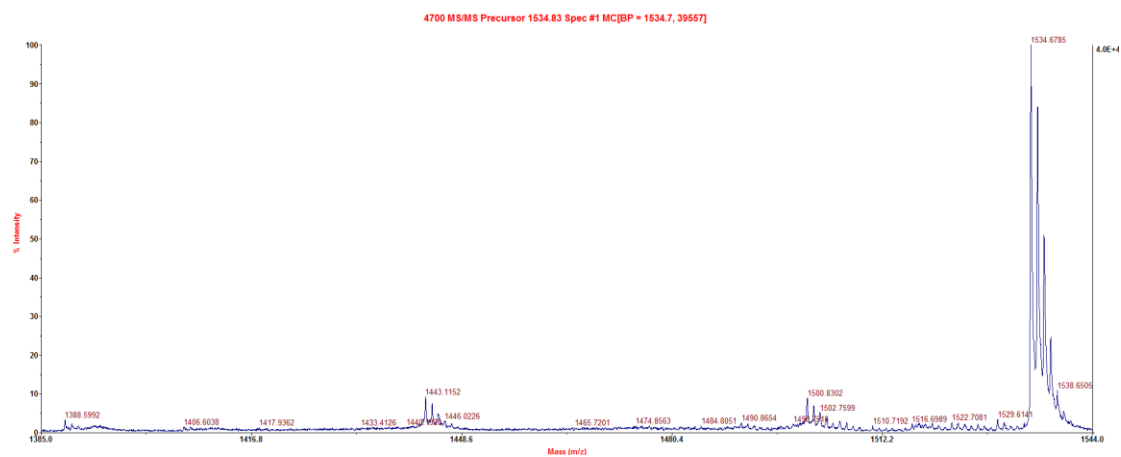
RHPYFYAPELLYYA b+18 ion



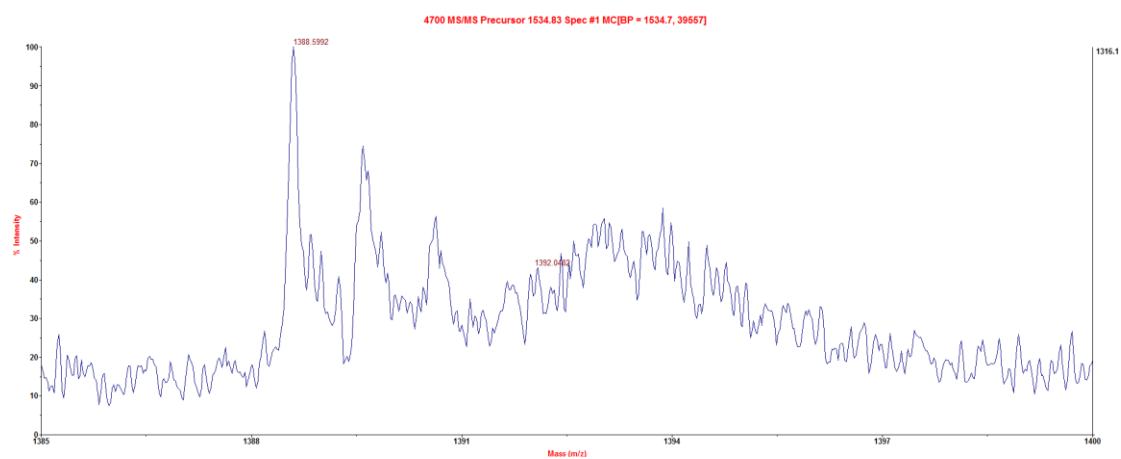
1534.83 LKECmcCmcDKPLLEK



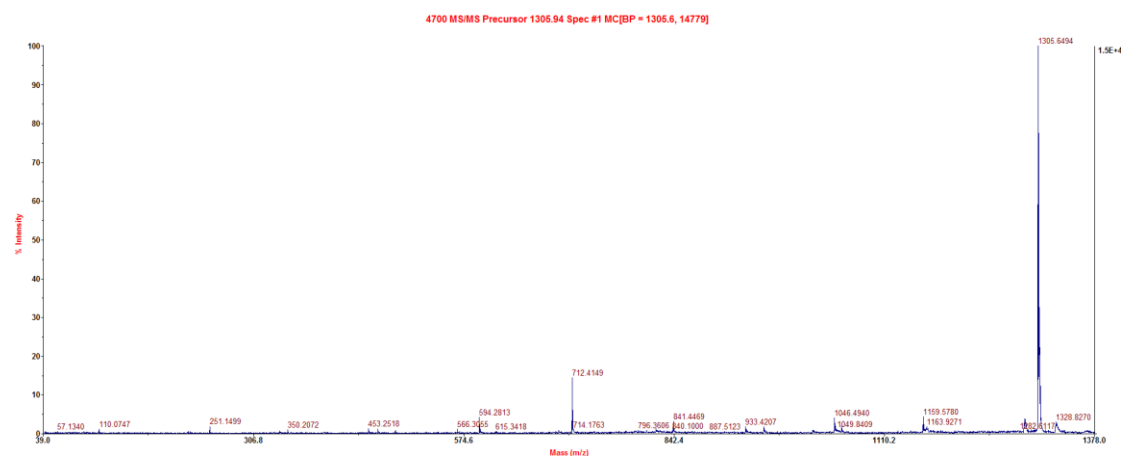
Precursor



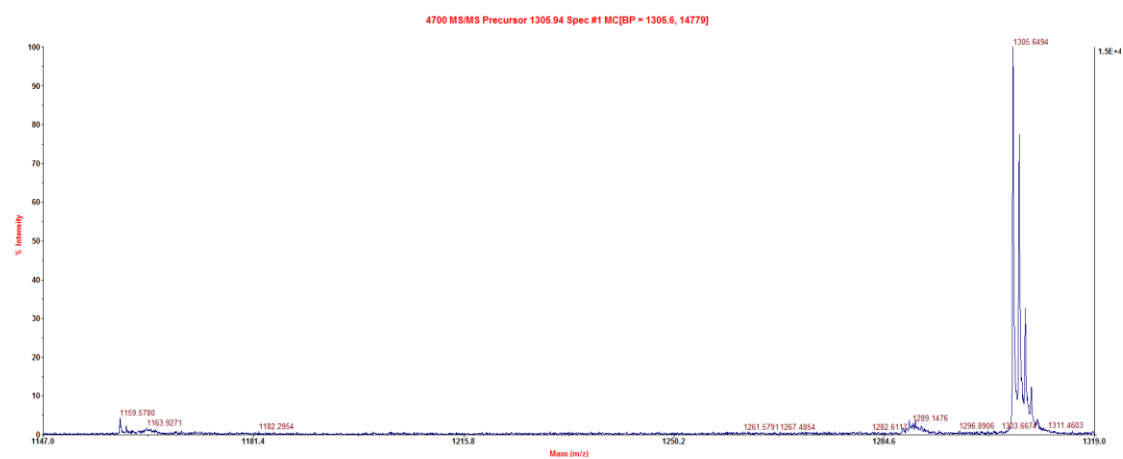
LKECmcCmcDKPLLE b ion



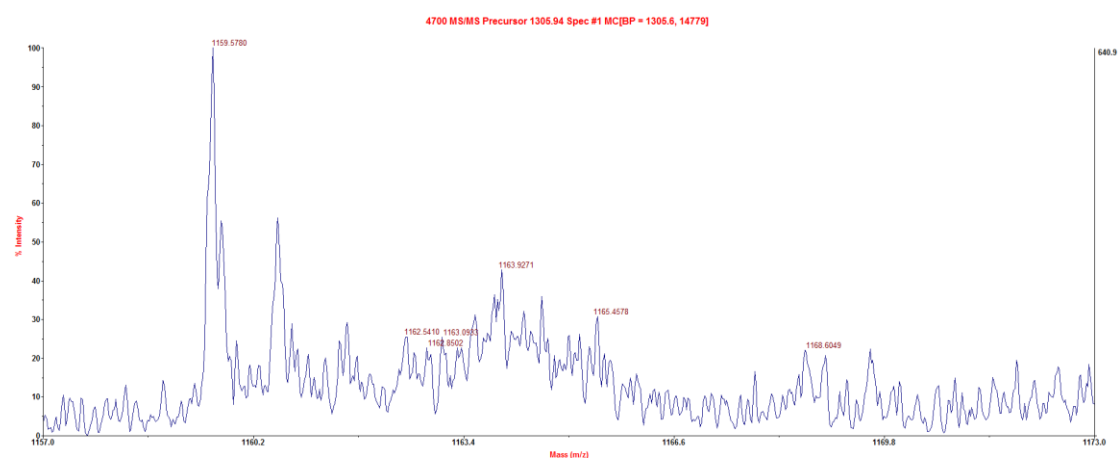
1305.94 HLVDEPQNLIK



Precursor

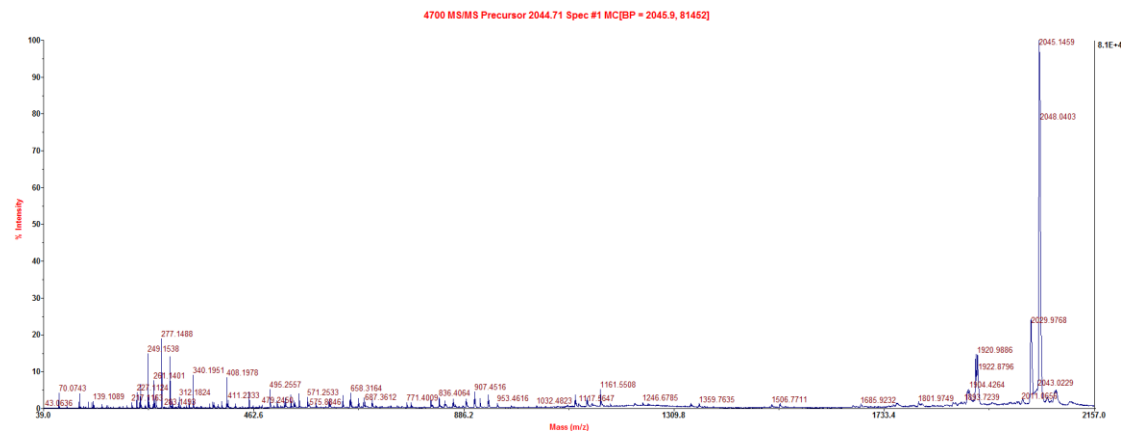


HLVDEPQNLI b ion

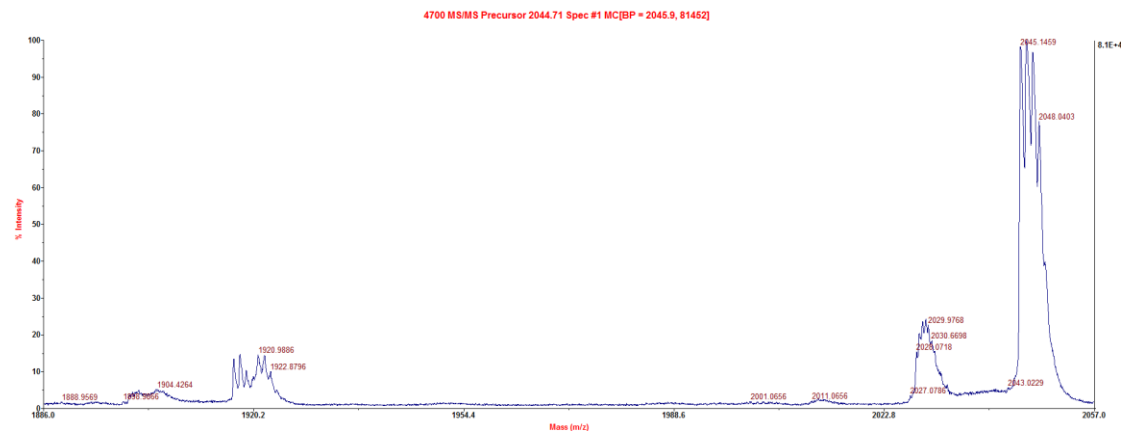


AspN digest

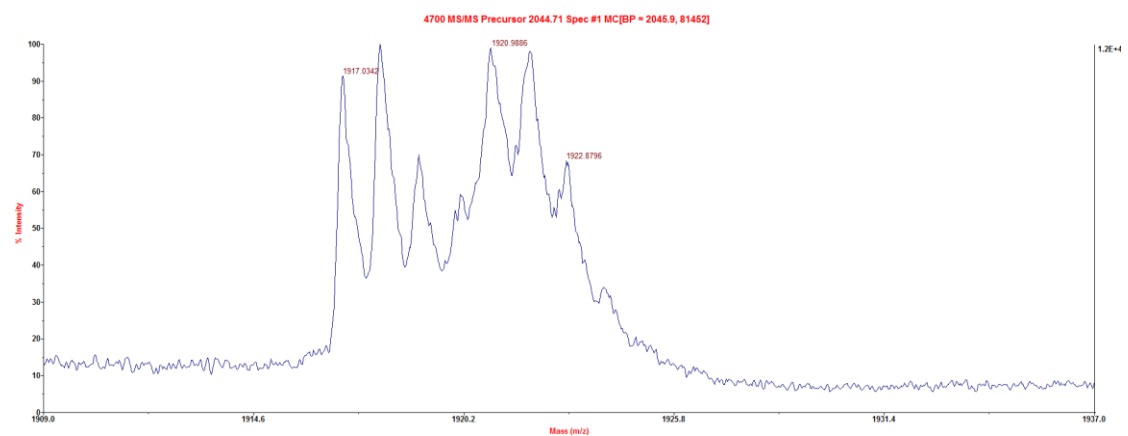
2044.71 RHPYFYAPELLYYANK



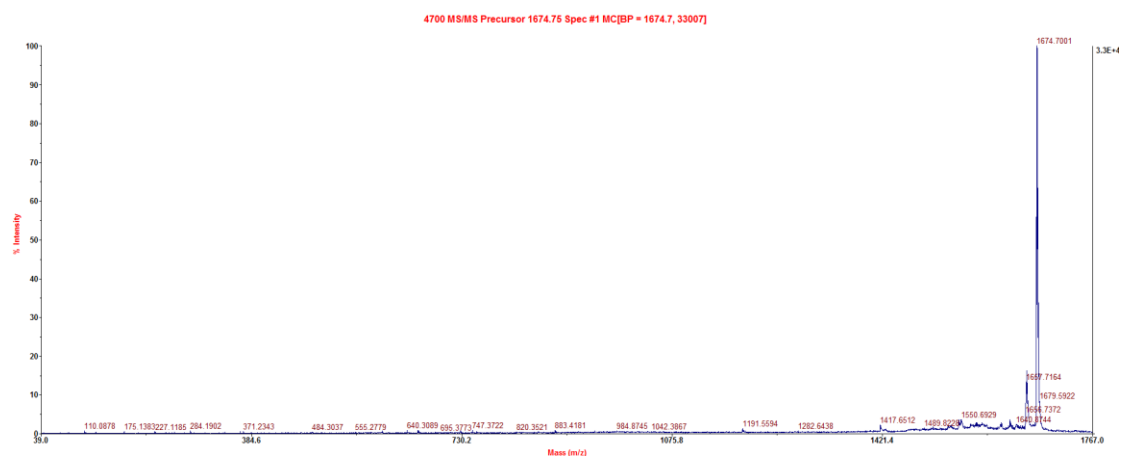
Precursor



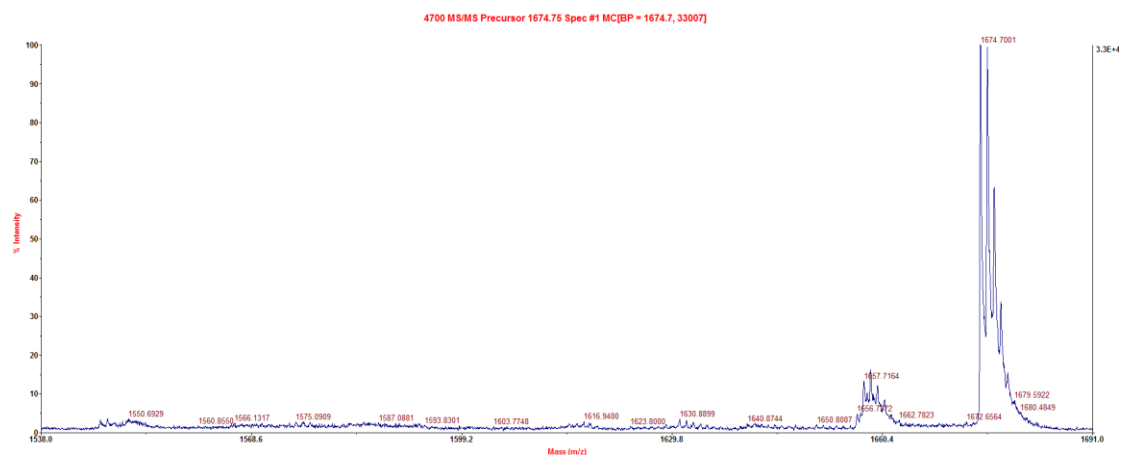
RHPYFYAPELLYYAN b+18 ion



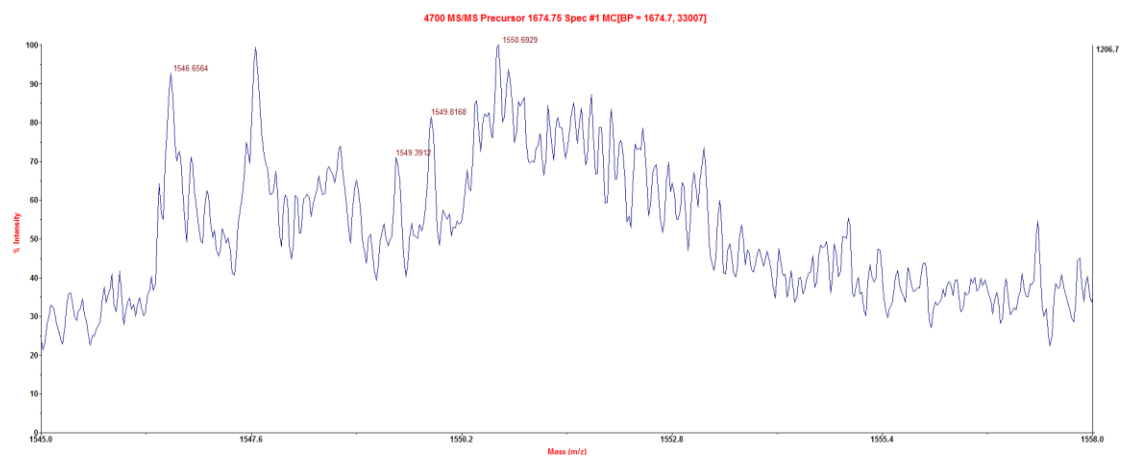
1674.75 RHPYFYAPELLYYAN



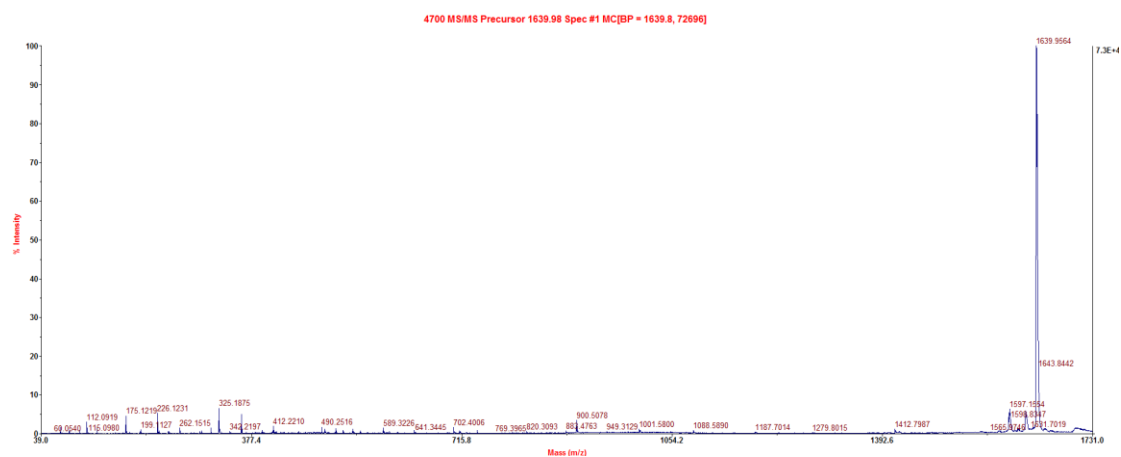
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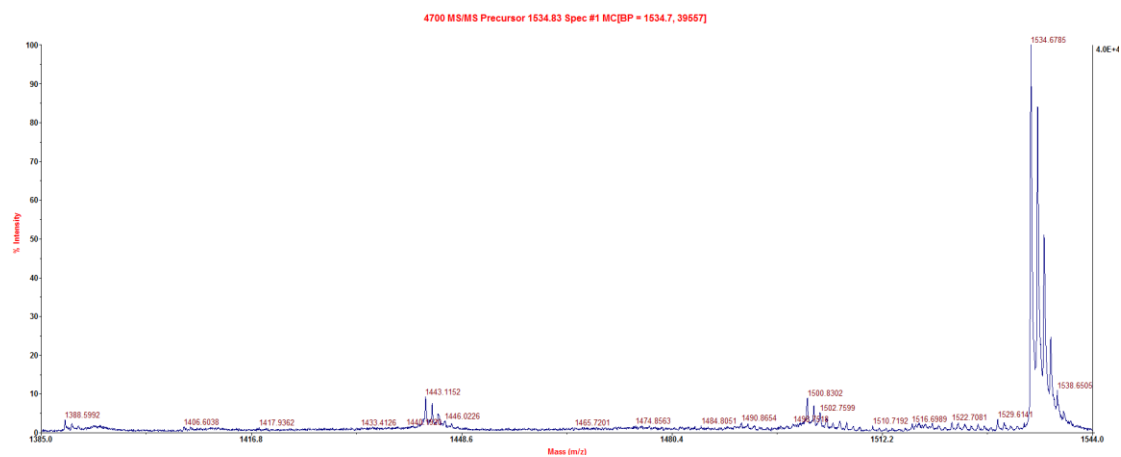
RHPYFYAPELLYYA b+18 ion



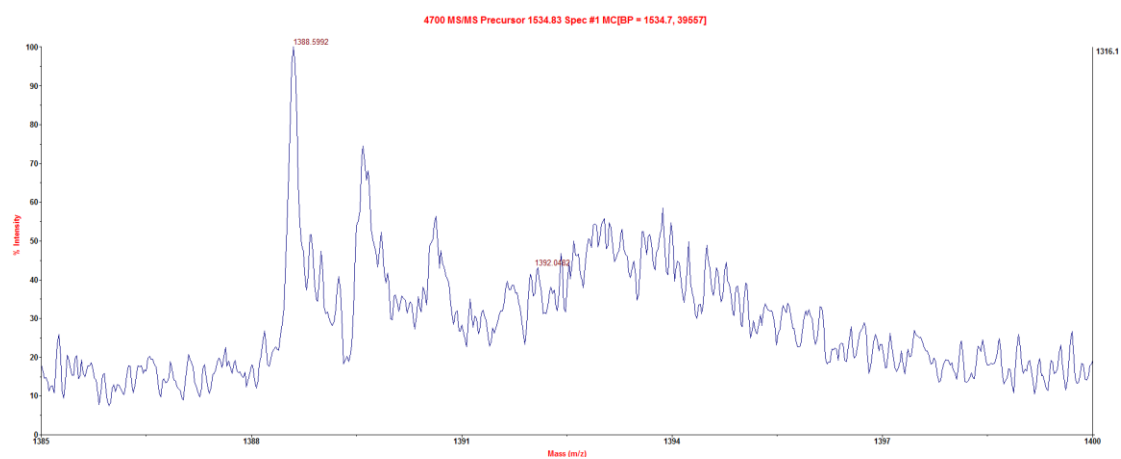
1534.83 LKECmcCmcDKPLLEK



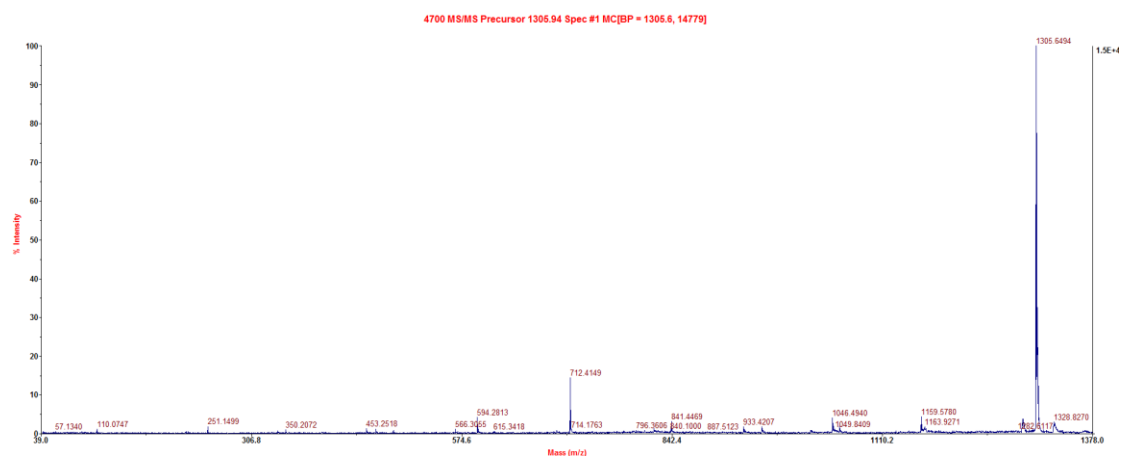
Precursor



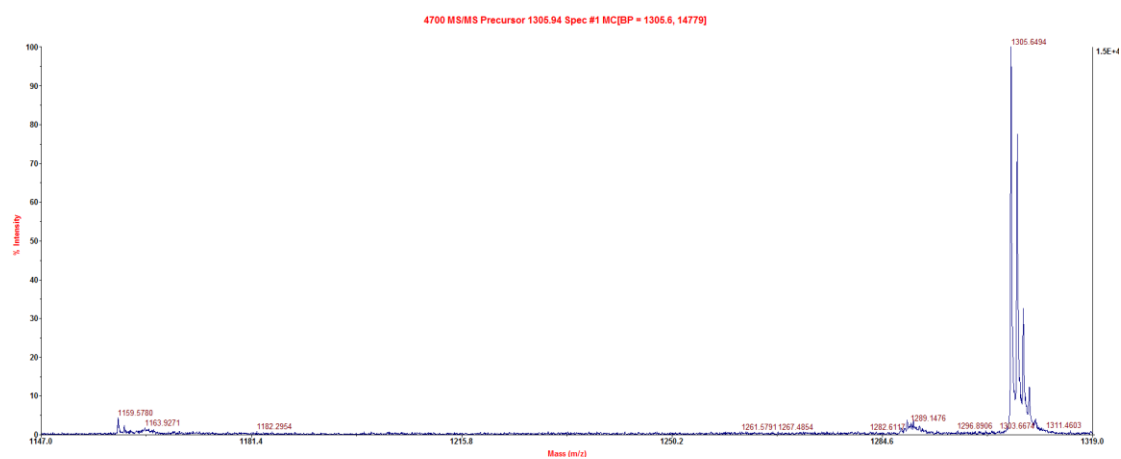
LKECmcCmcDKPLLE b ion



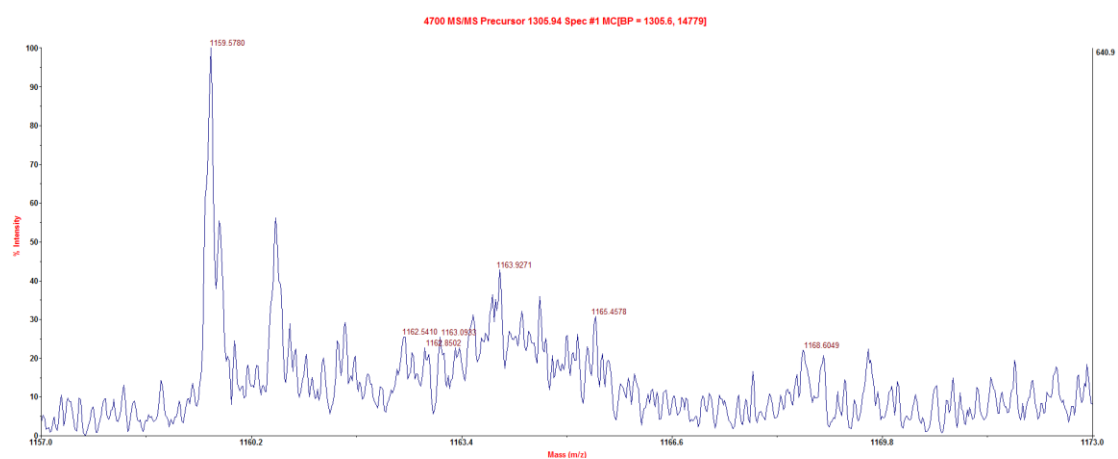
1305.94 HLVDEPQNLIK



Precursor

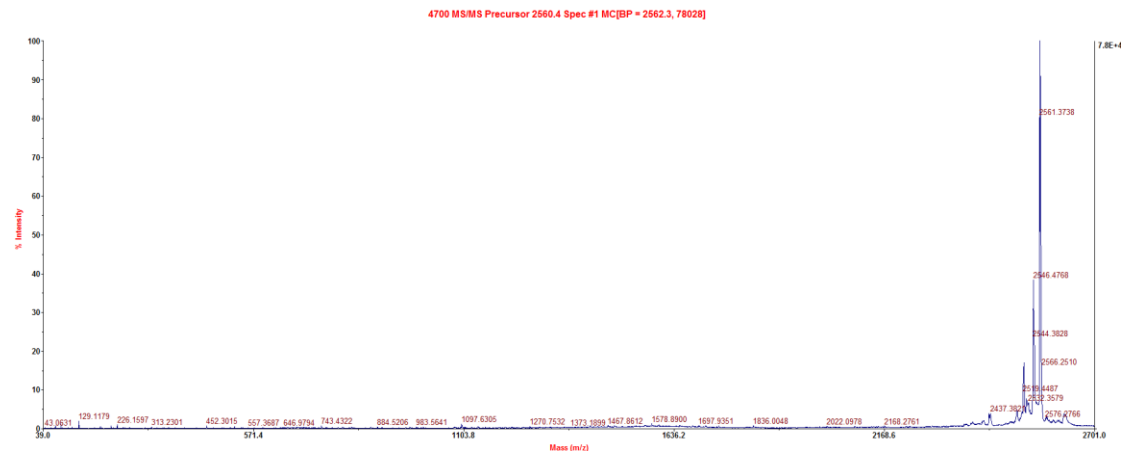


HLVDEPQNLI b ion

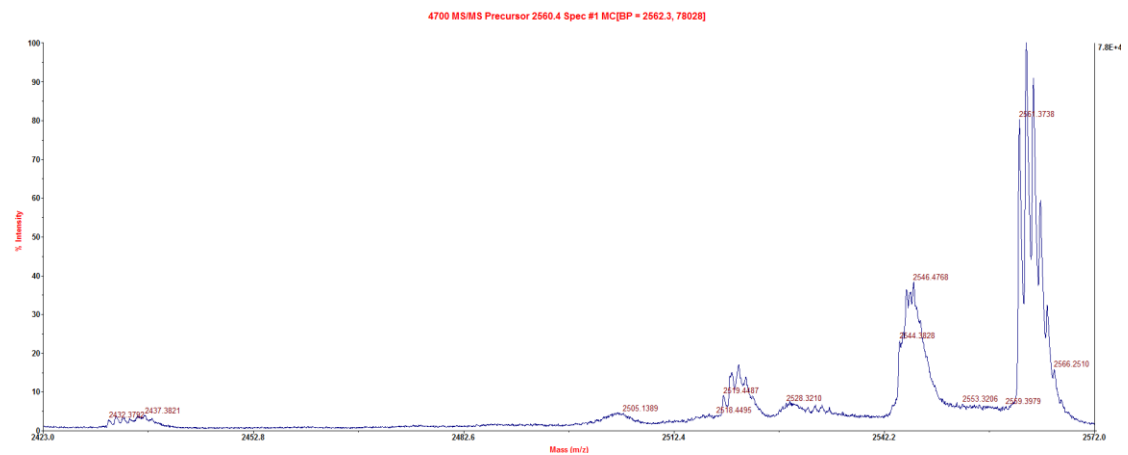


GluC digest

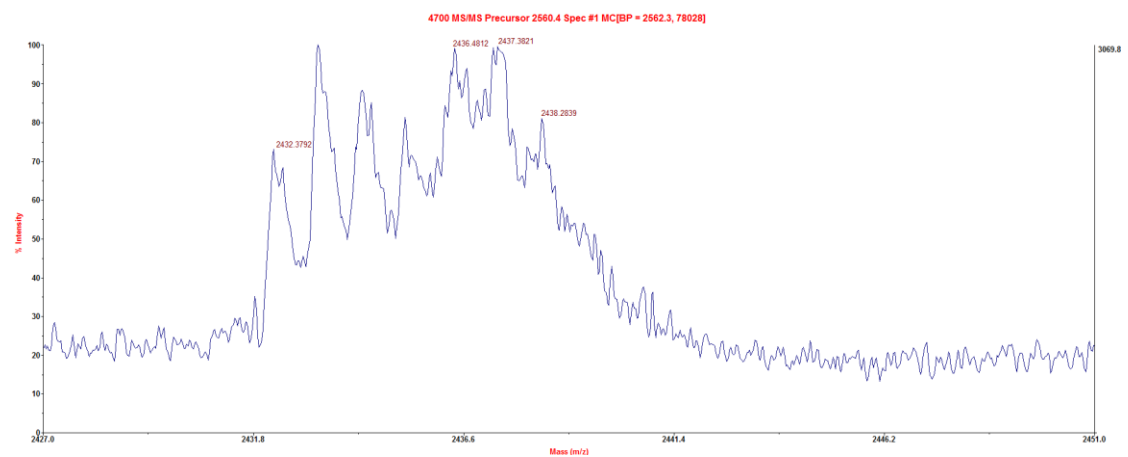
2560.40 RALKAWSVARLSQKFPKAEFVE



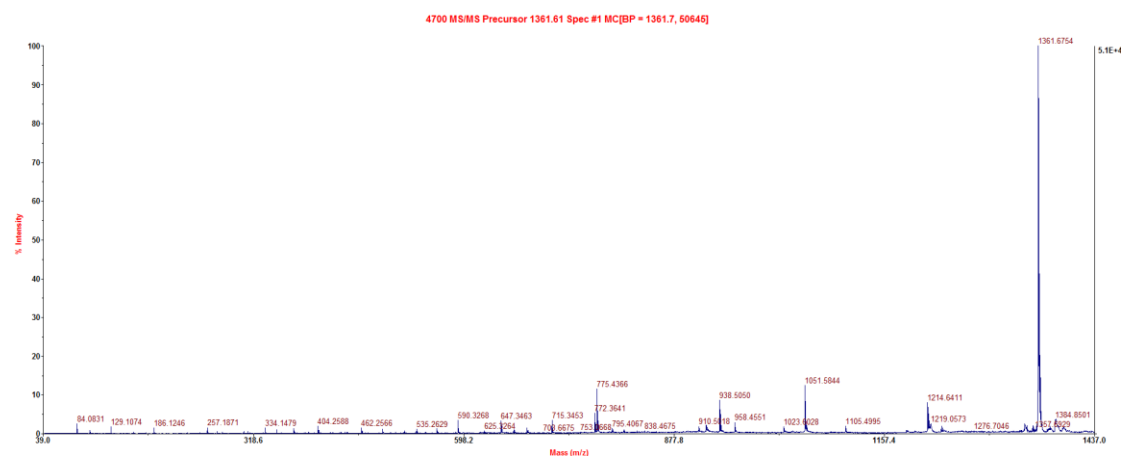
Precursor



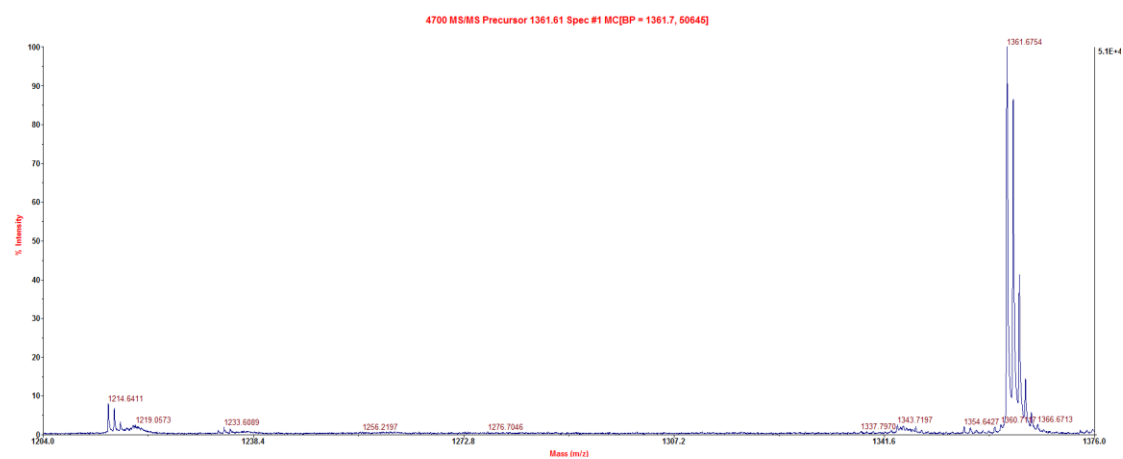
RALKAWSVARLSQKFPKAEFV b+18 ion



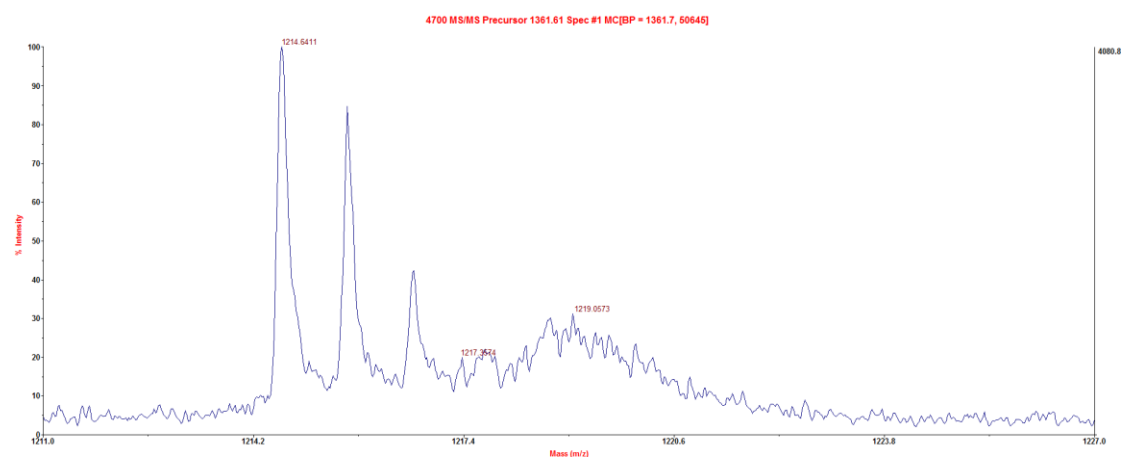
1361.61 KKFWGKYLYE



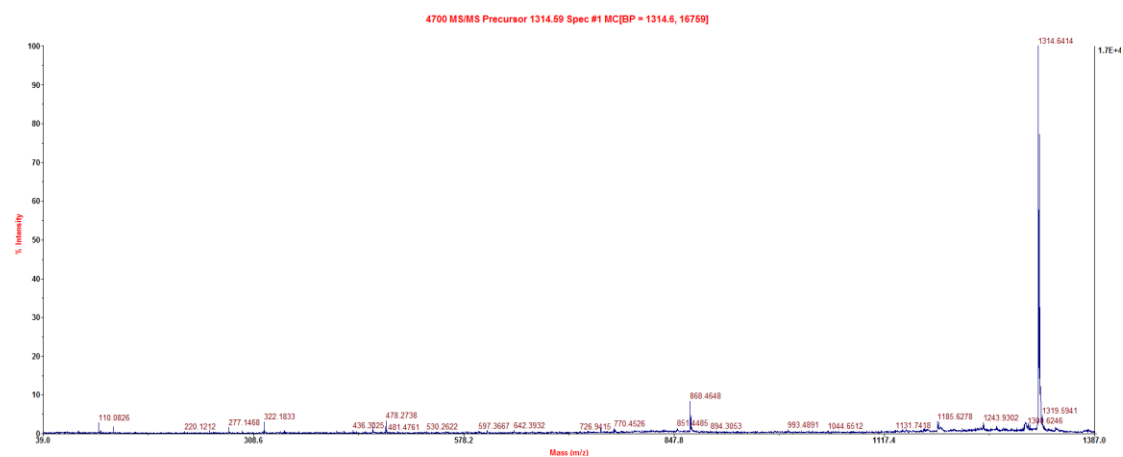
Precursor



KKFWGKYLY b ion



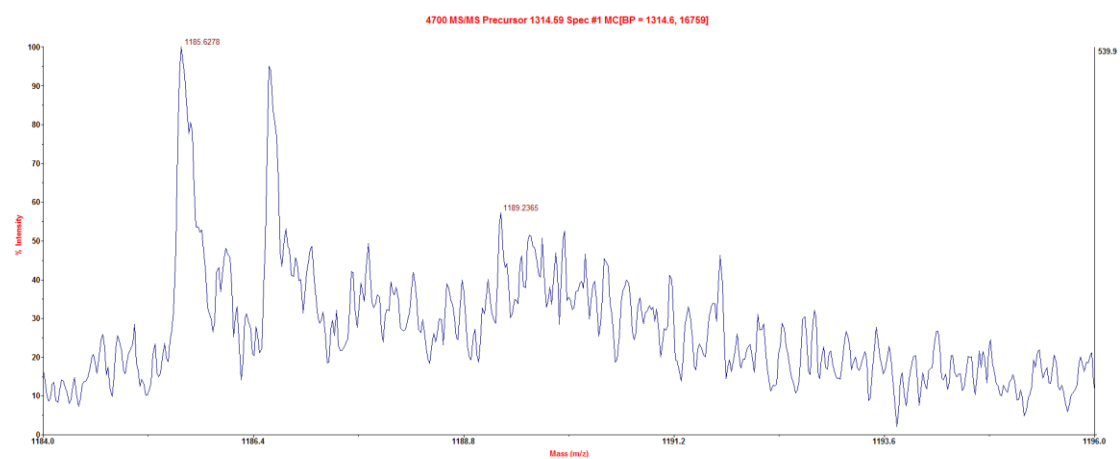
1314.59 IAHRFKDLGEE



Precursor



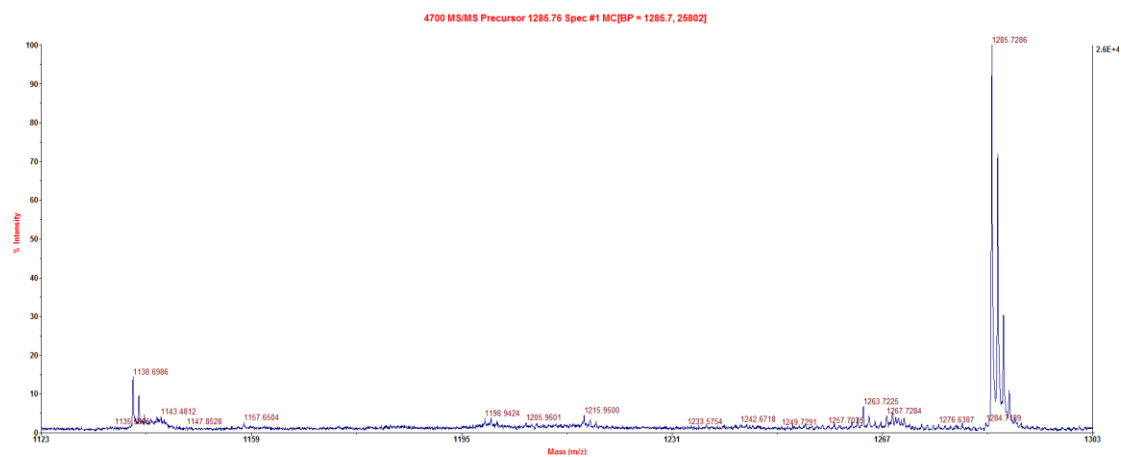
IAHRFKDLGE b+18 ion



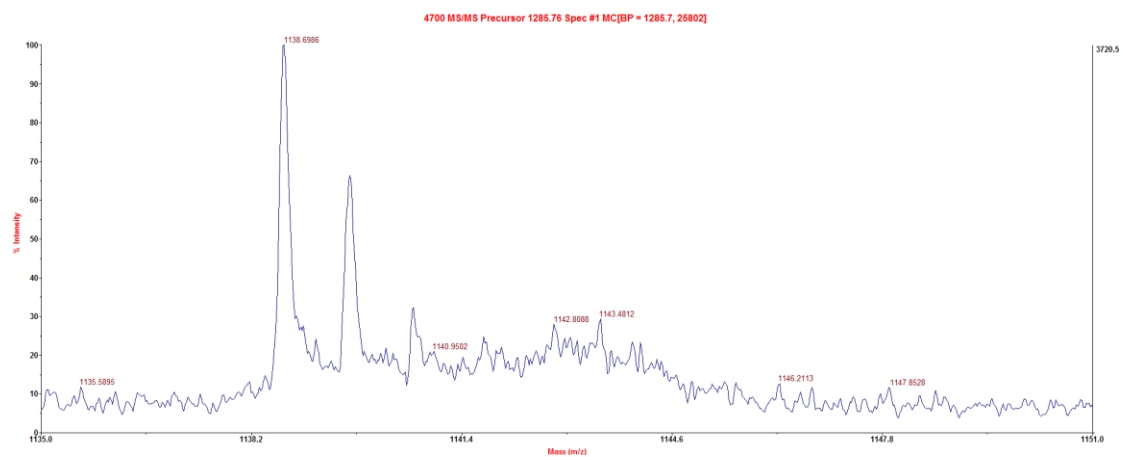
1285.76 KQIKKQTALVE



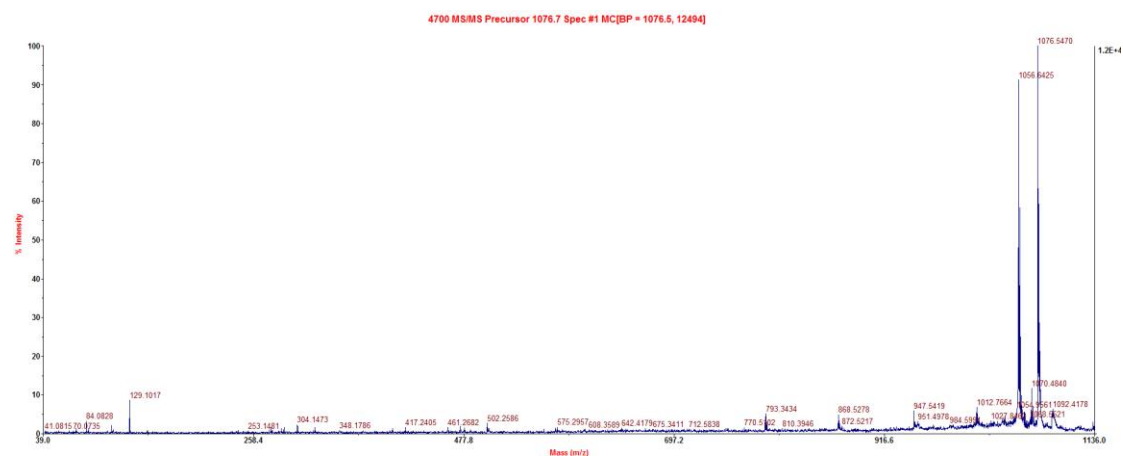
Precursor



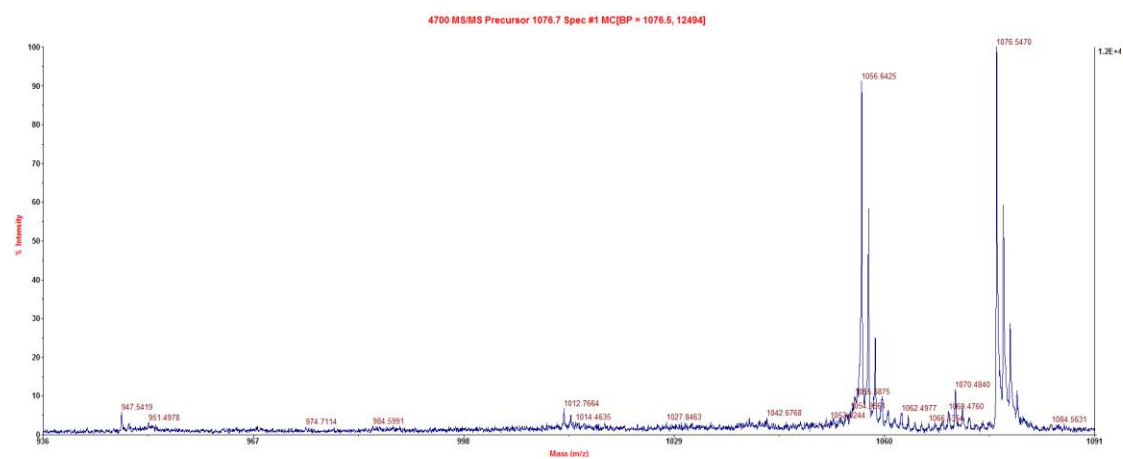
KQIKKQTALV b ion



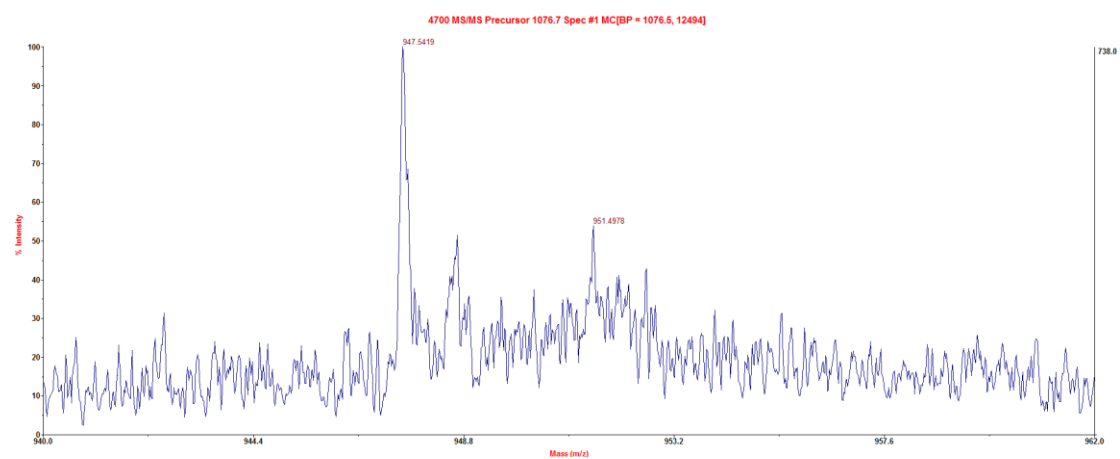
1076.70 LCmcKVASLRE



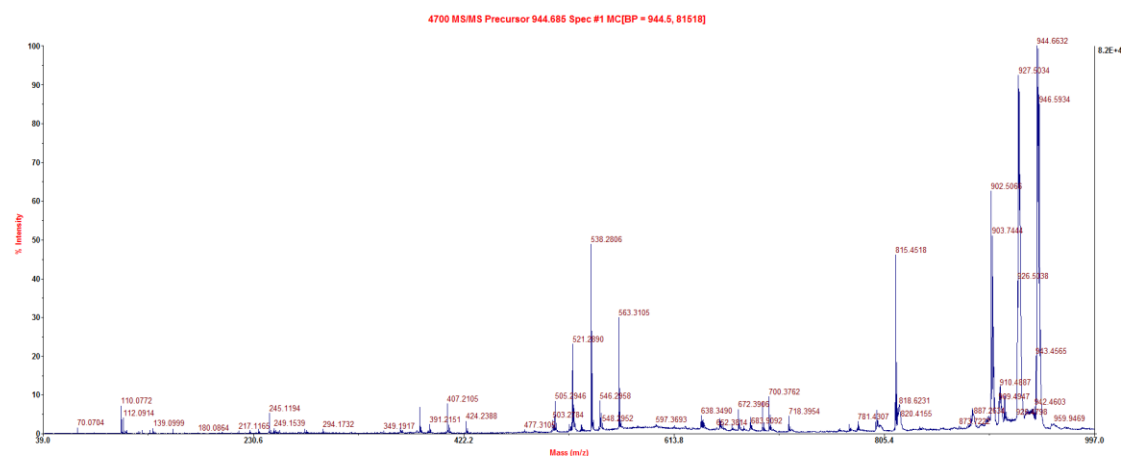
Precursor



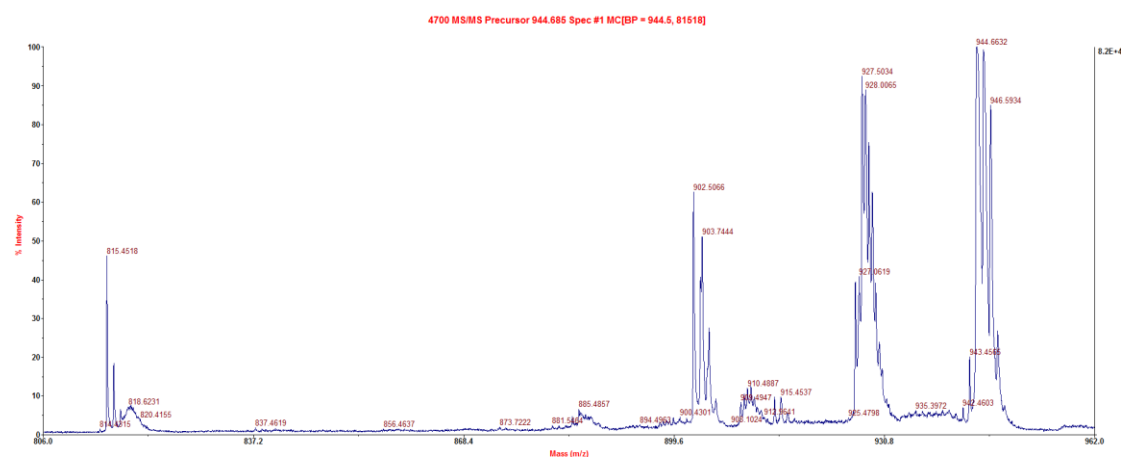
LCmcKVASLR b+18 ion



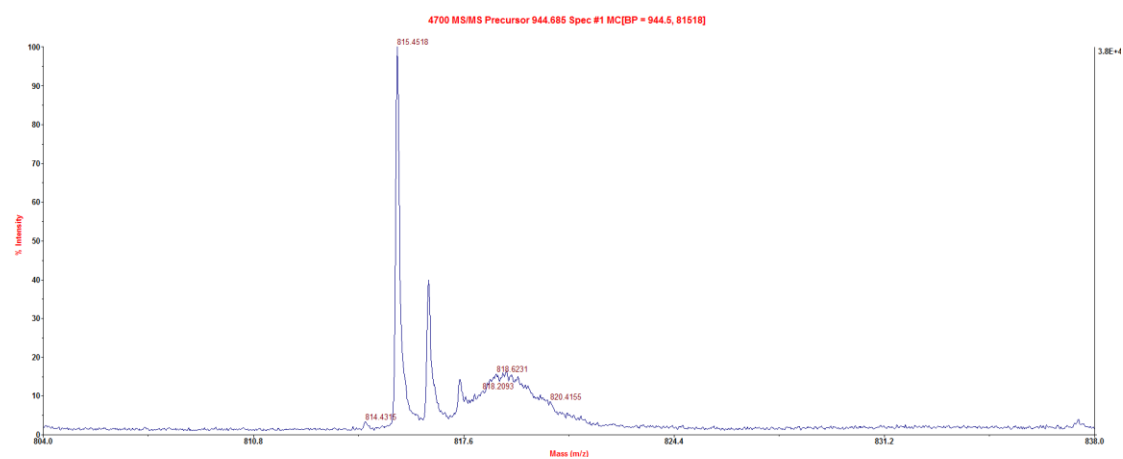
944.69 YSRRHPE



Precursor

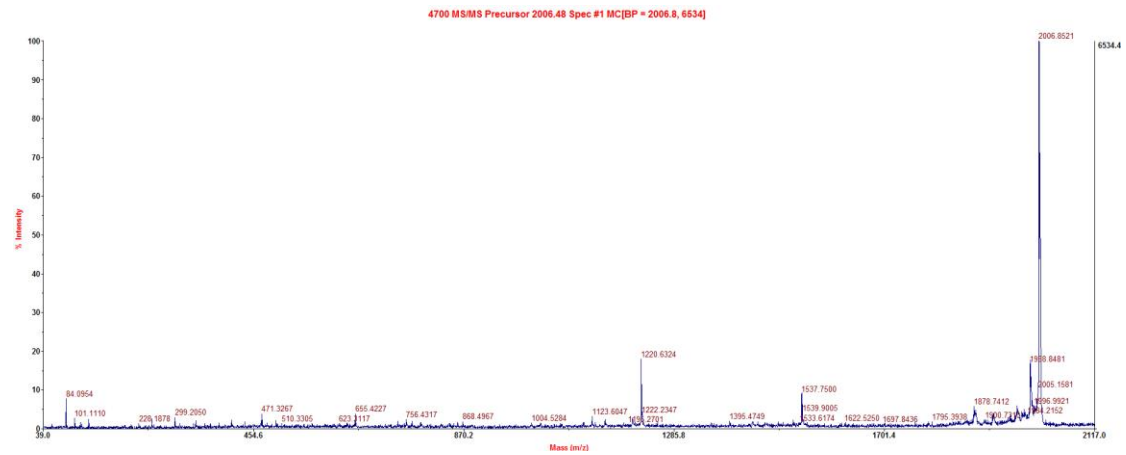


YSRRHP b+18 ion

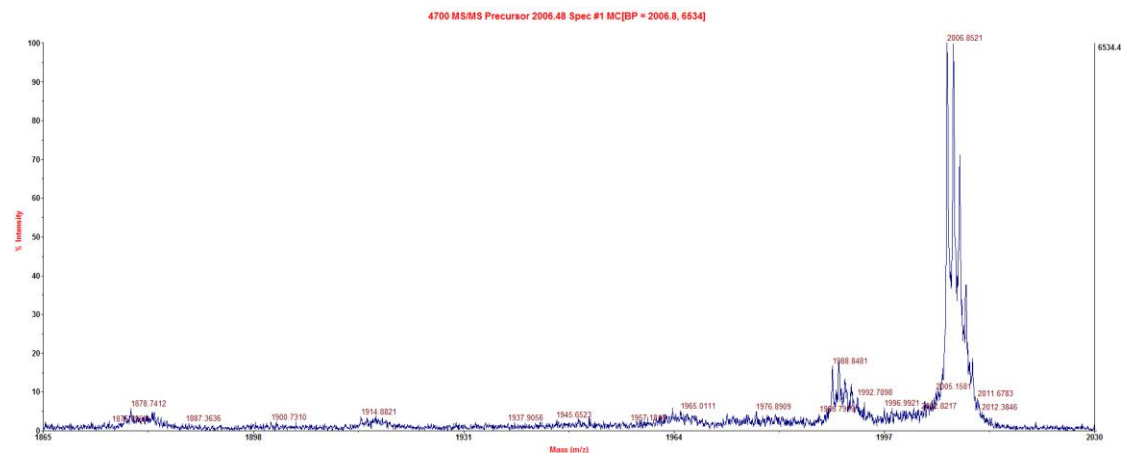


LysN digest

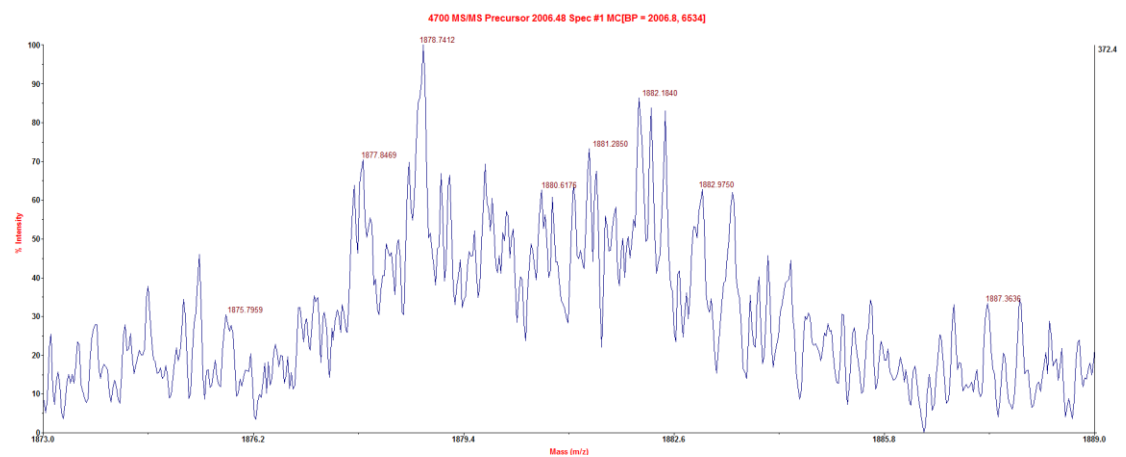
2006.48 KVASLRETYGDMADCmcCmcE



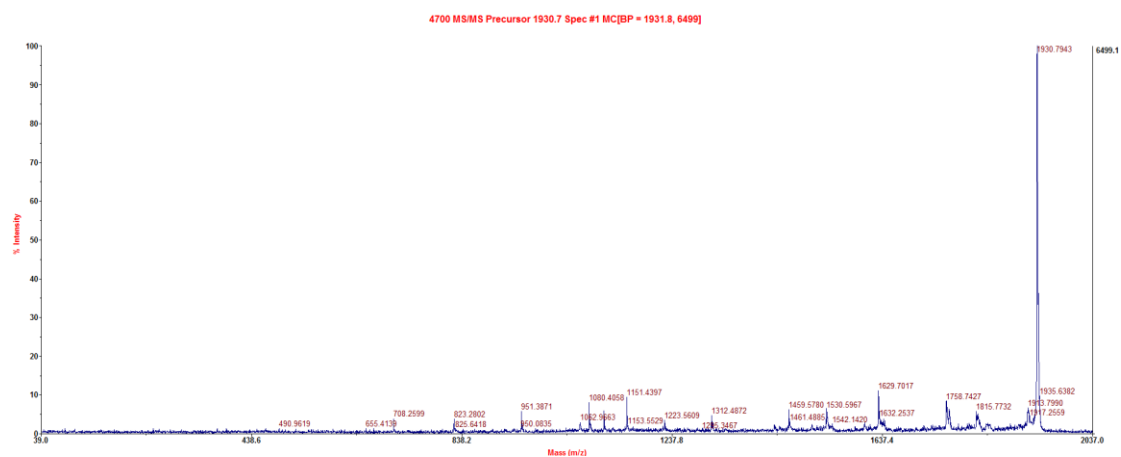
Precursor



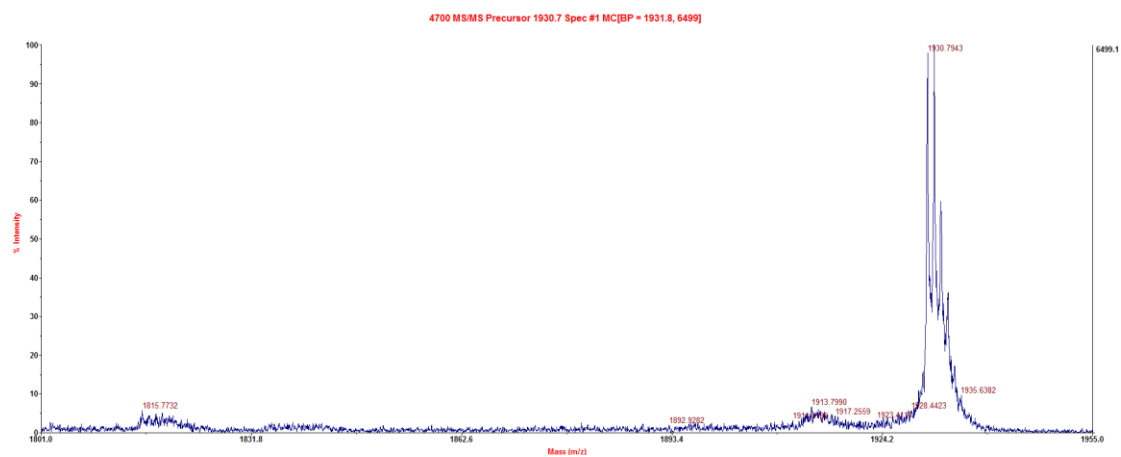
KVASLRETYGDMADCmcCmc b+18 ion



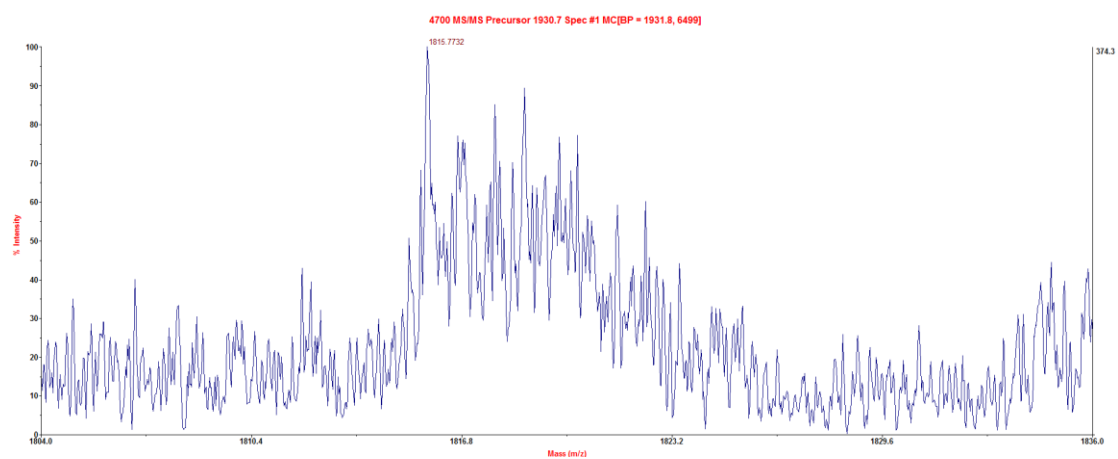
1930.70 KCmcCmcAADDKEACmcFAVEGP



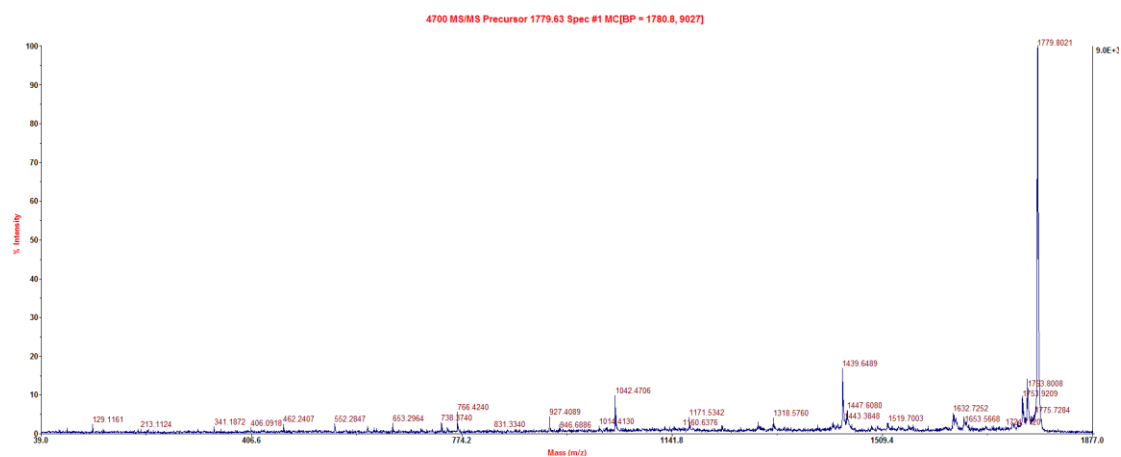
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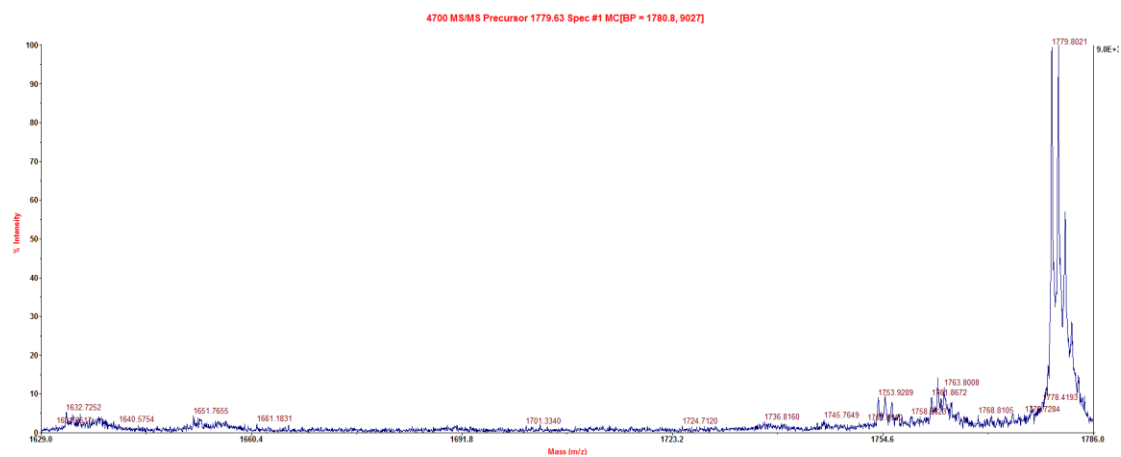
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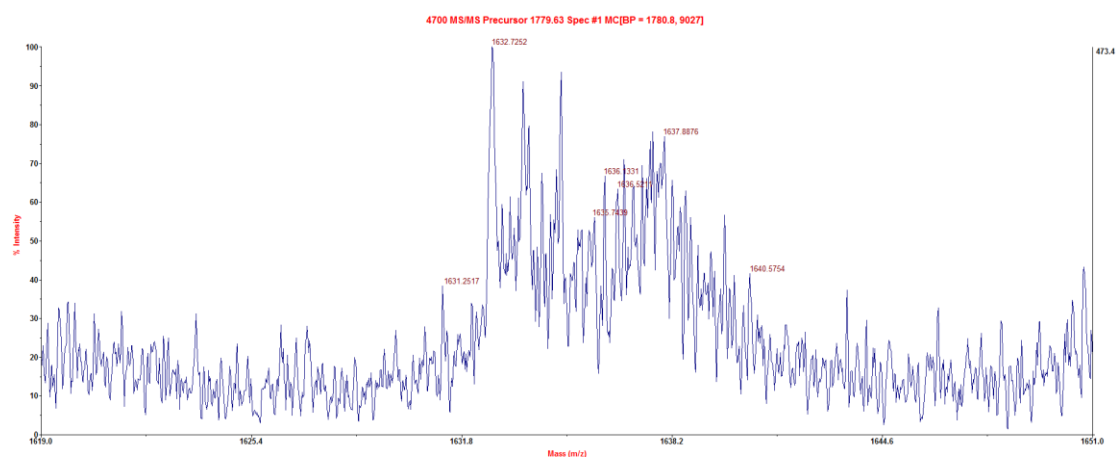
1779.63 KPDPNTLCmcDEFKADE



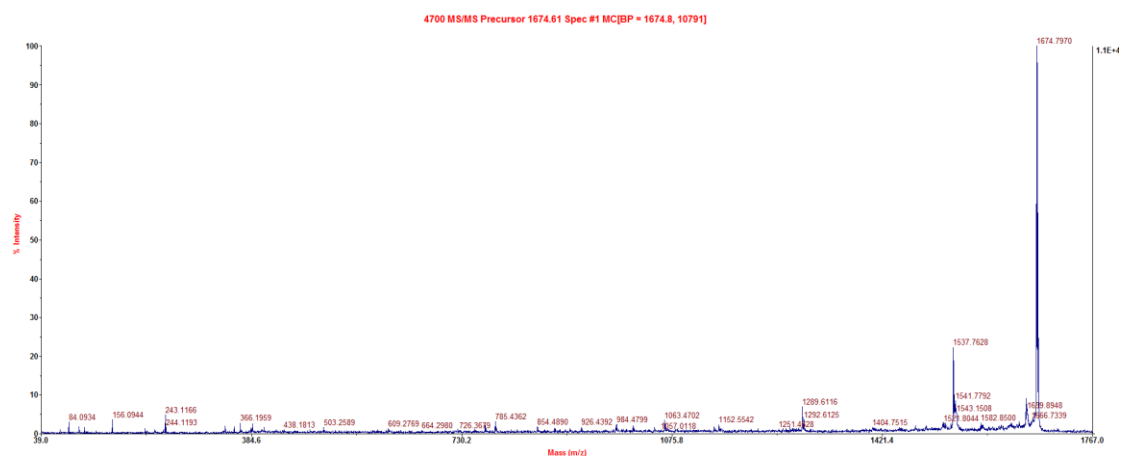
Precursor



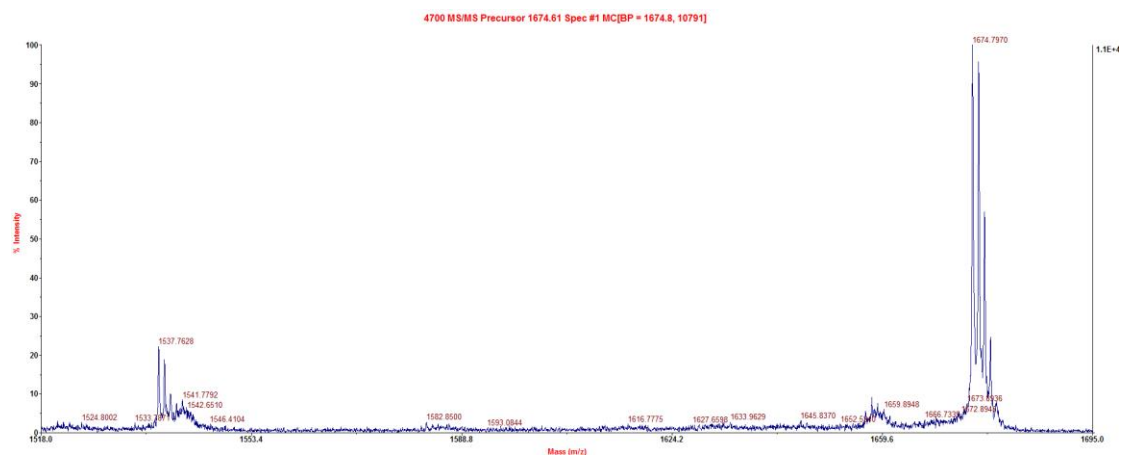
KPDPNTLCmcDEFKAD b ion



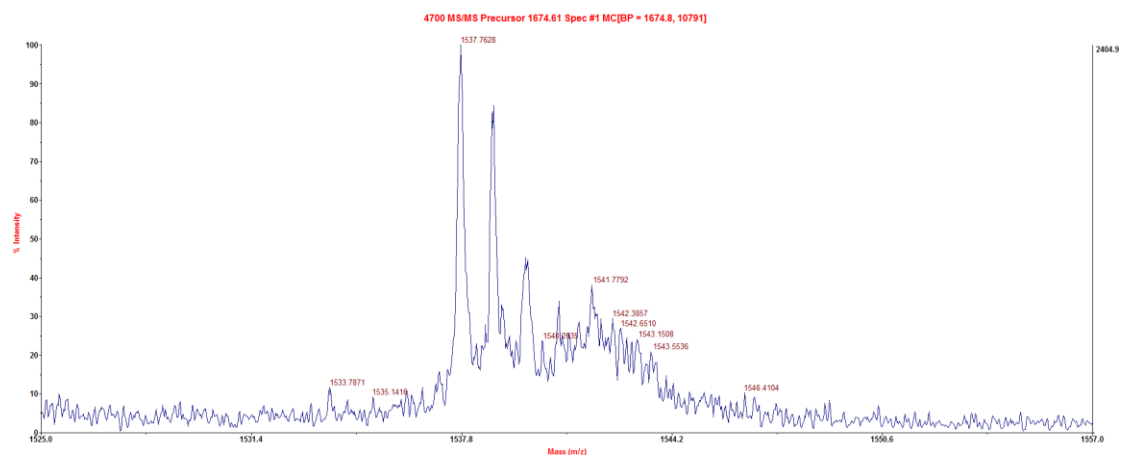
1764.61 KQEPERNECmcFLSH



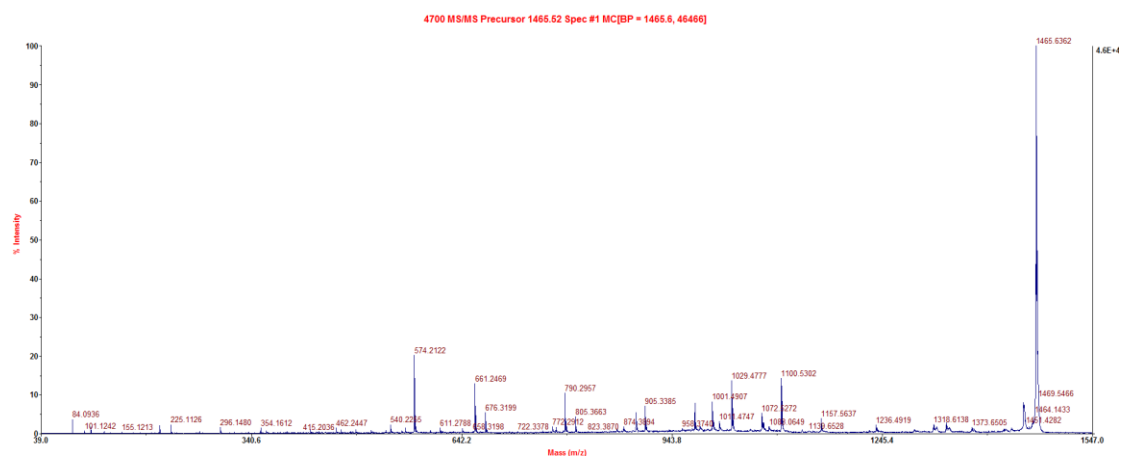
Precursor



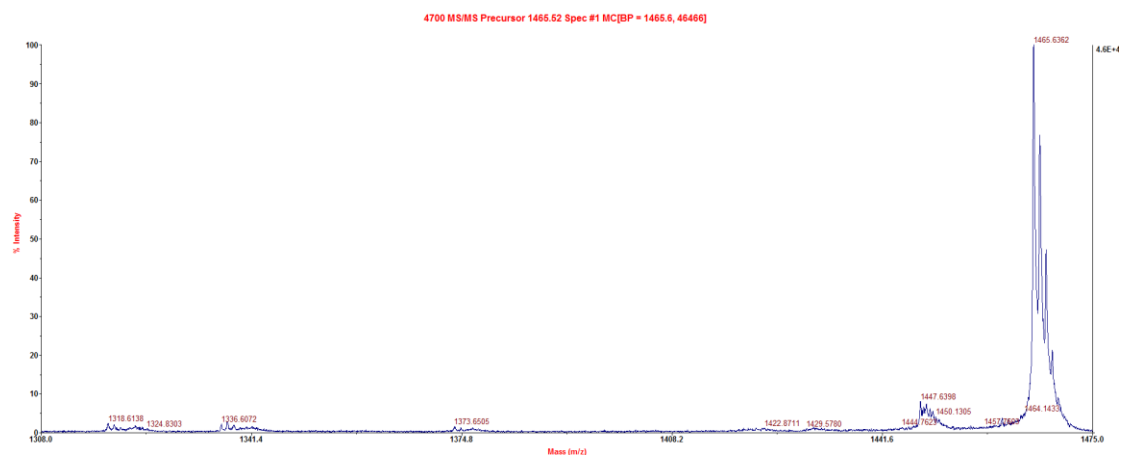
KQEPERNECmcFLS b+18 ion



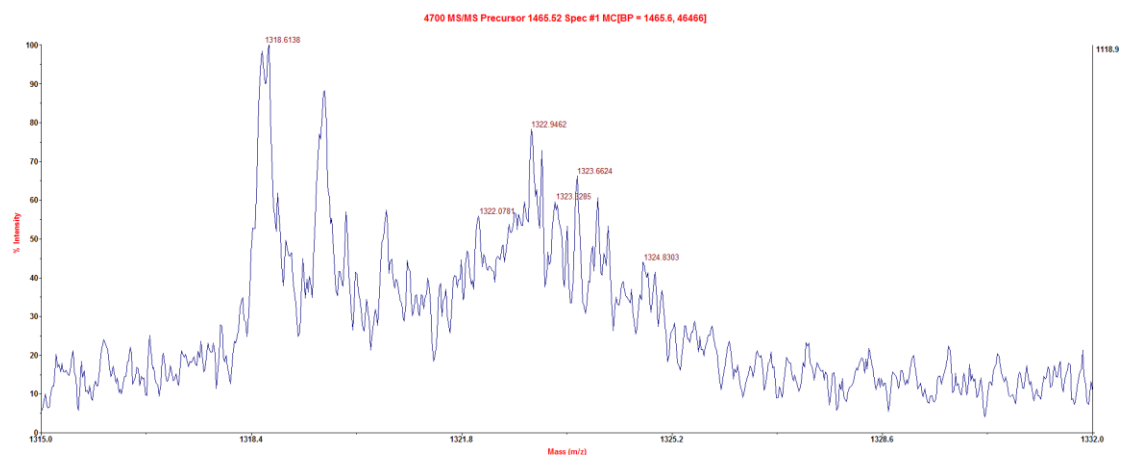
1465.52 KTCmcVADESHAGCmcE



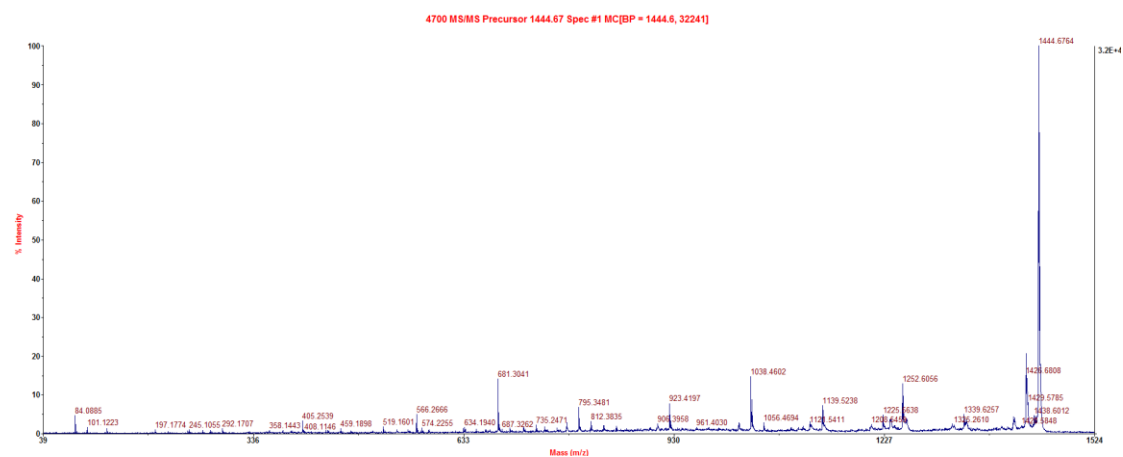
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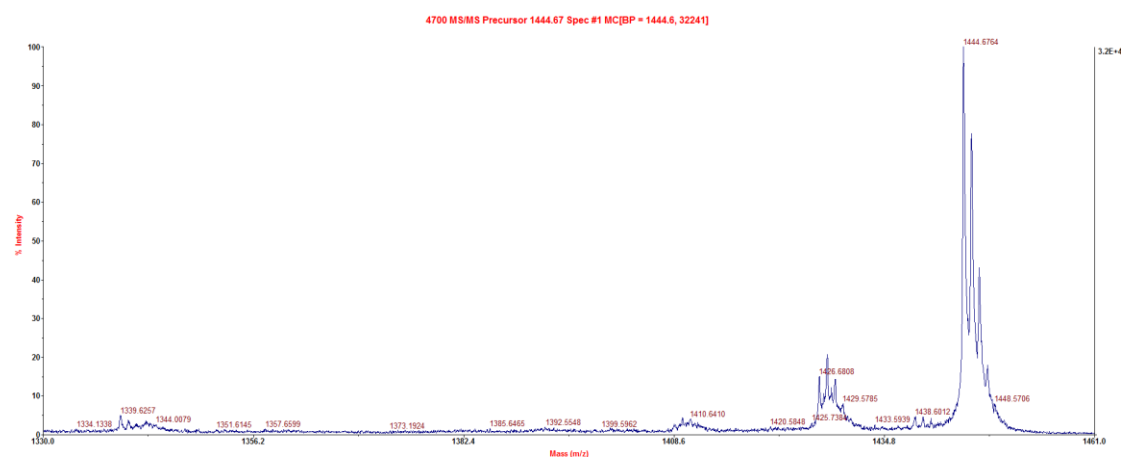
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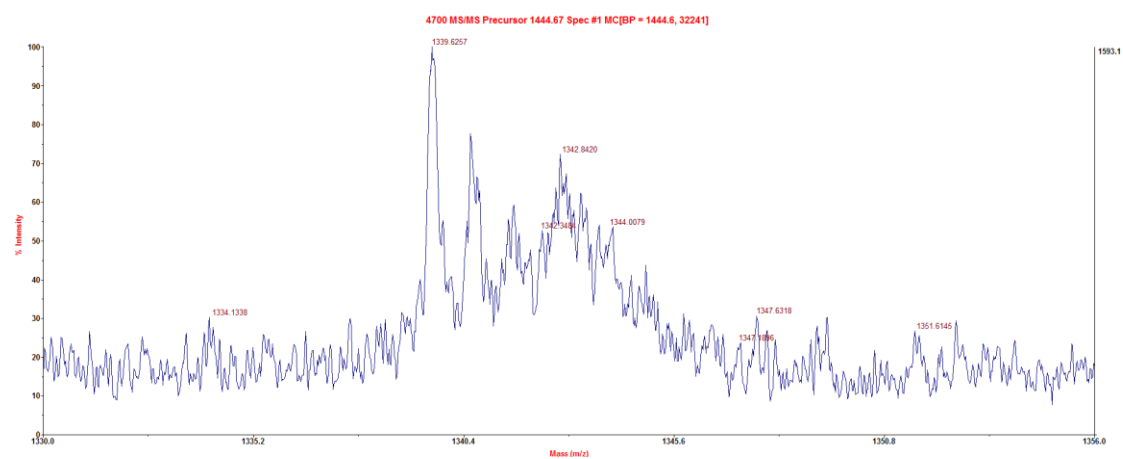
1443.67 KYICmcDNQDTISS



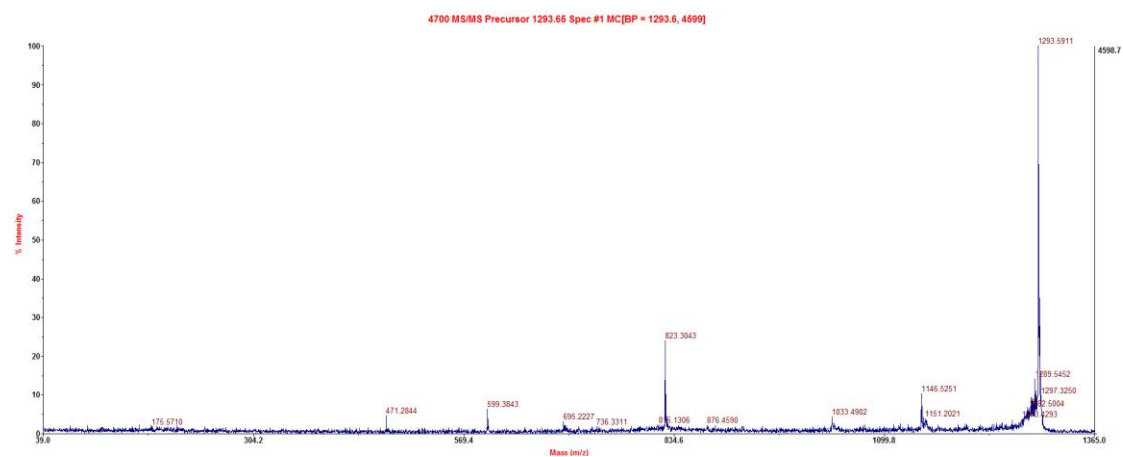
Precursor



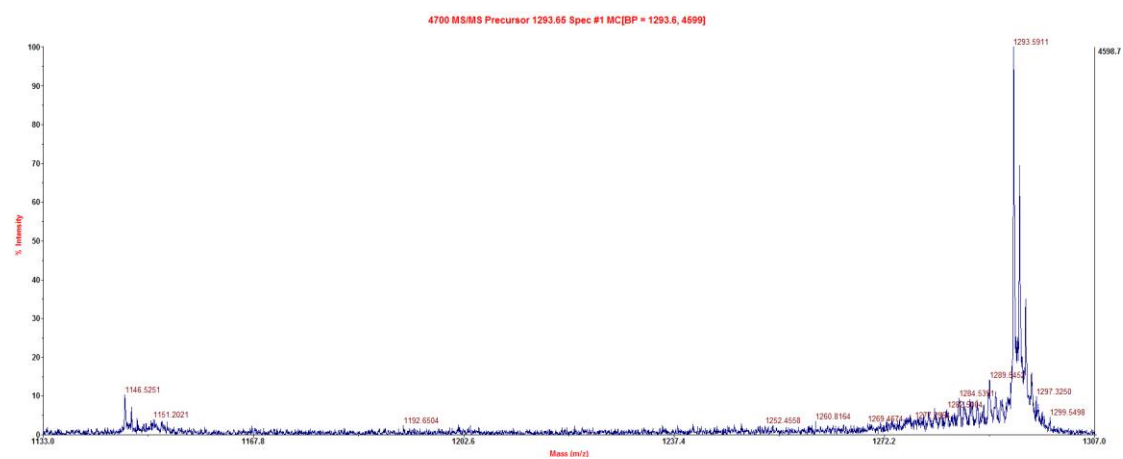
KYICmcDNQDTIS b ion



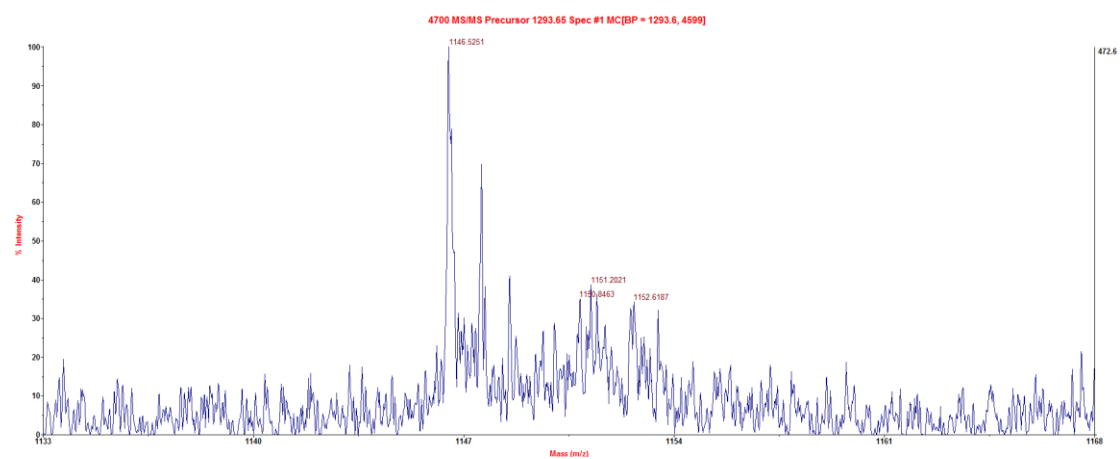
1293.65 KECmcCmcDKPLLE



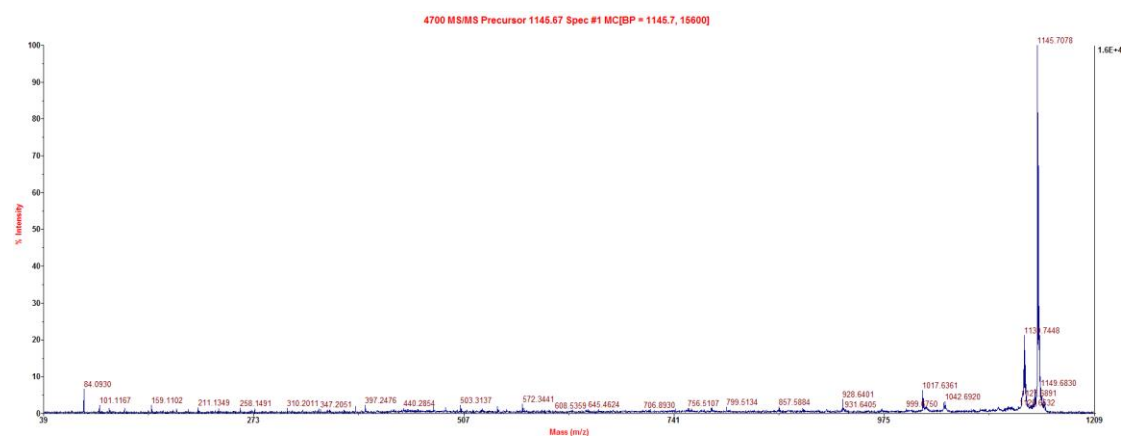
Precursor



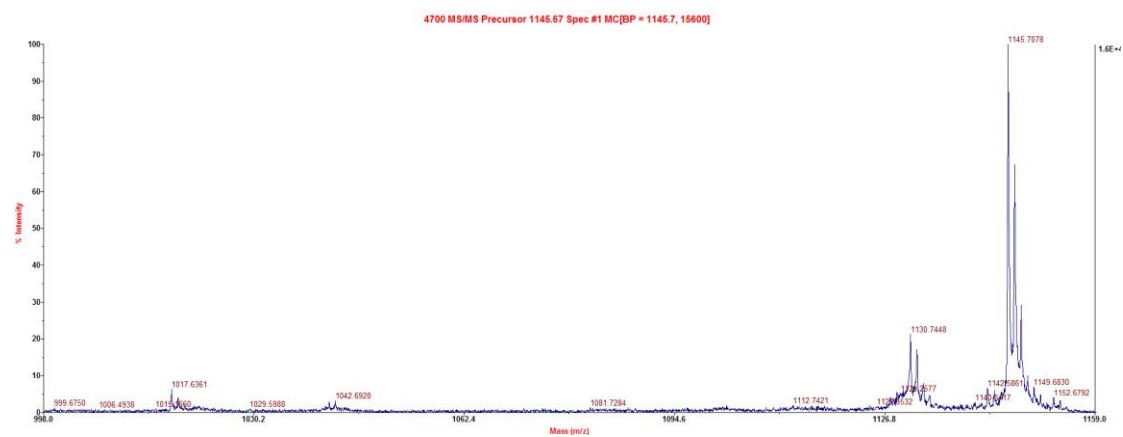
KECmcCmcDKPLL b ion



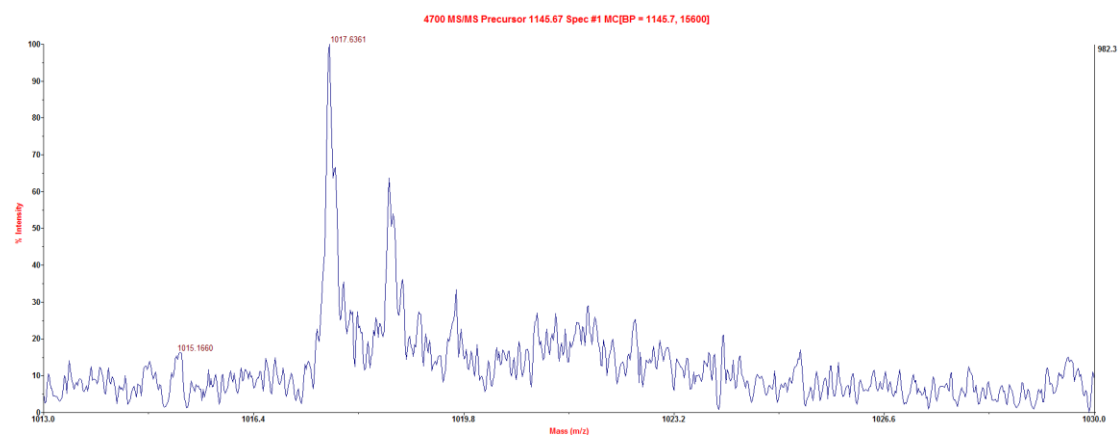
1145.67 KAWSVARLSQ



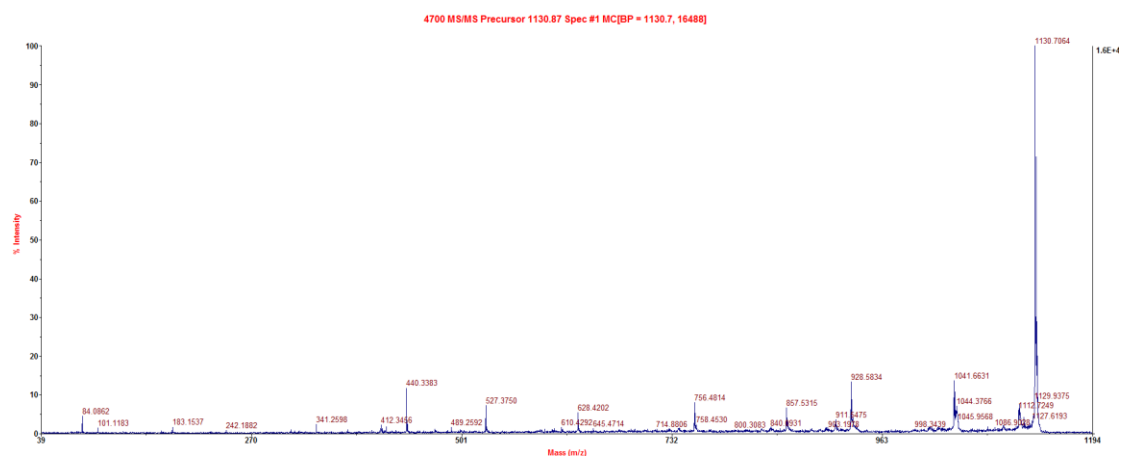
Precursor



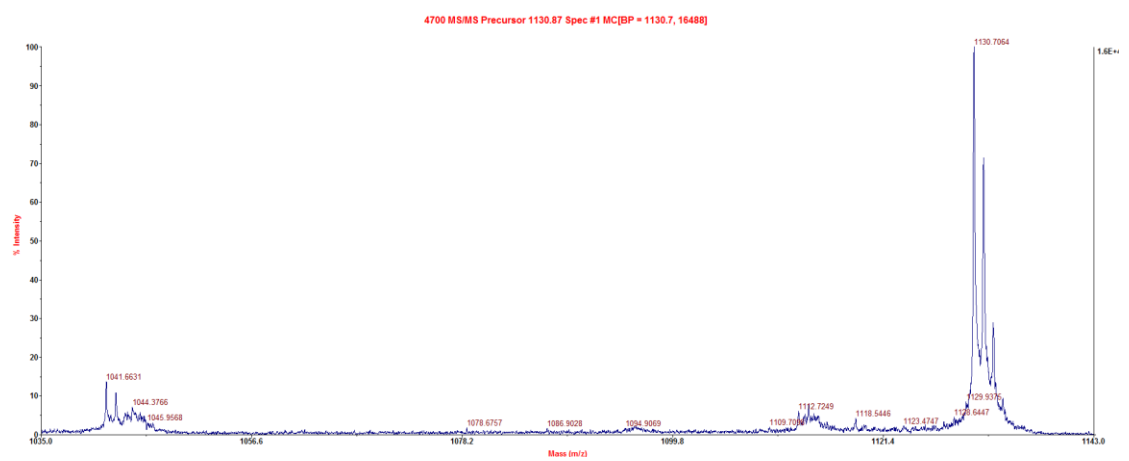
KAWSVARLS b+18 ion



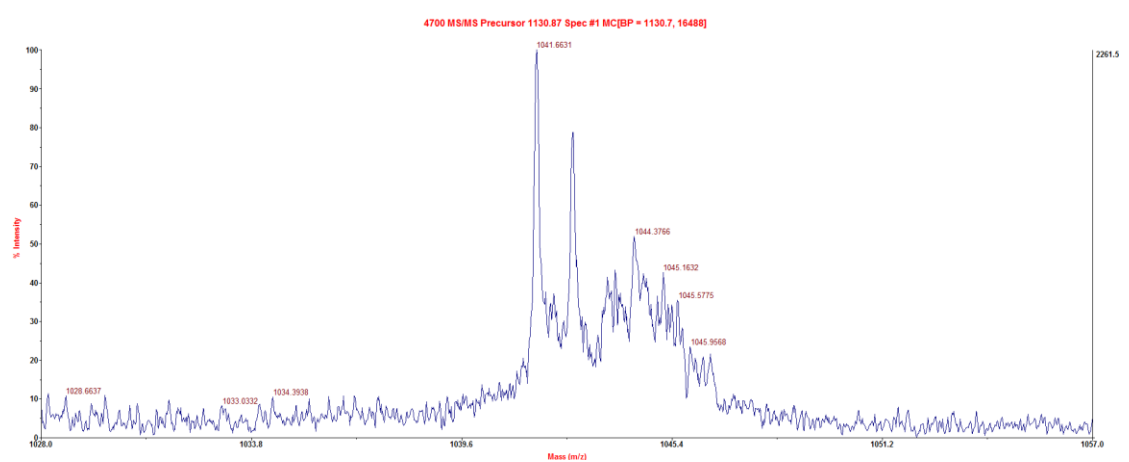
1130.87 KLVVSTQTALA



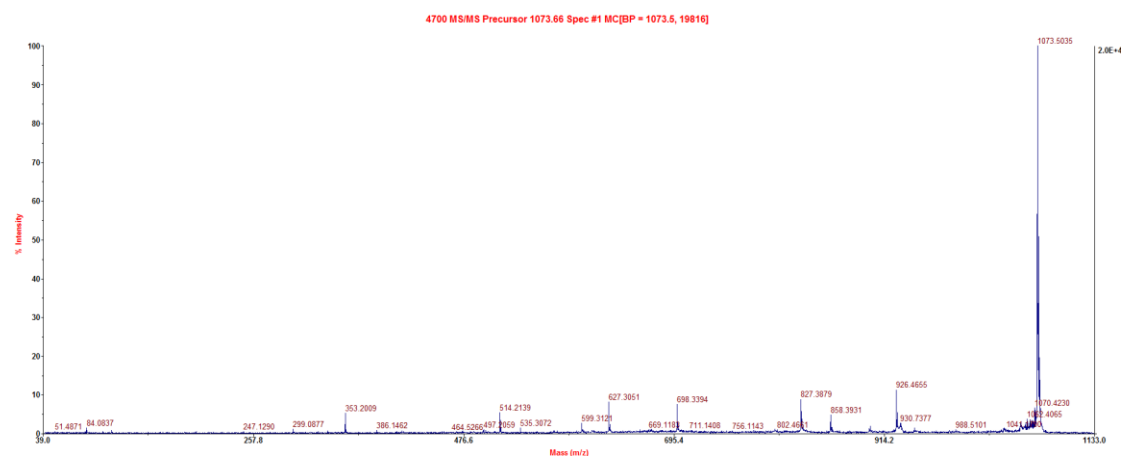
Precursor



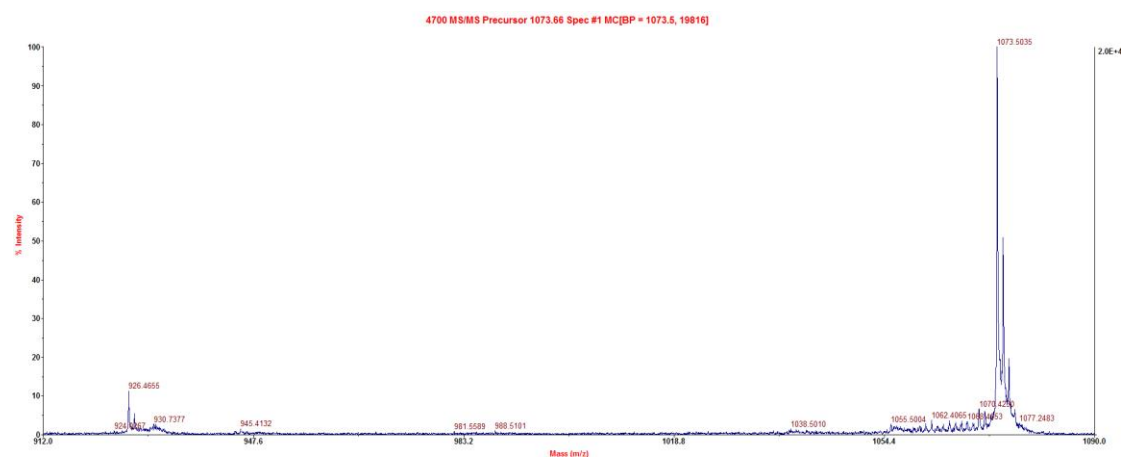
KLVVSTQTAL b ion



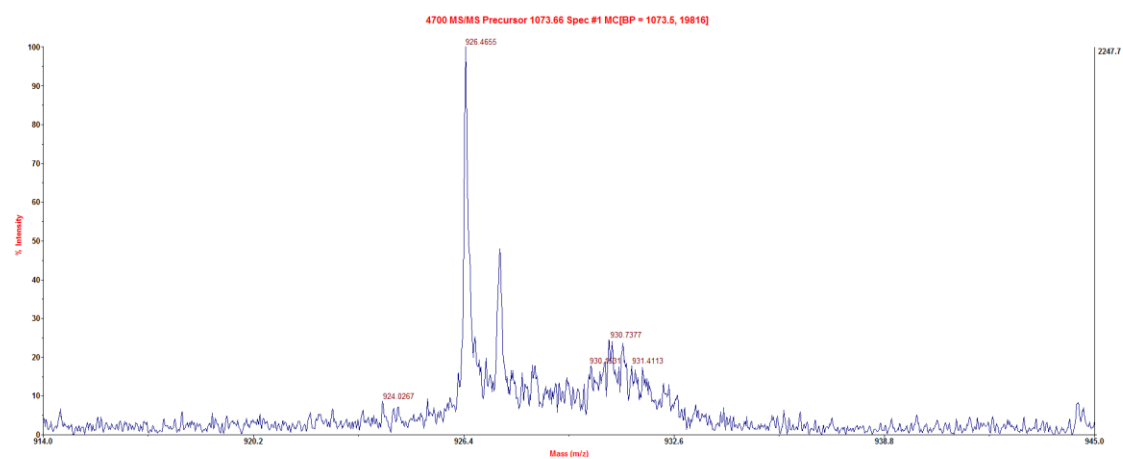
1073.66 KSHCmcIAEVE



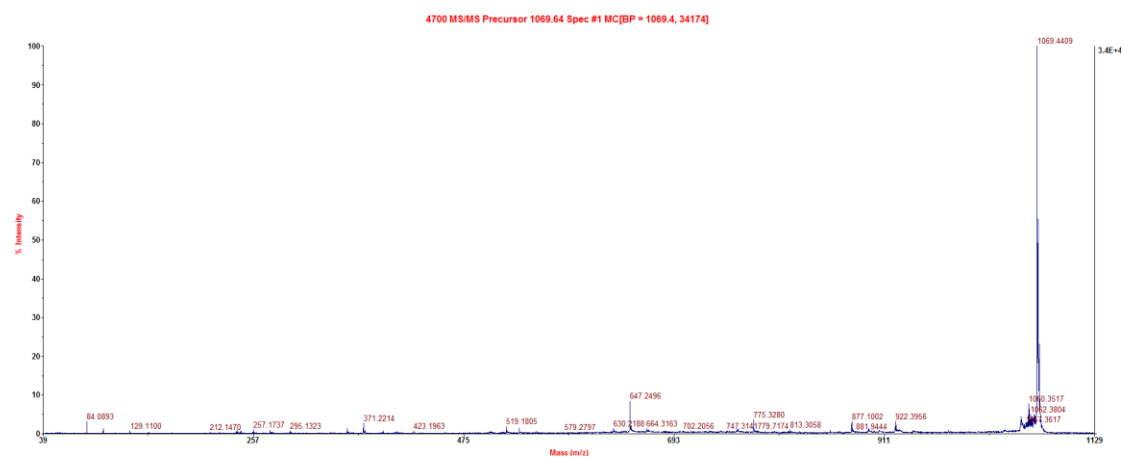
Precursor



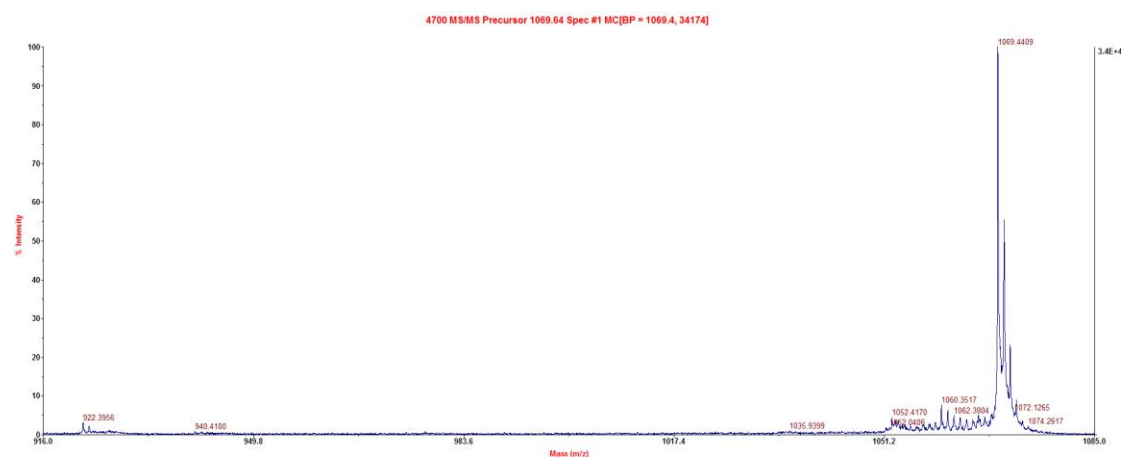
KSHCmcIAEV b ion



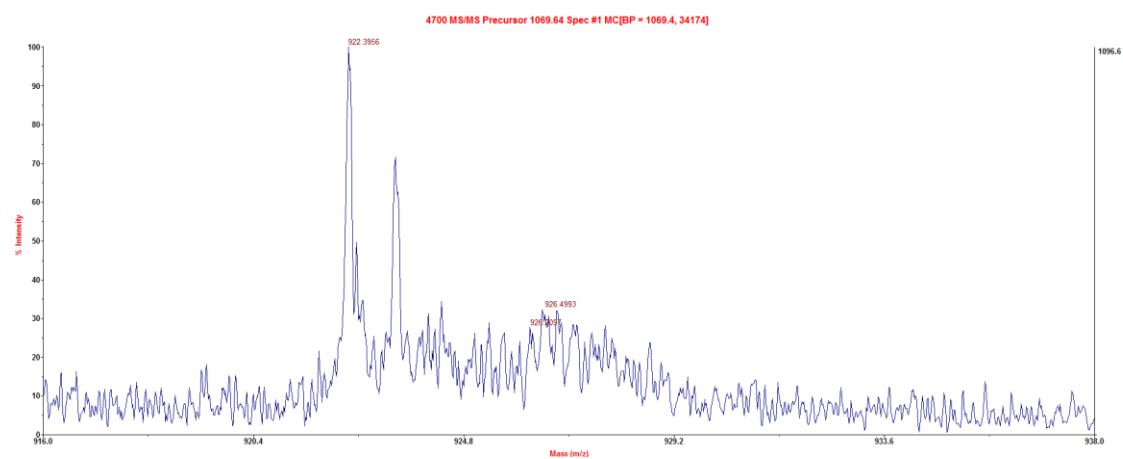
1069.64 KQNCmcDQFE



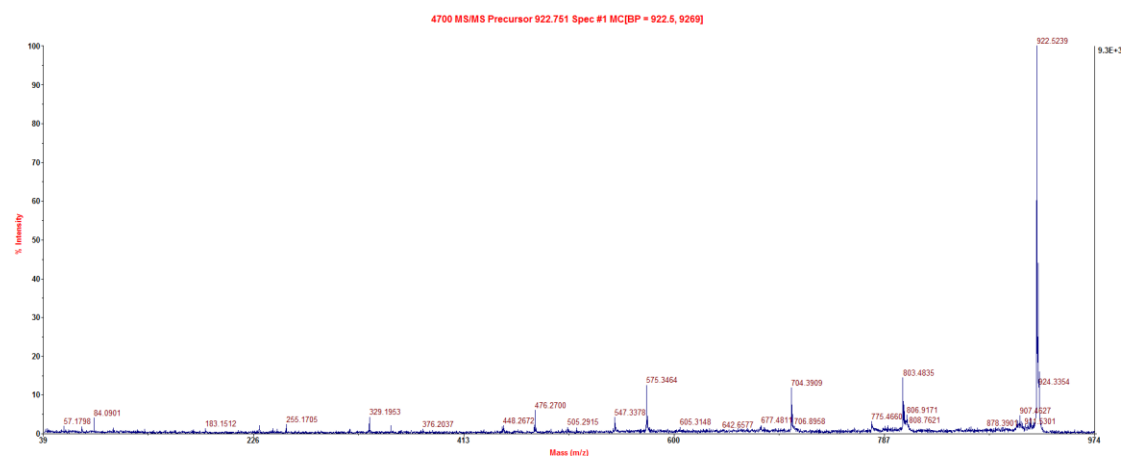
Precursor



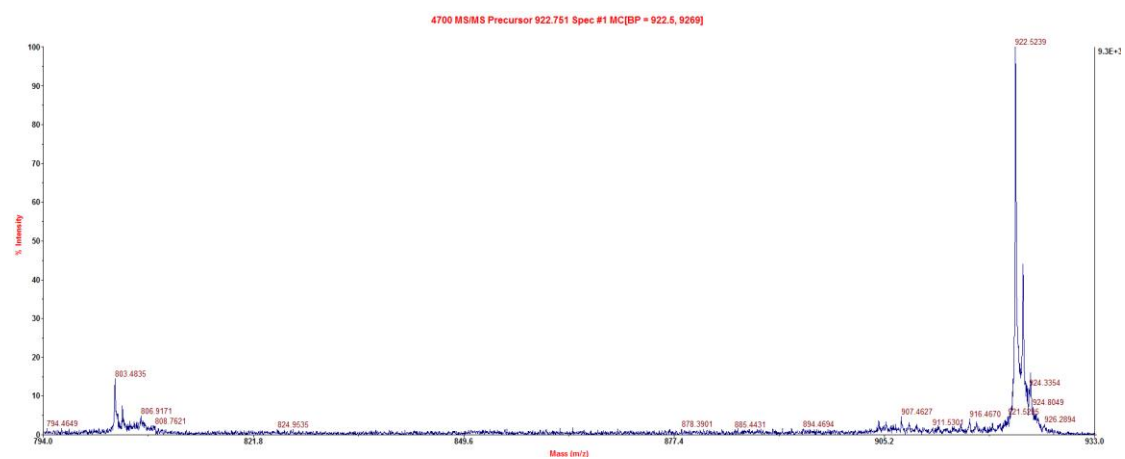
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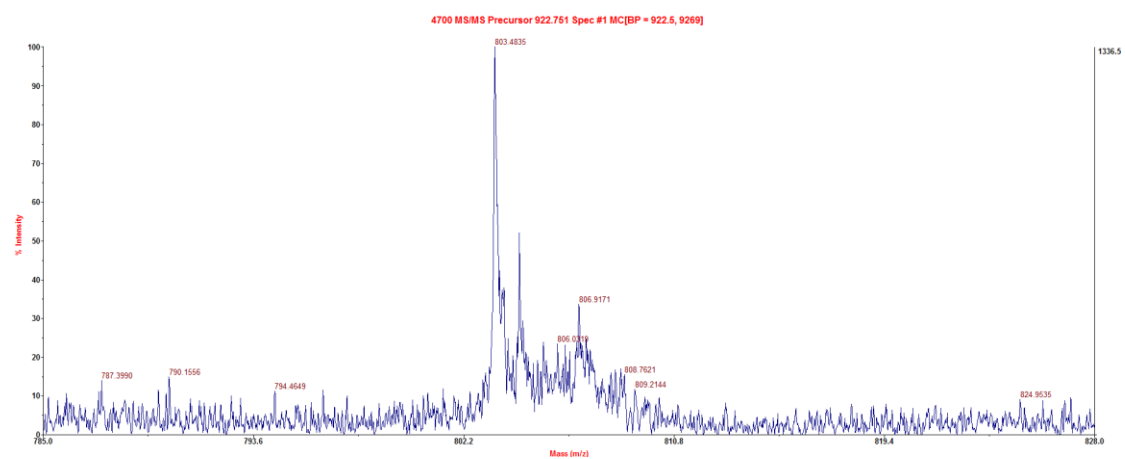
922.75 KAEFVEVT



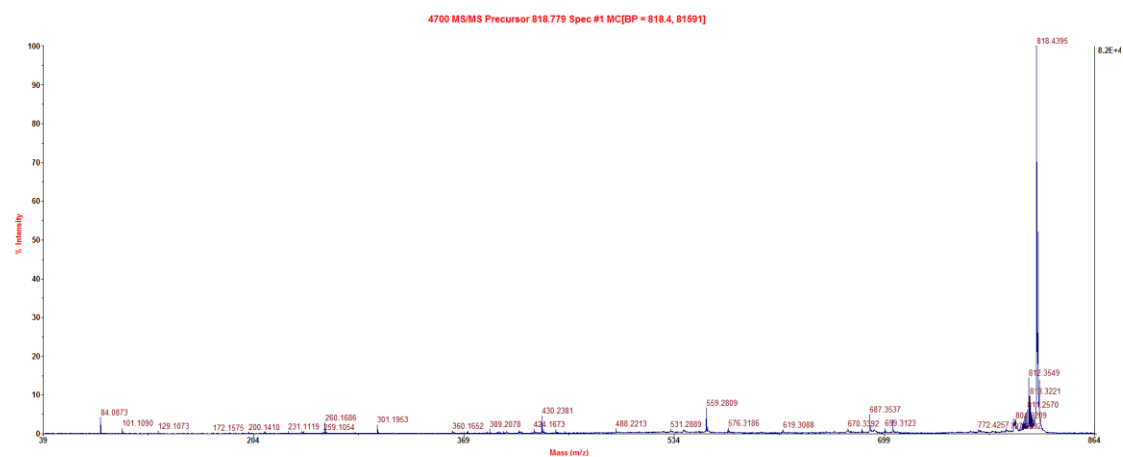
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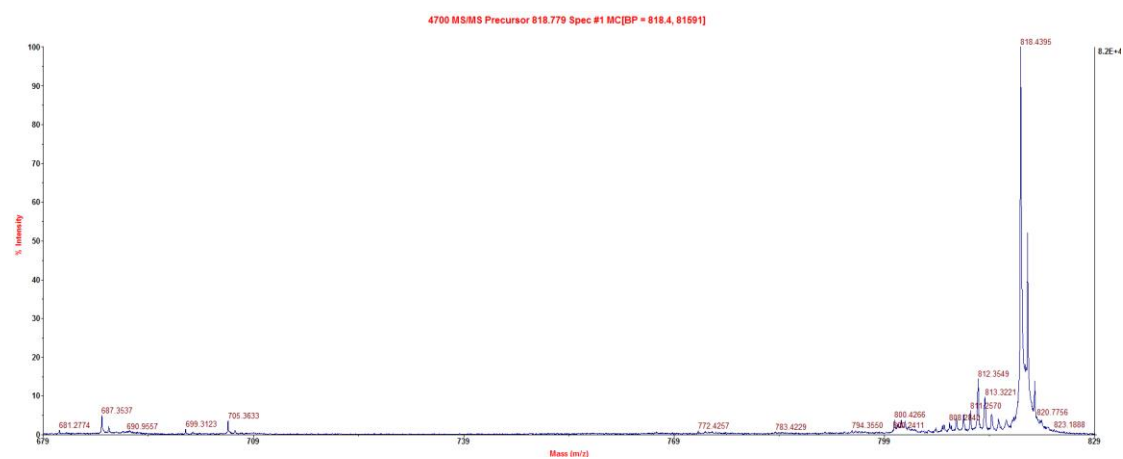
KAEFVEV b ion



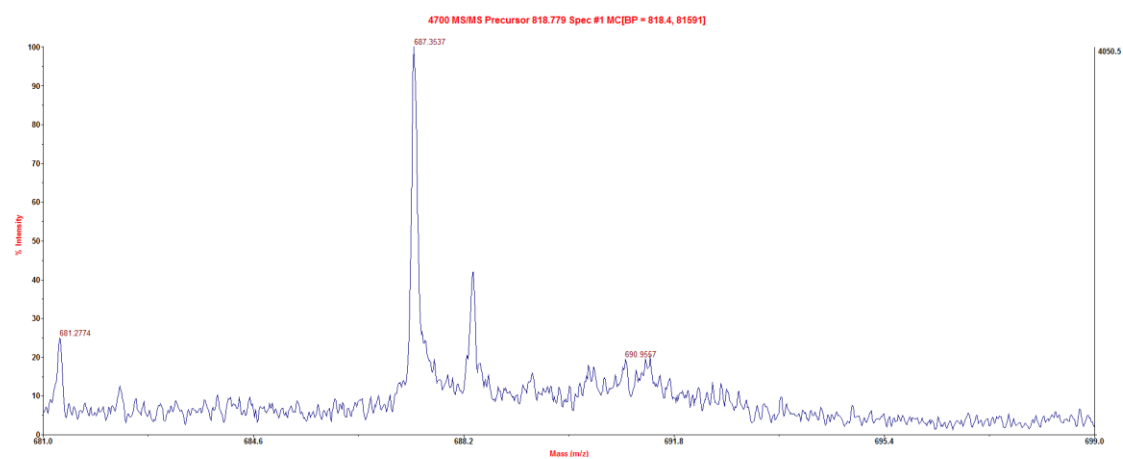
818.78 KATEEQL



Precursor

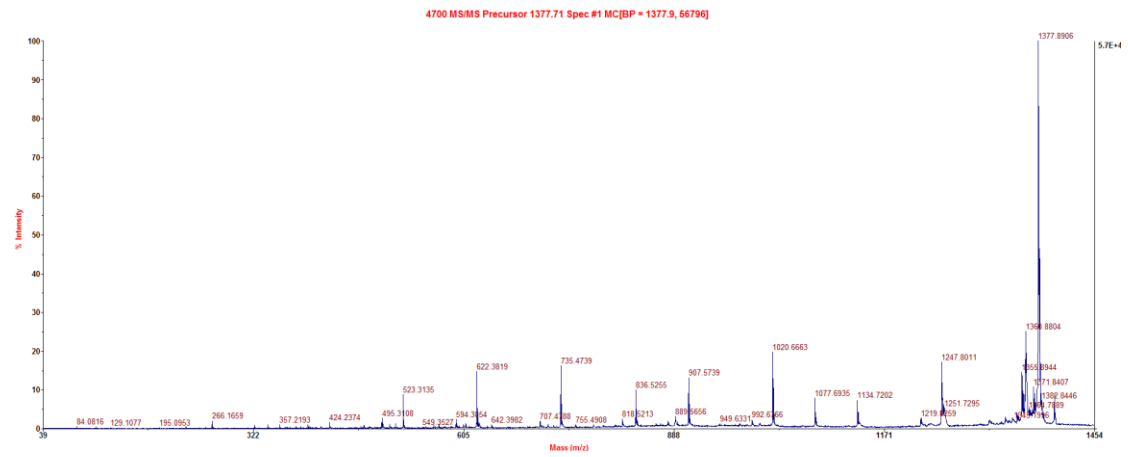


KATEEQ b ion

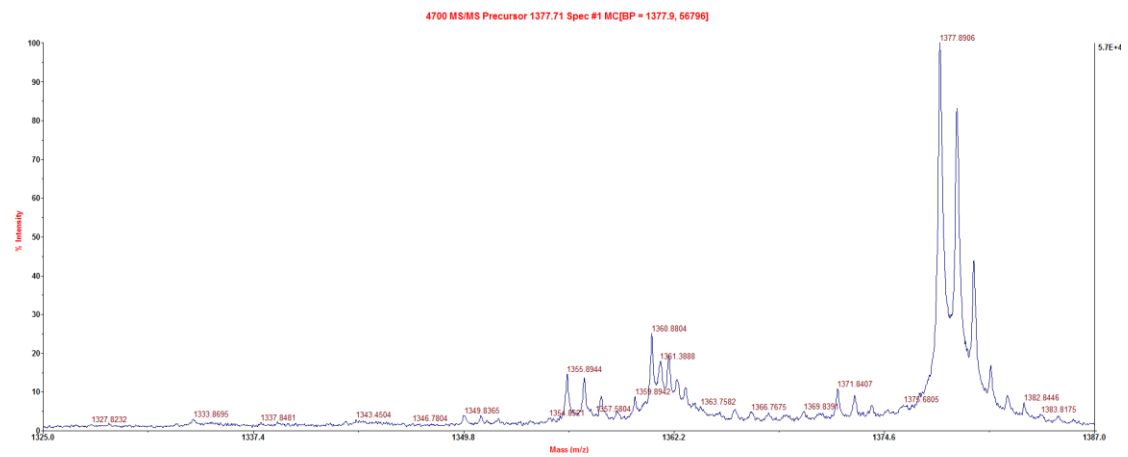


Spectra of peptides with C-terminal amide

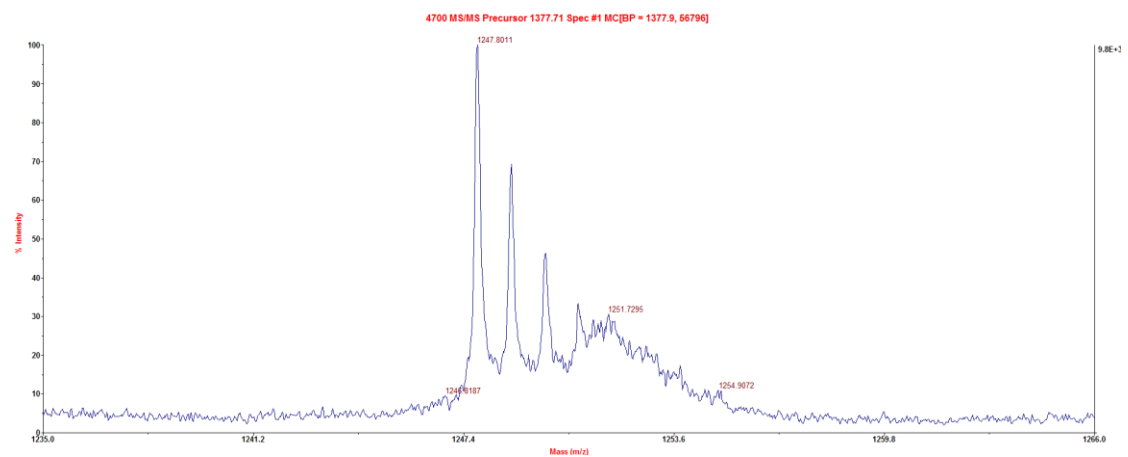
KHGTVVLTALGGIL-NH₂ 1377.71



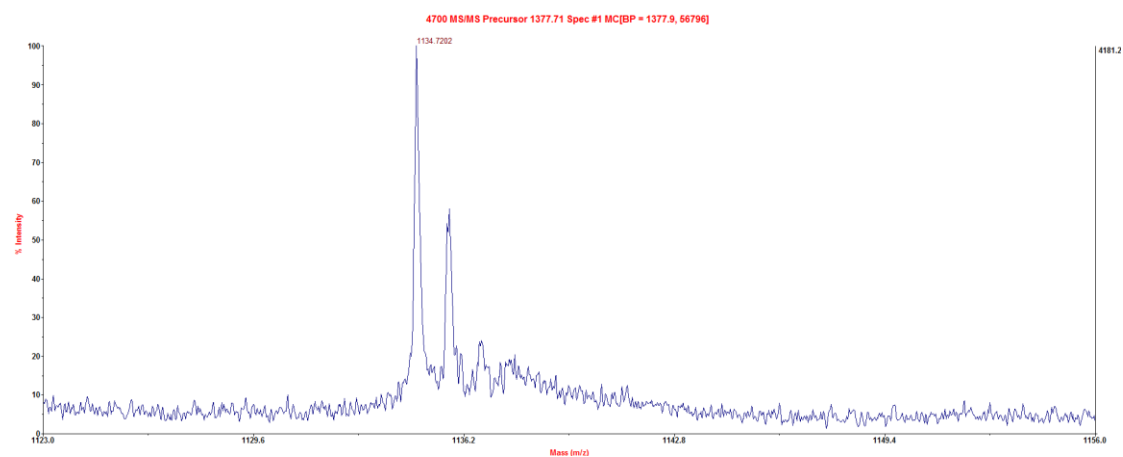
Precursor



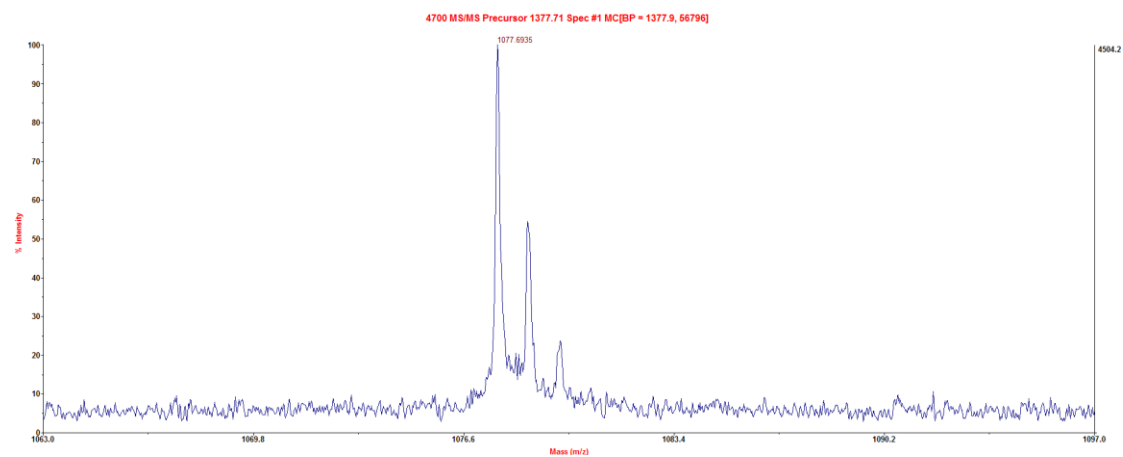
KHGTVVLTALGGI 1247.80 b-ion



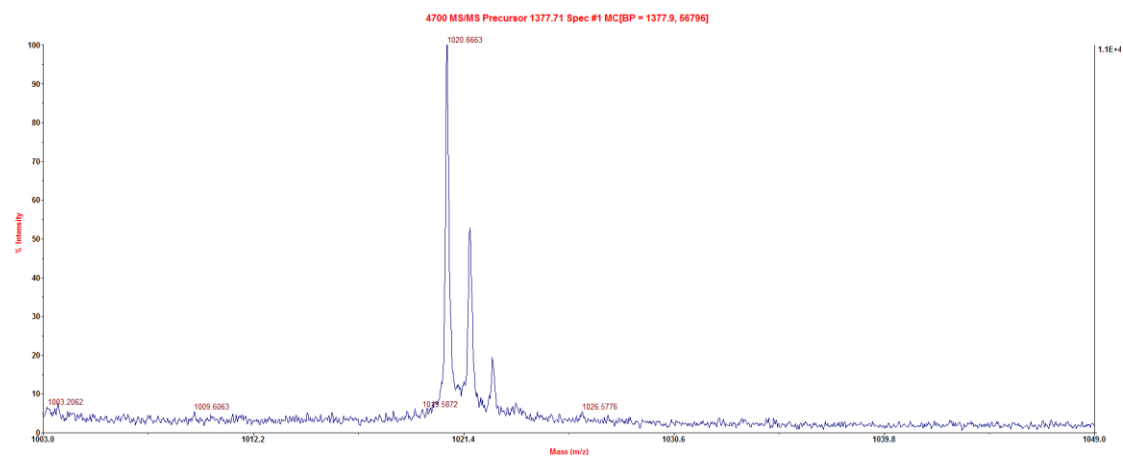
KHGTVVLTALGG 1134.72



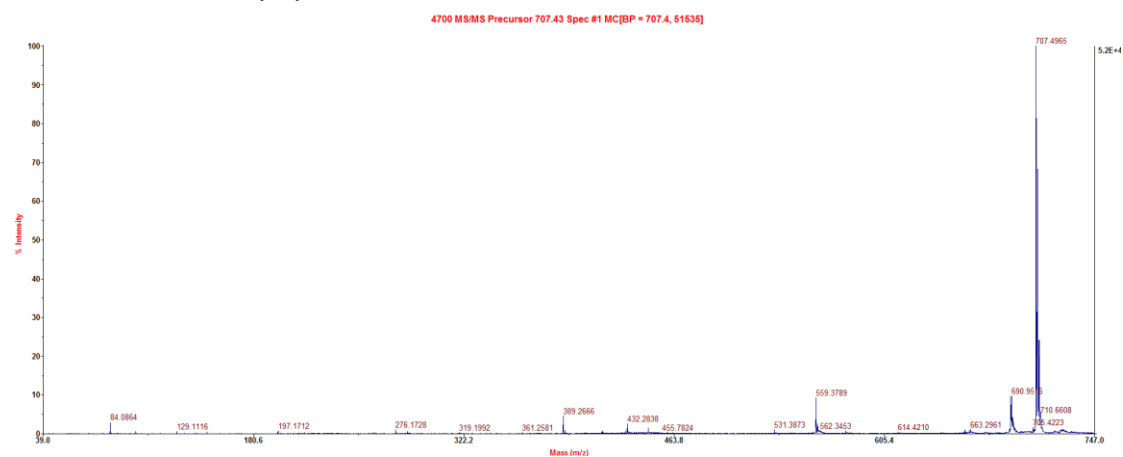
KHGTVVLTALG 1077.69



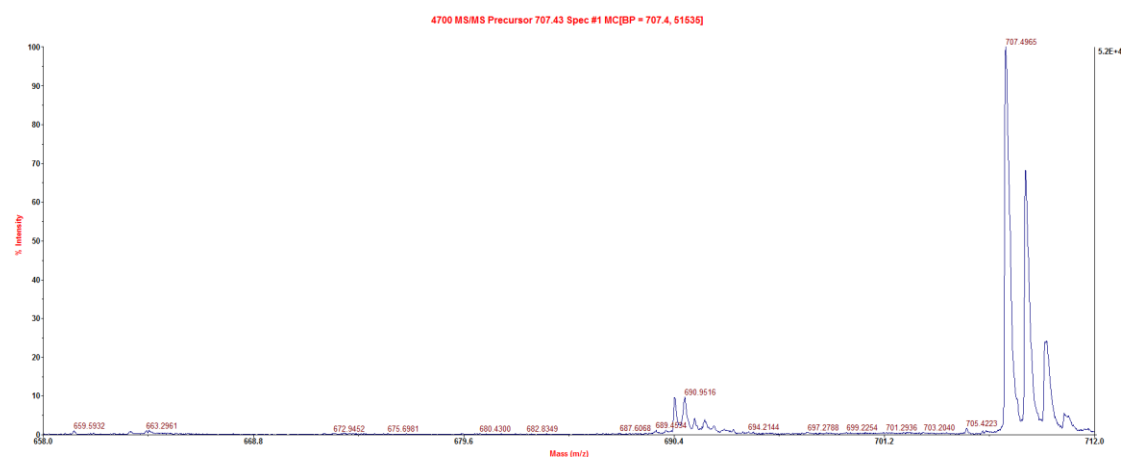
KHGTVVLTAL 1020.663



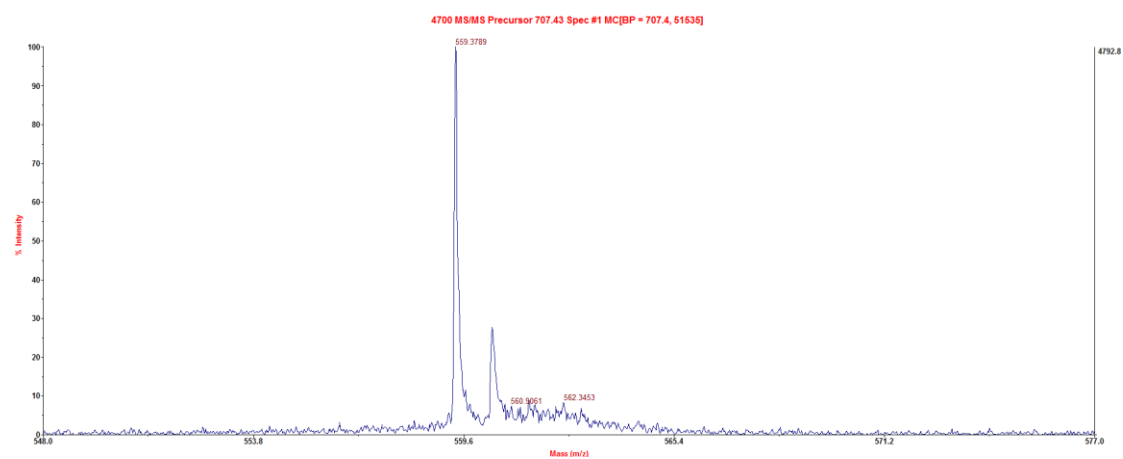
Eledoisin related peptide KFIGLM-NH₂ 707.43



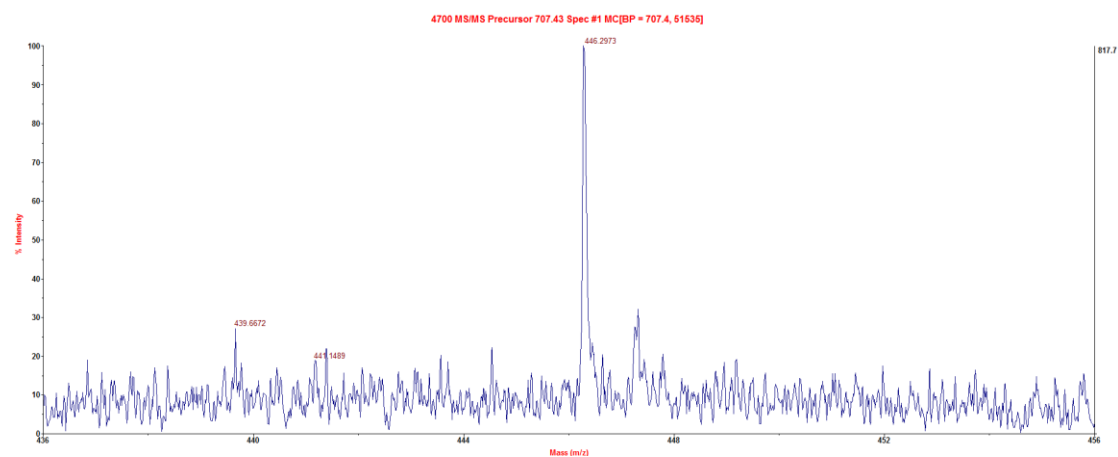
Precursor



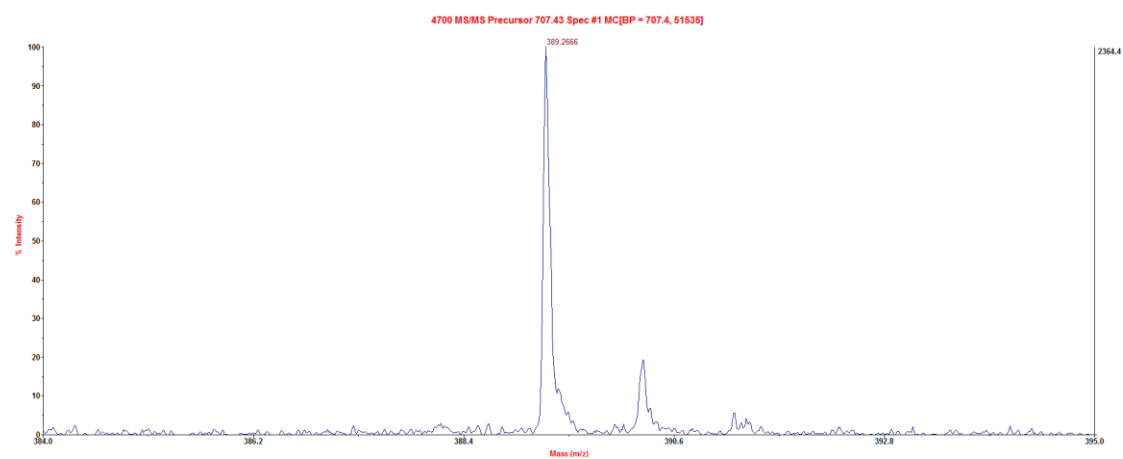
KFIGL 559.37 b-ion



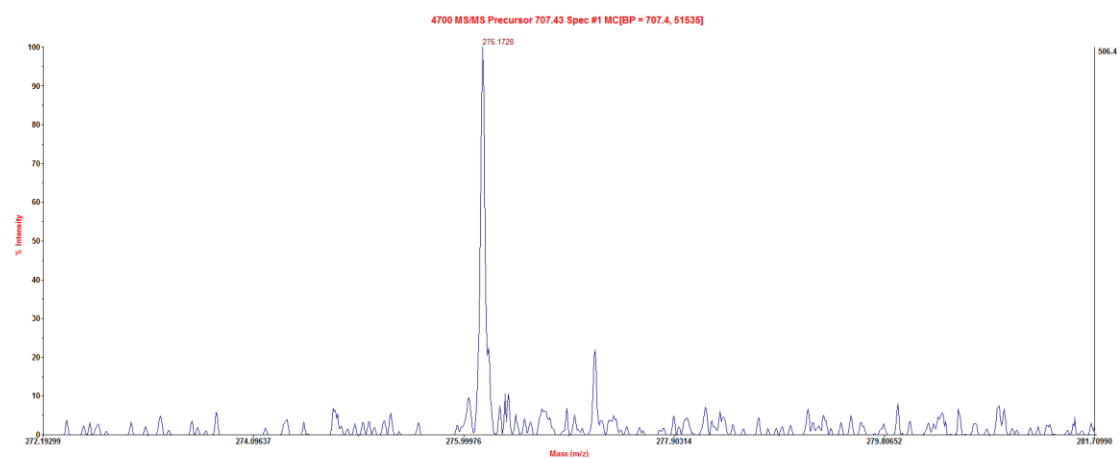
KFIG 446.30



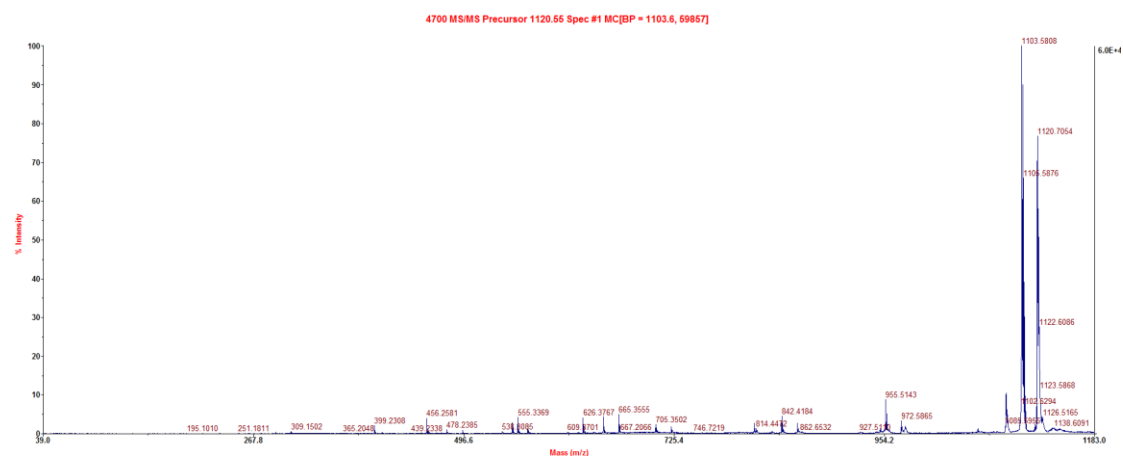
KFI 389.27



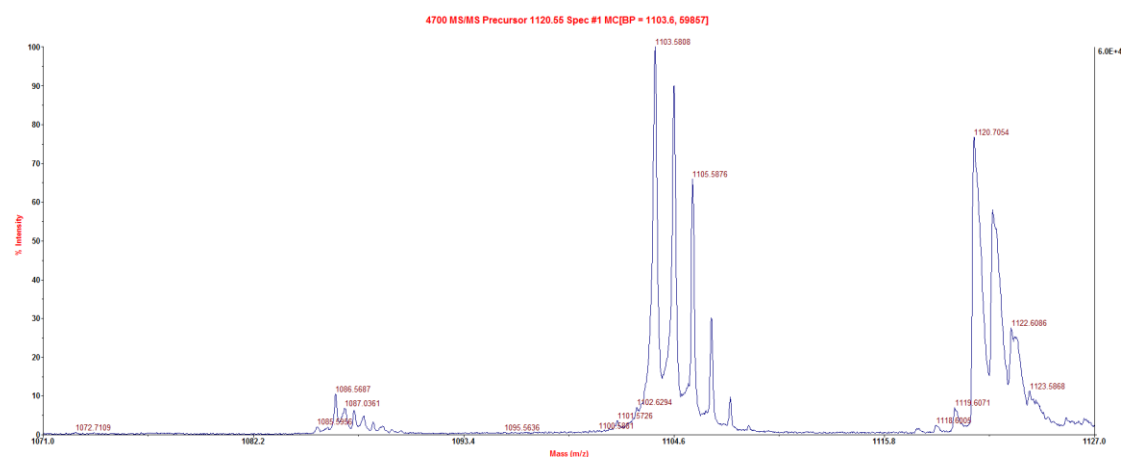
KF 276.37



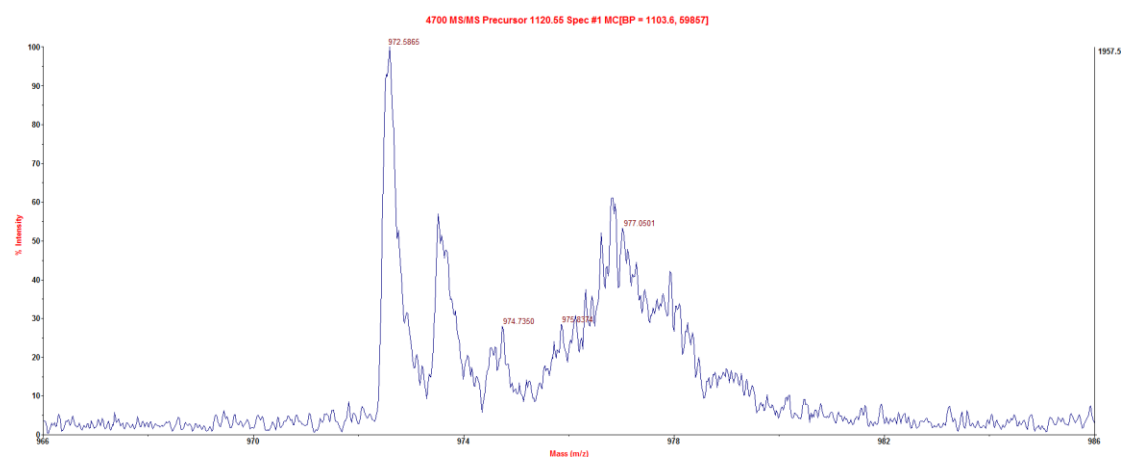
Neuromedin C GNHWAVGHLM-NH₂ 1120.55



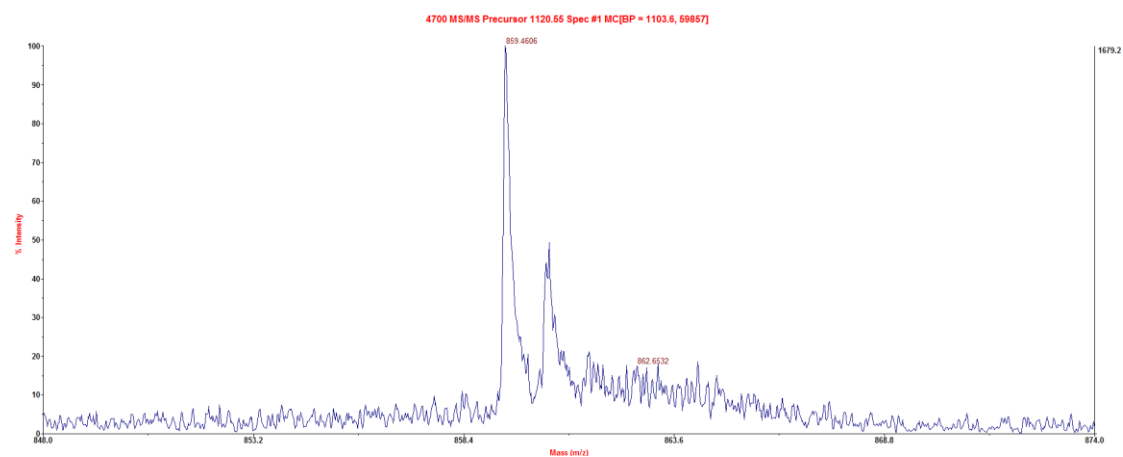
Precursor



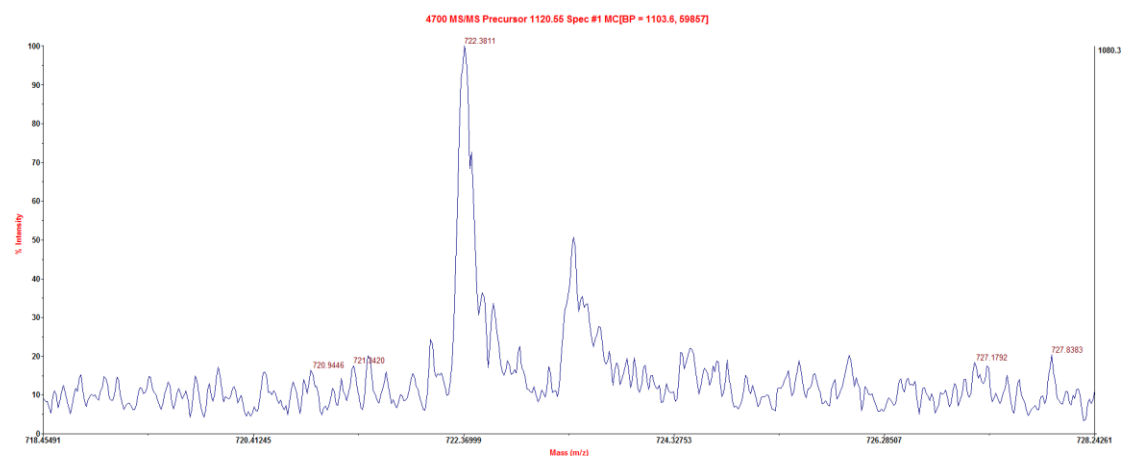
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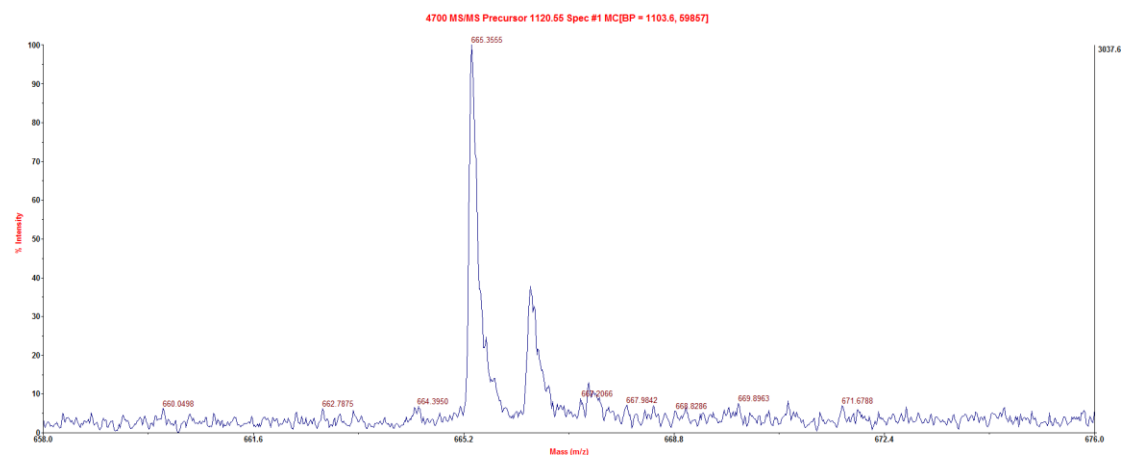
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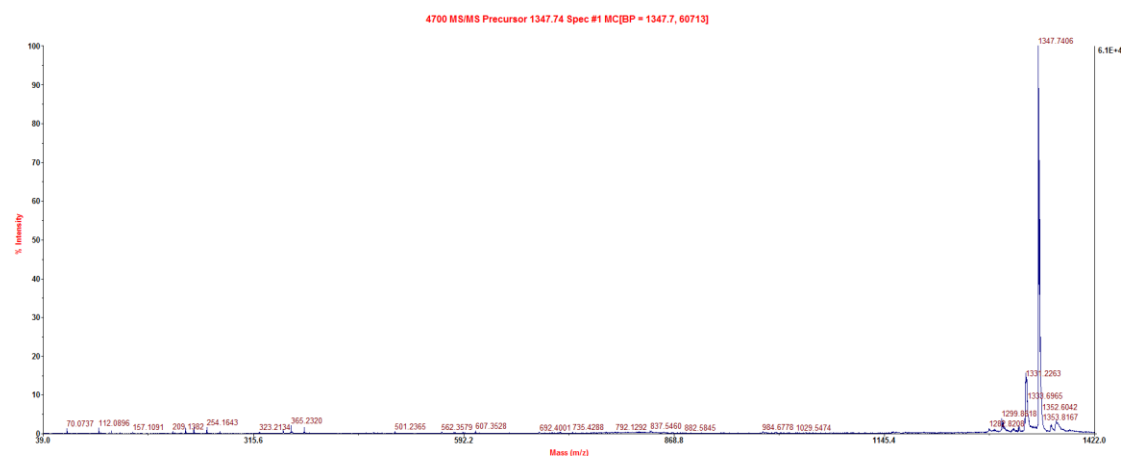
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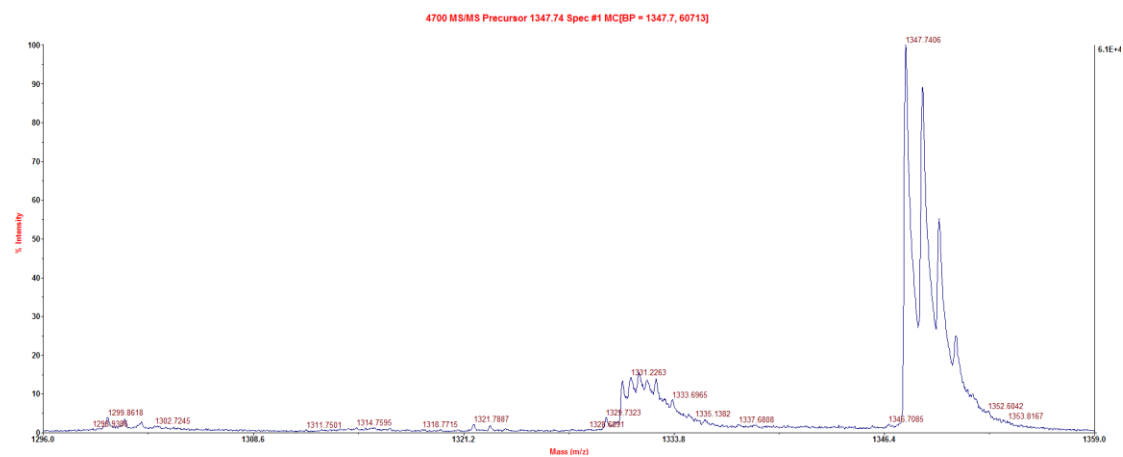
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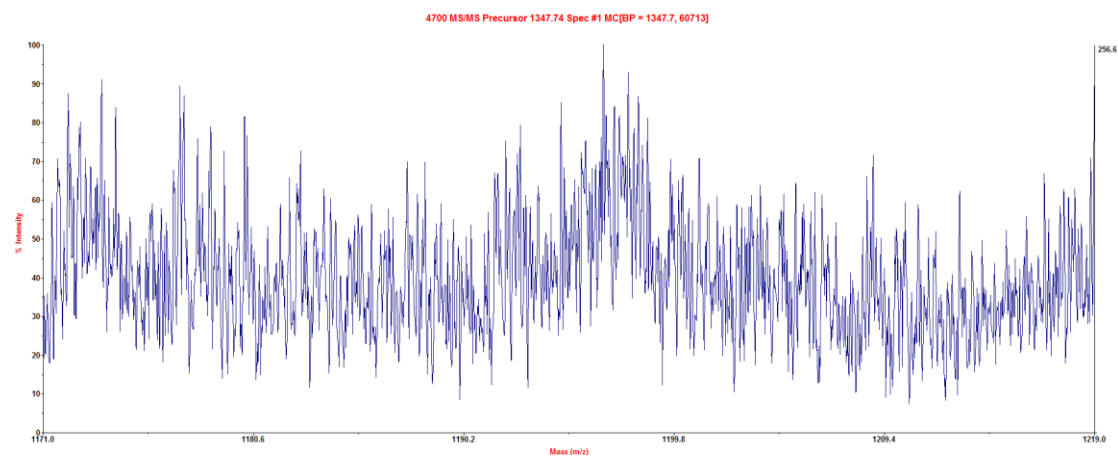
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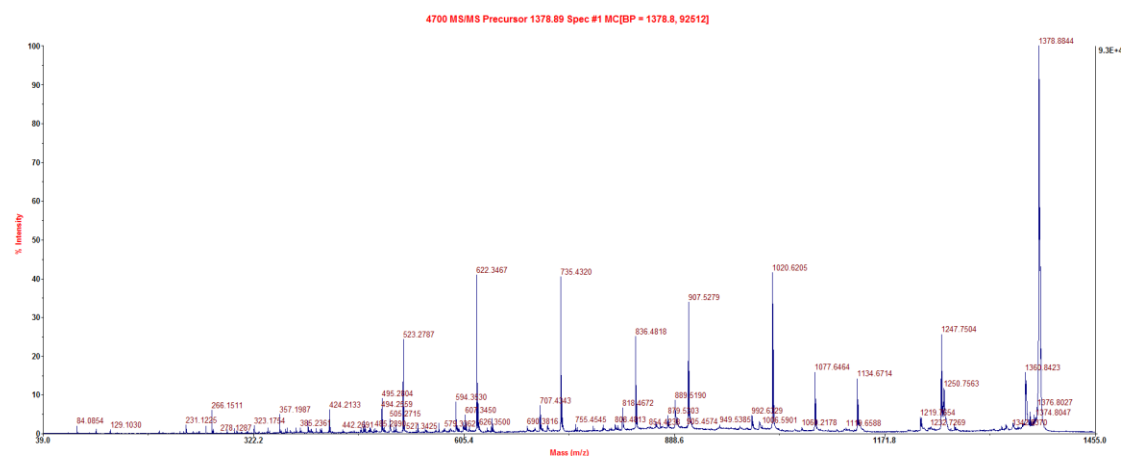
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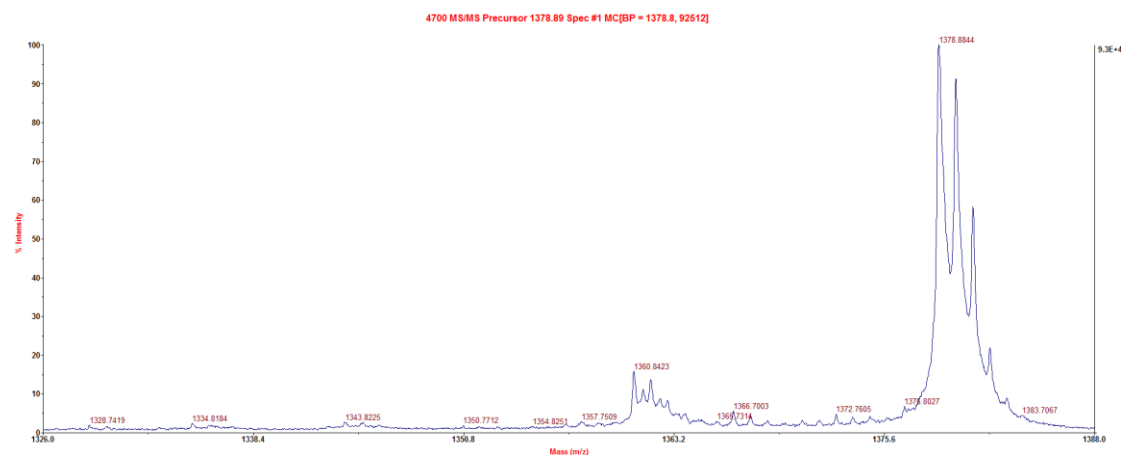
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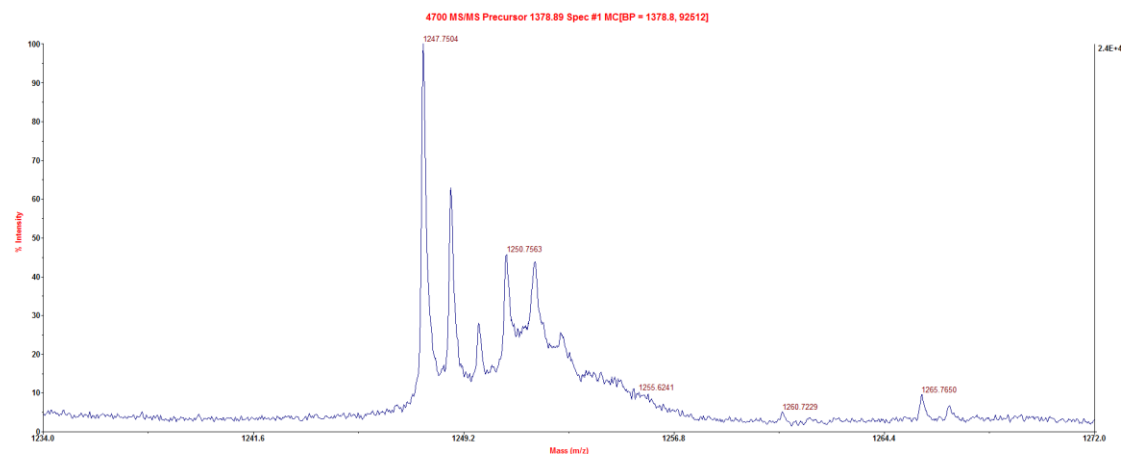
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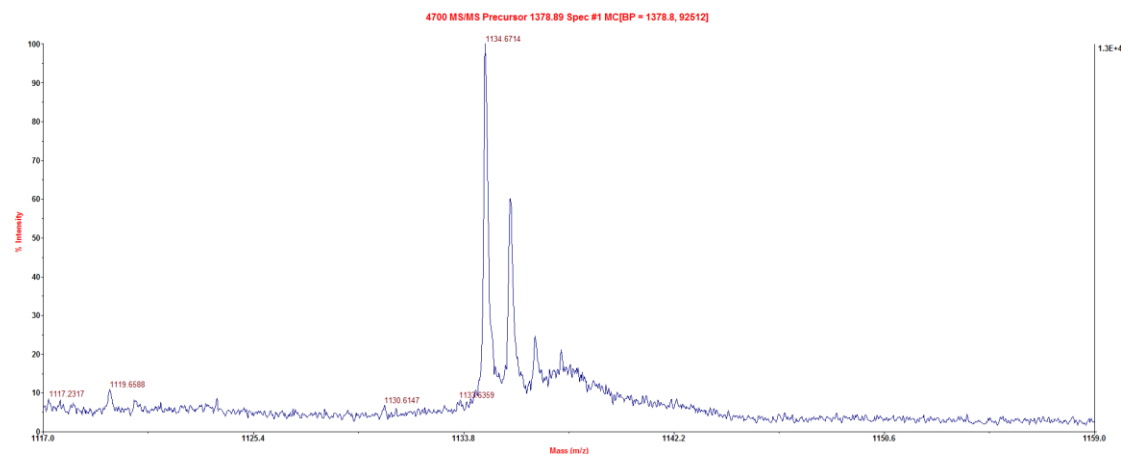
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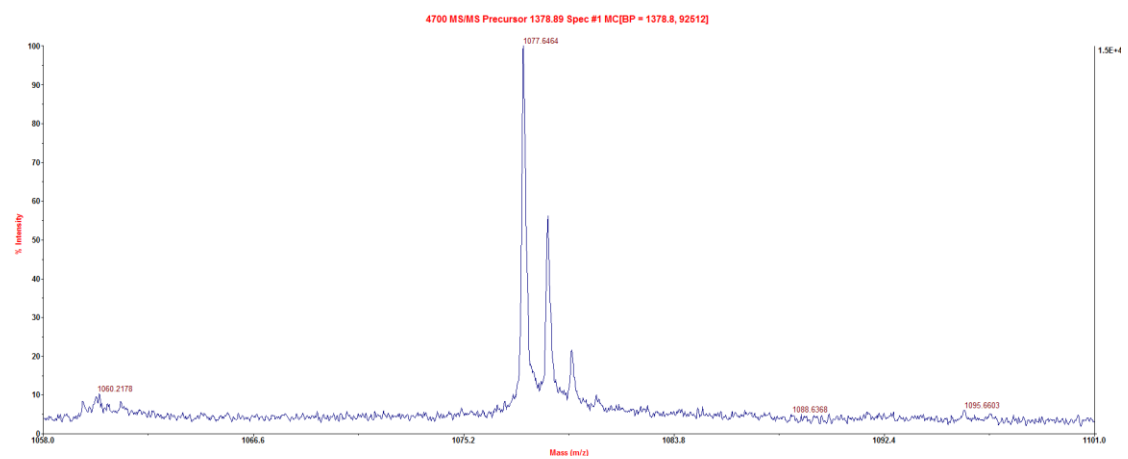
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