RESEARCH ARTICLE

2-D DIGE analysis of the proteome of extracts from peanut variants reveals striking differences in major allergen contents

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Over the last decade, an increasing prevalence of peanut allergies was observed worldwide. Peanuts are meanwhile categorized among the most dangerous food allergens. This is particularly relevant since peanut-derived ingredients are widely used in industrial food production. To minimize the problem of hidden food allergens causing severe anaphylactic reactions, pre-packaged food containing peanut components needs to be classified according to European ruling since 2005. Food companies search for strategies to reduce the allergenicity of peanut-derived food additives either by genetically altering the allergen content or by identifying peanut varieties with low levels of major allergens. In our study, we focused on peanut extracts from Indonesia that apparently contain lower levels of the major *Arachis hypogaea* allergen 1 (Ara h 1). Basic extracts of Virginia-type and Indonesian peanuts were compared by 1- and 2-DE . We identified more than hundred individual components in these extracts by MS and provide a high-resolution allergen map that also includes so far unknown fragments of major peanut allergens. The reduced level of Ara h 1 associated with a significantly lower abundance of the most potent peanut allergen Ara h 2 in various Indonesian peanuts was also confirmed by Western blotting with monoclonal antibodies and sera of allergic patients.

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1 Introduction

Peanuts (*Arachis hypogaea*) are groundnuts that belong to the pea family (Leguminosae) and originate from South America. Today, peanuts are a major agricultural crop and are cultivated in more than 80 countries worldwide. They serve as an inexpensive protein source and for the industrial production of oil. Peanuts are consumed either after roasting or boiling, as peanut butter or as ingredients in a wide range of food products. However, in recent years, peanuts developed to a major cause of IgE-mediated food allergies [1, 2] with the highest potential of any food allergen to induce anaphylactic shock [3, 4]. It is estimated that as many as 150 deaths occur in the US each year due to severe allergic or anaphylactic reactions to peanut allergens [5]. This food allergy affects children as well as adults. In contrast to allergies associated with egg and milk components, in the case of an early onset, peanut allergy persists into adulthood in the majority of patients. Thus, only 21.5%

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Abbreviations: ABC, ammonium bicarbonate; **Ara h,** Arachis hypogaea allergen (WHO nomenclature); **mAb,** monoclonal antibodies

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of the patients lose sensitivity over time [6]. In addition, recurrent peanut allergy has been observed in various cases to be associated with continued avoidance of the allergen [7]. In the US, approximately 0.6% of the population suffer from peanut allergy and in the UK 0.5% of the population [8]. It is important to stress that the only available ''treatment'' at the moment is the strict avoidance of all peanut containing products and a rapid counteraction of accidental ingestions with antihistamines and/or self-injectable epinephrine [4].

The diagnosis of peanut allergies includes medical history, physical examinations, prick tests and food challenges, which are time-consuming, require close supervision by medical personnel, and always carry a risk of inducing severe allergic responses [9]. To improve allergy diagnosis and therapy, potential peanut allergens have been identified and molecularly characterized over the past few years. According to the Allergen Nomenclature Sub-Committee of the International Union of Immunological Societies 11 peanut proteins were identified that elicit allergic reactions and/or are recognized by IgE antibodies from patients with peanut ingestion. Notably, most of the Ara h-type allergens form part of the major storage proteins of the peanut. Briefly, Ara h 1 (biochemical name: cupin; old name: vicilin-type 7S globulin) is a 63.5 kDa glycoprotein that belongs to the vicilin family and is recognized by IgE antibodies of 60–80% of the patients suffering from peanut allergy [10]. The two known isoforms of Ara h 2 (conglutin; 2S albumin) migrate at 16.6 and 18.0 kDa in SDS-PAGE gels and differ in a 12 amino acid insertion [11]. Of 40 peanut-allergic patients tested, 34 (85%) showed IgE binding to recombinant Ara h 2 on immunoblots. In ELISA of partially purified Ara h 2, all 6 peanut-allergic patients tested had Ara h 2-reactive IgE antibodies. Ara h 3 (cupin; legumin-type, 11S globulin, glycinin; 60 kDa) was originally identified as a 14 kDa breakdown fragment and later classified as glycinin [12, 13]. Of 18 peanut-allergic patients tested, 8 (44%) showed IgE binding to recombinant Ara h 3 on immunoblot. Ara h 3 shares 91.3% sequence identity with Ara h 4 (cupin; legumin-type, 11S globulin, glycinin; 61 kDa), another member of the glycinin family of storage proteins. Most glycinins are proteolytically processed from larger complexes yielding several isoforms between 58 and 62 kDa [14] that resolve under reducing conditions into two major subunits with 23 and 45 kDa [15]. Ara h 5 (profilin; 15 kDa) is a profilin-type protein and seems to play a minor role in peanut allergy (5 of 40 patients show IgE reactivity against the recombinant protein). However, due to its similarity to other plant profilins, Ara h 5 is discussed in the context of patient's cross reactivities to various pollen and food allergens [16, 17]. More recently, the heat- and digestion-stable Ara h 6 (conglutin; 2S albumin; 15 kDa) was identified which displays 59% amino acid sequence identity with Ara h 2 [18, 19] and is recognized by 30–40% of patient's IgE antibodies. Similar reactivities have been observed for the still poorly characterized Ara h 7 (conglutin; 2S albumin; 15 kDa) [16]. The Bet v 1 homologue Ara h 8 [20] was termed pathogenesis-related protein, PR-10, and is a major allergen in patients with combined birch pollen and peanut allergy (83% reactivity, inhibitable by Bet v 1) [21]. The list of peanut allergens is completed by the only recently described (Krause *et al., J. Allergy Clin. Immunol.,* in press) Ara h 9 (non-specific lipid-transfer protein 1; 9.8 kDa), Ara h 10 (oleosin; 16 kDa), and Ara h 11 (oleosin; 14 kDa).

As peanuts are widely used as industrial food ingredients and additives, researchers and companies started substantial efforts to reduce or eliminate the major allergens in peanuts. As an example, a patent filed in 2005 (US Pat. No. 20050114924) [22] describes the design of allergen-reduced transgenic peanut seed by recombinant cloning. Recently, a reduction in the allergens Ara h 2 and Ara h 6 by genetic engineering was achieved [23]. In this context, it previously has been noted that certain peanut variants apparently differ in the composition of allergy-causing storage proteins [24, 25].

In order to compare and molecularly define the protein composition of extracts obtained from such variants, we applied a proteomic approach using 2-D DIGE followed by mass spectrometric analyses of individual protein spots. We provide a comprehensive proteomic map of *A. hypogaea* kernel extracts. We demonstrate that peanut variants from Indonesia contain much lower levels of the major seed storage protein Ara h 1 and also differ substantially in the abundance of other potential allergenic storage proteins. 2-D DIGE technology is not only suited to characterize the overall composition of extracts from individual peanut variants, but also to detect minute amounts of contaminants, *e.g.* in purified allergen preparations from different sources.

2 Materials and methods

2.1 Extraction of peanut proteins

Peanuts were purchased from South East Asian suppliers (Kacang Asin from Manalagi, Denpasar, Bali Indonesia; Kacang Kulit and Biga from Garudafood, Jakarta, Indonesia) and from Seeberger, Ulm, Germany (Virginia-type peanuts). In most experiments, we used extracts of Kacang Asin kernels (occasionally also termed ''Balinese'' or ''Bali'' peanut) to represent the Indonesian peanut varieties. The extraction procedure was performed as described before [26]. Briefly, the frozen raw peanut kernels were ground and extracted overnight in 0.1 M ammonium hydrogen carbonate, pH 8.0. After centrifugation and decanting, the supernatant was filtered. Finally, the extracts were dialyzed against double-distilled water, lyophilized and stored at -20°C.

2.2 Allergen purification and antibody production

To purify Ara h 3/4, extracts of Kacang Asin Manalagi peanuts were subjected to an HPLC-coupled gel permeation

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chromatography on a Superdex S200 column (GE Healthcare, Munich, Germany) equilibrated with 200 mM NaCl, 50 mM Tris-HCl pH 7.5. Traces of Ara h 1 were removed by passing the Ara h 3/4 enriched eluate through a Con A sepharose column using the same equilibration buffer. The unbound fraction was dialyzed, concentrated in an Amicon device (10 kDa MWCO, Millipore, Billerica, MA, USA) and lyophilized. Purified Ara h 1 [27] and Ara h 3/4 were also used for immunization to generate respective antisera in rabbits. In addition to these polyclonal reagents, the monoclonal antibodies (mAb) anti-Ara h 1 (Pn-t) and anti-Ara h 2 (Pn-2) were used [27].

2.3 1-DE

Twenty-five micrograms of protein extracted from peanuts as described before or allergen preparations of Ara h 1 and Ara h 3/4, respectively, were separated by SDS-PAGE on a 12% gel. Protein bands were visualized by silver staining. Alternative protocols are described in the legends to the respective figures.

2.4 2-DE and Western blot analysis

The lyophilized peanut extracts were dissolved on ice for at least 30 min with lysis buffer (pH 8.5) containing 7 M urea, 2 M thiourea, 4% w/v CHAPS, 1% v/v IPG buffer pH 4–7 and 1% w/v DTT. They were then adjusted to a final protein concentration of 1 mg/mL. Thirty micrograms of protein were applied by cup loading on 13 cm IPG-strips (pH 4–7 linear), rehydrated at room temperature for at least 10 h in 250 µL DeStreak solution (GE Healthcare) with 0.5% v/v IPG buffer. Proteins were focused using the IPGphor 3 electrophoresis unit (GE Healthcare) at 20°C to reach 17 kV h, with a maximum voltage of 8000 V. Reduction and alkylation in equilibration buffer were performed as described elsewhere [28]. Subsequent PAGE separation was performed on 12.5 or 10% gels [29] using a Protean II cell (Bio-Rad, Munich, Germany). 2-D gels were transferred to 0.2 µm NC membranes (GE Healthcare) by tank-blotting [30]. Membranes were stained using Sypro Ruby Blot stain (Invitrogen) following the manufacturer's instructions. For Western blot matching, reference markers were placed on the membranes before fluorescent detection. After blocking with 5% non-fat dry milk in TBST (Tris-buffered saline (TBS) + 0.05% Tween), the membranes were probed with polyclonal anti-Ara h 1 or anti-Ara h 3/4 sera (both 1/7500) or with anti-Ara h 1 (Pn-t, 1/500) or anti-Ara h 2 (Pn-2, 1/1000) mAb, followed by HRP-conjugated goat anti-rabbit or goat anti-mouse secondary antibodies (1/7500, GE Healthcare). ECL detection reagents (GE Healthcare) were used for chemiluminescent detection using ECL Hyper Film (GE Healthcare). For reblotting, membranes were incubated in stripping solution (100 mM 2-mercaptoethanol, 2% SDS, 60 mM Tris) for 30 min at 56°C. Western blotting with sera from allergic patients was performed as detailed in the respective paragraphs of the Supporting Information.

2.5 Fluorescence labeling and 2-D DIGE

Lyophilized peanut extracts were dissolved for at least 30 min on ice in lysis buffer (pH 8.5) containing 7 M urea, 2 M thiourea, 30 mM Tris and 4% CHAPS [31]. The samples were adjusted to a protein concentration of approximately 5 mg/mL. The labeling with CyDyes and the subsequent 2-D separation was described elsewhere [28]. Briefly, 50 µg of protein *per* sample were labeled with equal amounts of Cy5 or Cy3 (CyDyes, GE Healthcare). Mixed samples were applied by cup loading on 24 cm IPG-strips rehydrated at 20°C in 450 µL DeStreak solution (GE Healthcare) with 0.5% v/v IPG buffer. IEF was carried out for a total of 50–55 kV h for pH 3–11 NL and 65–70 kV h for pH 4–7 L at 20°C, with gradual voltage increase (150 V for 2 h, 300 V for 2:30 h, 500 V for 3 h, gradient from 500 to 1000 V in 6 h, gradient from 1000 to 10 000 V for 4 h and 10 000 V) until total kV h were reached. After reduction and alkylation of the gel strips, the second dimension was performed on 12.5% polyacrylamide gels using Ettan Dalt 6 equipment (GE Healthcare) under continuous cooling at 16°C.

2.6 Image analysis and spot picking

The in-gel fluorescence was scanned on a Typhoon Trio (GE Healthcare) at appropriate wavelengths to detect Cy3 and Cy5-specific emissions corresponding to the protein concentration in every single spot [32]. The intra-gel spot detection of the multiplexed gel images was performed using differential in-gel analysis included in the DeCyder 6.5 software (GE Healthcare). Images for each gel were merged; spot boundaries were detected followed by a normalization of the spot volumes. For spot picking, gels were stained with Flamingo Pink (Bio-Rad) by following the manufacturer's instructions. Image Master 6.0 software was used for spot selection. Selected spots were picked automatically on an Ettan Spotpicker (GE Healthcare) using a 2 mm picking head. The picked gels were again scanned to document the locations of the punched spots.

2.7 In-gel tryptic digestion and MS

Isolated spots were washed three times with HPLC-grade water, dehydrated in a first step with 25 mM ammonium bicarbonate (ABC) in 50% ACN and shrunk in pure ACN as a second step, according to Gelhaus *et al.* [33]. The dry gel pieces were then rehydrated with 100 ng sequencing-grade modified porcine trypsin (Promega, Mannheim, Germany) or with bovine trypsin (Roche, Basel, Switzerland) in 10 µL of

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5 mM ABC. After rehydration, 10 μL of 5 mM ABC was added. For tryptic in-gel digestion, samples were incubated at 37°C overnight. To extract the peptides, 20 μL of 0.3% TFA in ACN was added and the samples were sonicated in a water bath (Sonorex Super RK100; Bandelin, Berlin, Germany) for 15 min. For some low abundant proteins, a second elution of rehydrated spots (in 0.1% TFA) was performed. Liquid phases were collected, lyophilized, redissolved in 0.8 μL MALDI matrix solution (8 mg/mL α-cyanohydroxycinnamic acid (Sigma) in 65% ACN/0.1% TFA), spotted on 192 well stainless steel MALDI plates and air-dried.

2.8 MS and database analysis

Mass spectrometric measurements of tryptic peptides were performed on a 4700 Proteomics analyzer MALDI-TOF/TOF instrument (Applied Biosystems, Framingham, MA, USA) using the 4000 Series Explorer Software V3.6. Protein identification was either performed by PMF or by combining MS and MS/MS spectral data for database searches. MS spectra were acquired in positive reflector mode by accumulation of 1000–2000 laser shots. For peak picking, a minimum signal-to-noise ratio of 30 was chosen. In addition, for selected samples, precursor ions were also fragmented by MS/MS to confirm and validate previous results of the PMF. Precursor ions were selected automatically according to the following criteria: a maximum of 5–7 masses *per* spot, and a signal-to-noise ratio >35. The precursor mass window was set to 50 (full width at half maximum). Peak intensity was used to select the most intense peaks excluding peaks from trypsin autolysis products with a 0.2 m/z precursor mass tolerance (see below). For MS and MS/MS measurements, the instrument default calibration was updated before the run. If internal calibration was applied in MS mode, the respective trypsin autolysis products were used at 25 ppm mass tolerance. In MS/MS mode, air was used as collision gas and the collision energy was set to 1 kV. A minimum of 5000 fragmentation spectra and a maximum of 8000 laser shots were accumulated *per* precursor depending on the signal-to-noise ratio of the fragment ions. Expected tryptic autolysis product peaks were excluded from the selection with 50 ppm precursor mass tolerance. A signal-to-noise ratio of >10 was selected for peak picking. Spectral data (PMF or combined MS and MS/MS spectral data) were processed by the GPS Explorer 3.6 software (Applied Biosystems), submitted to MASCOT server (version 2.0, Matrix Science, London, UK) for in-house search against proteins from green plants included in the NCBI non-redundant protein database or protein identification was performed by searching against an in-house database (NCBInr, date 26/02/2007) including all proteins from *A. hypogaea* found in the NCBI database (with 875 protein entries). MASCOT was used with the following parameters: Trypsin's enzymatic specificity was considered, autolysis products of trypsin were excluded from the searches, *i.e.* tryptic monoisotopic masses 842.5100, 870.5412, 1045.5642, 1126.5645, 1420.7225, 1940.9354, 2003.0734, 2211.1046, 2225.1202, 2283.1807, 2239.1358, 2299.1756, 2807.3145, 3337.7577, 3353.7526 (porcine trypsin), or 805.4166, 906.516, 1020.503, 1153.5740, 1433.7210, 2163.0568, 2227.2037, 2289.1503, 3153.5385, 3227.5663, 3323.487 (bovine trypsin). The modification on cysteine residues by carboxyamidomethylation was set as obligate, potential modification of methionine by oxidation, a maximum of one missed tryptic cleavage site in a peptide fragment, the mass tolerance of precursor was set to 50 ppm, and the fragment-ion mass tolerance was set to 0.2 Da (MS/MS). A protein or protein fragment was accepted to be identified when the total protein score reached or exceeded the MASCOT score threshold (≥ 42 with a probability of identification greater than 95%) and the theoretical molecular mass and p*I* matched the respective localization on the 2-D gels. In the case of combined MS and MS/MS searches, no cut-off score for accepting individual MS/MS spectra was set.

3 Results

Peanuts contain some of the most potent food allergens known to date. Most peanut allergens are classical seed storage proteins. Owing to the polypeptide heterogeneity within individual protein families, a detailed analysis of storage compartments turned out to be rather complex and requires high-resolution technologies that have been developed only recently. In addition, covalent co- and post-translational modifications lead to a variety of protein isoforms that may yield various indistinguishable protein bands in 1-DE approaches. Also, major storage proteins of legumes tend to form hexameric or heteromeric complexes with large molecular weights of 300–450 kDa or more [34]. In our study, these peculiarities were circumvented by a combination of two methods: First, the proteins were extracted in an alkaline environment [26], which was effective in solubilizing the storage proteins and other minor seed protein components to monomers [35]. Second, we applied a high-resolution 2-DE technique to be able to efficiently separate different isoforms at similar molecular masses.

3.1 Protein distribution in peanut extracts resolved by 1-D SDS-PAGE

The generation of peanut extracts can be achieved by different protocols including acidic extraction with sodium acetate buffer and alkaline extraction with ABC buffer. In our experiments, we analyzed proteins from four different peanut variants generated by basic extraction. This method mimics oral digestion and was shown to readily release most detectable allergens of peanut kernels [36]. In an initial experiment, we compared basic extracts from 'standard' Virginia-type and Indonesian peanuts

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with enriched Ara h 1 (purified from Virginia-type peanuts), and Ara h 3/4 (purified from Kacang Asin peanuts). Silver staining of the SDS gel revealed that the two variants differ massively in their overall protein composition (Fig. 1). While fairly few bands were stained equally in both extracts, the major components were clearly differentially represented. As an example, a band at 65 kDa is dominant in the extract of Virginia-type peanuts, but almost not detectable in the Indonesian variant. In line with previous characterizations of such extracts, the enrichment of protein in purified Ara h 1 preparations suggested that the band might in fact represent the major portion of this allergen. In contrast, a band with an approximate molecular weight around 40 kDa was almost absent in Virginia-type peanuts, but formed a major component of the Indonesian extract and purified Ara h 3/4.

3.2 2-D DIGE analyses of peanut varieties

To define differences between the two peanut varieties, we used a 2-D DIGE approach. We separated the individual protein bands at high-resolution and defined the proteome by subsequent mass spectrometric analyses. For analytical gels, a total of 100 μg of differentially labeled proteins were cup-loaded on IPG-strips covering pH ranges from 3 to 11 (non-linear) or from 4 to 7 (linear). On the basis of individually scanned fluorescence emissions, differences between the two peanut extracts became apparent. Red spots in Fig. 2A and D represent Cy5-marked proteins from Virginia-type peanut extracts (see Fig. 2B and E for individual scans), whereas green spots represent Cy3-labeled proteins from Kacang Asin peanut extracts (see Fig. 2C and F for individual scans). Similarly abundant protein spots appear in yellow in the overlay pictures (Fig. 2A and D). Gel analysis with the DeCyder software package resulted in the detection of 169 individual spots using a pH 3–11 NL IPG-strip. Of those, 32 (18.9%) were apparently more prominent in Virginia-type peanuts and 20 (11.8%) were more prominent in Indonesian peanuts. Based on the twofold square deviation of all included spots, only spots that differed more than 12.5-fold were classified as non-equal. Thus, the 2-D analyses clearly proved the initial observation and documented that the two variants massively differ in the distribution of selected seed storage proteins. Of note, the separation on pH 4–7 L strips (Fig. 2D, E) occasionally led to a streaky pattern near the anode. However, this might be due to underfocusing since we did not observe this phenomenon using shorter (13 cm) pH 4–7 L strips (see also Fig. 5A, B). IEF on pH 4–7 L strips nevertheless yielded a generally better separation of acidic proteins. To demonstrate that the observed differences are not brand-specific, additional experiments with two other Indonesian peanuts (Kacang Kulit and Biga) of the Kacang Garuda type were performed (Supporting Information Fig. S3 and Table S1). Moreover, similar results as shown in Fig. 2 were also obtained in five independent experiments with pH 3–11 NL strips and two with pH 4–7 L IPG-strips, (Supporting Information Fig. S4 and Table S2). Although the suppliers roasted all tested peanuts, we investigated whether the reduced level of Ara h 1 might be due to the different manufacturing procedures. Therefore, we also compared extracts of heat roasted and oil roasted (fried) Virginia-type peanuts in a separate DIGE experiment (Supporting Information Table S2). As described before by Beyer *et al.* [37], we also observed a reduction in the level of Ara h 1 in fried peanuts. However, in the basic extracts obtained from such kernels, Ara h 1 was still present and readily detectable by different means (Supporting Information, Fig. S5).

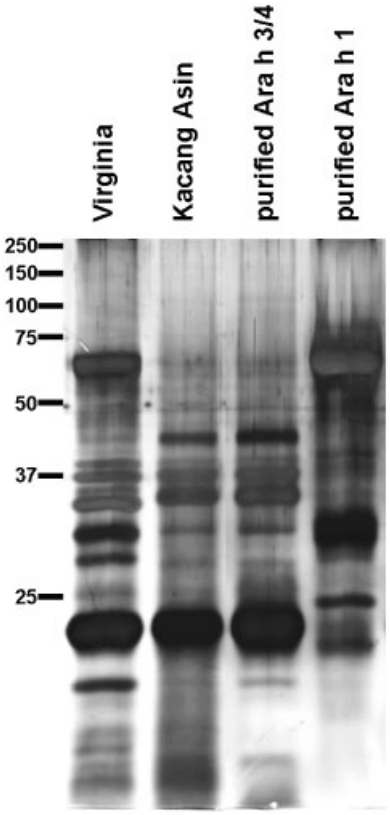


Figure 1. Protein distribution in peanut varieties. Twenty-five micrograms of total protein from Virginia-type and Balinese (Kacang Asin) peanut extracts and purified major allergens (Ara h 1 and Ara h 3/4) were separated on a 12% SDS gel. Proteins were visualized by silver staining.

3.3 Identification of the peanut proteome by MS

Since alterations in protein masses upon CyDye labeling have been previously observed [38], we decided to pick individual spots from 2-D gels stained with Flamingo Pink. The samples were washed, digested with trypsin and analyzed by MS. We identified a total of 108 spots from both peanut extracts. The identified spots are listed in Table 1 and correspond to an annotated spot map as shown in

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Fig. 3. This comprehensive analysis revealed peptides that cover different parts of the peanut proteins Ara h 1, Ara h 2, Ara h 3/4, Ara h 6 and their isoforms. For a better view and to delineate identical proteins, all identified fragments were assigned to their specific isoallergen in Table 1.

One of the major peanut allergens is Ara h 1. This allergen was detected as a full-length protein in spots 1–27 and in two distinct fragments. An acidic fragment (p*I* 5) was present in spots 55–57, whereas a basic fragment (p*I* 9–10) was detected in spots 82–84.

Ara h 2, regarded as a major disease-associated peanut allergen, was identified as full-length proteins in spots 77–81 and 85–89. In addition, we also identified low molecular C-terminal fragments of Ara h 2 in spots 99 and 100. A similar distribution was seen for Ara h 6 that is present in a full-length form in spots 93-97 and as fragments in spots 101 and 102. The other major peanut allergen is Ara h 3/4. Glycinin represents an isoallergen of Ara h 3/4 that was identified as full-length protein with peptides covering amino acids 23–507 of the 510-residue protein (spots 107 and 108). Fragments of glycinin were identified in spots 45–54, 58, 60, 64–67, 75, 76 and 106. More

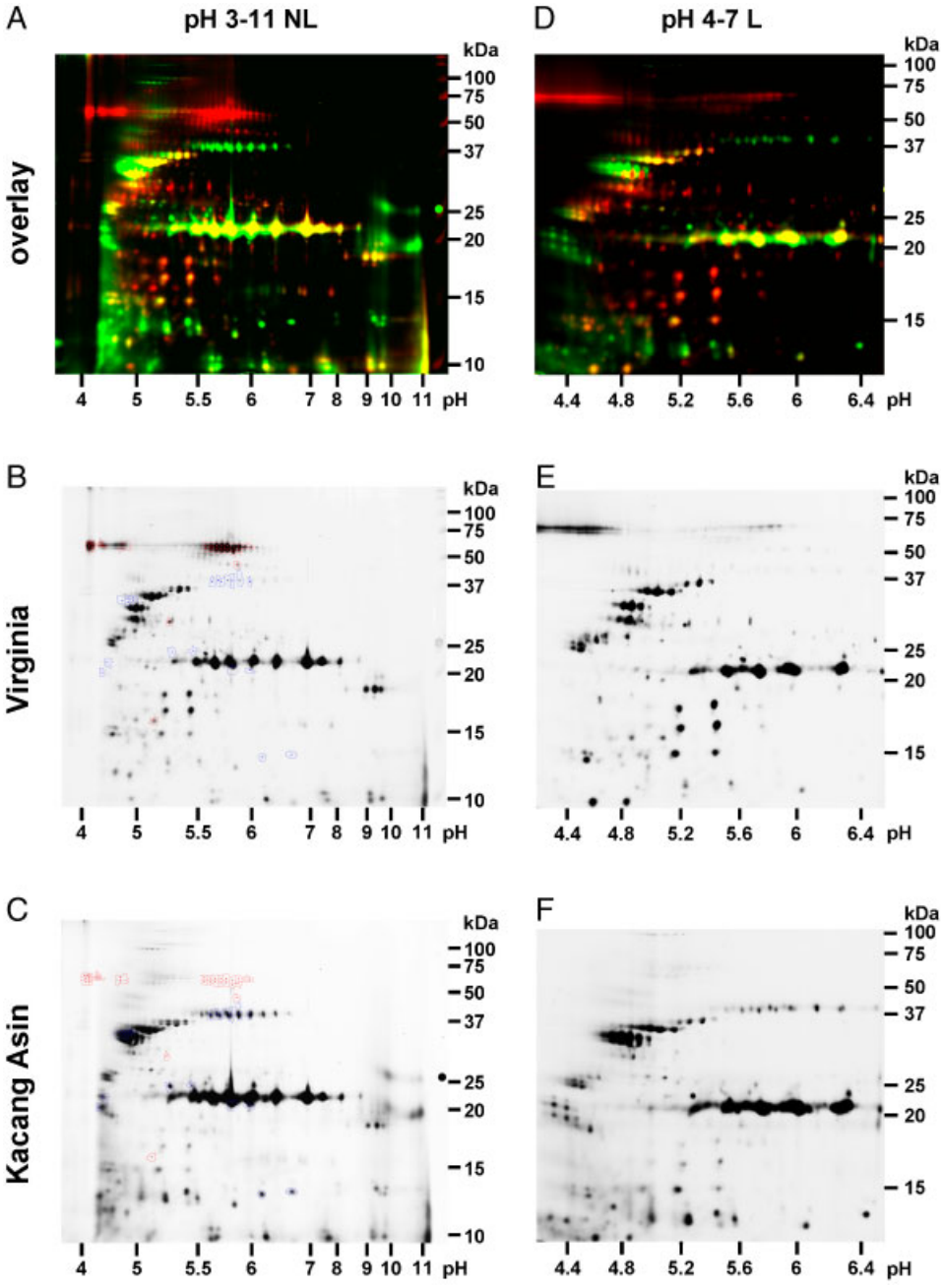


Figure 2. 2-D DIGE analyses of peanut extracts. Fifty micrograms of Virginia type (B, E) and Balinese (Kacang Asin; C, F) peanut extracts were labeled with Cy5 (red) and Cy3 (green), respectively. Samples were combined and separated in the first dimension on IPG-strips (pH 3–11 non-linear (A–C), pH 4–7 linear (D–F)). 12.5% Tris-glycine gels were used for the SDS-PAGE in the second dimension. Protein spots with a change in their relative abundance greater than 12.5-fold are marked in blue (increased) or red (decreased) for Kacang Asin extracts.

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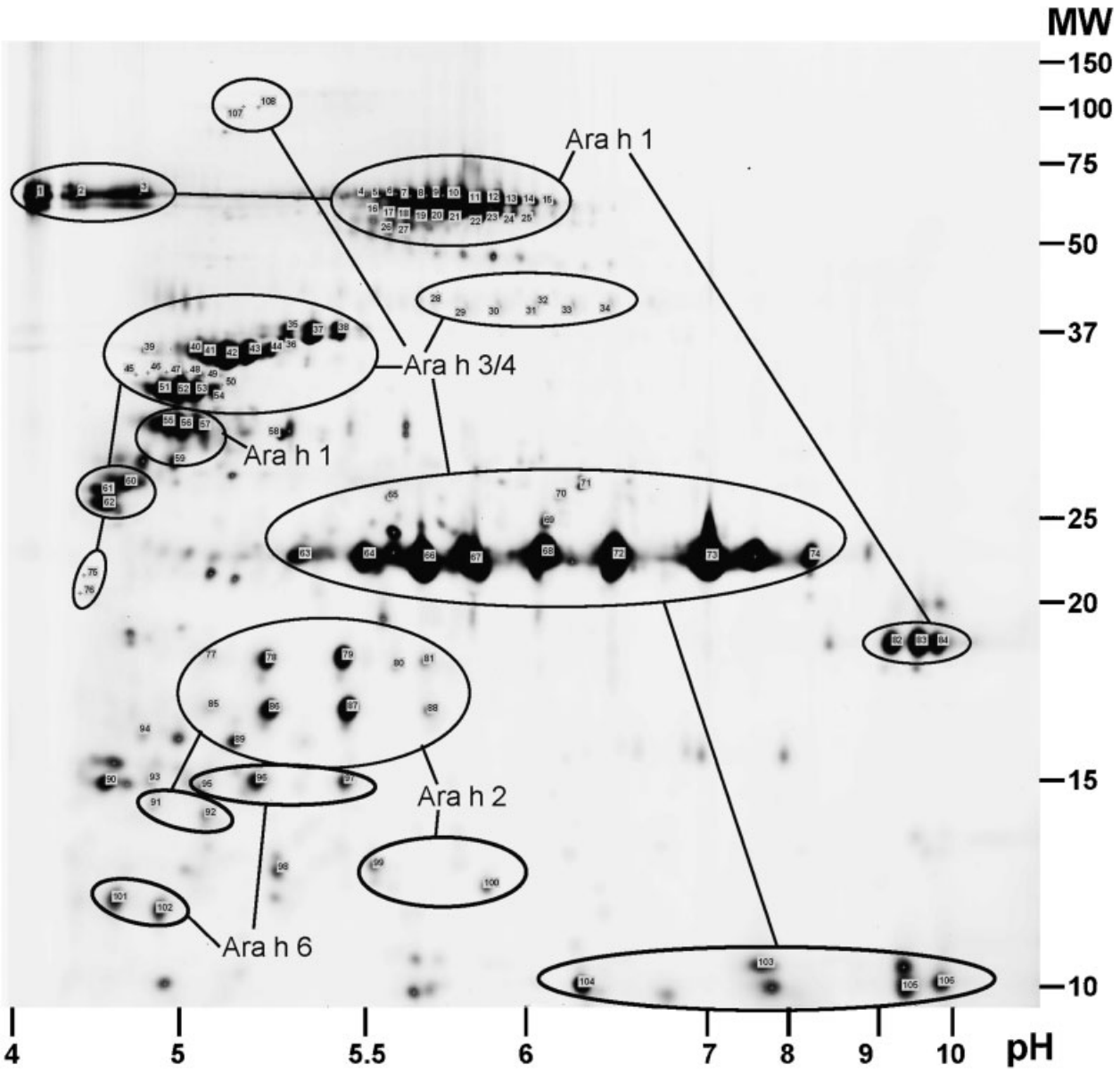


Figure 3. Proteome map of peanut extracts. Identified proteins and individual protein isoforms are annotated and grouped according to their homology with the respective major allergen (spot numbers correspond to numbers given in Table 1).

fragments of Ara h 3/4 isoallergens were also detected in different regions of the 2-D gel. Among these, spots 28–30, 32–34, 61 and 62 were identified as C-terminal parts of arachin 6. In contrast, spot 90 represents the middle part of this protein. Furthermore, Gly1, yet another isoform of Ara h 3/4, was detected in spots 31, 39–42, 68, 72 and 74. Other Ara h 3/4 homologous proteins are arachin Ahy-1 (spots 35-38), arachin Ahy-2 (spot 70), arachin Ahy-3 (spot 63) and arachin Ahy-4 (spots 43–44). Last but not least, in spots 103–105 we identified the putative low molecular trypsin inhibitor as yet another Ara h 3/4 family member.

3.4 Identification of differentially expressed proteins

As mentioned, the combination of 2-DE and MS led to the identification of 108 different proteins. Thus, we were able to go back to the initial comparison of the two peanut variants. As shown in Fig. 4, the complete lack of the full length Ara h 1 (spots 1–27 in Fig. 3) was most apparent in the Balinese peanut variety (Kacang Asin, Fig. 4A). However, both the acidic and basic fragments of Ara h 1 are still present (although at reduced levels). In the case of Ara h 2, one form represented by spot 89 was almost absent in the

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Table 1. Protein profile in peanut kernels[a)]

spot no.	NCBI acc. no.	Uni Prot No.	MW	PI	identified peptides	MASCOT Score	sequence coverage %	MS+MS/MS	protein	isoallergen[a)]	fragment	identified regions in full length protein by PMF in black	total length of protein in aa
1	gil46560478	Q6PSU3	66934	6.7	36	296	55	no	conarachin	Ara h 1	no		580
2	gil46560478	Q6PSU3	66934	6.7	21	189	38	no	conarachin	Ara h 1	no		580
3	gil46560478	Q6PSU3	66934	6.7	30	331	50	no	conarachin	Ara h 1	no		580
4	gil46560478	Q6PSU3	66934	6.7	21	154	33	no	conarachin	Ara h 1	no		580
5	gil46560478	Q6PSU3	66934	6.7	30	333	53	no	conarachin	Ara h 1	no		580
6	gil46560478	Q6PSU3	66934	6.7	31	349	53	no	conarachin	Ara h 1	no		580
7	gil46560478	Q6PSU3	66934	6.7	31	345	50	no	conarachin	Ara h 1	no		580
8	gil46560478	Q6PSU3	66934	6.7	31	339	55	no	conarachin	Ara h 1	no		580
9	gil46560478	Q6PSU3	66934	6.7	23	197	33	no	conarachin	Ara h 1	no		580
10	gil46560478	Q6PSU3	66934	6.7	29	241	47	no	conarachin	Ara h 1	no		580
11	gil46560478	Q6PSU3	66934	6.7	28	296	37	no	conarachin	Ara h 1	no		580
12	gil46560478	Q6PSU3	66934	6.7	24	405	30	no	conarachin	Ara h 1	no		580
13	gil46560478	Q6PSU3	66934	6.7	28	289	49	no	conarachin	Ara h 1	no		580
14	gil46560478	Q6PSU3	66934	6.7	27	265	45	no	conarachin	Ara h 1	no		580
15	gil46560478	Q6PSU3	66934	6.7	23	206	43	no	conarachin	Ara h 1	no		580
16	gil16612200	P43238	71701	6.6	9	54	15	no	major allergen Arah1	Ara h 1	no		626
17	gil16612200	P43238	71701	6.6	15	108	23	no	major allergen Arah1	Ara h 1	no		626
18	gil16612200	P43238	71701	6.6	29	301	40	no	major allergen Arah1	Ara h 1	no		626
19	gil16612200	P43238	71701	6.6	10	43	21	no	major allergen Arah1	Ara h 1	no		626
20	gil16612200	P43238	71701	6.6	14	85	21	no	major allergen Arah1	Ara h 1	no		626
21	gil16612200	P43238	71701	6.6	16	103	22	no	major allergen Arah1	Ara h 1	no		626
22	gil16612200	P43238	71701	6.6	13	373	19	yes	major allergen Arah1	Ara h 1	no		626
23	gil16612200	P43238	71701	6.6	13	65	19	no	major allergen Arah1	Ara h 1	no		626
24	gil16612200	P43238	71701	6.6	13	95	18	no	major allergen Arah1	Ara h 1	no		626
25	gil16612200	P43238	71701	6.6	10	62	14	no	major allergen Arah1	Ara h 1	no		626
26	gil46560478	Q6PSU3	66934	6.7	18	157	36	no	conarachin	Ara h 1	no		580
27	gil46560478	Q6PSU3	66934	6.7	13	91	24	no	conarachin	Ara h 1	no		580
28	gil118776570	A1DZF0	60681	5.4	8	50	16	no	arachin 6	Ara h 3/4	yes		529
29	gil118776570	A1DZF0	60681	5.4	12	82	23	no	arachin 6	Ara h 3/4	yes		529
30	gil118776570	A1DZF0	60681	5.4	8	48	20	no	arachin 6	Ara h 3/4	yes		529
31	gil9864777	Q9FZ11	60754	5.5	10	73	24	no	Gly1	Ara h 3/4	yes		529
32	gil118776570	A1DZF0	60681	5.4	9	51	20	no	arachin 6	Ara h 3/4	yes		529
33	gil118776570	A1DZF0	60681	5.4	11	75	23	no	arachin 6	Ara h 3/4	yes		529
34	gil118776570	A1DZF0	60681	5.4	10	67	21	no	arachin 6	Ara h 3/4	yes		529

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Table 1. Continued

spot no.	NCBI acc. no.	Uni Prot No.	MW	PI	identified peptides	MASCOT Score	sequence coverage %	MS+MS/MS	protein	isoallergen[a]	fragment	identified regions in full length protein by PMF in black	total length of protein in aa
35	gil52001219	Q647H4	61810	5.6	10	92	45	no[b]	arachin Ahy-1	Ara h 3/4	yes		538
36	gil52001219	Q647H4	61810	5.6	19	154	31	no[b]	arachin Ahy-1	Ara h 3/4	yes		538
37	gil52001219	Q647H4	61810	5.6	12	96	20	no[b]	arachin Ahy-1	Ara h 3/4	yes		538
38	gil52001219	Q647H4	61810	5.6	8	70	12	no[b]	arachin Ahy-1	Ara h 3/4	yes		538
39	gil9864777	Q9FZ11	60754	5.5	10	64	25	no[b]	Gly1	Ara h 3/4	yes		529
40	gil9864777	Q9FZ11	60754	5.5	14	98	32	no	Gly1	Ara h 3/4	yes		529
41	gil9864777	Q9FZ11	60754	5.5	16	131	39	no	Gly1	Ara h 3/4	yes		529
42	gil9864777	Q9FZ11	60754	5.5	17	134	43	no	Gly1	Ara h 3/4	yes		529
43	gil57669861	Q5I6T2	61041	5.4	15	107	24	no	arachin Ahy-4	Ara h 3/4	yes		531
44	gil57669861	Q5I6T2	61041	5.4	12	102	21	no	arachin Ahy-4	Ara h 3/4	yes		531
45	gil47933675	Q6IWG5	58368	5.4	16	138	32	no	glycinin	Ara h 3/4	yes		510
46	gil47933675	Q6IWG5	58368	5.4	14	128	20	no	glycinin	Ara h 3/4	yes		510
47	gil47933675	Q6IWG5	58368	5.4	15	110	26	no	glycinin	Ara h 3/4	yes		510
48	gil47933675	Q6IWG5	58368	5.4	8	47	18	no	glycinin	Ara h 3/4	yes		510
49	gil47933675	Q6IWG5	58368	5.4	8	76	19	no	glycinin	Ara h 3/4	yes		510
50	gil47933675	Q6IWG5	58368	5.4	11	100	30	no	glycinin	Ara h 3/4	yes		510
51	gil47933675	Q6IWG5	58368	5.4	16	138	32	no	glycinin	Ara h 3/4	yes		510
52	gil47933675	Q6IWG5	58368	5.4	15	127	21	no	glycinin	Ara h 3/4	yes		510
53	gil47933675	Q6IWG5	58368	5.4	15	133	32	no	glycinin	Ara h 3/4	yes		510
54	gil47933675	Q6IWG5	58368	5.4	17	161	34	no	glycinin	Ara h 3/4	yes		510
55	gil46560474	Q6PSU5	33641	5.1	8	58	30	no	conarachin fragment	Ara h 1	yes		614
56	gil46560474	Q6PSU5	33641	5.1	7	52	26	no	conarachin fragment	Ara h 1	yes		614
57	gil46560472	Q6PSU6	34169	5.1	15	139	44	no	conarachin fragment	Ara h 1	yes		614
58	gil47933675	Q0GM57	58368	5.4	3	116	6	yes	glycinin	Ara h 3/4	yes		510
59	gil46560472	Q6PSU6	34169	5.1	6	52	24	no	conarachin	Ara h 1	yes		580
60	gil5712199	Q9SQH7	61430	5.5	3	52	8	yes	glycinin	Ara h 3/4	yes		530
61	gil118776570	A1DZF0	60681	5.4	7	44	12	no	arachin 6	Ara h 3/4	yes		529
62	gil118776570	A1DZF0	60681	5.4	8	62	20	no	arachin 6	Ara h 3/4	yes		529
63	gil52001223	Q647H2	54991	5.4	5	100	14	yes	arachin Ahy-3 [chain beta]	Ara h 3/4	yes		484
64	gil47933675	Q6IWG5	58368	5.4	9	62	31	no	glycinin	Ara h 3/4	yes		510
65	gil47933675	Q6IWG5	58368	5.4	2	83	4	yes	glycinin	Ara h 3/4	yes		512
66	gil47933675	Q6IWG5	58368	5.4	8	74	21	no	glycinin	Ara h 3/4	yes		510
67	gil47933675	Q6IWG5	58368	5.4	12	82	31	no	glycinin	Ara h 3/4	yes		510
68	gil9864777	Q9FZ11	60754	5.5	10	53	20	no	Gly1	Ara h 3/4	yes		529
69	gil118776570	A1DZF0	60681	5.4	8	67	22	no	arachin 6	Ara h 3/4	yes		529

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Table 1. Continued

spot no.	NCBI acc. no.	Uni Prot No.	MW	PI	identified peptides	MASCOT Score	sequence coverage %	MS+MS/MS	protein	isoallergen[a]	fragment	identified regions in full length protein by PMF in black	total length of protein in aa
70	gil52001221	Q647H3	61836	5.5	7	445	17	yes	arachin Ahy-2	Ara h 3/4	yes		537
71	gil22135348	Q8LL03	25768	6.7	16	538	47	yes	trypsin inhibitor	Ara h 3/4	yes		530
72	gil9864777	Q9FZ11	60754	5.5	11	60	23	no	Gly1	Ara h 3/4	yes		529
73	gil118776570	A1DZF0	60681	5.4	6	348	17	yes	arachin 6	Ara h 3/4	yes		529
74	gil9864777	Q9FZ11	60754	5.5	6	108	8	yes	Gly1	Ara h 3/4	yes		529
75	gil47933675	Q6IWG5	58368	5.4	9	80	17	no	glycinin	Ara h 3/4	yes		510
76	gil47933675	Q6IWG5	58368	5.4	7	47	11	no	glycinin	Ara h 3/4	yes		510
77	gil31322017	Q7Y1C0	20212	5.7	10	108	56	no	allergen Ara h 2 isoform	Ara h 2	no		169
78	gil52001227	Q647H0	21293	7.1	10	87	64	no	2S protein 1	Ara h 2	no		172
79	gil15418705	Q941R0	18612	5.7	9	98	60	no	allergen II	Ara h 2	no		156
80	gil15418705	Q941R0	18612	5.7	8	79	44	no	allergen II	Ara h 2	no		156
81	gil52001227	Q647H0	21293	7.1	6	44	37	no	2S protein 1	Ara h 2	no		172
82	gil52001225	Q647H1	76343	5.2	3	146	6	yes	conarachin fragment	Ara h 1	yes		662
83	gil52001225	Q647H1	76343	5.2	6	315	12	yes	conarachin fra ment	Ara h 1	yes		662
84	gil52001225	Q647H1	76343	5.2	6	303	12	yes	conarachin fragment	Ara h 1	yes		662
85	gil15418705	Q941R0	18612	5.7	10	111	59	no	allergen II	Ara h 2	no		156
86	gil15418705	Q941R0	18612	5.7	10	116	60	no	allergen II	Ara h 2	no		156
87	gil15418705	Q941R0	18612	5.7	9	98	60	no	allergen II	Ara h 2	no		156
88	gil15418705	Q941R0	18612	5.7	7	66	36	no*	allergen II	Ara h 2	no		156
89	gil15418705	Q941R0	18612	5.7	9	100	44	no*	allergen II	Ara h 2	no		156
90	gil118776570	A1DZF0	60681	5.4	10	412	13	yes	arachin 6	Ara h 3/4	yes		529
91	gil46560482	Q6PSU1	20907	6.0	6	43	32	no	seed storage protein SSP2	Ara h 2	yes		175
92	gil46560482	Q6PSU1	20907	6.0	6	54	25	no	seed storage protein SSP2	Ara h 2	yes		175
93[c]	gil46560482	Q6PSU1	20907	6.0	6	58	36	no	seed storage protein SSP2	Ara h 2	yes		175
	gil52001229	Q647G9	17479	6.1	9	89	53	no	conglutin	Ara h 6	no		145
94	gil17225991	Q647G9	17349	5.7	5	45	47	no	conglutin	Ara h 6	no		145
95	gil17225991	Q647G9	17349	5.7	9	96	56	no	conglutin	Ara h 6	no		145
96	gil17225991	Q647G9	17349	5.7	9	81	70	no	conglutin	Ara h 6	no		145
97	gil52001229	Q647G9	17479	6.1	10	88	73	no	conglutin	Ara h 6	no		145
98	gil66735602	Q4U4M1	10408	5.3	7	82	61	no	LEA protein	n.d.	?		95
99	gil15418705	Q941R0	18612	5.7	8	54	35	no	allergen II	Ara h 2	yes		156
100	gil31322017	Q7Y1C0	20212	5.7	7	65	39	no	allergen Ara h 2 isoform [large chain]	Ara h 2	yes		169

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Table 1. Continued

spot no.	NCBI acc. no.	Uni Prot No.	MW	PI	identified peptides	MASCOT Score	sequence coverage %	MS+MS/MS	protein	isoallergen[a]	fragment	identified regions in full length protein by PMF in black	total length of protein in aa
101	gi|17225991	Q647G9	17349	5.7	8	74	37	no	conglutin	Ara h 6	yes		145
102	gi|52001229	Q647G9	17479	6.1	9	91	51	no	conglutin	Ara h 6	yes		145
103	gi|22135348	Q8LL03	25768	6.7	7	291	27	yes	trypsin inhibitor N-terminal fragment	Ara h 3/4	yes		529
104	gi|22135348	Q8LL03	25768	6.7	4	175	27	yes	trypsin inhibitor N-terminal fragment	Ara h 3/4	yes		529
105	gi|22135348	Q8LL03	25768	6.7	4	347	27	yes	trypsin inhibitor N-terminal fragment	Ara h 3/4	yes		529
106	gi|5712199	Q9SQH7	61430	5.5	6	376	13	yes	glycinin	Ara h 3/4	yes		529
107	gi|47933675	Q6IWG5	58368	5.4	11	81	23	no	glycinin	Ara h 3/4	no		510
108	gi|47933675	Q6IWG5	58368	5.4	11	82	25	no	glycinin	Ara h 3/4	no		510

[a]Spot numbers refer to the annotations in Fig. 3. Identified protein isoforms were further assigned to their allergen family. The sequence coverage and localization of the identified peptide fragments within the corresponding full-length proteins are displayed graphically.
[b]Exception of the identification rules for this protein, due to the more correct molecular weight of second ranked protein.
[c]Mixture of two proteins was identified in one single spot.

Balinese extract (Fig. 4) and other forms (spots 77–81 and 85–88) were much less abundant. Of note, at the same time, several proteins (*e.g.* 35–38, 40–44, 51–54, 66–68 and 72–74) were almost equally distributed in both extracts. Interestingly, as expected from the initial 1-D experiment, in contrast to Ara h 1, different isoallergens of the Ara h 3/4 family are relatively overrepresented in the Balinese peanut (Fig. 4B, spots 45–50 and 75, 76). Also arachin 6 (spots 28–34) appears to be present at much higher level in the Balinese variant as shown in the lower panel of Fig. 4B.

3.5 Comparative 2-D Western blot analyses of Ara h 1, Ara h 3/4 and Ara h 2

We confirmed several of these findings by Western blot analyses using allergen-specific polyclonal or mAb. Upon 2-DE, proteins were transferred to NC membranes and initially stained with Sypro Ruby blot stain to get an indication for transfer efficiency and to be able to allocate specific antibody signals to individual protein spots using reference markers (Fig. 5A, B; Fig. 6A, B). Blots were probed with rabbit-antisera against Ara h 1 and Ara h 3/4 as shown in Fig. 5 and in more detail in Supporting Information Fig. S1. Ara h 1 (spots 1–25) was only detected by the antiserum in the extract of Virginia-type peanuts. The same result was obtained using anti-Ara h 1 mAb (Supporting Information, Fig. S2 C, D). Notably, the acidic cleavage products (spots 55–57) were not detected using both reagents. By contrast, the Ara h 3/4-specific staining on the reprobed blots was fairly similar for both peanut varieties when applying the same exposure time. Figure S1 of the Supporting Information also includes overlays of individual immunoblots with whole protein stain. The relative overrepresentation and the appearance of further Ara h 3/4-related proteins (*e.g.* spots 107, 108; 28–34; 75–76) in the Balinese variety were also confirmed by Western blotting using the anti-Ara h 3/4-specific antiserum (Fig. S2 E, F).

In the case of Ara h 2, we verified the differential abundance by Western blotting using a specific mAb (Fig. 6). With the Ara h 2-specific mAb Pn-2 [27], a major reduction of Ara h 2 in Balinese peanuts was confirmed (Fig. 6B, lower panel). Interestingly, a recent epitope mapping for this antibody revealed that Pn-2 presumably recognizes the sequence EQQFKRELR of Ara h 2. Notably, the mAb displays a significant cross-reactivity to the similar sequence VQQFKRELM of Ara h 6 (unpublished data). Nevertheless, the antibody yielded a more prominent Western blot staining for Ara h 2 than for Ara h 6 (spots 95–97).

4 Discussion

Peanut proteins are a major cause of potentially fatal anaphylactic reactions associated with food allergies. It may therefore be useful to identify peanut variants that are naturally devoid of certain allergenic components in their kernels. To this end, however, the peanut storage proteins need to be analyzed at high resolution since already traces of allergens might elicit severe immune reactions. In order to identify and compare allergens in different peanut extracts, we used a 2-D DIGE approach followed by MS. As an initial proof of principle for the suitability of this technique to

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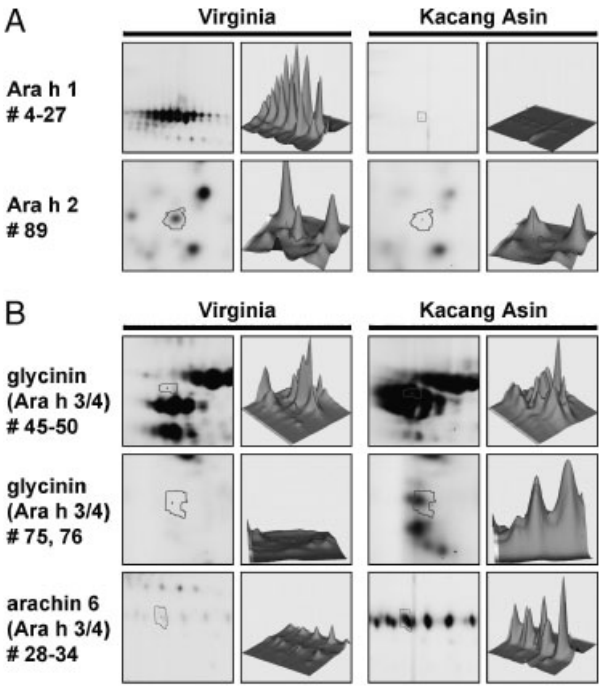


Figure 4. Direct comparison of selected differentially expressed proteins. Magnified gel regions and corresponding 3-D views of individual protein spots with a higher relative abundance in Virginia type (A) or Kacang Asin (B) peanuts.

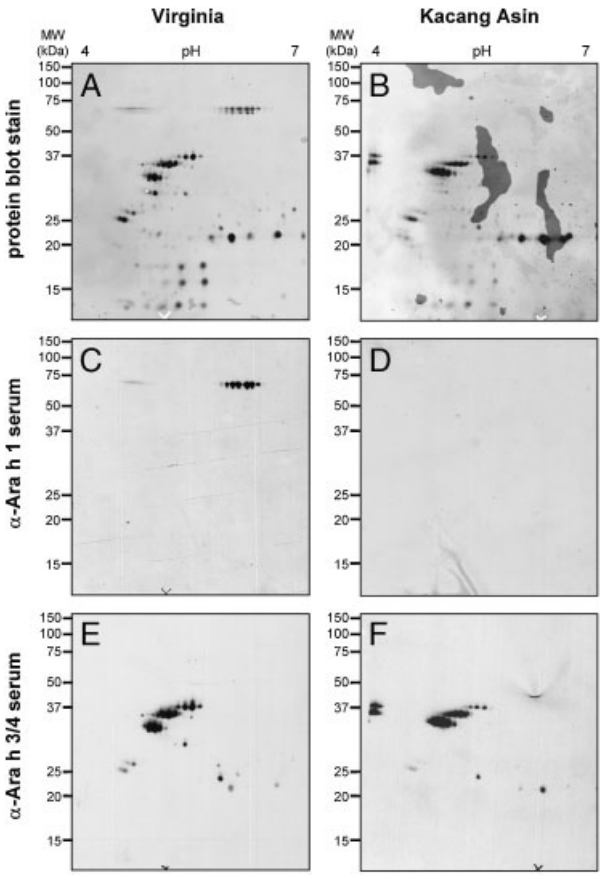


Figure 5. 2-D Western blotting of Virginia type (A, C, E) and Kacang Asin (B, D, F) peanut extracts. Thirty micrograms of total protein were separated (IEF pH 4–7, 10% Tris-glycine gels), transferred onto NC membranes and stained with Sypro Ruby blot stain. Subsequently, the blots were probed with a polyclonal antiserum against Ara h 1 (C, D), stripped, and reprobed with a polyclonal α-Ara h 3/4 antiserum (E, F). The exposure times were equal for both blots.

detect major and minor differences in peanut varieties or purified allergen preparations, we compared basic extracts from Indonesian- and Virginia-type peanut kernels and also individual allergen preparations derived thereof.

As expected from the initial SDS-PAGE (Fig. 1), we detected a major difference in the presence or absence of Ara h 1, which was seen as spot accumulation with a molecular weight of approximately 65 kDa only in extracts of Virginia type but not of Balinese peanuts. The subsequently performed analyses of individual spots by MS covered peptides in the range of amino acids 109–568, whereas no peptides corresponding to the N-terminal end of the protein were found. This is consistent with the observation that Ara h 1 mostly occurs as an N-terminally truncated protein lacking the first 78–84 amino acids due to proteolytic cleavage [39]. However, the short cleavage products representing the fragment from amino acid 85 to 108 of the Ara h 1 protein might not have been detected by our MALDI-TOF analysis due to their relatively high arginine content.

Interestingly, we identified several additional fragments of Ara h 1 by MS+MS/MS. For example, spots 82–84 represent basic fragments of conarachin (synonymously used for Ara h 1) with an apparent molecular mass of 18 kDa and an average p*I* of 9.5. Based on the identified peptides (see Supporting Information), the calculated p*I* of the C-terminal fragment (amino acids 469–662) of conarachin is 9.41. In addition, the acidic fragment (spots 55–57 and 59) represents a larger C-terminal part of conarachin with a molecular weight of 33 kDa and a theoretical p*I* of 5.1. This fragment showed IgE reactivity in immunoblots using patient's sera [40], but was not recognized by the polyclonal or monoclonal anti-Ara h 1 antibodies used in our experiments. Of note, when Marsh *et al.* [40] purified native Ara h 1 using lectin affinity chromatography, they also showed a major band of 67 kDa and a minor band around 33 kDa.

Based on our DIGE and Western blot analyses, the full-length conarachin is completely absent from the Balinese peanut extract, while the acidic and basic fragments seem to be still present (although reduced as compared with extracts from Virginia-type peanuts). As indicated in the Supporting Information Fig. S6, IgE reactivities to peanut extracts obtained after incubation with Tris buffer containing SDS and DTT were detectable in the molecular mass range of Ara h 1. This immunoreactivity, however, was only observed when polyclonal sera were used and was strongly reduced

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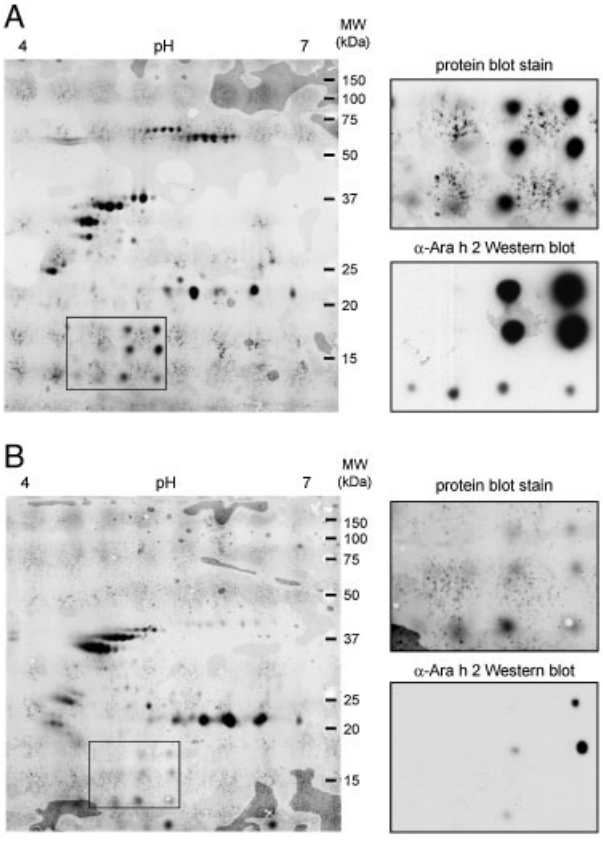


Figure 6. Presence of Ara h 2 in Virginia type (A) and Kacang Asin (B) peanuts. Thirty micrograms of total protein were separated (IEF pH 4–7, 10% Tris-glycine gels), transferred onto NC membranes and stained with Sypro Ruby blot stain. The membranes were probed with a mAb against Ara h 2 (Pn-2, 1/1000). Exposure times are equal for both blots. Rectangles represent the magnified regions for the protein stain and the α-Ara h 2 Western blots shown in the right panels.

when the Indonesian variants were tested in comparison with extracts of Virginia-type peanuts (Supporting Information, Fig. S6).

Along with the lack of the 65 kDa Ara h 1 isoforms, also Ara h 2 was found to be reduced in the basic extracts of Balinese (Indonesian) peanuts. Ara h 1 and Ara h 2 have long been regarded as the most relevant peanut allergens, as they are frequently recognized by sera from patients suffering from peanut allergy [41, 13, 42]. Moreover, a direct comparison of the relevance of Ara h 1, Ara h 2 and Ara h 3 in patients by analyzing IgE responses in Western blotting, histamine release and intra-cutaneous application, suggested that Ara h 2 in fact represents the most important peanut allergen [43, 44]. Ara h 2 has therefore been chosen as a target for genetic manipulation in order to generate allergen-deficient peanuts. Silencing of Ara h 2 and Ara h 6 are accompanied by a clear reduction in IgE binding [23]. In our analyses, fragments of Ara h 2 were also detected in spots 99 and 100. Based on the peptide characteristics, these spots seem to represent the heavy chain of Ara h 2 (Conglutin-7, UniProt No. Q6PSU2). Of particular interest and supporting the idea that the C-terminal part of this fragment ends with amino acid 172, we detected peptides covering the protein up to amino acid 169 in spot 100.

In peanuts, several conglutins are present that are related to so-called 2S albumins. One example is the 15 kDa Ara h 6, which was identified with sequence-coverages of 70% (spot 96) and 73% (spot 97), respectively, in our study. Notably, no peptides corresponding to the first 21 amino acids of the theoretical cDNA-based transcript were identified. This is, however, consistent with findings of Suhr *et al.* [19], who identified the N-terminus (MRRERGRQGDSSS) of natural Ara h 6 only starting at position 22 of the peptide sequence Q647G9 (UniProt). Ara h 6 contains five disulfide bonds and might be proteolytically processed at position 46–47 resulting in two parts spanning amino acids 1–45 and 48–124 that still remain linked by disulfide bonds [45]. As a consequence of the reduction and alkylation, applied during 2-DE, the longer part (48–124, MW of 9.15 kDa, calculated p*I* 5) is represented by spots 101 and 102 where we identified peptides covering amino acids 51–124. The first and smaller part of the protein with an approximate MW of 5.44 kDa was not detected.

Conarachin (Ara h 1) and arachin (Ara h 3/4) constitute the majority (about 87%) of seed storage proteins in peanuts [26]. The subunits of arachin are separated into acidic and basic fragments. We detected four major spot accumulations of Ara h 3/4 isoforms in the acidic part (pH range 4.5–5.5) of the immobilized pH gradient in Virginia-type peanut extracts. Interestingly, we describe two other spot accumulations representing Ara h 3/4 (spots 28–34 and 45–50) only in the Balinese type. One of these additional isoforms of Ara h 3/4 has an apparent molecular mass of 40 kDa and an average p*I* of 6. Six of seven spots of this pattern (28–34) were identified as the N-terminal region of arachin 6, a known isoform of Ara h 3/4. Although the other spot accumulation (45–50) was difficult to discriminate from the acidic parts of Ara h 3/4, which were also present in extracts from Virginia-type peanuts, we were able to separate these spots using a pH 4–7 gradient for IEF. The spots were then identified as the C-terminal fragment of glycinin with a MW of 35 kDa and a p*I* of 5.

Moreover, spots 75 and 76 represent another fragment of glycinin that was only detected in Balinese peanuts. In this case, we only found peptides of the middle part of the protein. Again, the observed p*I* of 4.6 was verified by theoretical calculation based on the identified fragment.

Unfortunately, using the obtained MS data, we cannot separate between glycinin and the recently discovered isoform iso-Ara h 3 [26], which apparently shares 70–85% sequence identity with Ara h 3/4, Ara h 4, Gly1 and a putative peanut trypsin inhibitor, respectively. The nature of the moderate but obvious molecular weight shift of this glycinin in the Balinese peanut is not understood at present. If it is due to post-translational modifications or alternative splicing, this might indicate that a single glycinin

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gene may be processed differently in individual peanut varieties [24].

In conclusion, we not only provided a detailed proteome profile of peanut extracts but also point to the potential of 2-D DIGE analyses for comparing different peanut variants and also allergen preparations. This will be of practical use if the generation of allergen-reduced peanut variants progresses and also for testing the purity and distribution of isoforms in given allergen preparations.

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The authors have declared no conflict of interest.

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PROTEOMICS

Supporting Information for Proteomics

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2-D DIGE analysis of the proteome of extracts from peanut variants reveals striking differences in major allergen contents

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Supplemental informations

Supplemental figures

Figure S1

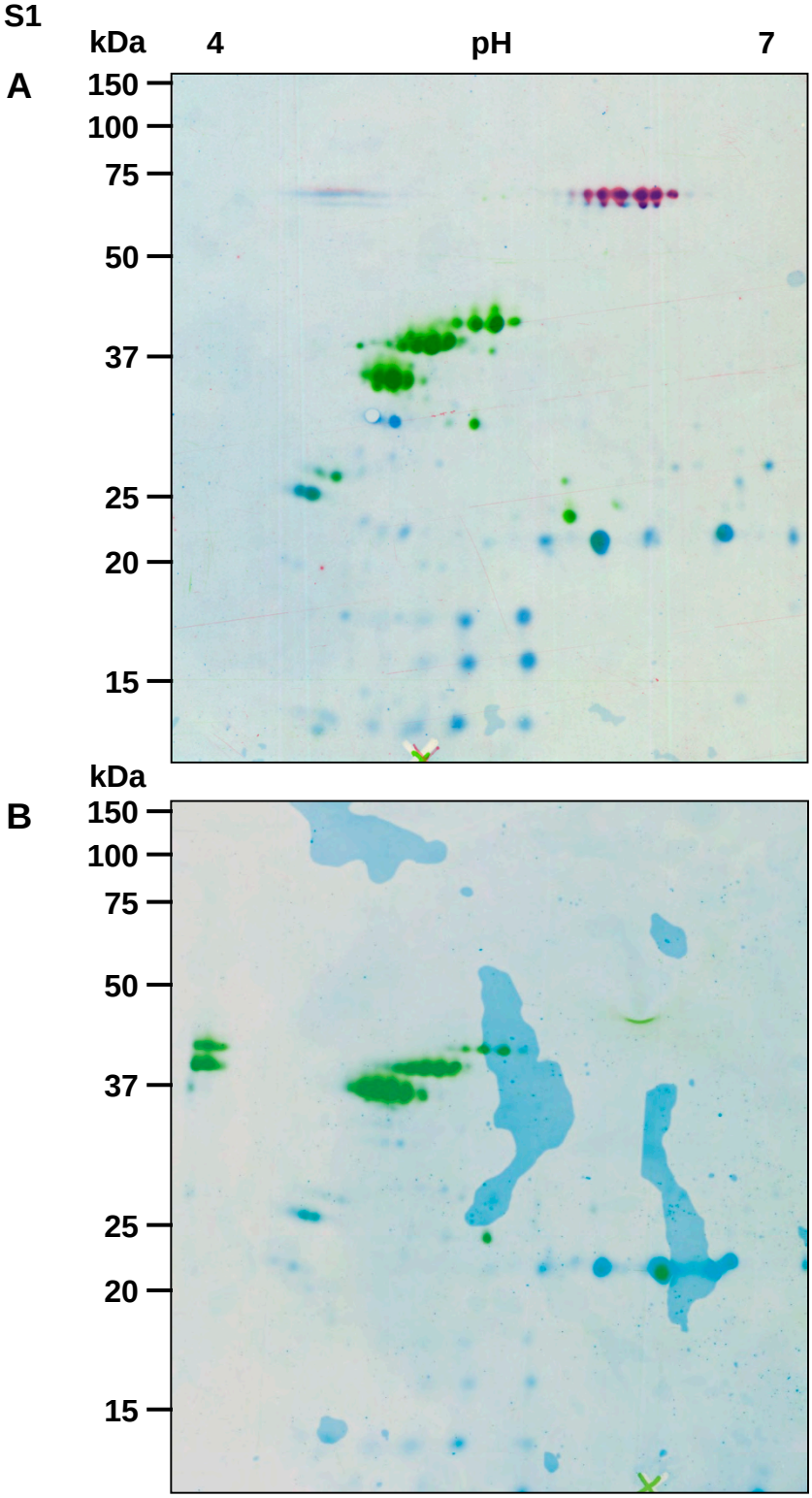


Fig. S1: 2D Western blot of Virginia (A) and Kacang Asin (B) peanut extracts. 30 µg of total protein were separated on pH 4-7 gradients and subsequent SDS-PAGE, transferred to NC membranes and stained with Sypro Ruby blot stain (blue). Both blots were probed with rabbit sera α-Ara h 1 (pink) and reprobed with α-Ara h 3/4 (green) (polyclonal rabbit sera, dilution 1/7500). Single Western blots are displayed in figure 5.

Figure S2

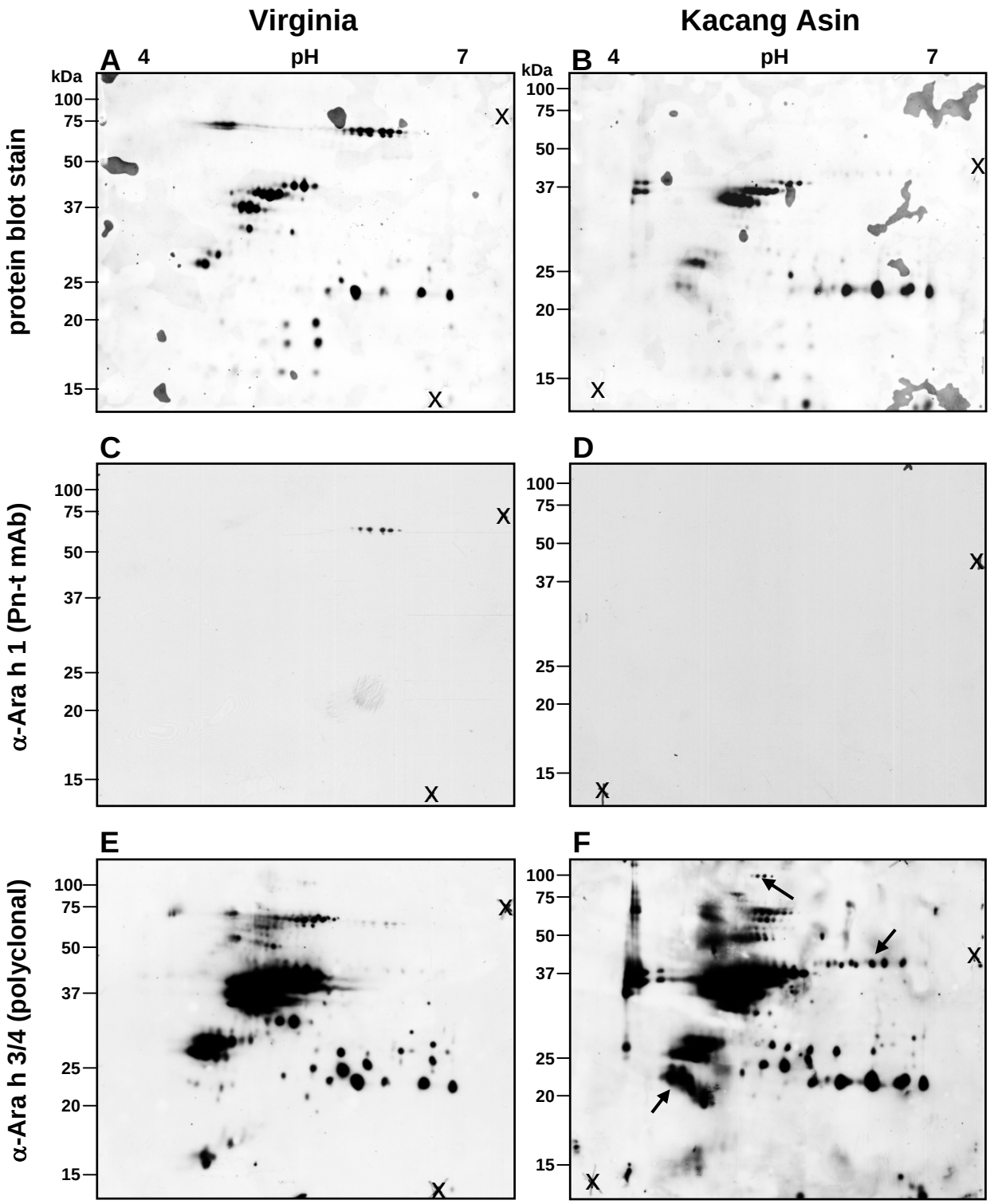


Fig. S2: 2D Western blot of Virginia and Kacang Asin peanut extracts. 40 µg of total protein were separated on pH 4-7 gradients followed by SDS-PAGE, transferred to NC membranes and stained with Sypro Ruby blot stain (**A**, **B**). The blots were probed with α-Ara h 1 mAb (Pn-t, 1/500) (**C**, **D**) and reprobed with α-Ara h 3/4 (rabbit serum, 1/7500) (**E**, **F**). Of note, even after longer exposure (20 min), no α-Ara h 1 signal was detected in extracts of Kacang Asin peanuts. After prolonged exposure, additional specifically stained spots were detected by the α-Ara h 3/4 serum only in the Indonesian variant (arrows). Importantly, no unspecific stainings of Ara h 1, Ara h 2 or Ara h 6 are visible.

Table S1. Experimental design for comparison of different biological samples in DIGE experiments, including dye swap labeling. (see also supplementary figure S3)

gel #	pH range	loading amount	loading type	labeling	
				Cy 5	Cy3
A	3-11NL	100µg	cup	Kacang Asin	Virginia
B	3-11NL	100µg	cup	Kacang Biga	Virginia
C	3-11NL	100µg	cup	Kacang Kulit	Virginia
D	3-11NL	100µg	cup	Virginia	Kacang Asin
E	3-11NL	100µg	cup	Virginia	Kacang Biga
F	3-11NL	100µg	cup	Virginia	Kacang Kulit

Figure S3

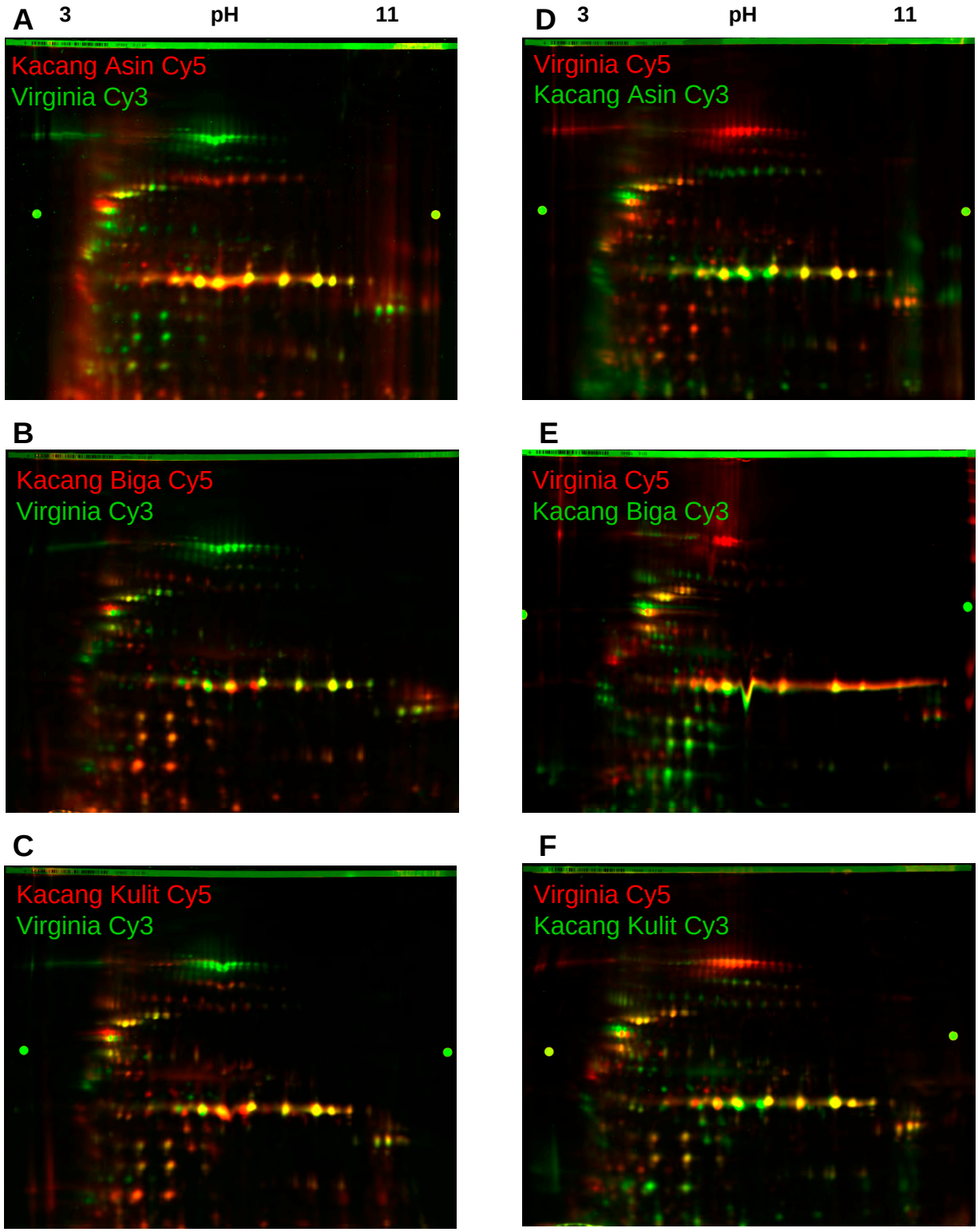


Fig. S3: Biological replicates of 2D-DIGE experiments. The characters A to F correspond to table S1. Three different Indonesian peanut varieties (Asin: **A**, **D**; Biga: **B**, **E**; Kulit: **C**, **F**) were labeled with Cy5 or Cy3, respectively and directly compared to Virginia type peanuts. In all three varieties, Ara h 1 is strongly reduced (Kulit) or even absent (Asin, Biga). Experiments were performed with dye swap to exclude preferential Cy-dye binding to individual proteins.

Table S2. Experimental design for different technical replicates in independent experiments, including dye swap labeling, different loading methods and amounts. (see also supplementary figures S4 and S5.)

exp. #	pH range	loading amount	loading type	labeling	
				Cy 5	Cy3
1	3-11NL	150 µg	cup	Virginia	Kacang Asin
2	3-11NL	100 µg	cup	Virginia	Kacang Asin
3	3-11NL	60 µg	cup	Kacang Asin	Virginia
4	3-11NL	700 µg	rehydration	Virginia	Kacang Asin
5	3-11NL	600 µg	rehydration	Virginia	Kacang Asin
6	4-7L	100 µg	cup	Kacang Asin	Virginia
7	4-7L	60 µg	cup	Virginia	Kacang Asin
8	3-11NL	100 µg	cup	Virginia	Virginia oil roasted

Figure S4

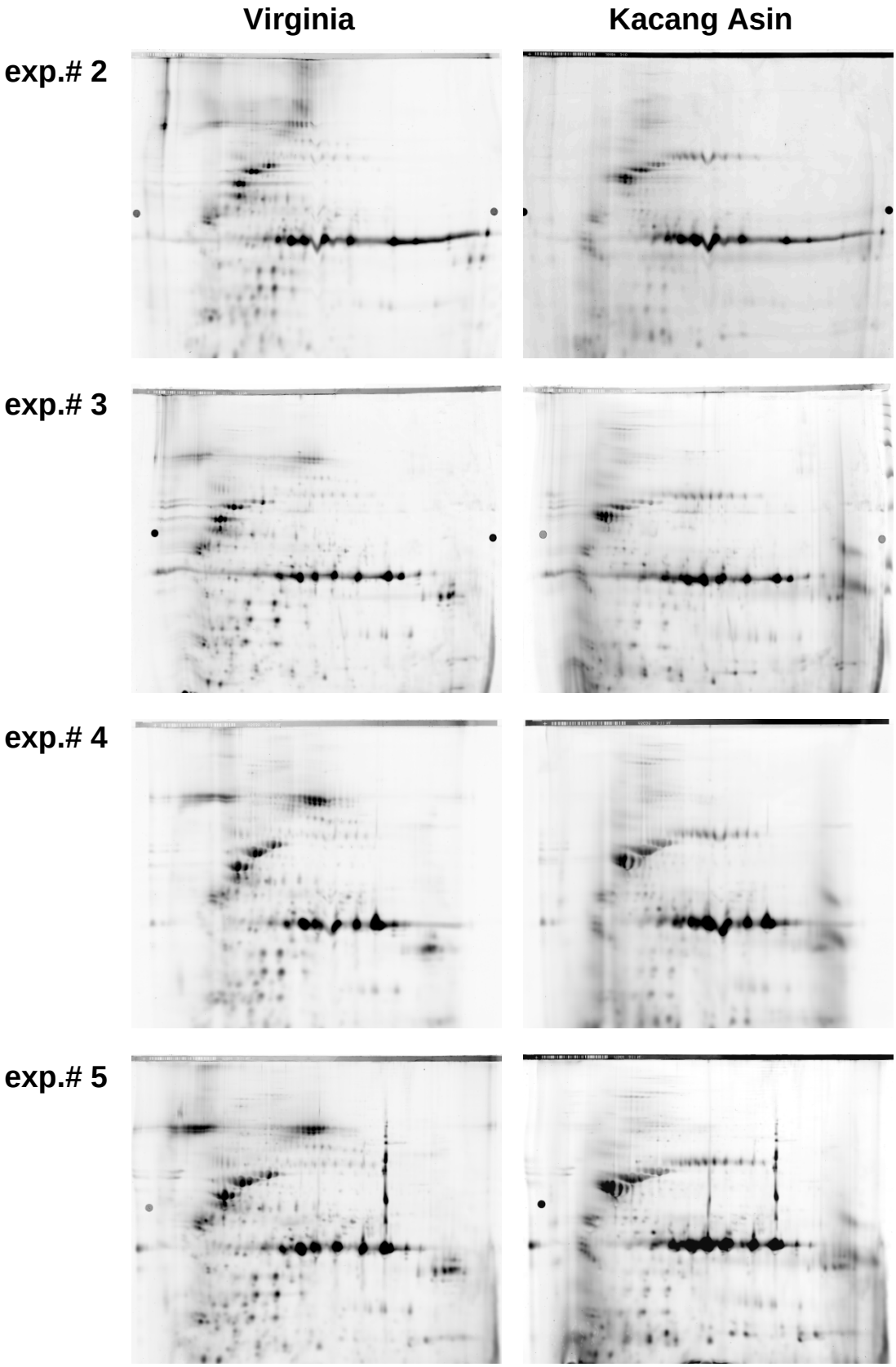


Fig. S4: Technical replicates of 2D-DIGE experiments. Experiment numbers refer to table S2. In all independent experiments, no Ara h 1 is visible in Kacang Asin extracts using pH 3-11NL IPG strips followed by SDS-PAGE. Please note the experimental variations including cup (# **2**, **3**) or rehydration loading (# **4**, **5**)

Figure S5

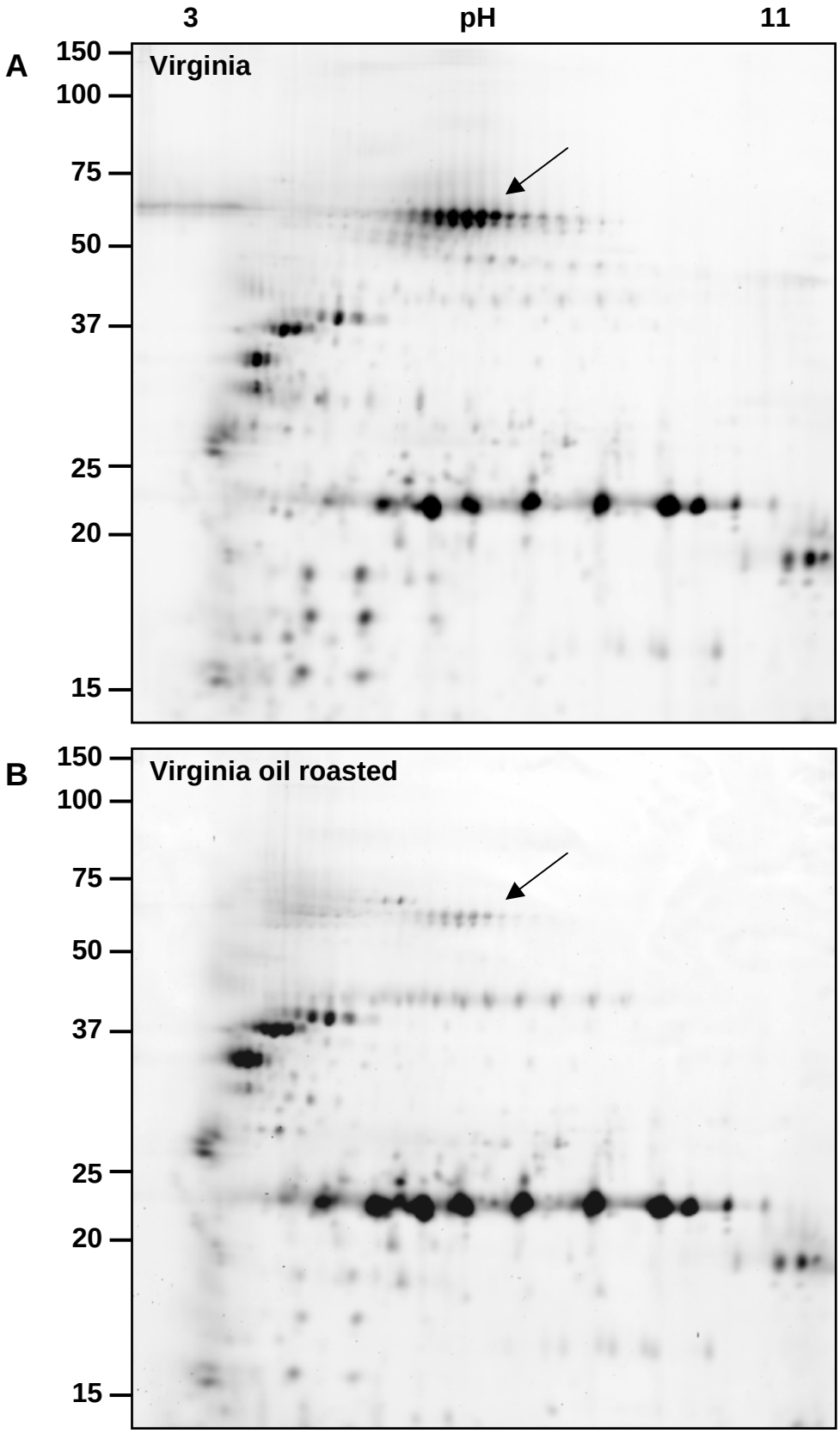


Fig. S5: Influence of oil roasting on the protein profile. Extracts of roasted (**A**) and fried (oil roasted, **B**) Virginia type peanuts (table S2, exp.# **8**) were separated on pH3-11NL IPG strips followed by SDS-PAGE. As expected, oil roasting leads to a selective reduction of various proteins including Ara h 1 (arrow). Nevertheless, Ara h 1 is still detectable even under these conditions.

Figure S6

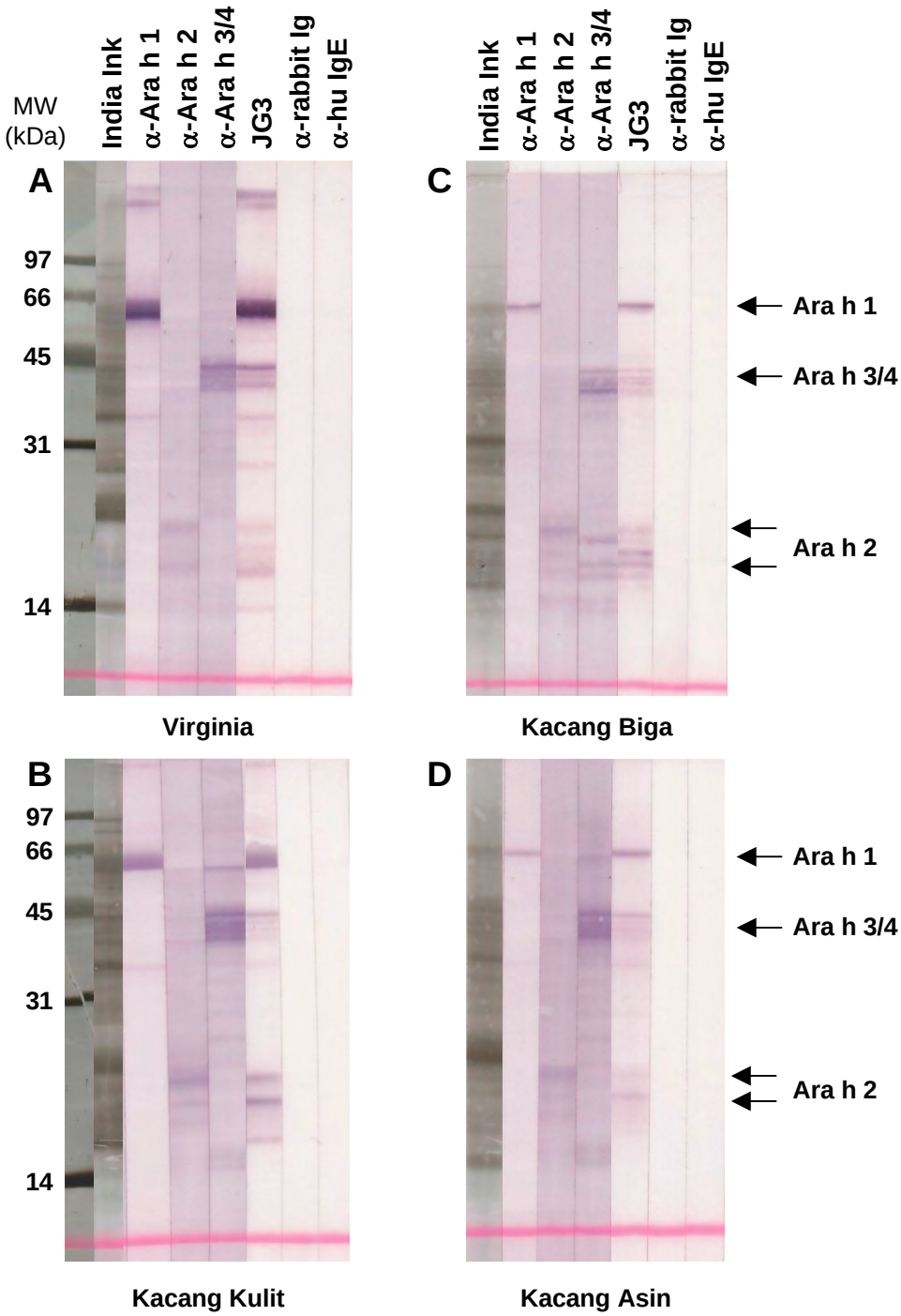


Fig. S6: Western blots of total peanut lysates. Kernels of Virgina type (**A**) and Indonesian peanuts (Kacang Kulit (**B**), Kacang Biga (**C**) and Kacang Asin (**D**) were frozen in liquid nitrogen and grinded. Peanut flour was extracted overnight at 4°C in 50 mM Tris, pH 8 with 1% SDS and 0.2% DTT. After centrifugation, the supernatants were filtered and equal amounts of protein were separated by SDS-PAGE (12% gel) and blotted to NC membranes. The membranes were cut and individual lanes were incubated with rabbit sera against Ara h 1, Ara h 2 and Ara h 3/4, the serum of an allergic patient (JG3) or respective AP-coupled 2nd step antibodies as control. The polyclonal α-Ara h 1 rabbit serum and the patient's serum show a very prominent immunoreactivity in the range of 65 kDa (presumably Ara h 1) in Virginia type peanuts that is much less apparent in Kacang Kulit and markedly reduced in Kacang Biga and Kacang Asin lysates.

Data set S1. Additional protein identification data.

Spot 1

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:35:15 GMT
Top Score : 296 for gi|46560478, conarachin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	296	conarachin [Arachis hypogaea]
2.	gi|620025	70639	289	Ara h I
3.	gi|1168390	70639	289	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	259	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	259	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	259	Ara h I
7.	gi|46560476	48122	182	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	77	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	58	conarachin [Arachis hypogaea]
10.	gi|62177652	10056	14	resistance protein PRG [Arachis hypogaea]

Results List

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conarachin [Arachis hypogaea]

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855.5306	854.5233	854.5086	0.0147	140	146	1	KIRPEGR
896.4416	895.4343	895.4260	0.0083	272	278	0	HDNQNLR
1005.5374	1004.5301	1004.5264	0.0037	132	139	0	RPSHQQPR
1019.4708	1018.4635	1018.4468	0.0167	118	124	1	EREEDWR
1061.5857	1060.5784	1060.5777	0.0007	189	196	1	VLQRFDQR
1115.5367	1114.5294	1114.5155	0.0139	120	127	1	EEDWRQPR
1128.6312	1127.6239	1127.6298	-0.0059	453	463	0	GTGNLELVAVR

1141.5520	1140.5447	1140.5352	0.0095	166 - 174	0	NNPFYFPSR
1184.5956	1183.5883	1183.5846	0.0037	199 - 207	0	QFQNLQNHR
1258.6229	1257.6156	1257.6101	0.0055	249 - 259	0	SFNLDEGHALR
1287.5997	1286.5924	1286.5891	0.0033	302 - 312	0	DQSSYLQGFSR
1297.6433	1296.6360	1296.6363	-0.0003	166 - 175	1	NNPFYFPSRR
1320.5875	1319.5802	1319.5741	0.0061	394 - 405	0	DGEPDLSNNFGR
1343.6753	1342.6680	1342.6703	-0.0023	432 - 443	0	EGALMLPHFNSK
1376.6713	1375.6640	1375.6619	0.0021	555 - 567	0	DLAFPGSGEQVEK
1379.7651	1378.7578	1378.7608	-0.0030	260 - 271	0	IPSGFISYILNR
1386.7150	1385.7077	1385.7051	0.0026	248 - 259	1	KSFNLDEGHALR
1399.7063	1398.6990	1398.7116	-0.0126	197 - 207	1	SKQFQNLQNHR
1560.6849	1559.6776	1559.6851	-0.0075	147 - 160	0	EGEQEWGTPGSEVR
1572.7430	1571.7357	1571.7426	-0.0069	329 - 342	0	VLLEENAGGEQEER
1586.7590	1585.7517	1585.7583	-0.0066	380 - 393	0	GSEEEDITNPINLR
1591.7788	1590.7715	1590.7763	-0.0048	128 - 139	1	EDWRRPSHQQPR
1691.0171	1690.0098	1690.0141	-0.0042	208 - 222	0	IVQIEARPNTLVLPK
1714.8562	1713.8489	1713.8533	-0.0043	379 - 393	1	KGSEEEDITNPINLR
1728.8522	1727.8449	1727.8437	0.0012	328 - 342	1	RVLLEENAGGEQEER
1738.8383	1737.8310	1737.8321	-0.0011	313 - 327	0	NTLEAAFNAEFNEIR
1817.9558	1816.9485	1816.9570	-0.0085	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9404	1893.9331	1893.9332	-0.0001	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2136	2081.2063	2081.2030	0.0034	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0754	2226.0681	2226.0415	0.0266	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0547	2242.0474	2242.0364	0.0110	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1572	2256.1499	2256.1763	-0.0263	260 - 278	1	IPSGFISYILNRHDNQNLR
2281.8589	2280.8516	2280.8414	0.0103	473 - 490	0	EQEWEEEEEDEEEEGSNR
2525.2075	2524.2002	2524.2420	-0.0417	279 - 301	1	VAKISMPVNTPGQFEDFFPASSR
2619.3550	2618.3477	2618.3604	-0.0127	249 - 271	1	SFNLDEGHALRIPSGFISYILNR
2747.4224	2746.4151	2746.4110	0.0042	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

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Ara h I

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855.5306	854.5233	854.5086	0.0147	140	146	1	KIRPEGR
896.4416	895.4343	895.4260	0.0083	272	278	0	HDNQNLR
1005.5374	1004.5301	1004.5264	0.0037	132	139	0	RPSHQQPR
1019.4708	1018.4635	1018.4468	0.0167	118	124	1	EREEDWR
1061.5857	1060.5784	1060.5777	0.0007	189	196	1	VLQRFDQR
1115.5367	1114.5294	1114.5155	0.0139	120	127	1	EEDWRQPR
1128.6312	1127.6239	1127.6298	-0.0059	453	463	0	GTGNLELVAVR
1141.5520	1140.5447	1140.5352	0.0095	166	174	0	NNPFYFPSR
1184.5956	1183.5883	1183.5846	0.0037	199	207	0	QFQNLQNHR
1258.6229	1257.6156	1257.6101	0.0055	249	259	0	SFNLDEGHALR
1287.5997	1286.5924	1286.5891	0.0033	302	312	0	DQSSYLQGFSR
1297.6433	1296.6360	1296.6363	-0.0003	166	175	1	NNPFYFPSRR
1320.5875	1319.5802	1319.5741	0.0061	394	405	0	DGEPDLSNNFGR
1343.6753	1342.6680	1342.6703	-0.0023	432	443	0	EGALMLPHFNSK
1376.6713	1375.6640	1375.6619	0.0021	555	567	0	DLAFPGSGEQVEK
1379.7651	1378.7578	1378.7608	-0.0030	260	271	0	IPSGFISYILNR
1386.7150	1385.7077	1385.7051	0.0026	248	259	1	KSFNLDEGHALR
1399.7063	1398.6990	1398.7116	-0.0126	197	207	1	SKQFQNLQNHR
1560.6849	1559.6776	1559.6851	-0.0075	147	160	0	EGEQEWGTPGSEVR
1572.7430	1571.7357	1571.7426	-0.0069	329	342	0	VLLEENAGGEQEER
1586.7590	1585.7517	1585.7583	-0.0066	380	393	0	GSEEEDITNPINLR
1591.7788	1590.7715	1590.7763	-0.0048	128	139	1	EDWRRPSHQQPR
1691.0171	1690.0098	1690.0141	-0.0042	208	222	0	IVQIEARPNTLVLPK
1714.8562	1713.8489	1713.8533	-0.0043	379	393	1	KGSEEEDITNPINLR
1728.8522	1727.8449	1727.8437	0.0012	328	342	1	RVLLEENAGGEQEER
1738.8383	1737.8310	1737.8321	-0.0011	313	327	0	NTLEAAFNAEFNEIR
1817.9558	1816.9485	1816.9570	-0.0085	536	551	1	IFLAGDKDNVIDQIEK
1894.9404	1893.9331	1893.9332	-0.0001	313	328	1	NTLEAAFNAEFNEIRR
2082.2136	2081.2063	2081.2030	0.0034	444	463	1	AMVIVVVNKGTGNLELVAVR
2227.0754	2226.0681	2226.0415	0.0266	282	301	0	ISMPVNTPGQFEDFFPASSR
2243.0547	2242.0474	2242.0364	0.0110	282	301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1572	2256.1499	2256.1763	-0.0263	260	278	1	IPSGFISYILNRHDNQNLR
2281.8589	2280.8516	2280.8414	0.0103	473	490	0	EQEWEEEEEDEEEEGSNR
2525.2075	2524.2002	2524.2420	-0.0417	279	301	1	VAKISMPVNTPGQFEDFFPASSR
2619.3550	2618.3477	2618.3604	-0.0127	249	271	1	SFNLDEGHALRIPSGFISYILNR
2747.4224	2746.4151	2746.4110	0.0042	223	248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 805.4622, 808.4086, 812.4315, 813.4330, 824.4281, 825.4193, 826.4116, 828.4656, 848.4346, 861.0914,

881.2838, 959.4822, 975.4969, 1021.5086, 1111.5630, 1144.5332, 1167.5745, 1304.6061, 1330.7548, 1424.7096, 1427.7218, 1440.7019, 1496.7299, 1512.7223, 1568.7040, 1590.7579, 1643.7795, 1685.8076, 1731.8743, 1771.8760, 1813.4187, 1830.8500, 1899.9332, 2051.0215, 2070.0386, 2116.0962, 2129.1279, 2145.1472, 2171.9956, 2185.0378, 2273.1658, 2295.1462, 2311.1328, 2333.1082, 2456.2361, 2514.3181, 2553.2390, 2568.2795, 2612.2229, 2662.4358, 2748.4390, 2751.4229, 2792.4922, 2974.3398, 2990.3176, 3016.4280, 3136.5017, 3211.5313, 3300.7397, 3317.7559, 3441.7615, 3451.5989

3. gi|1168390 **Mass:** 70639 **Score:** 289 **Expect:** 1.1e-026 **Queries matched:** 37

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4500	815.4427	815.4249	0.0178	464	469	1	KEQQQR
855.5306	854.5233	854.5086	0.0147	140	146	1	KIRPEGR
896.4416	895.4343	895.4260	0.0083	272	278	0	HDNQNLR
1005.5374	1004.5301	1004.5264	0.0037	132	139	0	RPSHQQPR
1019.4708	1018.4635	1018.4468	0.0167	118	124	1	EREEDWR
1061.5857	1060.5784	1060.5777	0.0007	189	196	1	VLQRFDQR
1115.5367	1114.5294	1114.5155	0.0139	120	127	1	EEDWRQPR
1128.6312	1127.6239	1127.6298	-0.0059	453	463	0	GTGNLELVAVR
1141.5520	1140.5447	1140.5352	0.0095	166	174	0	NNPFYFPSR
1184.5956	1183.5883	1183.5846	0.0037	199	207	0	QFQNLQNHR
1258.6229	1257.6156	1257.6101	0.0055	249	259	0	SFNLDEGHALR
1287.5997	1286.5924	1286.5891	0.0033	302	312	0	DQSSYLQGFSR
1297.6433	1296.6360	1296.6363	-0.0003	166	175	1	NNPFYFPSRR
1320.5875	1319.5802	1319.5741	0.0061	394	405	0	DGEPDLSNNFGR
1343.6753	1342.6680	1342.6703	-0.0023	432	443	0	EGALMLPHFNSK
1376.6713	1375.6640	1375.6619	0.0021	555	567	0	DLAFPGSGEQVEK
1379.7651	1378.7578	1378.7608	-0.0030	260	271	0	IPSGFISYILNR
1386.7150	1385.7077	1385.7051	0.0026	248	259	1	KSFNLDEGHALR
1399.7063	1398.6990	1398.7116	-0.0126	197	207	1	SKQFQNLQNHR
1560.6849	1559.6776	1559.6851	-0.0075	147	160	0	EGEQEWGTPGSEVR
1572.7430	1571.7357	1571.7426	-0.0069	329	342	0	VLLEENAGGEQEER
1586.7590	1585.7517	1585.7583	-0.0066	380	393	0	GSEEEDITNPINLR
1591.7788	1590.7715	1590.7763	-0.0048	128	139	1	EDWRRPSHQQPR
1691.0171	1690.0098	1690.0141	-0.0042	208	222	0	IVQIEARPNTLVLPK
1714.8562	1713.8489	1713.8533	-0.0043	379	393	1	KGSEEEDITNPINLR
1728.8522	1727.8449	1727.8437	0.0012	328	342	1	RVLLEENAGGEQEER
1738.8383	1737.8310	1737.8321	-0.0011	313	327	0	NTLEAAFNAEFNEIR
1817.9558	1816.9485	1816.9570	-0.0085	536	551	1	IFLAGDKDNVIDQIEK
1894.9404	1893.9331	1893.9332	-0.0001	313	328	1	NTLEAAFNAEFNEIRR
2082.2136	2081.2063	2081.2030	0.0034	444	463	1	AMVIVVVNKGTGNLELVAVR

2227.0754	2226.0681	2226.0415	0.0266	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0547	2242.0474	2242.0364	0.0110	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1572	2256.1499	2256.1763	-0.0263	260 - 278	1	IPSGFISYILNRHDNQNLR
2281.8589	2280.8516	2280.8414	0.0103	473 - 490	0	EQEWEEEEEDEEEEGSNR
2525.2075	2524.2002	2524.2420	-0.0417	279 - 301	1	VAKISMPVNTPGQFEDFFPASSR
2619.3550	2618.3477	2618.3604	-0.0127	249 - 271	1	SFNLDEGHALRIPSGFISYILNR
2747.4224	2746.4151	2746.4110	0.0042	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 805.4622, 808.4086, 812.4315, 813.4330, 824.4281, 825.4193, 826.4116, 828.4656, 848.4346, 861.0914, 881.2838, 959.4822, 975.4969, 1021.5086, 1111.5630, 1144.5332, 1167.5745, 1304.6061, 1330.7548, 1424.7096, 1427.7218, 1440.7019, 1496.7299, 1512.7223, 1568.7040, 1590.7579, 1643.7795, 1685.8076, 1731.8743, 1771.8760, 1813.4187, 1830.8500, 1899.9332, 2051.0215, 2070.0386, 2116.0962, 2129.1279, 2145.1472, 2171.9956, 2185.0378, 2273.1658, 2295.1462, 2311.1328, 2333.1082, 2456.2361, 2514.3181, 2553.2390, 2568.2795, 2612.2229, 2662.4358, 2748.4390, 2751.4229, 2792.4922, 2974.3398, 2990.3176, 3016.4280, 3136.5017, 3211.5313, 3300.7397, 3317.7559, 3441.7615, 3451.5989

4. gi|16612200 **Mass:** 71701 **Score:** 259 **Expect:** 1.1e-023 **Queries matched:** 35

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.4086	807.4013	807.3987	0.0026	199 - 204		1	FDQRSR
816.4500	815.4427	815.4249	0.0178	472 - 477		1	KEQQQR
855.5306	854.5233	854.5086	0.0147	146 - 152		1	KIRPEGR
896.4416	895.4343	895.4260	0.0083	278 - 284		0	HDNQNLR
1005.5374	1004.5301	1004.5264	0.0037	138 - 145		0	RPSHQQPR
1019.4708	1018.4635	1018.4468	0.0167	124 - 130		1	EREEDWR
1061.5857	1060.5784	1060.5777	0.0007	195 - 202		1	VLQRFDQR
1115.5367	1114.5294	1114.5155	0.0139	126 - 133		1	EEDWRQPR
1128.6312	1127.6239	1127.6298	-0.0059	461 - 471		0	GTGNLELVAVR
1141.5520	1140.5447	1140.5352	0.0095	172 - 180		0	NNPFYFPSR
1184.5956	1183.5883	1183.5846	0.0037	205 - 213		0	QFQNLQNHR
1258.6229	1257.6156	1257.6101	0.0055	255 - 265		0	SFNLDEGHALR
1287.5997	1286.5924	1286.5891	0.0033	308 - 318		0	DQSSYLQGFSR
1297.6433	1296.6360	1296.6363	-0.0003	172 - 181		1	NNPFYFPSRR
1343.6753	1342.6680	1342.6703	-0.0023	440 - 451		0	EGALMLPHFNSK
1376.6713	1375.6640	1375.6619	0.0021	560 - 572		0	DLAFPGSGEQVEK
1379.7651	1378.7578	1378.7608	-0.0030	266 - 277		0	IPSGFISYILNR
1386.7150	1385.7077	1385.7051	0.0026	254 - 265		1	KSFNLDEGHALR
1427.7218	1426.7145	1426.7177	-0.0032	203 - 213		1	SRQFQNLQNHR
1568.7040	1567.6967	1567.7015	-0.0047	153 - 166		0	EGEQEWGTPGSHVR
1572.7430	1571.7357	1571.7426	-0.0069	335 - 348		0	VLLEENAGGEQEER

1591.7788	1590.7715	1590.7763	-0.0048	134 - 145	1	EDWRRPSHQQPR
1643.7795	1642.7722	1642.7798	-0.0075	387 - 401	0	GSEEEGDITNPINLR
1728.8522	1727.8449	1727.8437	0.0012	334 - 348	1	RVLLEENAGGEQEER
1738.8383	1737.8310	1737.8321	-0.0011	319 - 333	0	NTLEAAFNAEFNEIR
1771.8760	1770.8687	1770.8747	-0.0060	386 - 401	1	KGSEEEGDITNPINLR
1817.9558	1816.9485	1816.9570	-0.0085	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9404	1893.9331	1893.9332	-0.0001	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2136	2081.2063	2081.2030	0.0034	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0754	2226.0681	2226.0415	0.0266	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0547	2242.0474	2242.0364	0.0110	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1572	2256.1499	2256.1763	-0.0263	266 - 284	1	IPSGFISYILNRHDNQNLR
2525.2075	2524.2002	2524.2420	-0.0417	285 - 307	1	VAKISMPVNTPGQFEDFFPASSR
2619.3550	2618.3477	2618.3604	-0.0127	255 - 277	1	SFNLDEGHALRIPSGFISYILNR
2747.4224	2746.4151	2746.4110	0.0042	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 805.4622, 812.4315, 813.4330, 824.4281, 825.4193, 826.4116, 828.4656, 848.4346, 861.0914, 881.2838, 959.4822, 975.4969, 1021.5086, 1111.5630, 1144.5332, 1167.5745, 1304.6061, 1320.5875, 1330.7548, 1399.7063, 1424.7096, 1440.7019, 1496.7299, 1512.7223, 1560.6849, 1586.7590, 1590.7579, 1685.8076, 1691.0171, 1714.8562, 1731.8743, 1813.4187, 1830.8500, 1899.9332, 2051.0215, 2070.0386, 2116.0962, 2129.1279, 2145.1472, 2171.9956, 2185.0378, 2273.1658, 2281.8589, 2295.1462, 2311.1328, 2333.1082, 2456.2361, 2514.3181, 2553.2390, 2568.2795, 2612.2229, 2662.4358, 2748.4390, 2751.4229, 2792.4922, 2974.3398, 2990.3176, 3016.4280, 3136.5017, 3211.5313, 3300.7397, 3317.7559, 3441.7615, 3451.5989

5. gi|1168391 **Mass:** 71701 **Score:** 259 **Expect:** 1.1e-023 **Queries matched:** 35

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.4086	807.4013	807.3987	0.0026	199 - 204		1	FDQRSR
816.4500	815.4427	815.4249	0.0178	472 - 477		1	KEQQQR
855.5306	854.5233	854.5086	0.0147	146 - 152		1	KIRPEGR
896.4416	895.4343	895.4260	0.0083	278 - 284		0	HDNQNLR
1005.5374	1004.5301	1004.5264	0.0037	138 - 145		0	RPSHQQPR
1019.4708	1018.4635	1018.4468	0.0167	124 - 130		1	EREEDWR
1061.5857	1060.5784	1060.5777	0.0007	195 - 202		1	VLQRFDQR
1115.5367	1114.5294	1114.5155	0.0139	126 - 133		1	EEDWRQPR
1128.6312	1127.6239	1127.6298	-0.0059	461 - 471		0	GTGNLELVAVR
1141.5520	1140.5447	1140.5352	0.0095	172 - 180		0	NNPFYFPSR
1184.5956	1183.5883	1183.5846	0.0037	205 - 213		0	QFQNLQNHR
1258.6229	1257.6156	1257.6101	0.0055	255 - 265		0	SFNLDEGHALR
1287.5997	1286.5924	1286.5891	0.0033	308 - 318		0	DQSSYLQGFSR
1297.6433	1296.6360	1296.6363	-0.0003	172 - 181		1	NNPFYFPSRR

1343.6753	1342.6680	1342.6703	-0.0023	440 - 451	0	EGALMLPHFNSK
1376.6713	1375.6640	1375.6619	0.0021	560 - 572	0	DLAFPGSGEQVEK
1379.7651	1378.7578	1378.7608	-0.0030	266 - 277	0	IPSGFISYILNR
1386.7150	1385.7077	1385.7051	0.0026	254 - 265	1	KSFNLDEGHALR
1427.7218	1426.7145	1426.7177	-0.0032	203 - 213	1	SRQFQNLQNHR
1568.7040	1567.6967	1567.7015	-0.0047	153 - 166	0	EGEQEWGTPGSHVR
1572.7430	1571.7357	1571.7426	-0.0069	335 - 348	0	VLLEENAGGEQEER
1591.7788	1590.7715	1590.7763	-0.0048	134 - 145	1	EDWRRPSHQQPR
1643.7795	1642.7722	1642.7798	-0.0075	387 - 401	0	GSEEEGDITNPINLR
1728.8522	1727.8449	1727.8437	0.0012	334 - 348	1	RVLLEENAGGEQEER
1738.8383	1737.8310	1737.8321	-0.0011	319 - 333	0	NTLEAAFNAEFNEIR
1771.8760	1770.8687	1770.8747	-0.0060	386 - 401	1	KGSEEEGDITNPINLR
1817.9558	1816.9485	1816.9570	-0.0085	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9404	1893.9331	1893.9332	-0.0001	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2136	2081.2063	2081.2030	0.0034	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0754	2226.0681	2226.0415	0.0266	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0547	2242.0474	2242.0364	0.0110	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1572	2256.1499	2256.1763	-0.0263	266 - 284	1	IPSGFISYILNRHDNQNLR
2525.2075	2524.2002	2524.2420	-0.0417	285 - 307	1	VAKISMPVNTPGQFEDFFPASSR
2619.3550	2618.3477	2618.3604	-0.0127	255 - 277	1	SFNLDEGHALRIPSGFISYILNR
2747.4224	2746.4151	2746.4110	0.0042	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 805.4622, 812.4315, 813.4330, 824.4281, 825.4193, 826.4116, 828.4656, 848.4346, 861.0914, 881.2838, 959.4822, 975.4969, 1021.5086, 1111.5630, 1144.5332, 1167.5745, 1304.6061, 1320.5875, 1330.7548, 1399.7063, 1424.7096, 1440.7019, 1496.7299, 1512.7223, 1560.6849, 1586.7590, 1590.7579, 1685.8076, 1691.0171, 1714.8562, 1731.8743, 1813.4187, 1830.8500, 1899.9332, 2051.0215, 2070.0386, 2116.0962, 2129.1279, 2145.1472, 2171.9956, 2185.0378, 2273.1658, 2281.8589, 2295.1462, 2311.1328, 2333.1082, 2456.2361, 2514.3181, 2553.2390, 2568.2795, 2612.2229, 2662.4358, 2748.4390, 2751.4229, 2792.4922, 2974.3398, 2990.3176, 3016.4280, 3136.5017, 3211.5313, 3300.7397, 3317.7559, 3441.7615, 3451.5989

6. gi|602436 **Mass:** 71701 **Score:** 259 **Expect:** 1.1e-023 **Queries matched:** 35

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
808.4086	807.4013	807.3987	0.0026	199 - 204	1	FDQRSR
816.4500	815.4427	815.4249	0.0178	472 - 477	1	KEQQQR
855.5306	854.5233	854.5086	0.0147	146 - 152	1	KIRPEGR
896.4416	895.4343	895.4260	0.0083	278 - 284	0	HDNQNLR
1005.5374	1004.5301	1004.5264	0.0037	138 - 145	0	RPSHQQPR
1019.4708	1018.4635	1018.4468	0.0167	124 - 130	1	EREEDWR
1061.5857	1060.5784	1060.5777	0.0007	195 - 202	1	VLQRFDQR

1115.5367	1114.5294	1114.5155	0.0139	126 - 133	1	EEDWRQPR
1128.6312	1127.6239	1127.6298	-0.0059	461 - 471	0	GTGNLELVAVR
1141.5520	1140.5447	1140.5352	0.0095	172 - 180	0	NNPFYFPSR
1184.5956	1183.5883	1183.5846	0.0037	205 - 213	0	QFQNLQNHR
1258.6229	1257.6156	1257.6101	0.0055	255 - 265	0	SFNLDEGHALR
1287.5997	1286.5924	1286.5891	0.0033	308 - 318	0	DQSSYLQGFSR
1297.6433	1296.6360	1296.6363	-0.0003	172 - 181	1	NNPFYFPSRR
1343.6753	1342.6680	1342.6703	-0.0023	440 - 451	0	EGALMLPHFNSK
1376.6713	1375.6640	1375.6619	0.0021	560 - 572	0	DLAFPGSGEQVEK
1379.7651	1378.7578	1378.7608	-0.0030	266 - 277	0	IPSGFISYILNR
1386.7150	1385.7077	1385.7051	0.0026	254 - 265	1	KSFNLDEGHALR
1427.7218	1426.7145	1426.7177	-0.0032	203 - 213	1	SRQFQNLQNHR
1568.7040	1567.6967	1567.7015	-0.0047	153 - 166	0	EGEQEWGTPGSHVR
1572.7430	1571.7357	1571.7426	-0.0069	335 - 348	0	VLLEENAGGEQEER
1591.7788	1590.7715	1590.7763	-0.0048	134 - 145	1	EDWRRPSHQQPR
1643.7795	1642.7722	1642.7798	-0.0075	387 - 401	0	GSEEEGDITNPINLR
1728.8522	1727.8449	1727.8437	0.0012	334 - 348	1	RVLLEENAGGEQEER
1738.8383	1737.8310	1737.8321	-0.0011	319 - 333	0	NTLEAAFNAEFNEIR
1771.8760	1770.8687	1770.8747	-0.0060	386 - 401	1	KGSEEEGDITNPINLR
1817.9558	1816.9485	1816.9570	-0.0085	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9404	1893.9331	1893.9332	-0.0001	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2136	2081.2063	2081.2030	0.0034	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0754	2226.0681	2226.0415	0.0266	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0547	2242.0474	2242.0364	0.0110	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1572	2256.1499	2256.1763	-0.0263	266 - 284	1	IPSGFISYILNRHDNQNLR
2525.2075	2524.2002	2524.2420	-0.0417	285 - 307	1	VAKISMPVNTPGQFEDFFPASSR
2619.3550	2618.3477	2618.3604	-0.0127	255 - 277	1	SFNLDEGHALRIPSGFISYILNR
2747.4224	2746.4151	2746.4110	0.0042	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 805.4622, 812.4315, 813.4330, 824.4281, 825.4193, 826.4116, 828.4656, 848.4346, 861.0914, 881.2838, 959.4822, 975.4969, 1021.5086, 1111.5630, 1144.5332, 1167.5745, 1304.6061, 1320.5875, 1330.7548, 1399.7063, 1424.7096, 1440.7019, 1496.7299, 1512.7223, 1560.6849, 1586.7590, 1590.7579, 1685.8076, 1691.0171, 1714.8562, 1731.8743, 1813.4187, 1830.8500, 1899.9332, 2051.0215, 2070.0386, 2116.0962, 2129.1279, 2145.1472, 2171.9956, 2185.0378, 2273.1658, 2281.8589, 2295.1462, 2311.1328, 2333.1082, 2456.2361, 2514.3181, 2553.2390, 2568.2795, 2612.2229, 2662.4358, 2748.4390, 2751.4229, 2792.4922, 2974.3398, 2990.3176, 3016.4280, 3136.5017, 3211.5313, 3300.7397, 3317.7559, 3441.7615, 3451.5989

7. gi|46560476 **Mass:** 48122 **Score:** 182 **Expect:** 5.5e-016 **Queries matched:** 23

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

816.4500	815.4427	815.4249	0.0178	274 - 279	1	KEQQQR
896.4416	895.4343	895.4260	0.0083	81 - 87	0	HDNQNLR
1128.6312	1127.6239	1127.6298	-0.0059	263 - 273	0	GTGNLELVAVR
1184.5956	1183.5883	1183.5846	0.0037	8 - 16	0	QFQNLQNHR
1258.6229	1257.6156	1257.6101	0.0055	58 - 68	0	SFNLDEGHALR
1287.5997	1286.5924	1286.5891	0.0033	111 - 121	0	DQSSYLQGFSR
1343.6753	1342.6680	1342.6703	-0.0023	242 - 253	0	EGALMLPHFNSK
1376.6713	1375.6640	1375.6619	0.0021	362 - 374	0	DLAFPGSGEQVEK
1379.7651	1378.7578	1378.7608	-0.0030	69 - 80	0	IPSGFISYILNR
1386.7150	1385.7077	1385.7051	0.0026	57 - 68	1	KSFNLDEGHALR
1427.7218	1426.7145	1426.7177	-0.0032	6 - 16	1	SRQFQNLQNHR
1572.7430	1571.7357	1571.7426	-0.0069	138 - 151	0	VLLEENAGGEQEER
1728.8522	1727.8449	1727.8437	0.0012	137 - 151	1	RVLLEENAGGEQEER
1738.8383	1737.8310	1737.8321	-0.0011	122 - 136	0	NTLEAAFNAEFNEIR
1817.9558	1816.9485	1816.9570	-0.0085	343 - 358	1	IFLAGDKDNVIDQIEK
1894.9404	1893.9331	1893.9332	-0.0001	122 - 137	1	NTLEAAFNAEFNEIRR
2082.2136	2081.2063	2081.2030	0.0034	254 - 273	1	AMVIVVVNKGTGNLELVAVR
2227.0754	2226.0681	2226.0415	0.0266	91 - 110	0	ISMPVNTPGQFEDFFPASSR
2243.0547	2242.0474	2242.0364	0.0110	91 - 110	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1572	2256.1499	2256.1763	-0.0263	69 - 87	1	IPSGFISYILNRHDNQNLR
2525.2075	2524.2002	2524.2420	-0.0417	88 - 110	1	VAKISMPVNTPGQFEDFFPASSR
2619.3550	2618.3477	2618.3604	-0.0127	58 - 80	1	SFNLDEGHALRIPSGFISYILNR
2747.4224	2746.4151	2746.4110	0.0042	32 - 57	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 805.4622, 808.4086, 812.4315, 813.4330, 824.4281, 825.4193, 826.4116, 828.4656, 848.4346, 855.5306, 861.0914, 881.2838, 959.4822, 975.4969, 1005.5374, 1019.4708, 1021.5086, 1061.5857, 1111.5630, 1115.5367, 1141.5520, 1144.5332, 1167.5745, 1297.6433, 1304.6061, 1320.5875, 1330.7548, 1399.7063, 1424.7096, 1440.7019, 1496.7299, 1512.7223, 1560.6849, 1568.7040, 1586.7590, 1590.7579, 1591.7788, 1643.7795, 1685.8076, 1691.0171, 1714.8562, 1731.8743, 1771.8760, 1813.4187, 1830.8500, 1899.9332, 2051.0215, 2070.0386, 2116.0962, 2129.1279, 2145.1472, 2171.9956, 2185.0378, 2273.1658, 2281.8589, 2295.1462, 2311.1328, 2333.1082, 2456.2361, 2514.3181, 2553.2390, 2568.2795, 2612.2229, 2662.4358, 2748.4390, 2751.4229, 2792.4922, 2974.3398, 2990.3176, 3016.4280, 3136.5017, 3211.5313, 3300.7397, 3317.7559, 3441.7615, 3451.5989

8. gi|46560472 **Mass:** 34169 **Score:** 77 **Expect:** 1.8e-005 **Queries matched:** 12

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
816.4500	815.4427	815.4249	0.0178	153 - 158	1	KEQQQR
1128.6312	1127.6239	1127.6298	-0.0059	142 - 152	0	GTGNLELVAVR
1320.5875	1319.5802	1319.5741	0.0061	83 - 94	0	DGEPDLSNNFGR
1343.6753	1342.6680	1342.6703	-0.0023	121 - 132	0	EGALMLPHFNSK

1376.6713	1375.6640	1375.6619	0.0021	244 - 256	0	DLAFPGSGEQVEK
1572.7430	1571.7357	1571.7426	-0.0069	18 - 31	0	VLLEENAGGEQEER
1586.7590	1585.7517	1585.7583	-0.0066	69 - 82	0	GSEEEDITNPINLR
1714.8562	1713.8489	1713.8533	-0.0043	68 - 82	1	KGSEEEDITNPINLR
1728.8522	1727.8449	1727.8437	0.0012	17 - 31	1	RVLLEENAGGEQEER
1817.9558	1816.9485	1816.9570	-0.0085	225 - 240	1	IFLAGDKDNVIDQIEK
2082.2136	2081.2063	2081.2030	0.0034	133 - 152	1	AMVIVVVNKGTGNLELVAVR
2281.8589	2280.8516	2280.8414	0.0103	162 - 179	0	EQEWEEEEEDEEEEGSNR

No match to: 805.4622, 808.4086, 812.4315, 813.4330, 824.4281, 825.4193, 826.4116, 828.4656, 848.4346, 855.5306, 861.0914, 881.2838, 896.4416, 959.4822, 975.4969, 1005.5374, 1019.4708, 1021.5086, 1061.5857, 1111.5630, 1115.5367, 1141.5520, 1144.5332, 1167.5745, 1184.5956, 1258.6229, 1287.5997, 1297.6433, 1304.6061, 1330.7548, 1379.7651, 1386.7150, 1399.7063, 1424.7096, 1427.7218, 1440.7019, 1496.7299, 1512.7223, 1560.6849, 1568.7040, 1590.7579, 1591.7788, 1643.7795, 1685.8076, 1691.0171, 1731.8743, 1738.8383, 1771.8760, 1813.4187, 1830.8500, 1894.9404, 1899.9332, 2051.0215, 2070.0386, 2116.0962, 2129.1279, 2145.1472, 2171.9956, 2185.0378, 2227.0754, 2243.0547, 2257.1572, 2273.1658, 2295.1462, 2311.1328, 2333.1082, 2456.2361, 2514.3181, 2525.2075, 2553.2390, 2568.2795, 2612.2229, 2619.3550, 2662.4358, 2747.4224, 2748.4390, 2751.4229, 2792.4922, 2974.3398, 2990.3176, 3016.4280, 3136.5017, 3211.5313, 3300.7397, 3317.7559, 3441.7615, 3451.5989

9. gi|46560474 **Mass:** 33641 **Score:** 58 **Expect:** 0.0015 **Queries matched:** 10

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4500	815.4427	815.4249	0.0178	152 - 157		1	KEQQQR
1128.6312	1127.6239	1127.6298	-0.0059	141 - 151		0	GTGNLELVAVR
1343.6753	1342.6680	1342.6703	-0.0023	120 - 131		0	EGALMLPHFNSK
1376.6713	1375.6640	1375.6619	0.0021	240 - 252		0	DLAFPGSGEQVEK
1572.7430	1571.7357	1571.7426	-0.0069	15 - 28		0	VLLEENAGGEQEER
1643.7795	1642.7722	1642.7798	-0.0075	67 - 81		0	GSEEEGDITNPINLR
1728.8522	1727.8449	1727.8437	0.0012	14 - 28		1	RVLLEENAGGEQEER
1771.8760	1770.8687	1770.8747	-0.0060	66 - 81		1	KGSEEEGDITNPINLR
1817.9558	1816.9485	1816.9570	-0.0085	221 - 236		1	IFLAGDKDNVIDQIEK
2082.2136	2081.2063	2081.2030	0.0034	132 - 151		1	AMVIVVVNKGTGNLELVAVR

No match to: 805.4622, 808.4086, 812.4315, 813.4330, 824.4281, 825.4193, 826.4116, 828.4656, 848.4346, 855.5306, 861.0914, 881.2838, 896.4416, 959.4822, 975.4969, 1005.5374, 1019.4708, 1021.5086, 1061.5857, 1111.5630, 1115.5367, 1141.5520, 1144.5332, 1167.5745, 1184.5956, 1258.6229, 1287.5997, 1297.6433, 1304.6061, 1320.5875, 1330.7548, 1379.7651, 1386.7150, 1399.7063, 1424.7096, 1427.7218, 1440.7019, 1496.7299, 1512.7223, 1560.6849, 1568.7040, 1586.7590, 1590.7579, 1591.7788, 1685.8076, 1691.0171, 1714.8562, 1731.8743, 1738.8383, 1813.4187, 1830.8500, 1894.9404, 1899.9332, 2051.0215, 2070.0386, 2116.0962, 2129.1279, 2145.1472, 2171.9956, 2185.0378, 2227.0754, 2243.0547, 2257.1572, 2273.1658, 2281.8589, 2295.1462, 2311.1328, 2333.1082, 2456.2361, 2514.3181, 2525.2075, 2553.2390, 2568.2795, 2612.2229, 2619.3550, 2662.4358, 2747.4224, 2748.4390, 2751.4229, 2792.4922, 2974.3398, 2990.3176, 3016.4280, 3136.5017, 3211.5313, 3300.7397, 3317.7559, 3441.7615, 3451.5989

10. gi|62177652 **Mass:** 10056 **Score:** 14 **Expect:** 37 **Queries matched:** 2
resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1379.7651	1378.7578	1378.7496	0.0083	77 -	89	1	EVVKYSGGLPFAL
1894.9404	1893.9331	1893.9009	0.0323	7 -	23	0	QLEYLGGEQAWFGPGSR

No match to: 805.4622, 808.4086, 812.4315, 813.4330, 816.4500, 824.4281, 825.4193, 826.4116, 828.4656, 848.4346, 855.5306, 861.0914, 881.2838, 896.4416, 959.4822, 975.4969, 1005.5374, 1019.4708, 1021.5086, 1061.5857, 1111.5630, 1115.5367, 1128.6312, 1141.5520, 1144.5332, 1167.5745, 1184.5956, 1258.6229, 1287.5997, 1297.6433, 1304.6061, 1320.5875, 1330.7548, 1343.6753, 1376.6713, 1386.7150, 1399.7063, 1424.7096, 1427.7218, 1440.7019, 1496.7299, 1512.7223, 1560.6849, 1568.7040, 1572.7430, 1586.7590, 1590.7579, 1591.7788, 1643.7795, 1685.8076, 1691.0171, 1714.8562, 1728.8522, 1731.8743, 1738.8383, 1771.8760, 1813.4187, 1817.9558, 1830.8500, 1899.9332, 2051.0215, 2070.0386, 2082.2136, 2116.0962, 2129.1279, 2145.1472, 2171.9956, 2185.0378, 2227.0754, 2243.0547, 2257.1572, 2273.1658, 2281.8589, 2295.1462, 2311.1328, 2333.1082, 2456.2361, 2514.3181, 2525.2075, 2553.2390, 2568.2795, 2612.2229, 2619.3550, 2662.4358, 2747.4224, 2748.4390, 2751.4229, 2792.4922, 2974.3398, 2990.3176, 3016.4280, 3136.5017, 3211.5313, 3300.7397, 3317.7559, 3441.7615, 3451.5989

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 99

Protein View

Match to: **gi|46560478** Score: **296** Expect: **2.2e-027**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **99**
Number of mass values matched: **37**
Sequence Coverage: **55%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
118 - 124	1019.4708	1018.4635	1018.4468	0.0167	1	EREEDWR
120 - 127	1115.5367	1114.5294	1114.5155	0.0139	1	EEDWRQPR
128 - 139	1591.7788	1590.7715	1590.7763	-0.0048	1	EDWRRPSHQQPR
132 - 139	1005.5374	1004.5301	1004.5264	0.0037	0	RPSHQQPR
140 - 146	855.5306	854.5233	854.5086	0.0147	1	KIRPEGR
147 - 160	1560.6849	1559.6776	1559.6851	-0.0075	0	EGEQEWGTPGSEVR
166 - 174	1141.5520	1140.5447	1140.5352	0.0095	0	NNPFYFPSR
166 - 175	1297.6433	1296.6360	1296.6363	-0.0003	1	NNPFYFPSRR
189 - 196	1061.5857	1060.5784	1060.5777	0.0007	1	VLQRFDQR
197 - 207	1399.7063	1398.6990	1398.7116	-0.0126	1	SKQFQNLQNHR
199 - 207	1184.5956	1183.5883	1183.5846	0.0037	0	QFQNLQNHR
208 - 222	1691.0171	1690.0098	1690.0141	-0.0042	0	IVQIEARPNTLVLPK
223 - 248	2747.4224	2746.4151	2746.4110	0.0042	1	HADADNILVIQQGQATVTVANGNNRK
248 - 259	1386.7150	1385.7077	1385.7051	0.0026	1	KSFNLDEGHALR
249 - 259	1258.6229	1257.6156	1257.6101	0.0055	0	SFNLDEGHALR
249 - 271	2619.3550	2618.3477	2618.3604	-0.0127	1	SFNLDEGHALRIPSGFISYILNR
260 - 271	1379.7651	1378.7578	1378.7608	-0.0030	0	IPSGFISYILNR
260 - 278	2257.1572	2256.1499	2256.1763	-0.0263	1	IPSGFISYILNRHDNQNLR
272 - 278	896.4416	895.4343	895.4260	0.0083	0	HDNQNLR
279 - 301	2525.2075	2524.2002	2524.2420	-0.0417	1	VAKISMPVNTPGQFEDFFPASSR

282 - 301	2227.0754	2226.0681	2226.0415	0.0266	0	ISMPVNTPGQFEDFFPASSR
282 - 301	2243.0547	2242.0474	2242.0364	0.0110	0	ISMPVNTPGQFEDFFPASSR Oxidation (M)
302 - 312	1287.5997	1286.5924	1286.5891	0.0033	0	DQSSYLQGFSR
313 - 327	1738.8383	1737.8310	1737.8321	-0.0011	0	NTLEAAFNAEFNEIR
313 - 328	1894.9404	1893.9331	1893.9332	-0.0001	1	NTLEAAFNAEFNEIRR
328 - 342	1728.8522	1727.8449	1727.8437	0.0012	1	RVLLEENAGGEQEER
329 - 342	1572.7430	1571.7357	1571.7426	-0.0069	0	VLLEENAGGEQEER
379 - 393	1714.8562	1713.8489	1713.8533	-0.0043	1	KGSEEEDITNPINLR
380 - 393	1586.7590	1585.7517	1585.7583	-0.0066	0	GSEEEDITNPINLR
394 - 405	1320.5875	1319.5802	1319.5741	0.0061	0	DGEPDLSNNFGR
432 - 443	1343.6753	1342.6680	1342.6703	-0.0023	0	EGALMLPHFNSK
444 - 463	2082.2136	2081.2063	2081.2030	0.0034	1	AMVIVVVNKGTGNLELVAVR
453 - 463	1128.6312	1127.6239	1127.6298	-0.0059	0	GTGNLELVAVR
464 - 469	816.4500	815.4427	815.4249	0.0178	1	KEQQQR
473 - 490	2281.8589	2280.8516	2280.8414	0.0103	0	EQEWEEEEEDEEEEGSNR
536 - 551	1817.9558	1816.9485	1816.9570	-0.0085	1	IFLAGDKDNVIDQIEK
555 - 567	1376.6713	1375.6640	1375.6619	0.0021	0	DLAFPGSGEQVEK

No match to: 805.4622, 808.4086, 812.4315, 813.4330, 824.4281, 825.4193, 826.4116, 828.4656, 848.4346, 861.0914, 881.2838, 959.4822, 975.4969, 1021.5086, 1111.5630, 1144.5332, 1167.5745, 1304.6061, 1330.7548, 1424.7096, 1427.7218, 1440.7019, 1496.7299, 1512.7223, 1568.7040, 1590.7579, 1643.7795, 1685.8076, 1731.8743, 1771.8760, 1813.4187, 1830.8500, 1899.9332, 2051.0215, 2070.0386, 2116.0962, 2129.1279, 2145.1472, 2171.9956, 2185.0378, 2273.1658, 2295.1462, 2311.1328, 2333.1082, 2456.2361, 2514.3181, 2553.2390, 2568.2795, 2612.2229, 2662.4358, 2748.4390, 2751.4229, 2792.4922, 2974.3398, 2990.3176, 3016.4280, 3136.5017, 3211.5313, 3300.7397, 3317.7559, 3441.7615, 3451.5989

Spot 2

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:30:21 GMT**
Top Score : **189 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	189	conarachin [Arachis hypogaea]
2.	gi|620025	70639	185	Ara h I
3.	gi|1168390	70639	185	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	129	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	129	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	129	Ara h I
7.	gi|46560476	48122	104	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	64	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	31	conarachin [Arachis hypogaea]
10.	gi|226258	10809	17	ferredoxin I

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 189 **Expect:** 1.1e-016 **Queries matched:** 22
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5209	1004.5136	1004.5264	-0.0128	132	139	0	RPSHQQPR
1019.4407	1018.4334	1018.4468	-0.0134	118	124	1	EREEDWR
1128.6384	1127.6311	1127.6298	0.0013	453	463	0	GTGNLELVAVR
1141.5490	1140.5417	1140.5352	0.0065	166	174	0	NNPFYFPSR
1184.6014	1183.5941	1183.5846	0.0095	199	207	0	QFQNLQNHR
1258.6328	1257.6255	1257.6101	0.0154	249	259	0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	302	312	0	DQSSYLQGFSR
1297.6639	1296.6566	1296.6363	0.0203	166	175	1	NNPFYFPSRR
1320.6044	1319.5971	1319.5741	0.0230	394	405	0	DGEPDLSNNFGR
1343.6971	1342.6898	1342.6703	0.0195	432	443	0	EGALMLPHFNSK
1376.6918	1375.6845	1375.6619	0.0226	555	567	0	DLAFPGSGEQVEK

1386.7302	1385.7229	1385.7051	0.0178	248 - 259	1	KSFNLDEGHALR
1399.7455	1398.7382	1398.7116	0.0266	197 - 207	1	SKQFQNLQNHR
1691.0543	1690.0470	1690.0141	0.0330	208 - 222	0	IVQIEARPNTLVLPK
1714.8909	1713.8836	1713.8533	0.0304	379 - 393	1	KGSEEEDITNPINLR
1728.8853	1727.8780	1727.8437	0.0343	328 - 342	1	RVLLEENAGGEQEER
1738.8719	1737.8646	1737.8321	0.0325	313 - 327	0	NTLEAAFNAEFNEIR
1817.9921	1816.9848	1816.9570	0.0278	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9635	1893.9562	1893.9332	0.0230	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0427	2226.0354	2226.0415	-0.0061	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0381	2242.0308	2242.0364	-0.0056	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8359	2280.8286	2280.8414	-0.0127	473 - 490	0	EQEWEEEEEDEEEEGSNR

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1167.5710, 1281.2159, 1304.6201, 1379.7982, 1560.7249, 1568.7400, 1572.7831, 1586.7999, 1643.8240, 1771.9196, 1830.8876, 2273.1592, 2619.2644, 2748.3149, 3211.2510

2. gi|620025 **Mass:** 70639 **Score:** 185 **Expect:** 2.8e-016 **Queries matched:** 22

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5209	1004.5136	1004.5264	-0.0128	132 - 139		0	RPSHQQPR
1019.4407	1018.4334	1018.4468	-0.0134	118 - 124		1	EREEDWR
1128.6384	1127.6311	1127.6298	0.0013	453 - 463		0	GTGNLELVAVR
1141.5490	1140.5417	1140.5352	0.0065	166 - 174		0	NNPFYFPSR
1184.6014	1183.5941	1183.5846	0.0095	199 - 207		0	QFQNLQNHR
1258.6328	1257.6255	1257.6101	0.0154	249 - 259		0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	302 - 312		0	DQSSYLQGFSR
1297.6639	1296.6566	1296.6363	0.0203	166 - 175		1	NNPFYFPSRR
1320.6044	1319.5971	1319.5741	0.0230	394 - 405		0	DGEPDLSNNFGR
1343.6971	1342.6898	1342.6703	0.0195	432 - 443		0	EGALMLPHFNSK
1376.6918	1375.6845	1375.6619	0.0226	555 - 567		0	DLAFPGSGEQVEK
1386.7302	1385.7229	1385.7051	0.0178	248 - 259		1	KSFNLDEGHALR
1399.7455	1398.7382	1398.7116	0.0266	197 - 207		1	SKQFQNLQNHR
1691.0543	1690.0470	1690.0141	0.0330	208 - 222		0	IVQIEARPNTLVLPK
1714.8909	1713.8836	1713.8533	0.0304	379 - 393		1	KGSEEEDITNPINLR
1728.8853	1727.8780	1727.8437	0.0343	328 - 342		1	RVLLEENAGGEQEER
1738.8719	1737.8646	1737.8321	0.0325	313 - 327		0	NTLEAAFNAEFNEIR
1817.9921	1816.9848	1816.9570	0.0278	536 - 551		1	IFLAGDKDNVIDQIEK
1894.9635	1893.9562	1893.9332	0.0230	313 - 328		1	NTLEAAFNAEFNEIRR
2227.0427	2226.0354	2226.0415	-0.0061	282 - 301		0	ISMPVNTPGQFEDFFPASSR
2243.0381	2242.0308	2242.0364	-0.0056	282 - 301		0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8359	2280.8286	2280.8414	-0.0127	473 - 490		0	EQEWEEEEEDEEEEGSNR

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1167.5710, 1281.2159, 1304.6201, 1379.7982, 1560.7249, 1568.7400, 1572.7831, 1586.7999, 1643.8240, 1771.9196, 1830.8876, 2273.1592, 2619.2644, 2748.3149, 3211.2510

3. gi|1168390 **Mass:** 70639 **Score:** 185 **Expect:** 2.8e-016 **Queries matched:** 22

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5209	1004.5136	1004.5264	-0.0128	132	139	0	RPSHQQPR
1019.4407	1018.4334	1018.4468	-0.0134	118	124	1	EREEDWR
1128.6384	1127.6311	1127.6298	0.0013	453	463	0	GTGNLELVAVR
1141.5490	1140.5417	1140.5352	0.0065	166	174	0	NNPFYFPSR
1184.6014	1183.5941	1183.5846	0.0095	199	207	0	QFQNLQNHR
1258.6328	1257.6255	1257.6101	0.0154	249	259	0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	302	312	0	DQSSYLQGFSR
1297.6639	1296.6566	1296.6363	0.0203	166	175	1	NNPFYFPSRR
1320.6044	1319.5971	1319.5741	0.0230	394	405	0	DGEPDLSNNFGR
1343.6971	1342.6898	1342.6703	0.0195	432	443	0	EGALMLPHFNSK
1376.6918	1375.6845	1375.6619	0.0226	555	567	0	DLAFPGSGEQVEK
1386.7302	1385.7229	1385.7051	0.0178	248	259	1	KSFNLDEGHALR
1399.7455	1398.7382	1398.7116	0.0266	197	207	1	SKQFQNLQNHR
1691.0543	1690.0470	1690.0141	0.0330	208	222	0	IVQIEARPNTLVLPK
1714.8909	1713.8836	1713.8533	0.0304	379	393	1	KGSEEEDITNPINLR
1728.8853	1727.8780	1727.8437	0.0343	328	342	1	RVLLEENAGGEQEER
1738.8719	1737.8646	1737.8321	0.0325	313	327	0	NTLEAAFNAEFNEIR
1817.9921	1816.9848	1816.9570	0.0278	536	551	1	IFLAGDKDNVIDQIEK
1894.9635	1893.9562	1893.9332	0.0230	313	328	1	NTLEAAFNAEFNEIRR
2227.0427	2226.0354	2226.0415	-0.0061	282	301	0	ISMPVNTPGQFEDFFPASSR
2243.0381	2242.0308	2242.0364	-0.0056	282	301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8359	2280.8286	2280.8414	-0.0127	473	490	0	EQEWEEEEEDEEEEGSNR

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1167.5710, 1281.2159, 1304.6201, 1379.7982, 1560.7249, 1568.7400, 1572.7831, 1586.7999, 1643.8240, 1771.9196, 1830.8876, 2273.1592, 2619.2644, 2748.3149, 3211.2510

4. gi|16612200 **Mass:** 71701 **Score:** 129 **Expect:** 1.1e-010 **Queries matched:** 18

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5209	1004.5136	1004.5264	-0.0128	138	145	0	RPSHQQPR
1019.4407	1018.4334	1018.4468	-0.0134	124	130	1	EREEDWR
1128.6384	1127.6311	1127.6298	0.0013	461	471	0	GTGNLELVAVR
1141.5490	1140.5417	1140.5352	0.0065	172	180	0	NNPFYFPSR
1184.6014	1183.5941	1183.5846	0.0095	205	213	0	QFQNLQNHR

1258.6328	1257.6255	1257.6101	0.0154	255 - 265	0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	308 - 318	0	DQSSYLQGFSR
1297.6639	1296.6566	1296.6363	0.0203	172 - 181	1	NNPFYFPSRR
1343.6971	1342.6898	1342.6703	0.0195	440 - 451	0	EGALMLPHFNSK
1376.6918	1375.6845	1375.6619	0.0226	560 - 572	0	DLAFPGSGEQVEK
1386.7302	1385.7229	1385.7051	0.0178	254 - 265	1	KSFNLDEGHALR
1568.7400	1567.7327	1567.7015	0.0313	153 - 166	0	EGEQEWGTPGSHVR
1728.8853	1727.8780	1727.8437	0.0343	334 - 348	1	RVLLEENAGGEQEER
1738.8719	1737.8646	1737.8321	0.0325	319 - 333	0	NTLEAAFNAEFNEIR
1817.9921	1816.9848	1816.9570	0.0278	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9635	1893.9562	1893.9332	0.0230	319 - 334	1	NTLEAAFNAEFNEIRR
2227.0427	2226.0354	2226.0415	-0.0061	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0381	2242.0308	2242.0364	-0.0056	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1167.5710, 1281.2159, 1304.6201, 1320.6044, 1379.7982, 1399.7455, 1560.7249, 1572.7831, 1586.7999, 1643.8240, 1691.0543, 1714.8909, 1771.9196, 1830.8876, 2273.1592, 2281.8359, 2619.2644, 2748.3149, 3211.2510

5. gi|1168391 **Mass:** 71701 **Score:** 129 **Expect:** 1.1e-010 **Queries matched:** 18

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5209	1004.5136	1004.5264	-0.0128	138 - 145		0	RPSHQQPR
1019.4407	1018.4334	1018.4468	-0.0134	124 - 130		1	EREEDWR
1128.6384	1127.6311	1127.6298	0.0013	461 - 471		0	GTGNLELVAVR
1141.5490	1140.5417	1140.5352	0.0065	172 - 180		0	NNPFYFPSR
1184.6014	1183.5941	1183.5846	0.0095	205 - 213		0	QFQNLQNHR
1258.6328	1257.6255	1257.6101	0.0154	255 - 265		0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	308 - 318		0	DQSSYLQGFSR
1297.6639	1296.6566	1296.6363	0.0203	172 - 181		1	NNPFYFPSRR
1343.6971	1342.6898	1342.6703	0.0195	440 - 451		0	EGALMLPHFNSK
1376.6918	1375.6845	1375.6619	0.0226	560 - 572		0	DLAFPGSGEQVEK
1386.7302	1385.7229	1385.7051	0.0178	254 - 265		1	KSFNLDEGHALR
1568.7400	1567.7327	1567.7015	0.0313	153 - 166		0	EGEQEWGTPGSHVR
1728.8853	1727.8780	1727.8437	0.0343	334 - 348		1	RVLLEENAGGEQEER
1738.8719	1737.8646	1737.8321	0.0325	319 - 333		0	NTLEAAFNAEFNEIR
1817.9921	1816.9848	1816.9570	0.0278	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9635	1893.9562	1893.9332	0.0230	319 - 334		1	NTLEAAFNAEFNEIRR
2227.0427	2226.0354	2226.0415	-0.0061	288 - 307		0	ISMPVNTPGQFEDFFPASSR
2243.0381	2242.0308	2242.0364	-0.0056	288 - 307		0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1167.5710, 1281.2159, 1304.6201, 1320.6044, 1379.7982, 1399.7455, 1560.7249,

1572.7831, 1586.7999, 1643.8240, 1691.0543, 1714.8909, 1771.9196, 1830.8876, 2273.1592, 2281.8359, 2619.2644, 2748.3149, 3211.2510

6. gi|602436 **Mass:** 71701 **Score:** 129 **Expect:** 1.1e-010 **Queries matched:** 18

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5209	1004.5136	1004.5264	-0.0128	138	145	0	RPSHQQPR
1019.4407	1018.4334	1018.4468	-0.0134	124	130	1	EREEDWR
1128.6384	1127.6311	1127.6298	0.0013	461	471	0	GTGNLELVAVR
1141.5490	1140.5417	1140.5352	0.0065	172	180	0	NNPFYFPSR
1184.6014	1183.5941	1183.5846	0.0095	205	213	0	QFQNLQNHR
1258.6328	1257.6255	1257.6101	0.0154	255	265	0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	308	318	0	DQSSYLQGFSR
1297.6639	1296.6566	1296.6363	0.0203	172	181	1	NNPFYFPSRR
1343.6971	1342.6898	1342.6703	0.0195	440	451	0	EGALMLPHFNSK
1376.6918	1375.6845	1375.6619	0.0226	560	572	0	DLAFPGSGEQVEK
1386.7302	1385.7229	1385.7051	0.0178	254	265	1	KSFNLDEGHALR
1568.7400	1567.7327	1567.7015	0.0313	153	166	0	EGEQEWGTPGSHVR
1728.8853	1727.8780	1727.8437	0.0343	334	348	1	RVLLEENAGGEQEER
1738.8719	1737.8646	1737.8321	0.0325	319	333	0	NTLEAAFNAEFNEIR
1817.9921	1816.9848	1816.9570	0.0278	541	556	1	IFLAGDKDNVIDQIEK
1894.9635	1893.9562	1893.9332	0.0230	319	334	1	NTLEAAFNAEFNEIRR
2227.0427	2226.0354	2226.0415	-0.0061	288	307	0	ISMPVNTPGQFEDFFPASSR
2243.0381	2242.0308	2242.0364	-0.0056	288	307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1167.5710, 1281.2159, 1304.6201, 1320.6044, 1379.7982, 1399.7455, 1560.7249, 1572.7831, 1586.7999, 1643.8240, 1691.0543, 1714.8909, 1771.9196, 1830.8876, 2273.1592, 2281.8359, 2619.2644, 2748.3149, 3211.2510

7. gi|46560476 **Mass:** 48122 **Score:** 104 **Expect:** 3.5e-008 **Queries matched:** 13

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6384	1127.6311	1127.6298	0.0013	263	273	0	GTGNLELVAVR
1184.6014	1183.5941	1183.5846	0.0095	8	16	0	QFQNLQNHR
1258.6328	1257.6255	1257.6101	0.0154	58	68	0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	111	121	0	DQSSYLQGFSR
1343.6971	1342.6898	1342.6703	0.0195	242	253	0	EGALMLPHFNSK
1376.6918	1375.6845	1375.6619	0.0226	362	374	0	DLAFPGSGEQVEK
1386.7302	1385.7229	1385.7051	0.0178	57	68	1	KSFNLDEGHALR
1728.8853	1727.8780	1727.8437	0.0343	137	151	1	RVLLEENAGGEQEER
1738.8719	1737.8646	1737.8321	0.0325	122	136	0	NTLEAAFNAEFNEIR

1817.9921	1816.9848	1816.9570	0.0278	343 - 358	1	IFLAGDKDNVIDQIEK
1894.9635	1893.9562	1893.9332	0.0230	122 - 137	1	NTLEAAFNAEFNEIRR
2227.0427	2226.0354	2226.0415	-0.0061	91 - 110	0	ISMPVNTPGQFEDFFPASSR
2243.0381	2242.0308	2242.0364	-0.0056	91 - 110	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1005.5209, 1019.4407, 1141.5490, 1167.5710, 1281.2159, 1297.6639, 1304.6201, 1320.6044, 1379.7982, 1399.7455, 1560.7249, 1568.7400, 1572.7831, 1586.7999, 1643.8240, 1691.0543, 1714.8909, 1771.9196, 1830.8876, 2273.1592, 2281.8359, 2619.2644, 2748.3149, 3211.2510

8. gi|46560472 **Mass:** 34169 **Score:** 64 **Expect:** 0.00037 **Queries matched:** 8

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6384	1127.6311	1127.6298	0.0013	142 -	152	0	GTGNLELVAVR
1320.6044	1319.5971	1319.5741	0.0230	83 -	94	0	DGEPDLSNNFGR
1343.6971	1342.6898	1342.6703	0.0195	121 -	132	0	EGALMLPHFNSK
1376.6918	1375.6845	1375.6619	0.0226	244 -	256	0	DLAFPGSGEQVEK
1714.8909	1713.8836	1713.8533	0.0304	68 -	82	1	KGSEEEDITNPINLR
1728.8853	1727.8780	1727.8437	0.0343	17 -	31	1	RVLLEENAGGEQEER
1817.9921	1816.9848	1816.9570	0.0278	225 -	240	1	IFLAGDKDNVIDQIEK
2281.8359	2280.8286	2280.8414	-0.0127	162 -	179	0	EQEWEEEEEDEEEEGSNR

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1005.5209, 1019.4407, 1141.5490, 1167.5710, 1184.6014, 1258.6328, 1281.2159, 1287.6149, 1297.6639, 1304.6201, 1379.7982, 1386.7302, 1399.7455, 1560.7249, 1568.7400, 1572.7831, 1586.7999, 1643.8240, 1691.0543, 1738.8719, 1771.9196, 1830.8876, 1894.9635, 2227.0427, 2243.0381, 2273.1592, 2619.2644, 2748.3149, 3211.2510

9. gi|46560474 **Mass:** 33641 **Score:** 31 **Expect:** 0.7 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6384	1127.6311	1127.6298	0.0013	141 -	151	0	GTGNLELVAVR
1343.6971	1342.6898	1342.6703	0.0195	120 -	131	0	EGALMLPHFNSK
1376.6918	1375.6845	1375.6619	0.0226	240 -	252	0	DLAFPGSGEQVEK
1728.8853	1727.8780	1727.8437	0.0343	14 -	28	1	RVLLEENAGGEQEER
1817.9921	1816.9848	1816.9570	0.0278	221 -	236	1	IFLAGDKDNVIDQIEK

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1005.5209, 1019.4407, 1141.5490, 1167.5710, 1184.6014, 1258.6328, 1281.2159, 1287.6149, 1297.6639, 1304.6201, 1320.6044, 1379.7982, 1386.7302, 1399.7455, 1560.7249, 1568.7400, 1572.7831, 1586.7999, 1643.8240, 1691.0543, 1714.8909, 1738.8719, 1771.9196, 1830.8876, 1894.9635, 2227.0427, 2243.0381, 2273.1592, 2281.8359, 2619.2644, 2748.3149, 3211.2510

10. gi|226258 **Mass:** 10809 **Score:** 17 **Expect:** 19 **Queries matched:** 2

ferredoxin I

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1141.5490	1140.5417	1140.5484	-0.0067	16	-	26	0	GDLAVAMASYK + Oxidation (M)
1297.6639	1296.6566	1296.6496	0.0071	15	-	26	1	RGDLAVAMASYK + Oxidation (M)

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1005.5209, 1019.4407, 1128.6384, 1167.5710, 1184.6014, 1258.6328, 1281.2159, 1287.6149, 1304.6201, 1320.6044, 1343.6971, 1376.6918, 1379.7982, 1386.7302, 1399.7455, 1560.7249, 1568.7400, 1572.7831, 1586.7999, 1643.8240, 1691.0543, 1714.8909, 1728.8853, 1738.8719, 1771.9196, 1817.9921, 1830.8876, 1894.9635, 2227.0427, 2243.0381, 2273.1592, 2281.8359, 2619.2644, 2748.3149, 3211.2510

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|46560478** Score: **189** Expect: **1.1e-016**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **22**
Sequence Coverage: **38%**

Matched peptides shown in **Bold Red**

```
  1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
 51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
118 - 124	1019.4407	1018.4334	1018.4468	-0.0134	1	EREEDWR	
132 - 139	1005.5209	1004.5136	1004.5264	-0.0128	0	RPSHQQPR	
166 - 174	1141.5490	1140.5417	1140.5352	0.0065	0	NNPFYFPSR	
166 - 175	1297.6639	1296.6566	1296.6363	0.0203	1	NNPFYFPSRR	
197 - 207	1399.7455	1398.7382	1398.7116	0.0266	1	SKQFQNLQNHR	
199 - 207	1184.6014	1183.5941	1183.5846	0.0095	0	QFQNLQNHR	
208 - 222	1691.0543	1690.0470	1690.0141	0.0330	0	IVQIEARPNTLVLPK	
248 - 259	1386.7302	1385.7229	1385.7051	0.0178	1	KSFNLDEGHALR	
249 - 259	1258.6328	1257.6255	1257.6101	0.0154	0	SFNLDEGHALR	
282 - 301	2227.0427	2226.0354	2226.0415	-0.0061	0	ISMPVNTPGQFEDFFPASSR	
282 - 301	2243.0381	2242.0308	2242.0364	-0.0056	0	ISMPVNTPGQFEDFFPASSR	Oxidation (M)
302 - 312	1287.6149	1286.6076	1286.5891	0.0185	0	DQSSYLQGFSR	
313 - 327	1738.8719	1737.8646	1737.8321	0.0325	0	NTLEAAFNAEFNEIR	
313 - 328	1894.9635	1893.9562	1893.9332	0.0230	1	NTLEAAFNAEFNEIRR	
328 - 342	1728.8853	1727.8780	1727.8437	0.0343	1	RVLLEENAGGEQEER	
379 - 393	1714.8909	1713.8836	1713.8533	0.0304	1	KGSEEEDITNPINLR	
394 - 405	1320.6044	1319.5971	1319.5741	0.0230	0	DGEPDLSNNFGR	
432 - 443	1343.6971	1342.6898	1342.6703	0.0195	0	EGALMLPHFNSK	
453 - 463	1128.6384	1127.6311	1127.6298	0.0013	0	GTGNLELVAVR	
473 - 490	2281.8359	2280.8286	2280.8414	-0.0127	0	EQEWEEEEEDEEEEGSNR	
536 - 551	1817.9921	1816.9848	1816.9570	0.0278	1	IFLAGDKDNVIDQIEK	
555 - 567	1376.6918	1375.6845	1375.6619	0.0226	0	DLAFPGSGEQVEK	

No match to: 740.3239, 756.3257, 805.3765, 808.3265, 811.3682, 812.3633, 816.3852, 828.4266, 845.3820, 848.4102, 855.4824, 896.4025, 959.4588, 1167.5710, 1281.2159, 1304.6201, 1379.7982, 1560.7249, 1568.7400, 1572.7831, 1586.7999, 1643.8240, 1771.9196, 1830.8876, 2273.1592, 2619.2644, 2748.3149, 3211.2510

Spot 3

Mascot Search Results

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:30:25 GMT**
Top Score : **331 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	331	conarachin [Arachis hypogaea]
2.	gi|620025	70639	324	Ara h I
3.	gi|1168390	70639	324	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	243	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	243	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	243	Ara h I
7.	gi|46560476	48122	177	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	98	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	61	conarachin [Arachis hypogaea]
10.	gi|226258	10809	17	ferredoxin I

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 331 **Expect:** 7e-031 **Queries matched:** 31
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3653	807.3580	807.3623	-0.0043	180	186	0	YGNQNGR
812.3934	811.3861	811.3976	-0.0115	109	115	0	WGPAEPR
816.4187	815.4114	815.4249	-0.0135	464	469	1	KEQQQR
896.4249	895.4176	895.4260	-0.0084	272	278	0	HDNQNLR
972.5858	971.5785	971.5837	-0.0052	444	452	0	AMVIVVVNK
1005.5331	1004.5258	1004.5264	-0.0006	132	139	0	RPSHQQPR
1019.4503	1018.4430	1018.4468	-0.0038	118	124	1	EREEDWR
1128.6398	1127.6325	1127.6298	0.0027	453	463	0	GTGNLELVAVR
1141.5453	1140.5380	1140.5352	0.0028	166	174	0	NNPFYFPSR

1184.5962	1183.5889	1183.5846	0.0043	199 - 207	0	QFQNLQNHR
1258.6266	1257.6193	1257.6101	0.0092	249 - 259	0	SFNLDEGHALR
1287.6062	1286.5989	1286.5891	0.0098	302 - 312	0	DQSSYLQGFSR
1297.6533	1296.6460	1296.6363	0.0097	166 - 175	1	NNPFYFPSRR
1320.6023	1319.5950	1319.5741	0.0209	394 - 405	0	DGEPDLSNNFGR
1343.6831	1342.6758	1342.6703	0.0055	432 - 443	0	EGALMLPHFNSK
1379.7795	1378.7722	1378.7608	0.0114	260 - 271	0	IPSGFISYILNR
1399.7209	1398.7136	1398.7116	0.0020	197 - 207	1	SKQFQNLQNHR
1560.7031	1559.6958	1559.6851	0.0107	147 - 160	0	EGEQEWGTPGSEVR
1572.7605	1571.7532	1571.7426	0.0106	329 - 342	0	VLLEENAGGEQEER
1586.7841	1585.7768	1585.7583	0.0185	380 - 393	0	GSEEEDITNPINLR
1691.0313	1690.0240	1690.0141	0.0100	208 - 222	0	IVQIEARPNTLVLPK
1714.8712	1713.8639	1713.8533	0.0107	379 - 393	1	KGSEEEDITNPINLR
1738.8503	1737.8430	1737.8321	0.0109	313 - 327	0	NTLEAAFNAEFNEIR
1817.9713	1816.9640	1816.9570	0.0070	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9484	1893.9411	1893.9332	0.0079	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2087	2081.2014	2081.2030	-0.0015	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0398	2242.0325	2242.0364	-0.0039	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8420	2280.8347	2280.8414	-0.0066	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.3123	2618.3050	2618.3160	-0.0110	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3884	2746.3811	2746.4110	-0.0298	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3703, 828.4621, 1111.5690, 1167.5709, 1281.2159, 1319.6281, 1376.6979, 1534.8389, 1568.7194, 1771.8945, 2185.0420, 2192.9956, 2273.1609, 2295.1414, 2311.1304, 2612.1484, 2748.3806, 3153.3743, 3211.4016

2. gi|620025 **Mass:** 70639 **Score:** 324 **Expect:** 3.5e-030 **Queries matched:** 31

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3653	807.3580	807.3623	-0.0043	180 - 186		0	YGNQNGR
812.3934	811.3861	811.3976	-0.0115	109 - 115		0	WGPAEPR
816.4187	815.4114	815.4249	-0.0135	464 - 469		1	KEQQQR
896.4249	895.4176	895.4260	-0.0084	272 - 278		0	HDNQNLR
972.5858	971.5785	971.5837	-0.0052	444 - 452		0	AMVIVVVNK
1005.5331	1004.5258	1004.5264	-0.0006	132 - 139		0	RPSHQQPR
1019.4503	1018.4430	1018.4468	-0.0038	118 - 124		1	EREEDWR
1128.6398	1127.6325	1127.6298	0.0027	453 - 463		0	GTGNLELVAVR
1141.5453	1140.5380	1140.5352	0.0028	166 - 174		0	NNPFYFPSR
1184.5962	1183.5889	1183.5846	0.0043	199 - 207		0	QFQNLQNHR
1258.6266	1257.6193	1257.6101	0.0092	249 - 259		0	SFNLDEGHALR
1287.6062	1286.5989	1286.5891	0.0098	302 - 312		0	DQSSYLQGFSR

1297.6533	1296.6460	1296.6363	0.0097	166 - 175	1	NNPFYFPSRR
1320.6023	1319.5950	1319.5741	0.0209	394 - 405	0	DGEPDLSNNFGR
1343.6831	1342.6758	1342.6703	0.0055	432 - 443	0	EGALMLPHFNSK
1379.7795	1378.7722	1378.7608	0.0114	260 - 271	0	IPSGFISYILNR
1399.7209	1398.7136	1398.7116	0.0020	197 - 207	1	SKQFQNLQNHR
1560.7031	1559.6958	1559.6851	0.0107	147 - 160	0	EGEQEWGTPGSEVR
1572.7605	1571.7532	1571.7426	0.0106	329 - 342	0	VLLEENAGGEQEER
1586.7841	1585.7768	1585.7583	0.0185	380 - 393	0	GSEEEDITNPINLR
1691.0313	1690.0240	1690.0141	0.0100	208 - 222	0	IVQIEARPNTLVLPK
1714.8712	1713.8639	1713.8533	0.0107	379 - 393	1	KGSEEEDITNPINLR
1738.8503	1737.8430	1737.8321	0.0109	313 - 327	0	NTLEAAFNAEFNEIR
1817.9713	1816.9640	1816.9570	0.0070	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9484	1893.9411	1893.9332	0.0079	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2087	2081.2014	2081.2030	-0.0015	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0398	2242.0325	2242.0364	-0.0039	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8420	2280.8347	2280.8414	-0.0066	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.3123	2618.3050	2618.3160	-0.0110	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3884	2746.3811	2746.4110	-0.0298	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3703, 828.4621, 1111.5690, 1167.5709, 1281.2159, 1319.6281, 1376.6979, 1534.8389, 1568.7194, 1771.8945, 2185.0420, 2192.9956, 2273.1609, 2295.1414, 2311.1304, 2612.1484, 2748.3806, 3153.3743, 3211.4016

3. gi|1168390 **Mass:** 70639 **Score:** 324 **Expect:** 3.5e-030 **Queries matched:** 31

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3653	807.3580	807.3623	-0.0043	180 - 186		0	YGNQNGR
812.3934	811.3861	811.3976	-0.0115	109 - 115		0	WGPAEPR
816.4187	815.4114	815.4249	-0.0135	464 - 469		1	KEQQQR
896.4249	895.4176	895.4260	-0.0084	272 - 278		0	HDNQNLR
972.5858	971.5785	971.5837	-0.0052	444 - 452		0	AMVIVVVNK
1005.5331	1004.5258	1004.5264	-0.0006	132 - 139		0	RPSHQQPR
1019.4503	1018.4430	1018.4468	-0.0038	118 - 124		1	EREEDWR
1128.6398	1127.6325	1127.6298	0.0027	453 - 463		0	GTGNLELVAVR
1141.5453	1140.5380	1140.5352	0.0028	166 - 174		0	NNPFYFPSR
1184.5962	1183.5889	1183.5846	0.0043	199 - 207		0	QFQNLQNHR
1258.6266	1257.6193	1257.6101	0.0092	249 - 259		0	SFNLDEGHALR
1287.6062	1286.5989	1286.5891	0.0098	302 - 312		0	DQSSYLQGFSR
1297.6533	1296.6460	1296.6363	0.0097	166 - 175		1	NNPFYFPSRR
1320.6023	1319.5950	1319.5741	0.0209	394 - 405		0	DGEPDLSNNFGR
1343.6831	1342.6758	1342.6703	0.0055	432 - 443		0	EGALMLPHFNSK

1379.7795	1378.7722	1378.7608	0.0114	260 - 271	0	IPSGFISYILNR
1399.7209	1398.7136	1398.7116	0.0020	197 - 207	1	SKQFQNLQNHR
1560.7031	1559.6958	1559.6851	0.0107	147 - 160	0	EGEQEWGTPGSEVR
1572.7605	1571.7532	1571.7426	0.0106	329 - 342	0	VLLEENAGGEQEER
1586.7841	1585.7768	1585.7583	0.0185	380 - 393	0	GSEEEDITNPINLR
1691.0313	1690.0240	1690.0141	0.0100	208 - 222	0	IVQIEARPNTLVLPK
1714.8712	1713.8639	1713.8533	0.0107	379 - 393	1	KGSEEEDITNPINLR
1738.8503	1737.8430	1737.8321	0.0109	313 - 327	0	NTLEAAFNAEFNEIR
1817.9713	1816.9640	1816.9570	0.0070	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9484	1893.9411	1893.9332	0.0079	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2087	2081.2014	2081.2030	-0.0015	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0398	2242.0325	2242.0364	-0.0039	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8420	2280.8347	2280.8414	-0.0066	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.3123	2618.3050	2618.3160	-0.0110	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3884	2746.3811	2746.4110	-0.0298	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3703, 828.4621, 1111.5690, 1167.5709, 1281.2159, 1319.6281, 1376.6979, 1534.8389, 1568.7194, 1771.8945, 2185.0420, 2192.9956, 2273.1609, 2295.1414, 2311.1304, 2612.1484, 2748.3806, 3153.3743, 3211.4016

4. gi|16612200 **Mass:** 71701 **Score:** 243 **Expect:** 4.4e-022 **Queries matched:** 26

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3703	739.3630	739.3765	-0.0135	115 - 121		0	WGPAGPR
808.3653	807.3580	807.3623	-0.0043	186 - 192		0	YGNQNGR
816.4187	815.4114	815.4249	-0.0135	472 - 477		1	KEQQQR
896.4249	895.4176	895.4260	-0.0084	278 - 284		0	HDNQNLR
972.5858	971.5785	971.5837	-0.0052	452 - 460		0	AMVIVVVNK
1005.5331	1004.5258	1004.5264	-0.0006	138 - 145		0	RPSHQQPR
1019.4503	1018.4430	1018.4468	-0.0038	124 - 130		1	EREEDWR
1128.6398	1127.6325	1127.6298	0.0027	461 - 471		0	GTGNLELVAVR
1141.5453	1140.5380	1140.5352	0.0028	172 - 180		0	NNPFYFPSR
1184.5962	1183.5889	1183.5846	0.0043	205 - 213		0	QFQNLQNHR
1258.6266	1257.6193	1257.6101	0.0092	255 - 265		0	SFNLDEGHALR
1287.6062	1286.5989	1286.5891	0.0098	308 - 318		0	DQSSYLQGFSR
1297.6533	1296.6460	1296.6363	0.0097	172 - 181		1	NNPFYFPSRR
1343.6831	1342.6758	1342.6703	0.0055	440 - 451		0	EGALMLPHFNSK
1379.7795	1378.7722	1378.7608	0.0114	266 - 277		0	IPSGFISYILNR
1568.7194	1567.7121	1567.7015	0.0107	153 - 166		0	EGEQEWGTPGSHVR
1572.7605	1571.7532	1571.7426	0.0106	335 - 348		0	VLLEENAGGEQEER
1738.8503	1737.8430	1737.8321	0.0109	319 - 333		0	NTLEAAFNAEFNEIR

1771.8945	1770.8872	1770.8747	0.0125	386 - 401	1	KGSEEEGDITNPINLR
1817.9713	1816.9640	1816.9570	0.0070	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9484	1893.9411	1893.9332	0.0079	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2087	2081.2014	2081.2030	-0.0015	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0398	2242.0325	2242.0364	-0.0039	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3123	2618.3050	2618.3160	-0.0110	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.3884	2746.3811	2746.4110	-0.0298	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 812.3934, 828.4621, 1111.5690, 1167.5709, 1281.2159, 1319.6281, 1320.6023, 1376.6979, 1399.7209, 1534.8389, 1560.7031, 1586.7841, 1691.0313, 1714.8712, 2185.0420, 2192.9956, 2273.1609, 2281.8420, 2295.1414, 2311.1304, 2612.1484, 2748.3806, 3153.3743, 3211.4016

5. gi|1168391 **Mass:** 71701 **Score:** 243 **Expect:** 4.4e-022 **Queries matched:** 26

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3703	739.3630	739.3765	-0.0135	115 - 121		0	WGPAGPR
808.3653	807.3580	807.3623	-0.0043	186 - 192		0	YGNQNGR
816.4187	815.4114	815.4249	-0.0135	472 - 477		1	KEQQQR
896.4249	895.4176	895.4260	-0.0084	278 - 284		0	HDNQNLR
972.5858	971.5785	971.5837	-0.0052	452 - 460		0	AMVIVVVNK
1005.5331	1004.5258	1004.5264	-0.0006	138 - 145		0	RPSHQQPR
1019.4503	1018.4430	1018.4468	-0.0038	124 - 130		1	EREEDWR
1128.6398	1127.6325	1127.6298	0.0027	461 - 471		0	GTGNLELVAVR
1141.5453	1140.5380	1140.5352	0.0028	172 - 180		0	NNPFYFPSR
1184.5962	1183.5889	1183.5846	0.0043	205 - 213		0	QFQNLQNHR
1258.6266	1257.6193	1257.6101	0.0092	255 - 265		0	SFNLDEGHALR
1287.6062	1286.5989	1286.5891	0.0098	308 - 318		0	DQSSYLQGFSR
1297.6533	1296.6460	1296.6363	0.0097	172 - 181		1	NNPFYFPSRR
1343.6831	1342.6758	1342.6703	0.0055	440 - 451		0	EGALMLPHFNSK
1379.7795	1378.7722	1378.7608	0.0114	266 - 277		0	IPSGFISYILNR
1568.7194	1567.7121	1567.7015	0.0107	153 - 166		0	EGEQEWGTPGSHVR
1572.7605	1571.7532	1571.7426	0.0106	335 - 348		0	VLLEENAGGEQEER
1738.8503	1737.8430	1737.8321	0.0109	319 - 333		0	NTLEAAFNAEFNEIR
1771.8945	1770.8872	1770.8747	0.0125	386 - 401		1	KGSEEEGDITNPINLR
1817.9713	1816.9640	1816.9570	0.0070	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9484	1893.9411	1893.9332	0.0079	319 - 334		1	NTLEAAFNAEFNEIRR
2082.2087	2081.2014	2081.2030	-0.0015	452 - 471		1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	288 - 307		0	ISMPVNTPGQFEDFFPASSR
2243.0398	2242.0325	2242.0364	-0.0039	288 - 307		0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3123	2618.3050	2618.3160	-0.0110	229 - 253		0	HADADNILVIQQGQATVTVANGNNR

2747.3884	2746.3811	2746.4110	-0.0298	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 812.3934, 828.4621, 1111.5690, 1167.5709, 1281.2159, 1319.6281, 1320.6023, 1376.6979, 1399.7209, 1534.8389, 1560.7031, 1586.7841, 1691.0313, 1714.8712, 2185.0420, 2192.9956, 2273.1609, 2281.8420, 2295.1414, 2311.1304, 2612.1484, 2748.3806, 3153.3743, 3211.4016

6. gi|602436 **Mass:** 71701 **Score:** 243 **Expect:** 4.4e-022 **Queries matched:** 26

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3703	739.3630	739.3765	-0.0135	115 -	121	0	WGPAGPR
808.3653	807.3580	807.3623	-0.0043	186 -	192	0	YGNQNGR
816.4187	815.4114	815.4249	-0.0135	472 -	477	1	KEQQQR
896.4249	895.4176	895.4260	-0.0084	278 -	284	0	HDNQNLR
972.5858	971.5785	971.5837	-0.0052	452 -	460	0	AMVIVVVNK
1005.5331	1004.5258	1004.5264	-0.0006	138 -	145	0	RPSHQQPR
1019.4503	1018.4430	1018.4468	-0.0038	124 -	130	1	EREEDWR
1128.6398	1127.6325	1127.6298	0.0027	461 -	471	0	GTGNLELVAVR
1141.5453	1140.5380	1140.5352	0.0028	172 -	180	0	NNPFYFPSR
1184.5962	1183.5889	1183.5846	0.0043	205 -	213	0	QFQNLQNHR
1258.6266	1257.6193	1257.6101	0.0092	255 -	265	0	SFNLDEGHALR
1287.6062	1286.5989	1286.5891	0.0098	308 -	318	0	DQSSYLQGFSR
1297.6533	1296.6460	1296.6363	0.0097	172 -	181	1	NNPFYFPSRR
1343.6831	1342.6758	1342.6703	0.0055	440 -	451	0	EGALMLPHFNSK
1379.7795	1378.7722	1378.7608	0.0114	266 -	277	0	IPSGFISYILNR
1568.7194	1567.7121	1567.7015	0.0107	153 -	166	0	EGEQEWGTPGSHVR
1572.7605	1571.7532	1571.7426	0.0106	335 -	348	0	VLLEENAGGEQEER
1738.8503	1737.8430	1737.8321	0.0109	319 -	333	0	NTLEAAFNAEFNEIR
1771.8945	1770.8872	1770.8747	0.0125	386 -	401	1	KGSEEEGDITNPINLR
1817.9713	1816.9640	1816.9570	0.0070	541 -	556	1	IFLAGDKDNVIDQIEK
1894.9484	1893.9411	1893.9332	0.0079	319 -	334	1	NTLEAAFNAEFNEIRR
2082.2087	2081.2014	2081.2030	-0.0015	452 -	471	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	288 -	307	0	ISMPVNTPGQFEDFFPASSR
2243.0398	2242.0325	2242.0364	-0.0039	288 -	307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3123	2618.3050	2618.3160	-0.0110	229 -	253	0	HADADNILVIQQGQATVTVANGNNR
2747.3884	2746.3811	2746.4110	-0.0298	229 -	254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 812.3934, 828.4621, 1111.5690, 1167.5709, 1281.2159, 1319.6281, 1320.6023, 1376.6979, 1399.7209, 1534.8389, 1560.7031, 1586.7841, 1691.0313, 1714.8712, 2185.0420, 2192.9956, 2273.1609, 2281.8420, 2295.1414, 2311.1304, 2612.1484, 2748.3806, 3153.3743, 3211.4016

7. gi|46560476 **Mass:** 48122 **Score:** 177 **Expect:** 1.7e-015 **Queries matched:** 18

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

816.4187	815.4114	815.4249	-0.0135	274 - 279	1	KEQQQR
896.4249	895.4176	895.4260	-0.0084	81 - 87	0	HDNQNLR
972.5858	971.5785	971.5837	-0.0052	254 - 262	0	AMVIVVVNK
1128.6398	1127.6325	1127.6298	0.0027	263 - 273	0	GTGNLELVAVR
1184.5962	1183.5889	1183.5846	0.0043	8 - 16	0	QFQNLQNHR
1258.6266	1257.6193	1257.6101	0.0092	58 - 68	0	SFNLDEGHALR
1287.6062	1286.5989	1286.5891	0.0098	111 - 121	0	DQSSYLQGFSR
1343.6831	1342.6758	1342.6703	0.0055	242 - 253	0	EGALMLPHFNSK
1379.7795	1378.7722	1378.7608	0.0114	69 - 80	0	IPSGFISYILNR
1572.7605	1571.7532	1571.7426	0.0106	138 - 151	0	VLLEENAGGEQEER
1738.8503	1737.8430	1737.8321	0.0109	122 - 136	0	NTLEAAFNAEFNEIR
1817.9713	1816.9640	1816.9570	0.0070	343 - 358	1	IFLAGDKDNVIDQIEK
1894.9484	1893.9411	1893.9332	0.0079	122 - 137	1	NTLEAAFNAEFNEIRR
2082.2087	2081.2014	2081.2030	-0.0015	254 - 273	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	91 - 110	0	ISMPVNTPGQFEDFFPASSR
2243.0398	2242.0325	2242.0364	-0.0039	91 - 110	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3123	2618.3050	2618.3160	-0.0110	32 - 56	0	HADADNILVIQQGQATVTVANGNNR
2747.3884	2746.3811	2746.4110	-0.0298	32 - 57	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3703, 808.3653, 812.3934, 828.4621, 1005.5331, 1019.4503, 1111.5690, 1141.5453, 1167.5709, 1281.2159, 1297.6533, 1319.6281, 1320.6023, 1376.6979, 1399.7209, 1534.8389, 1560.7031, 1568.7194, 1586.7841, 1691.0313, 1714.8712, 1771.8945, 2185.0420, 2192.9956, 2273.1609, 2281.8420, 2295.1414, 2311.1304, 2612.1484, 2748.3806, 3153.3743, 3211.4016

8. gi|46560472 **Mass:** 34169 **Score:** 98 **Expect:** 1.3e-007 **Queries matched:** 11

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4187	815.4114	815.4249	-0.0135	153 - 158		1	KEQQQR
972.5858	971.5785	971.5837	-0.0052	133 - 141		0	AMVIVVVNK
1128.6398	1127.6325	1127.6298	0.0027	142 - 152		0	GTGNLELVAVR
1320.6023	1319.5950	1319.5741	0.0209	83 - 94		0	DGEPDLSNNFGR
1343.6831	1342.6758	1342.6703	0.0055	121 - 132		0	EGALMLPHFNSK
1572.7605	1571.7532	1571.7426	0.0106	18 - 31		0	VLLEENAGGEQEER
1586.7841	1585.7768	1585.7583	0.0185	69 - 82		0	GSEEEDITNPINLR
1714.8712	1713.8639	1713.8533	0.0107	68 - 82		1	KGSEEEDITNPINLR
1817.9713	1816.9640	1816.9570	0.0070	225 - 240		1	IFLAGDKDNVIDQIEK
2082.2087	2081.2014	2081.2030	-0.0015	133 - 152		1	AMVIVVVNKGTGNLELVAVR
2281.8420	2280.8347	2280.8414	-0.0066	162 - 179		0	EQEWEEEEEDEEEEGSNR

No match to: 740.3703, 808.3653, 812.3934, 828.4621, 896.4249, 1005.5331, 1019.4503, 1111.5690, 1141.5453, 1167.5709, 1184.5962, 1258.6266, 1281.2159, 1287.6062, 1297.6533, 1319.6281, 1376.6979, 1379.7795, 1399.7209, 1534.8389, 1560.7031, 1568.7194, 1691.0313, 1738.8503, 1771.8945, 1894.9484, 2185.0420, 2192.9956, 2227.0444, 2243.0398, 2273.1609, 2295.1414, 2311.1304, 2612.1484, 2619.3123, 2747.3884, 2748.3806, 3153.3743, 3211.4016

9. gi|46560474 **Mass:** 33641 **Score:** 61 **Expect:** 0.00071 **Queries matched:** 8

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4187	815.4114	815.4249	-0.0135	152	157	1	KEQQQR
972.5858	971.5785	971.5837	-0.0052	132	140	0	AMVIVVVNK
1128.6398	1127.6325	1127.6298	0.0027	141	151	0	GTGNLELVAVR
1343.6831	1342.6758	1342.6703	0.0055	120	131	0	EGALMLPHFNSK
1572.7605	1571.7532	1571.7426	0.0106	15	28	0	VLLEENAGGEQEER
1771.8945	1770.8872	1770.8747	0.0125	66	81	1	KGSEEEGDITNPINLR
1817.9713	1816.9640	1816.9570	0.0070	221	236	1	IFLAGDKDNVIDQIEK
2082.2087	2081.2014	2081.2030	-0.0015	132	151	1	AMVIVVVNKGTGNLELVAVR

No match to: 740.3703, 808.3653, 812.3934, 828.4621, 896.4249, 1005.5331, 1019.4503, 1111.5690, 1141.5453, 1167.5709, 1184.5962, 1258.6266, 1281.2159, 1287.6062, 1297.6533, 1319.6281, 1320.6023, 1376.6979, 1379.7795, 1399.7209, 1534.8389, 1560.7031, 1568.7194, 1586.7841, 1691.0313, 1714.8712, 1738.8503, 1894.9484, 2185.0420, 2192.9956, 2227.0444, 2243.0398, 2273.1609, 2281.8420, 2295.1414, 2311.1304, 2612.1484, 2619.3123, 2747.3884, 2748.3806, 3153.3743, 3211.4016

10. gi|226258 **Mass:** 10809 **Score:** 17 **Expect:** 20 **Queries matched:** 2

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Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1141.5453	1140.5380	1140.5484	-0.0104	16	26	0	GDLAVAMASYK + Oxidation (M)
1297.6533	1296.6460	1296.6496	-0.0035	15	26	1	RGDLAVAMASYK + Oxidation (M)

No match to: 740.3703, 808.3653, 812.3934, 816.4187, 828.4621, 896.4249, 972.5858, 1005.5331, 1019.4503, 1111.5690, 1128.6398, 1167.5709, 1184.5962, 1258.6266, 1281.2159, 1287.6062, 1319.6281, 1320.6023, 1343.6831, 1376.6979, 1379.7795, 1399.7209, 1534.8389, 1560.7031, 1568.7194, 1572.7605, 1586.7841, 1691.0313, 1714.8712, 1738.8503, 1771.8945, 1817.9713, 1894.9484, 2082.2087, 2185.0420, 2192.9956, 2227.0444, 2243.0398, 2273.1609, 2281.8420, 2295.1414, 2311.1304, 2612.1484, 2619.3123, 2747.3884, 2748.3806, 3153.3743, 3211.4016

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|46560478** Score: **331** Expect: **7e-031**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **31**
Sequence Coverage: **50%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
109 - 115	812.3934	811.3861	811.3976	-0.0115	0	WGPAEPR
118 - 124	1019.4503	1018.4430	1018.4468	-0.0038	1	EREEDWR
132 - 139	1005.5331	1004.5258	1004.5264	-0.0006	0	RPSHQQPR
147 - 160	1560.7031	1559.6958	1559.6851	0.0107	0	EGEQEWGTPGSEVR
166 - 174	1141.5453	1140.5380	1140.5352	0.0028	0	NNPFYFPSR
166 - 175	1297.6533	1296.6460	1296.6363	0.0097	1	NNPFYFPSRR
180 - 186	808.3653	807.3580	807.3623	-0.0043	0	YGNQNGR

197 - 207	1399.7209	1398.7136	1398.7116	0.0020	1	SKQFQNLQNHR
199 - 207	1184.5962	1183.5889	1183.5846	0.0043	0	QFQNLQNHR
208 - 222	1691.0313	1690.0240	1690.0141	0.0100	0	IVQIEARPNTLVLPK
223 - 247	2619.3123	2618.3050	2618.3160	-0.0110	0	HADADNILVIQQGQATVTVANGNNR
223 - 248	2747.3884	2746.3811	2746.4110	-0.0298	1	HADADNILVIQQGQATVTVANGNNRK
249 - 259	1258.6266	1257.6193	1257.6101	0.0092	0	SFNLDEGHALR
260 - 271	1379.7795	1378.7722	1378.7608	0.0114	0	IPSGFISYILNR
272 - 278	896.4249	895.4176	895.4260	-0.0084	0	HDNQNLR
282 - 301	2227.0444	2226.0371	2226.0415	-0.0044	0	ISMPVNTPGQFEDFFPASSR
282 - 301	2243.0398	2242.0325	2242.0364	-0.0039	0	ISMPVNTPGQFEDFFPASSR Oxidation (M)
302 - 312	1287.6062	1286.5989	1286.5891	0.0098	0	DQSSYLQGFSR
313 - 327	1738.8503	1737.8430	1737.8321	0.0109	0	NTLEAAFNAEFNEIR
313 - 328	1894.9484	1893.9411	1893.9332	0.0079	1	NTLEAAFNAEFNEIRR
329 - 342	1572.7605	1571.7532	1571.7426	0.0106	0	VLLEENAGGEQEER
379 - 393	1714.8712	1713.8639	1713.8533	0.0107	1	KGSEEEDITNPINLR
380 - 393	1586.7841	1585.7768	1585.7583	0.0185	0	GSEEEDITNPINLR
394 - 405	1320.6023	1319.5950	1319.5741	0.0209	0	DGEPDLSNNFGR
432 - 443	1343.6831	1342.6758	1342.6703	0.0055	0	EGALMLPHFNSK
444 - 452	972.5858	971.5785	971.5837	-0.0052	0	AMVIVVVNK
444 - 463	2082.2087	2081.2014	2081.2030	-0.0015	1	AMVIVVVNKGTGNLELVAVR
453 - 463	1128.6398	1127.6325	1127.6298	0.0027	0	GTGNLELVAVR
464 - 469	816.4187	815.4114	815.4249	-0.0135	1	KEQQQR
473 - 490	2281.8420	2280.8347	2280.8414	-0.0066	0	EQEWEEEEEDEEEEGSNR
536 - 551	1817.9713	1816.9640	1816.9570	0.0070	1	IFLAGDKDNVIDQIEK

No match to: 740.3703, 828.4621, 1111.5690, 1167.5709, 1281.2159, 1319.6281, 1376.6979, 1534.8389, 1568.7194, 1771.8945, 2185.0420, 2192.9956, 2273.1609, 2295.1414, 2311.1304, 2612.1484, 2748.3806, 3153.3743, 3211.4016

Spot 4

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:37:32 GMT**
Top Score : **154 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	154	conarachin [Arachis hypogaea]
2.	gi|620025	70639	150	Ara h I
3.	gi|1168390	70639	150	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	116	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	116	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	116	Ara h I
7.	gi|46560476	48122	86	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	42	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	34	conarachin [Arachis hypogaea]
10.	gi|230338	23975	20	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|46560478 **Mass:** 66934 **Score:** **154** **Expect:** 3.5e-013 **Queries matched:** 21
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
855.5212	854.5139	854.5086	0.0053	140	146	1	KIRPEGR
896.4462	895.4389	895.4260	0.0129	272	278	0	HDNQNLR
1005.5402	1004.5329	1004.5264	0.0065	132	139	0	RPSHQQPR
1141.5549	1140.5476	1140.5352	0.0124	166	174	0	NNPFYFPSR
1184.6013	1183.5940	1183.5846	0.0094	199	207	0	QFQNLQNHR
1258.6156	1257.6083	1257.6101	-0.0018	249	259	0	SFNLDEGHALR
1287.6045	1286.5972	1286.5891	0.0081	302	312	0	DQSSYLQGFSR
1297.6490	1296.6417	1296.6363	0.0054	166	175	1	NNPFYFPSRR
1320.5898	1319.5825	1319.5741	0.0084	394	405	0	DGEPDLSNNFGR

1359.6471	1358.6398	1358.6652	-0.0254	432 - 443	0	EGALMLPHFNSK + Oxidation (M)
1376.6614	1375.6541	1375.6619	-0.0078	555 - 567	0	DLAFPGSGEQVEK
1399.7281	1398.7208	1398.7116	0.0092	197 - 207	1	SKQFQNLQNHR
1560.6843	1559.6770	1559.6851	-0.0081	147 - 160	0	EGEQEWGTPGSEVR
1572.7523	1571.7450	1571.7426	0.0024	329 - 342	0	VLLEENAGGEQEER
1586.7634	1585.7561	1585.7583	-0.0022	380 - 393	0	GSEEEDITNPINLR
1691.0221	1690.0148	1690.0141	0.0008	208 - 222	0	IVQIEARPNTLVLPK
1714.8658	1713.8585	1713.8533	0.0053	379 - 393	1	KGSEEEDITNPINLR
1728.8468	1727.8395	1727.8437	-0.0042	328 - 342	1	RVLLEENAGGEQEER
1738.8414	1737.8341	1737.8321	0.0020	313 - 327	0	NTLEAAFNAEFNEIR
1894.9250	1893.9177	1893.9332	-0.0155	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0920	2226.0847	2226.0415	0.0432	282 - 301	0	ISMPVNTPGQFEDFFPASSR

No match to: 805.4588, 855.0504, 861.0752, 877.0366, 959.4948, 1046.6029, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1145.0525, 1145.5836, 1167.5779, 1175.5732, 1234.6892, 1296.6444, 1309.6244, 1493.7371, 1496.7352, 1529.7163, 1568.7136, 1771.8705, 1774.8541, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2273.1582, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2514.3491, 2515.3472, 2530.3721, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

2. gi|620025 **Mass:** 70639 **Score:** 150 **Expect:** 8.8e-013 **Queries matched:** 21

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
855.5212	854.5139	854.5086	0.0053	140 - 146		1	KIRPEGR
896.4462	895.4389	895.4260	0.0129	272 - 278		0	HDNQNLR
1005.5402	1004.5329	1004.5264	0.0065	132 - 139		0	RPSHQQPR
1141.5549	1140.5476	1140.5352	0.0124	166 - 174		0	NNPFYFPSR
1184.6013	1183.5940	1183.5846	0.0094	199 - 207		0	QFQNLQNHR
1258.6156	1257.6083	1257.6101	-0.0018	249 - 259		0	SFNLDEGHALR
1287.6045	1286.5972	1286.5891	0.0081	302 - 312		0	DQSSYLQGFSR
1297.6490	1296.6417	1296.6363	0.0054	166 - 175		1	NNPFYFPSRR
1320.5898	1319.5825	1319.5741	0.0084	394 - 405		0	DGEPDLSNNFGR
1359.6471	1358.6398	1358.6652	-0.0254	432 - 443		0	EGALMLPHFNSK + Oxidation (M)
1376.6614	1375.6541	1375.6619	-0.0078	555 - 567		0	DLAFPGSGEQVEK
1399.7281	1398.7208	1398.7116	0.0092	197 - 207		1	SKQFQNLQNHR
1560.6843	1559.6770	1559.6851	-0.0081	147 - 160		0	EGEQEWGTPGSEVR
1572.7523	1571.7450	1571.7426	0.0024	329 - 342		0	VLLEENAGGEQEER
1586.7634	1585.7561	1585.7583	-0.0022	380 - 393		0	GSEEEDITNPINLR
1691.0221	1690.0148	1690.0141	0.0008	208 - 222		0	IVQIEARPNTLVLPK
1714.8658	1713.8585	1713.8533	0.0053	379 - 393		1	KGSEEEDITNPINLR
1728.8468	1727.8395	1727.8437	-0.0042	328 - 342		1	RVLLEENAGGEQEER

1738.8414	1737.8341	1737.8321	0.0020	313 - 327	0	NTLEAAFNAEFNEIR
1894.9250	1893.9177	1893.9332	-0.0155	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0920	2226.0847	2226.0415	0.0432	282 - 301	0	ISMPVNTPGQFEDFFPASSR

No match to: 805.4588, 855.0504, 861.0752, 877.0366, 959.4948, 1046.6029, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1145.0525, 1145.5836, 1167.5779, 1175.5732, 1234.6892, 1296.6444, 1309.6244, 1493.7371, 1496.7352, 1529.7163, 1568.7136, 1771.8705, 1774.8541, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2273.1582, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2514.3491, 2515.3472, 2530.3721, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

3. gi|1168390 **Mass:** 70639 **Score:** 150 **Expect:** 8.8e-013 **Queries matched:** 21

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
855.5212	854.5139	854.5086	0.0053	140 - 146		1	KIRPEGR
896.4462	895.4389	895.4260	0.0129	272 - 278		0	HDNQNLR
1005.5402	1004.5329	1004.5264	0.0065	132 - 139		0	RPSHQQPR
1141.5549	1140.5476	1140.5352	0.0124	166 - 174		0	NNPFYFPSR
1184.6013	1183.5940	1183.5846	0.0094	199 - 207		0	QFQNLQNHR
1258.6156	1257.6083	1257.6101	-0.0018	249 - 259		0	SFNLDEGHALR
1287.6045	1286.5972	1286.5891	0.0081	302 - 312		0	DQSSYLQGFSR
1297.6490	1296.6417	1296.6363	0.0054	166 - 175		1	NNPFYFPSRR
1320.5898	1319.5825	1319.5741	0.0084	394 - 405		0	DGEPDLSNNFGR
1359.6471	1358.6398	1358.6652	-0.0254	432 - 443		0	EGALMLPHFNSK + Oxidation (M)
1376.6614	1375.6541	1375.6619	-0.0078	555 - 567		0	DLAFPGSGEQVEK
1399.7281	1398.7208	1398.7116	0.0092	197 - 207		1	SKQFQNLQNHR
1560.6843	1559.6770	1559.6851	-0.0081	147 - 160		0	EGEQEWGTPGSEVR
1572.7523	1571.7450	1571.7426	0.0024	329 - 342		0	VLLEENAGGEQEER
1586.7634	1585.7561	1585.7583	-0.0022	380 - 393		0	GSEEEDITNPINLR
1691.0221	1690.0148	1690.0141	0.0008	208 - 222		0	IVQIEARPNTLVLPK
1714.8658	1713.8585	1713.8533	0.0053	379 - 393		1	KGSEEEDITNPINLR
1728.8468	1727.8395	1727.8437	-0.0042	328 - 342		1	RVLLEENAGGEQEER
1738.8414	1737.8341	1737.8321	0.0020	313 - 327		0	NTLEAAFNAEFNEIR
1894.9250	1893.9177	1893.9332	-0.0155	313 - 328		1	NTLEAAFNAEFNEIRR
2227.0920	2226.0847	2226.0415	0.0432	282 - 301		0	ISMPVNTPGQFEDFFPASSR

No match to: 805.4588, 855.0504, 861.0752, 877.0366, 959.4948, 1046.6029, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1145.0525, 1145.5836, 1167.5779, 1175.5732, 1234.6892, 1296.6444, 1309.6244, 1493.7371, 1496.7352, 1529.7163, 1568.7136, 1771.8705, 1774.8541, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2273.1582, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2514.3491, 2515.3472, 2530.3721, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

4. gi|16612200 **Mass:** 71701 **Score:** 116 **Expect:** 2.2e-009 **Queries matched:** 18

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
855.5212	854.5139	854.5086	0.0053	146	-	152	1	KIRPEGR
896.4462	895.4389	895.4260	0.0129	278	-	284	0	HDNQNLR
1005.5402	1004.5329	1004.5264	0.0065	138	-	145	0	RPSHQQPR
1141.5549	1140.5476	1140.5352	0.0124	172	-	180	0	NNPFYFPSR
1175.5732	1174.5659	1174.5829	-0.0170	357	-	367	0	SSENNEGVIVK
1184.6013	1183.5940	1183.5846	0.0094	205	-	213	0	QFQNLQNHR
1258.6156	1257.6083	1257.6101	-0.0018	255	-	265	0	SFNLDEGHALR
1287.6045	1286.5972	1286.5891	0.0081	308	-	318	0	DQSSYLQGFSR
1297.6490	1296.6417	1296.6363	0.0054	172	-	181	1	NNPFYFPSRR
1359.6471	1358.6398	1358.6652	-0.0254	440	-	451	0	EGALMLPHFNSK + Oxidation (M)
1376.6614	1375.6541	1375.6619	-0.0078	560	-	572	0	DLAFPGSGEQVEK
1568.7136	1567.7063	1567.7015	0.0049	153	-	166	0	EGEQEWGTPGSHVR
1572.7523	1571.7450	1571.7426	0.0024	335	-	348	0	VLLEENAGGEQEER
1728.8468	1727.8395	1727.8437	-0.0042	334	-	348	1	RVLLEENAGGEQEER
1738.8414	1737.8341	1737.8321	0.0020	319	-	333	0	NTLEAAFNAEFNEIR
1771.8705	1770.8632	1770.8747	-0.0115	386	-	401	1	KGSEEEGDITNPINLR
1894.9250	1893.9177	1893.9332	-0.0155	319	-	334	1	NTLEAAFNAEFNEIRR
2227.0920	2226.0847	2226.0415	0.0432	288	-	307	0	ISMPVNTPGQFEDFFPASSR

No match to: 805.4588, 855.0504, 861.0752, 877.0366, 959.4948, 1046.6029, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1145.0525, 1145.5836, 1167.5779, 1234.6892, 1296.6444, 1309.6244, 1320.5898, 1399.7281, 1493.7371, 1496.7352, 1529.7163, 1560.6843, 1586.7634, 1691.0221, 1714.8658, 1774.8541, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2273.1582, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2514.3491, 2515.3472, 2530.3721, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

5. gi|1168391 **Mass:** 71701 **Score:** 116 **Expect:** 2.2e-009 **Queries matched:** 18

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
855.5212	854.5139	854.5086	0.0053	146	-	152	1	KIRPEGR
896.4462	895.4389	895.4260	0.0129	278	-	284	0	HDNQNLR
1005.5402	1004.5329	1004.5264	0.0065	138	-	145	0	RPSHQQPR
1141.5549	1140.5476	1140.5352	0.0124	172	-	180	0	NNPFYFPSR
1175.5732	1174.5659	1174.5829	-0.0170	357	-	367	0	SSENNEGVIVK
1184.6013	1183.5940	1183.5846	0.0094	205	-	213	0	QFQNLQNHR
1258.6156	1257.6083	1257.6101	-0.0018	255	-	265	0	SFNLDEGHALR

1287.6045	1286.5972	1286.5891	0.0081	308 - 318	0	DQSSYLQGFSR
1297.6490	1296.6417	1296.6363	0.0054	172 - 181	1	NNPFYFPSRR
1359.6471	1358.6398	1358.6652	-0.0254	440 - 451	0	EGALMLPHFNSK + Oxidation (M)
1376.6614	1375.6541	1375.6619	-0.0078	560 - 572	0	DLAFPGSGEQVEK
1568.7136	1567.7063	1567.7015	0.0049	153 - 166	0	EGEQEWGTPGSHVR
1572.7523	1571.7450	1571.7426	0.0024	335 - 348	0	VLLEENAGGEQEER
1728.8468	1727.8395	1727.8437	-0.0042	334 - 348	1	RVLLEENAGGEQEER
1738.8414	1737.8341	1737.8321	0.0020	319 - 333	0	NTLEAAFNAEFNEIR
1771.8705	1770.8632	1770.8747	-0.0115	386 - 401	1	KGSEEEGDITNPINLR
1894.9250	1893.9177	1893.9332	-0.0155	319 - 334	1	NTLEAAFNAEFNEIRR
2227.0920	2226.0847	2226.0415	0.0432	288 - 307	0	ISMPVNTPGQFEDFFPASSR

No match to: 805.4588, 855.0504, 861.0752, 877.0366, 959.4948, 1046.6029, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1145.0525, 1145.5836, 1167.5779, 1234.6892, 1296.6444, 1309.6244, 1320.5898, 1399.7281, 1493.7371, 1496.7352, 1529.7163, 1560.6843, 1586.7634, 1691.0221, 1714.8658, 1774.8541, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2273.1582, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2514.3491, 2515.3472, 2530.3721, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

6. gi|602436 **Mass:** 71701 **Score:** 116 **Expect:** 2.2e-009 **Queries matched:** 18

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
855.5212	854.5139	854.5086	0.0053	146 - 152		1	KIRPEGR
896.4462	895.4389	895.4260	0.0129	278 - 284		0	HDNQNLR
1005.5402	1004.5329	1004.5264	0.0065	138 - 145		0	RPSHQQPR
1141.5549	1140.5476	1140.5352	0.0124	172 - 180		0	NNPFYFPSR
1175.5732	1174.5659	1174.5829	-0.0170	357 - 367		0	SSENNEGVIVK
1184.6013	1183.5940	1183.5846	0.0094	205 - 213		0	QFQNLQNHR
1258.6156	1257.6083	1257.6101	-0.0018	255 - 265		0	SFNLDEGHALR
1287.6045	1286.5972	1286.5891	0.0081	308 - 318		0	DQSSYLQGFSR
1297.6490	1296.6417	1296.6363	0.0054	172 - 181		1	NNPFYFPSRR
1359.6471	1358.6398	1358.6652	-0.0254	440 - 451		0	EGALMLPHFNSK + Oxidation (M)
1376.6614	1375.6541	1375.6619	-0.0078	560 - 572		0	DLAFPGSGEQVEK
1568.7136	1567.7063	1567.7015	0.0049	153 - 166		0	EGEQEWGTPGSHVR
1572.7523	1571.7450	1571.7426	0.0024	335 - 348		0	VLLEENAGGEQEER
1728.8468	1727.8395	1727.8437	-0.0042	334 - 348		1	RVLLEENAGGEQEER
1738.8414	1737.8341	1737.8321	0.0020	319 - 333		0	NTLEAAFNAEFNEIR
1771.8705	1770.8632	1770.8747	-0.0115	386 - 401		1	KGSEEEGDITNPINLR
1894.9250	1893.9177	1893.9332	-0.0155	319 - 334		1	NTLEAAFNAEFNEIRR
2227.0920	2226.0847	2226.0415	0.0432	288 - 307		0	ISMPVNTPGQFEDFFPASSR

No match to: 805.4588, 855.0504, 861.0752, 877.0366, 959.4948, 1046.6029, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1145.0525, 1145.5836, 1167.5779, 1234.6892, 1296.6444, 1309.6244, 1320.5898, 1399.7281, 1493.7371, 1496.7352, 1529.7163, 1560.6843, 1586.7634, 1691.0221, 1714.8658, 1774.8541, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2273.1582, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2514.3491, 2515.3472, 2530.3721, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

7. gi|46560476 **Mass:** 48122 **Score:** 86 **Expect:** 2e-006 **Queries matched:** 12

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
896.4462	895.4389	895.4260	0.0129	81	-	87	0	HDNQNLR
1175.5732	1174.5659	1174.5829	-0.0170	160	-	170	0	SSENNEGVIVK
1184.6013	1183.5940	1183.5846	0.0094	8	-	16	0	QFQNLQNHR
1258.6156	1257.6083	1257.6101	-0.0018	58	-	68	0	SFNLDEGHALR
1287.6045	1286.5972	1286.5891	0.0081	111	-	121	0	DQSSYLQGFSR
1359.6471	1358.6398	1358.6652	-0.0254	242	-	253	0	EGALMLPHFNSK + Oxidation (M)
1376.6614	1375.6541	1375.6619	-0.0078	362	-	374	0	DLAFPGSGEQVEK
1572.7523	1571.7450	1571.7426	0.0024	138	-	151	0	VLLEENAGGEQEER
1728.8468	1727.8395	1727.8437	-0.0042	137	-	151	1	RVLLEENAGGEQEER
1738.8414	1737.8341	1737.8321	0.0020	122	-	136	0	NTLEAAFNAEFNEIR
1894.9250	1893.9177	1893.9332	-0.0155	122	-	137	1	NTLEAAFNAEFNEIRR
2227.0920	2226.0847	2226.0415	0.0432	91	-	110	0	ISMPVNTPGQFEDFFPASSR

No match to: 805.4588, 855.0504, 855.5212, 861.0752, 877.0366, 959.4948, 1005.5402, 1046.6029, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1141.5549, 1145.0525, 1145.5836, 1167.5779, 1234.6892, 1296.6444, 1297.6490, 1309.6244, 1320.5898, 1399.7281, 1493.7371, 1496.7352, 1529.7163, 1560.6843, 1568.7136, 1586.7634, 1691.0221, 1714.8658, 1771.8705, 1774.8541, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2273.1582, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2514.3491, 2515.3472, 2530.3721, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

8. gi|46560472 **Mass:** 34169 **Score:** 42 **Expect:** 0.05 **Queries matched:** 7

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1320.5898	1319.5825	1319.5741	0.0084	83	-	94	0	DGEPDLSNNFGR
1359.6471	1358.6398	1358.6652	-0.0254	121	-	132	0	EGALMLPHFNSK + Oxidation (M)
1376.6614	1375.6541	1375.6619	-0.0078	244	-	256	0	DLAFPGSGEQVEK
1572.7523	1571.7450	1571.7426	0.0024	18	-	31	0	VLLEENAGGEQEER
1586.7634	1585.7561	1585.7583	-0.0022	69	-	82	0	GSEEEDITNPINLR
1714.8658	1713.8585	1713.8533	0.0053	68	-	82	1	KGSEEEDITNPINLR
1728.8468	1727.8395	1727.8437	-0.0042	17	-	31	1	RVLLEENAGGEQEER

No match to: 805.4588, 855.0504, 855.5212, 861.0752, 877.0366, 896.4462, 959.4948, 1005.5402, 1046.6029, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1141.5549, 1145.0525, 1145.5836, 1167.5779, 1175.5732, 1184.6013, 1234.6892, 1258.6156, 1287.6045, 1296.6444, 1297.6490, 1309.6244, 1399.7281, 1493.7371, 1496.7352, 1529.7163, 1560.6843, 1568.7136, 1691.0221, 1738.8414, 1771.8705, 1774.8541, 1894.9250, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2227.0920, 2273.1582, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2514.3491, 2515.3472, 2530.3721, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

9. gi|46560474 **Mass:** 33641 **Score:** 34 **Expect:** 0.35 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1175.5732	1174.5659	1174.5829	-0.0170	37	-	47	0	SSENNEGVIVK
1359.6471	1358.6398	1358.6652	-0.0254	120	-	131	0	EGALMLPHFNSK + Oxidation (M)
1376.6614	1375.6541	1375.6619	-0.0078	240	-	252	0	DLAFPGSGEQVEK
1572.7523	1571.7450	1571.7426	0.0024	15	-	28	0	VLLEENAGGEQEER
1728.8468	1727.8395	1727.8437	-0.0042	14	-	28	1	RVLLEENAGGEQEER
1771.8705	1770.8632	1770.8747	-0.0115	66	-	81	1	KGSEEEGDITNPINLR

No match to: 805.4588, 855.0504, 855.5212, 861.0752, 877.0366, 896.4462, 959.4948, 1005.5402, 1046.6029, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1141.5549, 1145.0525, 1145.5836, 1167.5779, 1184.6013, 1234.6892, 1258.6156, 1287.6045, 1296.6444, 1297.6490, 1309.6244, 1320.5898, 1399.7281, 1493.7371, 1496.7352, 1529.7163, 1560.6843, 1568.7136, 1586.7634, 1691.0221, 1714.8658, 1738.8414, 1774.8541, 1894.9250, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2227.0920, 2273.1582, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2514.3491, 2515.3472, 2530.3721, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

10. gi|230338 **Mass:** 23975 **Score:** 20 **Expect:** 9 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1046.6029	1045.5956	1045.5880	0.0077	90	-	99	1	LKSAASLNSR
2273.1582	2272.1509	2272.1521	-0.0012	70	-	89	0	SIVHPSYNSNTLNNDIMLIK
2514.3491	2513.3418	2513.3311	0.0107	70	-	91	1	SIVHPSYNSNTLNNDIMLIKLK
2530.3721	2529.3648	2529.3260	0.0388	70	-	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4588, 855.0504, 855.5212, 861.0752, 877.0366, 896.4462, 959.4948, 1005.5402, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1141.5549, 1145.0525, 1145.5836, 1167.5779, 1175.5732, 1184.6013, 1234.6892, 1258.6156, 1287.6045, 1296.6444, 1297.6490, 1309.6244, 1320.5898, 1359.6471, 1376.6614, 1399.7281, 1493.7371, 1496.7352, 1529.7163, 1560.6843, 1568.7136, 1572.7523, 1586.7634, 1691.0221, 1714.8658, 1728.8468, 1738.8414, 1771.8705, 1774.8541, 1894.9250, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2227.0920, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2515.3472, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 66

Protein View

Match to: **gi|46560478** Score: **154** Expect: **3.5e-013**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **66**
Number of mass values matched: **21**
Sequence Coverage: **33%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
132 - 139	1005.5402	1004.5329	1004.5264	0.0065	0	RPSHQQPR	
140 - 146	855.5212	854.5139	854.5086	0.0053	1	KIRPEGR	
147 - 160	1560.6843	1559.6770	1559.6851	-0.0081	0	EGEQEWGTPGSEVR	
166 - 174	1141.5549	1140.5476	1140.5352	0.0124	0	NNPFYFPSR	
166 - 175	1297.6490	1296.6417	1296.6363	0.0054	1	NNPFYFPSRR	
197 - 207	1399.7281	1398.7208	1398.7116	0.0092	1	SKQFQNLQNHR	
199 - 207	1184.6013	1183.5940	1183.5846	0.0094	0	QFQNLQNHR	
208 - 222	1691.0221	1690.0148	1690.0141	0.0008	0	IVQIEARPNTLVLPK	
249 - 259	1258.6156	1257.6083	1257.6101	-0.0018	0	SFNLDEGHALR	
272 - 278	896.4462	895.4389	895.4260	0.0129	0	HDNQNLR	
282 - 301	2227.0920	2226.0847	2226.0415	0.0432	0	ISMPVNTPGQFEDFFPASSR	
302 - 312	1287.6045	1286.5972	1286.5891	0.0081	0	DQSSYLQGFSR	
313 - 327	1738.8414	1737.8341	1737.8321	0.0020	0	NTLEAAFNAEFNEIR	
313 - 328	1894.9250	1893.9177	1893.9332	-0.0155	1	NTLEAAFNAEFNEIRR	
328 - 342	1728.8468	1727.8395	1727.8437	-0.0042	1	RVLLEENAGGEQEER	
329 - 342	1572.7523	1571.7450	1571.7426	0.0024	0	VLLEENAGGEQEER	
379 - 393	1714.8658	1713.8585	1713.8533	0.0053	1	KGSEEEDITNPINLR	
380 - 393	1586.7634	1585.7561	1585.7583	-0.0022	0	GSEEEDITNPINLR	
394 - 405	1320.5898	1319.5825	1319.5741	0.0084	0	DGEPDLSNNFGR	
432 - 443	1359.6471	1358.6398	1358.6652	-0.0254	0	EGALMLPHFNSK	Oxidation (M)
555 - 567	1376.6614	1375.6541	1375.6619	-0.0078	0	DLAFPGSGEQVEK	

No match to: 805.4588, 855.0504, 861.0752, 877.0366, 959.4948, 1046.6029, 1061.6160, 1066.0944, 1080.5375, 1107.5436, 1137.0753, 1137.5823, 1145.0525, 1145.5836, 1167.5779, 1175.5732, 1234.6892, 1296.6444, 1309.6244, 1493.7371, 1496.7352, 1529.7163, 1568.7136, 1771.8705, 1774.8541, 2145.0510, 2146.6096, 2185.0483, 2224.9932, 2273.1582, 2295.1597, 2305.1582, 2311.1331, 2335.0916, 2351.0854, 2513.3235, 2514.3491, 2515.3472, 2530.3721, 2612.1514, 2974.3386, 3136.4609, 3211.5166, 3227.4519, 3300.7529

Spot 5

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:30:29 GMT**
Top Score : **333 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	333	conarachin [Arachis hypogaea]
2.	gi|620025	70639	327	Ara h I
3.	gi|1168390	70639	327	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	262	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	262	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	262	Ara h I
7.	gi|46560476	48122	179	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	101	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	76	conarachin [Arachis hypogaea]
10.	gi|62177652	10056	19	resistance protein PRG [Arachis hypogaea]

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 333 **Expect:** 4.4e-031 **Queries matched:** 31
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3676	807.3603	807.3623	-0.0020	180	186	0	YGNQNGR
812.3965	811.3892	811.3976	-0.0084	109	115	0	WGPAEPR
816.4172	815.4099	815.4249	-0.0150	464	469	1	KEQQQR
896.4340	895.4267	895.4260	0.0007	272	278	0	HDNQNLR
1005.5334	1004.5261	1004.5264	-0.0003	132	139	0	RPSHQQPR
1019.4505	1018.4432	1018.4468	-0.0036	118	124	1	EREEDWR
1128.6376	1127.6303	1127.6298	0.0005	453	463	0	GTGNLELVAVR
1141.5393	1140.5320	1140.5352	-0.0032	166	174	0	NNPFYFPSR
1184.6030	1183.5957	1183.5846	0.0111	199	207	0	QFQNLQNHR
1258.6211	1257.6138	1257.6101	0.0037	249	259	0	SFNLDEGHALR

1287.5975	1286.5902	1286.5891	0.0011	302 - 312	0	DQSSYLQGFSR
1297.6462	1296.6389	1296.6363	0.0026	166 - 175	1	NNPFYFPSRR
1320.5856	1319.5783	1319.5741	0.0042	394 - 405	0	DGEPDLSNNFGR
1343.6843	1342.6770	1342.6703	0.0067	432 - 443	0	EGALMLPHFNSK
1379.7729	1378.7656	1378.7608	0.0048	260 - 271	0	IPSGFISYILNR
1399.7240	1398.7167	1398.7116	0.0051	197 - 207	1	SKQFQNLQNHR
1560.6948	1559.6875	1559.6851	0.0024	147 - 160	0	EGEQEWGTPGSEVR
1572.7526	1571.7453	1571.7426	0.0027	329 - 342	0	VLLEENAGGEQEER
1586.7717	1585.7644	1585.7583	0.0061	380 - 393	0	GSEEEDITNPINLR
1691.0267	1690.0194	1690.0141	0.0054	208 - 222	0	IVQIEARPNTLVLPK
1714.8563	1713.8490	1713.8533	-0.0042	379 - 393	1	KGSEEEDITNPINLR
1738.8428	1737.8355	1737.8321	0.0034	313 - 327	0	NTLEAAFNAEFNEIR
1817.9559	1816.9486	1816.9570	-0.0084	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9409	1893.9336	1893.9332	0.0004	313 - 328	1	NTLEAAFNAEFNEIRR
2047.9816	2046.9743	2046.9788	-0.0045	415 - 431	0	NPQLQDLDMMLTCVEIK
2082.2026	2081.1953	2081.2030	-0.0076	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0413	2226.0340	2226.0415	-0.0075	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0532	2242.0459	2242.0364	0.0095	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8521	2280.8448	2280.8414	0.0035	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.3130	2618.3057	2618.3160	-0.0103	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.4236	2746.4163	2746.4110	0.0054	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3702, 828.4715, 1111.5609, 1167.5664, 1568.7104, 1643.7865, 1771.8815, 1878.4956, 2193.0002, 2210.3008, 2273.1589, 2612.1492, 2620.3257, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

2. gi|620025 **Mass:** 70639 **Score:** 327 **Expect:** 1.7e-030 **Queries matched:** 31

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3676	807.3603	807.3623	-0.0020	180	186	0	YGNQNGR
812.3965	811.3892	811.3976	-0.0084	109	115	0	WGPAEPR
816.4172	815.4099	815.4249	-0.0150	464	469	1	KEQQQR
896.4340	895.4267	895.4260	0.0007	272	278	0	HDNQNLR
1005.5334	1004.5261	1004.5264	-0.0003	132	139	0	RPSHQQPR
1019.4505	1018.4432	1018.4468	-0.0036	118	124	1	EREEDWR
1128.6376	1127.6303	1127.6298	0.0005	453	463	0	GTGNLELVAVR
1141.5393	1140.5320	1140.5352	-0.0032	166	174	0	NNPFYFPSR
1184.6030	1183.5957	1183.5846	0.0111	199	207	0	QFQNLQNHR
1258.6211	1257.6138	1257.6101	0.0037	249	259	0	SFNLDEGHALR
1287.5975	1286.5902	1286.5891	0.0011	302	312	0	DQSSYLQGFSR
1297.6462	1296.6389	1296.6363	0.0026	166	175	1	NNPFYFPSRR
1320.5856	1319.5783	1319.5741	0.0042	394	405	0	DGEPDLSNNFGR

1343.6843	1342.6770	1342.6703	0.0067	432 - 443	0	EGALMLPHFNSK
1379.7729	1378.7656	1378.7608	0.0048	260 - 271	0	IPSGFISYILNR
1399.7240	1398.7167	1398.7116	0.0051	197 - 207	1	SKQFQNLQNHR
1560.6948	1559.6875	1559.6851	0.0024	147 - 160	0	EGEQEWGTPGSEVR
1572.7526	1571.7453	1571.7426	0.0027	329 - 342	0	VLLEENAGGEQEER
1586.7717	1585.7644	1585.7583	0.0061	380 - 393	0	GSEEEDITNPINLR
1691.0267	1690.0194	1690.0141	0.0054	208 - 222	0	IVQIEARPNTLVLPK
1714.8563	1713.8490	1713.8533	-0.0042	379 - 393	1	KGSEEEDITNPINLR
1738.8428	1737.8355	1737.8321	0.0034	313 - 327	0	NTLEAAFNAEFNEIR
1817.9559	1816.9486	1816.9570	-0.0084	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9409	1893.9336	1893.9332	0.0004	313 - 328	1	NTLEAAFNAEFNEIRR
2047.9816	2046.9743	2046.9788	-0.0045	415 - 431	0	NPQLQDLDMMLTCVEIK
2082.2026	2081.1953	2081.2030	-0.0076	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0413	2226.0340	2226.0415	-0.0075	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0532	2242.0459	2242.0364	0.0095	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8521	2280.8448	2280.8414	0.0035	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.3130	2618.3057	2618.3160	-0.0103	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.4236	2746.4163	2746.4110	0.0054	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3702, 828.4715, 1111.5609, 1167.5664, 1568.7104, 1643.7865, 1771.8815, 1878.4956, 2193.0002, 2210.3008, 2273.1589, 2612.1492, 2620.3257, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

3. gi|1168390 **Mass:** 70639 **Score:** 327 **Expect:** 1.7e-030 **Queries matched:** 31

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
808.3676	807.3603	807.3623	-0.0020	180 - 186	0	YGNQNGR
812.3965	811.3892	811.3976	-0.0084	109 - 115	0	WGPAEPR
816.4172	815.4099	815.4249	-0.0150	464 - 469	1	KEQQQR
896.4340	895.4267	895.4260	0.0007	272 - 278	0	HDNQNLR
1005.5334	1004.5261	1004.5264	-0.0003	132 - 139	0	RPSHQQPR
1019.4505	1018.4432	1018.4468	-0.0036	118 - 124	1	EREEDWR
1128.6376	1127.6303	1127.6298	0.0005	453 - 463	0	GTGNLELVAVR
1141.5393	1140.5320	1140.5352	-0.0032	166 - 174	0	NNPFYFPSR
1184.6030	1183.5957	1183.5846	0.0111	199 - 207	0	QFQNLQNHR
1258.6211	1257.6138	1257.6101	0.0037	249 - 259	0	SFNLDEGHALR
1287.5975	1286.5902	1286.5891	0.0011	302 - 312	0	DQSSYLQGFSR
1297.6462	1296.6389	1296.6363	0.0026	166 - 175	1	NNPFYFPSRR
1320.5856	1319.5783	1319.5741	0.0042	394 - 405	0	DGEPDLSNNFGR
1343.6843	1342.6770	1342.6703	0.0067	432 - 443	0	EGALMLPHFNSK
1379.7729	1378.7656	1378.7608	0.0048	260 - 271	0	IPSGFISYILNR
1399.7240	1398.7167	1398.7116	0.0051	197 - 207	1	SKQFQNLQNHR

1560.6948	1559.6875	1559.6851	0.0024	147 - 160	0	EGEQEWGTPGSEVR
1572.7526	1571.7453	1571.7426	0.0027	329 - 342	0	VLLEENAGGEQEER
1586.7717	1585.7644	1585.7583	0.0061	380 - 393	0	GSEEEDITNPINLR
1691.0267	1690.0194	1690.0141	0.0054	208 - 222	0	IVQIEARPNTLVLPK
1714.8563	1713.8490	1713.8533	-0.0042	379 - 393	1	KGSEEEDITNPINLR
1738.8428	1737.8355	1737.8321	0.0034	313 - 327	0	NTLEAAFNAEFNEIR
1817.9559	1816.9486	1816.9570	-0.0084	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9409	1893.9336	1893.9332	0.0004	313 - 328	1	NTLEAAFNAEFNEIRR
2047.9816	2046.9743	2046.9788	-0.0045	415 - 431	0	NPQLQDLDMMLTCVEIK
2082.2026	2081.1953	2081.2030	-0.0076	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0413	2226.0340	2226.0415	-0.0075	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0532	2242.0459	2242.0364	0.0095	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8521	2280.8448	2280.8414	0.0035	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.3130	2618.3057	2618.3160	-0.0103	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.4236	2746.4163	2746.4110	0.0054	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3702, 828.4715, 1111.5609, 1167.5664, 1568.7104, 1643.7865, 1771.8815, 1878.4956, 2193.0002, 2210.3008, 2273.1589, 2612.1492, 2620.3257, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

4. gi|16612200 **Mass:** 71701 **Score:** 262 **Expect:** 5.5e-024 **Queries matched:** 27

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3702	739.3629	739.3765	-0.0136	115 - 121		0	WGPAGPR
808.3676	807.3603	807.3623	-0.0020	186 - 192		0	YGNQNGR
816.4172	815.4099	815.4249	-0.0150	472 - 477		1	KEQQQR
896.4340	895.4267	895.4260	0.0007	278 - 284		0	HDNQNLR
1005.5334	1004.5261	1004.5264	-0.0003	138 - 145		0	RPSHQQPR
1019.4505	1018.4432	1018.4468	-0.0036	124 - 130		1	EREEDWR
1128.6376	1127.6303	1127.6298	0.0005	461 - 471		0	GTGNLELVAVR
1141.5393	1140.5320	1140.5352	-0.0032	172 - 180		0	NNPFYFPSR
1184.6030	1183.5957	1183.5846	0.0111	205 - 213		0	QFQNLQNHR
1258.6211	1257.6138	1257.6101	0.0037	255 - 265		0	SFNLDEGHALR
1287.5975	1286.5902	1286.5891	0.0011	308 - 318		0	DQSSYLQGFSR
1297.6462	1296.6389	1296.6363	0.0026	172 - 181		1	NNPFYFPSRR
1343.6843	1342.6770	1342.6703	0.0067	440 - 451		0	EGALMLPHFNSK
1379.7729	1378.7656	1378.7608	0.0048	266 - 277		0	IPSGFISYILNR
1568.7104	1567.7031	1567.7015	0.0017	153 - 166		0	EGEQEWGTPGSHVR
1572.7526	1571.7453	1571.7426	0.0027	335 - 348		0	VLLEENAGGEQEER
1643.7865	1642.7792	1642.7798	-0.0005	387 - 401		0	GSEEEGDITNPINLR
1738.8428	1737.8355	1737.8321	0.0034	319 - 333		0	NTLEAAFNAEFNEIR
1771.8815	1770.8742	1770.8747	-0.0005	386 - 401		1	KGSEEEGDITNPINLR

1817.9559	1816.9486	1816.9570	-0.0084	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9409	1893.9336	1893.9332	0.0004	319 - 334	1	NTLEAAFNAEFNEIRR
2047.9816	2046.9743	2046.9788	-0.0045	423 - 439	0	NPQLQDLDMMLTCVEIK
2082.2026	2081.1953	2081.2030	-0.0076	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0413	2226.0340	2226.0415	-0.0075	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0532	2242.0459	2242.0364	0.0095	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3130	2618.3057	2618.3160	-0.0103	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.4236	2746.4163	2746.4110	0.0054	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 812.3965, 828.4715, 1111.5609, 1167.5664, 1320.5856, 1399.7240, 1560.6948, 1586.7717, 1691.0267, 1714.8563, 1878.4956, 2193.0002, 2210.3008, 2273.1589, 2281.8521, 2612.1492, 2620.3257, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

5. gi|1168391 **Mass:** 71701 **Score:** 262 **Expect:** 5.5e-024 **Queries matched:** 27

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3702	739.3629	739.3765	-0.0136	115 - 121		0	WGPAGPR
808.3676	807.3603	807.3623	-0.0020	186 - 192		0	YGNQNGR
816.4172	815.4099	815.4249	-0.0150	472 - 477		1	KEQQQR
896.4340	895.4267	895.4260	0.0007	278 - 284		0	HDNQNLR
1005.5334	1004.5261	1004.5264	-0.0003	138 - 145		0	RPSHQQPR
1019.4505	1018.4432	1018.4468	-0.0036	124 - 130		1	EREEDWR
1128.6376	1127.6303	1127.6298	0.0005	461 - 471		0	GTGNLELVAVR
1141.5393	1140.5320	1140.5352	-0.0032	172 - 180		0	NNPFYFPSR
1184.6030	1183.5957	1183.5846	0.0111	205 - 213		0	QFQNLQNHR
1258.6211	1257.6138	1257.6101	0.0037	255 - 265		0	SFNLDEGHALR
1287.5975	1286.5902	1286.5891	0.0011	308 - 318		0	DQSSYLQGFSR
1297.6462	1296.6389	1296.6363	0.0026	172 - 181		1	NNPFYFPSRR
1343.6843	1342.6770	1342.6703	0.0067	440 - 451		0	EGALMLPHFNSK
1379.7729	1378.7656	1378.7608	0.0048	266 - 277		0	IPSGFISYILNR
1568.7104	1567.7031	1567.7015	0.0017	153 - 166		0	EGEQEWGTPGSHVR
1572.7526	1571.7453	1571.7426	0.0027	335 - 348		0	VLLEENAGGEQEER
1643.7865	1642.7792	1642.7798	-0.0005	387 - 401		0	GSEEEGDITNPINLR
1738.8428	1737.8355	1737.8321	0.0034	319 - 333		0	NTLEAAFNAEFNEIR
1771.8815	1770.8742	1770.8747	-0.0005	386 - 401		1	KGSEEEGDITNPINLR
1817.9559	1816.9486	1816.9570	-0.0084	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9409	1893.9336	1893.9332	0.0004	319 - 334		1	NTLEAAFNAEFNEIRR
2047.9816	2046.9743	2046.9788	-0.0045	423 - 439		0	NPQLQDLDMMLTCVEIK
2082.2026	2081.1953	2081.2030	-0.0076	452 - 471		1	AMVIVVVNKGTGNLELVAVR
2227.0413	2226.0340	2226.0415	-0.0075	288 - 307		0	ISMPVNTPGQFEDFFPASSR
2243.0532	2242.0459	2242.0364	0.0095	288 - 307		0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)

2619.3130	2618.3057	2618.3160	-0.0103	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.4236	2746.4163	2746.4110	0.0054	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 812.3965, 828.4715, 1111.5609, 1167.5664, 1320.5856, 1399.7240, 1560.6948, 1586.7717, 1691.0267, 1714.8563, 1878.4956, 2193.0002, 2210.3008, 2273.1589, 2281.8521, 2612.1492, 2620.3257, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

6. gi|602436 **Mass:** 71701 **Score:** 262 **Expect:** 5.5e-024 **Queries matched:** 27

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3702	739.3629	739.3765	-0.0136	115	121	0	WGPAGPR
808.3676	807.3603	807.3623	-0.0020	186	192	0	YGNQNGR
816.4172	815.4099	815.4249	-0.0150	472	477	1	KEQQQR
896.4340	895.4267	895.4260	0.0007	278	284	0	HDNQNLR
1005.5334	1004.5261	1004.5264	-0.0003	138	145	0	RPSHQQPR
1019.4505	1018.4432	1018.4468	-0.0036	124	130	1	EREEDWR
1128.6376	1127.6303	1127.6298	0.0005	461	471	0	GTGNLELVAVR
1141.5393	1140.5320	1140.5352	-0.0032	172	180	0	NNPFYFPSR
1184.6030	1183.5957	1183.5846	0.0111	205	213	0	QFQNLQNHR
1258.6211	1257.6138	1257.6101	0.0037	255	265	0	SFNLDEGHALR
1287.5975	1286.5902	1286.5891	0.0011	308	318	0	DQSSYLQGFSR
1297.6462	1296.6389	1296.6363	0.0026	172	181	1	NNPFYFPSRR
1343.6843	1342.6770	1342.6703	0.0067	440	451	0	EGALMLPHFNSK
1379.7729	1378.7656	1378.7608	0.0048	266	277	0	IPSGFISYILNR
1568.7104	1567.7031	1567.7015	0.0017	153	166	0	EGEQEWGTPGSHVR
1572.7526	1571.7453	1571.7426	0.0027	335	348	0	VLLEENAGGEQEER
1643.7865	1642.7792	1642.7798	-0.0005	387	401	0	GSEEEGDITNPINLR
1738.8428	1737.8355	1737.8321	0.0034	319	333	0	NTLEAAFNAEFNEIR
1771.8815	1770.8742	1770.8747	-0.0005	386	401	1	KGSEEEGDITNPINLR
1817.9559	1816.9486	1816.9570	-0.0084	541	556	1	IFLAGDKDNVIDQIEK
1894.9409	1893.9336	1893.9332	0.0004	319	334	1	NTLEAAFNAEFNEIRR
2047.9816	2046.9743	2046.9788	-0.0045	423	439	0	NPQLQDLDMMLTCVEIK
2082.2026	2081.1953	2081.2030	-0.0076	452	471	1	AMVIVVVNKGTGNLELVAVR
2227.0413	2226.0340	2226.0415	-0.0075	288	307	0	ISMPVNTPGQFEDFFPASSR
2243.0532	2242.0459	2242.0364	0.0095	288	307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3130	2618.3057	2618.3160	-0.0103	229	253	0	HADADNILVIQQGQATVTVANGNNR
2747.4236	2746.4163	2746.4110	0.0054	229	254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 812.3965, 828.4715, 1111.5609, 1167.5664, 1320.5856, 1399.7240, 1560.6948, 1586.7717, 1691.0267, 1714.8563, 1878.4956, 2193.0002, 2210.3008, 2273.1589, 2281.8521, 2612.1492, 2620.3257, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

7. gi|46560476 **Mass:** 48122 **Score:** 179 **Expect:** 1.1e-015 **Queries matched:** 18

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4172	815.4099	815.4249	-0.0150	274	279	1	KEQQQR
896.4340	895.4267	895.4260	0.0007	81	87	0	HDNQNLR
1128.6376	1127.6303	1127.6298	0.0005	263	273	0	GTGNLELVAVR
1184.6030	1183.5957	1183.5846	0.0111	8	16	0	QFQNLQNHR
1258.6211	1257.6138	1257.6101	0.0037	58	68	0	SFNLDEGHALR
1287.5975	1286.5902	1286.5891	0.0011	111	121	0	DQSSYLQGFSR
1343.6843	1342.6770	1342.6703	0.0067	242	253	0	EGALMLPHFNSK
1379.7729	1378.7656	1378.7608	0.0048	69	80	0	IPSGFISYILNR
1572.7526	1571.7453	1571.7426	0.0027	138	151	0	VLLEENAGGEQEER
1738.8428	1737.8355	1737.8321	0.0034	122	136	0	NTLEAAFNAEFNEIR
1817.9559	1816.9486	1816.9570	-0.0084	343	358	1	IFLAGDKDNVIDQIEK
1894.9409	1893.9336	1893.9332	0.0004	122	137	1	NTLEAAFNAEFNEIRR
2047.9816	2046.9743	2046.9788	-0.0045	225	241	0	NPQLQDLDMMLTCVEIK
2082.2026	2081.1953	2081.2030	-0.0076	254	273	1	AMVIVVVNKGTGNLELVAVR
2227.0413	2226.0340	2226.0415	-0.0075	91	110	0	ISMPVNTPGQFEDFFPASSR
2243.0532	2242.0459	2242.0364	0.0095	91	110	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3130	2618.3057	2618.3160	-0.0103	32	56	0	HADADNILVIQQGQATVTVANGNNR
2747.4236	2746.4163	2746.4110	0.0054	32	57	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3702, 808.3676, 812.3965, 828.4715, 1005.5334, 1019.4505, 1111.5609, 1141.5393, 1167.5664, 1297.6462, 1320.5856, 1399.7240, 1560.6948, 1568.7104, 1586.7717, 1643.7865, 1691.0267, 1714.8563, 1771.8815, 1878.4956, 2193.0002, 2210.3008, 2273.1589, 2281.8521, 2612.1492, 2620.3257, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

8. gi|46560472 **Mass:** 34169 **Score:** 101 **Expect:** 7e-008 **Queries matched:** 11

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4172	815.4099	815.4249	-0.0150	153	158	1	KEQQQR
1128.6376	1127.6303	1127.6298	0.0005	142	152	0	GTGNLELVAVR
1320.5856	1319.5783	1319.5741	0.0042	83	94	0	DGEPDLSNNFGR
1343.6843	1342.6770	1342.6703	0.0067	121	132	0	EGALMLPHFNSK
1572.7526	1571.7453	1571.7426	0.0027	18	31	0	VLLEENAGGEQEER
1586.7717	1585.7644	1585.7583	0.0061	69	82	0	GSEEEDITNPINLR
1714.8563	1713.8490	1713.8533	-0.0042	68	82	1	KGSEEEDITNPINLR
1817.9559	1816.9486	1816.9570	-0.0084	225	240	1	IFLAGDKDNVIDQIEK
2047.9816	2046.9743	2046.9788	-0.0045	104	120	0	NPQLQDLDMMLTCVEIK
2082.2026	2081.1953	2081.2030	-0.0076	133	152	1	AMVIVVVNKGTGNLELVAVR
2281.8521	2280.8448	2280.8414	0.0035	162	179	0	EQEWEEEEEDEEEEGSNR

No match to: 740.3702, 808.3676, 812.3965, 828.4715, 896.4340, 1005.5334, 1019.4505, 1111.5609, 1141.5393, 1167.5664, 1184.6030, 1258.6211, 1287.5975, 1297.6462, 1379.7729, 1399.7240, 1560.6948, 1568.7104, 1643.7865,

1691.0267, 1738.8428, 1771.8815, 1878.4956, 1894.9409, 2193.0002, 2210.3008, 2227.0413, 2243.0532, 2273.1589, 2612.1492, 2619.3130, 2620.3257, 2747.4236, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

9. gi|46560474 **Mass:** 33641 **Score:** 76 **Expect:** 2.2e-005 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4172	815.4099	815.4249	-0.0150	152	157	1	KEQQQR
1128.6376	1127.6303	1127.6298	0.0005	141	151	0	GTGNLELVAVR
1343.6843	1342.6770	1342.6703	0.0067	120	131	0	EGALMLPHFNSK
1572.7526	1571.7453	1571.7426	0.0027	15	28	0	VLLEENAGGEQEER
1643.7865	1642.7792	1642.7798	-0.0005	67	81	0	GSEEEGDITNPINLR
1771.8815	1770.8742	1770.8747	-0.0005	66	81	1	KGSEEEGDITNPINLR
1817.9559	1816.9486	1816.9570	-0.0084	221	236	1	IFLAGDKDNVIDQIEK
2047.9816	2046.9743	2046.9788	-0.0045	103	119	0	NPQLQDLDMMLTCVEIK
2082.2026	2081.1953	2081.2030	-0.0076	132	151	1	AMVIVVVNKGTGNLELVAVR

No match to: 740.3702, 808.3676, 812.3965, 828.4715, 896.4340, 1005.5334, 1019.4505, 1111.5609, 1141.5393, 1167.5664, 1184.6030, 1258.6211, 1287.5975, 1297.6462, 1320.5856, 1379.7729, 1399.7240, 1560.6948, 1568.7104, 1586.7717, 1691.0267, 1714.8563, 1738.8428, 1878.4956, 1894.9409, 2193.0002, 2210.3008, 2227.0413, 2243.0532, 2273.1589, 2281.8521, 2612.1492, 2619.3130, 2620.3257, 2747.4236, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

10. gi|62177652 **Mass:** 10056 **Score:** 19 **Expect:** 11 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1379.7729	1378.7656	1378.7496	0.0161	77	89	1	EVVKYSGGLPFAL
1894.9409	1893.9336	1893.9009	0.0328	7	23	0	QLEYLGGEQAWFGPGSR

No match to: 740.3702, 808.3676, 812.3965, 816.4172, 828.4715, 896.4340, 1005.5334, 1019.4505, 1111.5609, 1128.6376, 1141.5393, 1167.5664, 1184.6030, 1258.6211, 1287.5975, 1297.6462, 1320.5856, 1343.6843, 1399.7240, 1560.6948, 1568.7104, 1572.7526, 1586.7717, 1643.7865, 1691.0267, 1714.8563, 1738.8428, 1771.8815, 1817.9559, 1878.4956, 2047.9816, 2082.2026, 2193.0002, 2210.3008, 2227.0413, 2243.0532, 2273.1589, 2281.8521, 2612.1492, 2619.3130, 2620.3257, 2747.4236, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1

Number of queries : 50

Protein View

Match to: **gi|46560478** Score: **333** Expect: **4.4e-031**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **31**
Sequence Coverage: **53%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
109 - 115	812.3965	811.3892	811.3976	-0.0084	0	WGPAEPR
118 - 124	1019.4505	1018.4432	1018.4468	-0.0036	1	EREEDWR
132 - 139	1005.5334	1004.5261	1004.5264	-0.0003	0	RPSHQQPR
147 - 160	1560.6948	1559.6875	1559.6851	0.0024	0	EGEQEWGTPGSEVR
166 - 174	1141.5393	1140.5320	1140.5352	-0.0032	0	NNPFYFPSR
166 - 175	1297.6462	1296.6389	1296.6363	0.0026	1	NNPFYFPSRR

180 - 186	808.3676	807.3603	807.3623	-0.0020	0	YGNQNGR
197 - 207	1399.7240	1398.7167	1398.7116	0.0051	1	SKQFQNLQNHR
199 - 207	1184.6030	1183.5957	1183.5846	0.0111	0	QFQNLQNHR
208 - 222	1691.0267	1690.0194	1690.0141	0.0054	0	IVQIEARPNTLVLPK
223 - 247	2619.3130	2618.3057	2618.3160	-0.0103	0	HADADNILVIQQGQATVTVANGNNR
223 - 248	2747.4236	2746.4163	2746.4110	0.0054	1	HADADNILVIQQGQATVTVANGNNRK
249 - 259	1258.6211	1257.6138	1257.6101	0.0037	0	SFNLDEGHALR
260 - 271	1379.7729	1378.7656	1378.7608	0.0048	0	IPSGFISYILNR
272 - 278	896.4340	895.4267	895.4260	0.0007	0	HDNQNLR
282 - 301	2227.0413	2226.0340	2226.0415	-0.0075	0	ISMPVNTPGQFEDFFPASSR
282 - 301	2243.0532	2242.0459	2242.0364	0.0095	0	ISMPVNTPGQFEDFFPASSR Oxidation (M)
302 - 312	1287.5975	1286.5902	1286.5891	0.0011	0	DQSSYLQGFSR
313 - 327	1738.8428	1737.8355	1737.8321	0.0034	0	NTLEAAFNAEFNEIR
313 - 328	1894.9409	1893.9336	1893.9332	0.0004	1	NTLEAAFNAEFNEIRR
329 - 342	1572.7526	1571.7453	1571.7426	0.0027	0	VLLEENAGGEQEER
379 - 393	1714.8563	1713.8490	1713.8533	-0.0042	1	KGSEEEDITNPINLR
380 - 393	1586.7717	1585.7644	1585.7583	0.0061	0	GSEEEDITNPINLR
394 - 405	1320.5856	1319.5783	1319.5741	0.0042	0	DGEPDLSNNFGR
415 - 431	2047.9816	2046.9743	2046.9788	-0.0045	0	NPQLQDLDMMLTCVEIK
432 - 443	1343.6843	1342.6770	1342.6703	0.0067	0	EGALMLPHFNSK
444 - 463	2082.2026	2081.1953	2081.2030	-0.0076	1	AMVIVVVNKGTGNLELVAVR
453 - 463	1128.6376	1127.6303	1127.6298	0.0005	0	GTGNLELVAVR
464 - 469	816.4172	815.4099	815.4249	-0.0150	1	KEQQQR
473 - 490	2281.8521	2280.8448	2280.8414	0.0035	0	EQEWEEEEEDEEEEGSNR
536 - 551	1817.9559	1816.9486	1816.9570	-0.0084	1	IFLAGDKDNVIDQIEK

No match to: 740.3702, 828.4715, 1111.5609, 1167.5664, 1568.7104, 1643.7865, 1771.8815, 1878.4956, 2193.0002, 2210.3008, 2273.1589, 2612.1492, 2620.3257, 2748.4048, 2926.2878, 3136.4138, 3153.4343, 3211.4753, 3300.7119

Spot 6

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:30:33 GMT**
Top Score : **349 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	349	conarachin [Arachis hypogaea]
2.	gi|620025	70639	343	Ara h I
3.	gi|1168390	70639	343	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	277	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	277	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	277	Ara h I
7.	gi|46560476	48122	193	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	100	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	75	conarachin [Arachis hypogaea]
10.	gi|62177652	10056	19	resistance protein PRG [Arachis hypogaea]

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 349 **Expect:** 1.1e-032 **Queries matched:** 32
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
812.4179	811.4106	811.3976	0.0130	109	115	0	WGPAEPR
816.4457	815.4384	815.4249	0.0135	464	469	1	KEQQQR
855.5270	854.5197	854.5086	0.0111	140	146	1	KIRPEGR
896.4477	895.4404	895.4260	0.0144	272	278	0	HDNQNLR
1005.5445	1004.5372	1004.5264	0.0108	132	139	0	RPSHQQPR
1019.4675	1018.4602	1018.4468	0.0134	118	124	1	EREEDWR
1128.6503	1127.6430	1127.6298	0.0132	453	463	0	GTGNLELVAVR
1141.5558	1140.5485	1140.5352	0.0133	166	174	0	NNPFYFPSR

1184.6049	1183.5976	1183.5846	0.0130	199 - 207	0	QFQNLQNHR
1258.6267	1257.6194	1257.6101	0.0093	249 - 259	0	SFNLDEGHALR
1287.6078	1286.6005	1286.5891	0.0114	302 - 312	0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	166 - 175	1	NNPFYFPSRR
1320.5917	1319.5844	1319.5741	0.0103	394 - 405	0	DGEPDLSNNFGR
1343.6807	1342.6734	1342.6703	0.0031	432 - 443	0	EGALMLPHFNSK
1376.6738	1375.6665	1375.6619	0.0046	555 - 567	0	DLAFPGSGEQVEK
1379.7811	1378.7738	1378.7608	0.0130	260 - 271	0	IPSGFISYILNR
1386.7233	1385.7160	1385.7051	0.0109	248 - 259	1	KSFNLDEGHALR
1399.7314	1398.7241	1398.7116	0.0125	197 - 207	1	SKQFQNLQNHR
1560.6963	1559.6890	1559.6851	0.0039	147 - 160	0	EGEQEWGTPGSEVR
1572.7555	1571.7482	1571.7426	0.0056	329 - 342	0	VLLEENAGGEQEER
1586.7666	1585.7593	1585.7583	0.0010	380 - 393	0	GSEEEDITNPINLR
1691.0289	1690.0216	1690.0141	0.0076	208 - 222	0	IVQIEARPNTLVLPK
1714.8617	1713.8544	1713.8533	0.0012	379 - 393	1	KGSEEEDITNPINLR
1738.8445	1737.8372	1737.8321	0.0051	313 - 327	0	NTLEAAFNAEFNEIR
1817.9626	1816.9553	1816.9570	-0.0017	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9393	1893.9320	1893.9332	-0.0012	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2083	2081.2010	2081.2030	-0.0019	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0347	2226.0274	2226.0415	-0.0141	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0430	2242.0357	2242.0364	-0.0007	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8374	2280.8301	2280.8414	-0.0112	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.3030	2618.2957	2618.3160	-0.0203	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3936	2746.3863	2746.4110	-0.0246	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3958, 756.3921, 795.3989, 805.4335, 808.3868, 828.4940, 959.4940, 1167.5803, 1281.2028, 1568.7139, 1643.7926, 1771.8853, 2185.0300, 2273.1587, 2620.3003, 2748.3792, 3153.4365, 3211.4670

2. gi|620025 **Mass:** 70639 **Score:** 343 **Expect:** 4.4e-032 **Queries matched:** 32

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
812.4179	811.4106	811.3976	0.0130	109 - 115		0	WGPAEPR
816.4457	815.4384	815.4249	0.0135	464 - 469		1	KEQQQR
855.5270	854.5197	854.5086	0.0111	140 - 146		1	KIRPEGR
896.4477	895.4404	895.4260	0.0144	272 - 278		0	HDNQNLR
1005.5445	1004.5372	1004.5264	0.0108	132 - 139		0	RPSHQQPR
1019.4675	1018.4602	1018.4468	0.0134	118 - 124		1	EREEDWR
1128.6503	1127.6430	1127.6298	0.0132	453 - 463		0	GTGNLELVAVR
1141.5558	1140.5485	1140.5352	0.0133	166 - 174		0	NNPFYFPSR
1184.6049	1183.5976	1183.5846	0.0130	199 - 207		0	QFQNLQNHR
1258.6267	1257.6194	1257.6101	0.0093	249 - 259		0	SFNLDEGHALR

1287.6078	1286.6005	1286.5891	0.0114	302 - 312	0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	166 - 175	1	NNPFYFPSRR
1320.5917	1319.5844	1319.5741	0.0103	394 - 405	0	DGEPDLSNNFGR
1343.6807	1342.6734	1342.6703	0.0031	432 - 443	0	EGALMLPHFNSK
1376.6738	1375.6665	1375.6619	0.0046	555 - 567	0	DLAFPGSGEQVEK
1379.7811	1378.7738	1378.7608	0.0130	260 - 271	0	IPSGFISYILNR
1386.7233	1385.7160	1385.7051	0.0109	248 - 259	1	KSFNLDEGHALR
1399.7314	1398.7241	1398.7116	0.0125	197 - 207	1	SKQFQNLQNHR
1560.6963	1559.6890	1559.6851	0.0039	147 - 160	0	EGEQEWGTPGSEVR
1572.7555	1571.7482	1571.7426	0.0056	329 - 342	0	VLLEENAGGEQEER
1586.7666	1585.7593	1585.7583	0.0010	380 - 393	0	GSEEEDITNPINLR
1691.0289	1690.0216	1690.0141	0.0076	208 - 222	0	IVQIEARPNTLVLPK
1714.8617	1713.8544	1713.8533	0.0012	379 - 393	1	KGSEEEDITNPINLR
1738.8445	1737.8372	1737.8321	0.0051	313 - 327	0	NTLEAAFNAEFNEIR
1817.9626	1816.9553	1816.9570	-0.0017	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9393	1893.9320	1893.9332	-0.0012	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2083	2081.2010	2081.2030	-0.0019	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0347	2226.0274	2226.0415	-0.0141	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0430	2242.0357	2242.0364	-0.0007	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8374	2280.8301	2280.8414	-0.0112	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.3030	2618.2957	2618.3160	-0.0203	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3936	2746.3863	2746.4110	-0.0246	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3958, 756.3921, 795.3989, 805.4335, 808.3868, 828.4940, 959.4940, 1167.5803, 1281.2028, 1568.7139, 1643.7926, 1771.8853, 2185.0300, 2273.1587, 2620.3003, 2748.3792, 3153.4365, 3211.4670

3. gi|1168390 **Mass:** 70639 **Score:** 343 **Expect:** 4.4e-032 **Queries matched:** 32

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
812.4179	811.4106	811.3976	0.0130	109 - 115		0	WGPAEPR
816.4457	815.4384	815.4249	0.0135	464 - 469		1	KEQQQR
855.5270	854.5197	854.5086	0.0111	140 - 146		1	KIRPEGR
896.4477	895.4404	895.4260	0.0144	272 - 278		0	HDNQNLR
1005.5445	1004.5372	1004.5264	0.0108	132 - 139		0	RPSHQQPR
1019.4675	1018.4602	1018.4468	0.0134	118 - 124		1	EREEDWR
1128.6503	1127.6430	1127.6298	0.0132	453 - 463		0	GTGNLELVAVR
1141.5558	1140.5485	1140.5352	0.0133	166 - 174		0	NNPFYFPSR
1184.6049	1183.5976	1183.5846	0.0130	199 - 207		0	QFQNLQNHR
1258.6267	1257.6194	1257.6101	0.0093	249 - 259		0	SFNLDEGHALR
1287.6078	1286.6005	1286.5891	0.0114	302 - 312		0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	166 - 175		1	NNPFYFPSRR

1320.5917	1319.5844	1319.5741	0.0103	394 - 405	0	DGEPDLSNNFGR
1343.6807	1342.6734	1342.6703	0.0031	432 - 443	0	EGALMLPHFNSK
1376.6738	1375.6665	1375.6619	0.0046	555 - 567	0	DLAFPGSGEQVEK
1379.7811	1378.7738	1378.7608	0.0130	260 - 271	0	IPSGFISYILNR
1386.7233	1385.7160	1385.7051	0.0109	248 - 259	1	KSFNLDEGHALR
1399.7314	1398.7241	1398.7116	0.0125	197 - 207	1	SKQFQNLQNHR
1560.6963	1559.6890	1559.6851	0.0039	147 - 160	0	EGEQEWGTPGSEVR
1572.7555	1571.7482	1571.7426	0.0056	329 - 342	0	VLLEENAGGEQEER
1586.7666	1585.7593	1585.7583	0.0010	380 - 393	0	GSEEEDITNPINLR
1691.0289	1690.0216	1690.0141	0.0076	208 - 222	0	IVQIEARPNTLVLPK
1714.8617	1713.8544	1713.8533	0.0012	379 - 393	1	KGSEEEDITNPINLR
1738.8445	1737.8372	1737.8321	0.0051	313 - 327	0	NTLEAAFNAEFNEIR
1817.9626	1816.9553	1816.9570	-0.0017	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9393	1893.9320	1893.9332	-0.0012	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2083	2081.2010	2081.2030	-0.0019	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0347	2226.0274	2226.0415	-0.0141	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0430	2242.0357	2242.0364	-0.0007	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8374	2280.8301	2280.8414	-0.0112	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.3030	2618.2957	2618.3160	-0.0203	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3936	2746.3863	2746.4110	-0.0246	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3958, 756.3921, 795.3989, 805.4335, 808.3868, 828.4940, 959.4940, 1167.5803, 1281.2028, 1568.7139, 1643.7926, 1771.8853, 2185.0300, 2273.1587, 2620.3003, 2748.3792, 3153.4365, 3211.4670

4. gi|16612200 **Mass:** 71701 **Score:** 277 **Expect:** 1.7e-025 **Queries matched:** 28

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3958	739.3885	739.3765	0.0120	115 - 121		0	WGPAGPR
816.4457	815.4384	815.4249	0.0135	472 - 477		1	KEQQQR
855.5270	854.5197	854.5086	0.0111	146 - 152		1	KIRPEGR
896.4477	895.4404	895.4260	0.0144	278 - 284		0	HDNQNLR
1005.5445	1004.5372	1004.5264	0.0108	138 - 145		0	RPSHQQPR
1019.4675	1018.4602	1018.4468	0.0134	124 - 130		1	EREEDWR
1128.6503	1127.6430	1127.6298	0.0132	461 - 471		0	GTGNLELVAVR
1141.5558	1140.5485	1140.5352	0.0133	172 - 180		0	NNPFYFPSR
1184.6049	1183.5976	1183.5846	0.0130	205 - 213		0	QFQNLQNHR
1258.6267	1257.6194	1257.6101	0.0093	255 - 265		0	SFNLDEGHALR
1287.6078	1286.6005	1286.5891	0.0114	308 - 318		0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	172 - 181		1	NNPFYFPSRR
1343.6807	1342.6734	1342.6703	0.0031	440 - 451		0	EGALMLPHFNSK
1376.6738	1375.6665	1375.6619	0.0046	560 - 572		0	DLAFPGSGEQVEK

1379.7811	1378.7738	1378.7608	0.0130	266 - 277	0	IPSGFISYILNR
1386.7233	1385.7160	1385.7051	0.0109	254 - 265	1	KSFNLDEGHALR
1568.7139	1567.7066	1567.7015	0.0052	153 - 166	0	EGEQEWGTPGSHVR
1572.7555	1571.7482	1571.7426	0.0056	335 - 348	0	VLLEENAGGEQEER
1643.7926	1642.7853	1642.7798	0.0056	387 - 401	0	GSEEEGDITNPINLR
1738.8445	1737.8372	1737.8321	0.0051	319 - 333	0	NTLEAAFNAEFNEIR
1771.8853	1770.8780	1770.8747	0.0033	386 - 401	1	KGSEEEGDITNPINLR
1817.9626	1816.9553	1816.9570	-0.0017	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9393	1893.9320	1893.9332	-0.0012	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2083	2081.2010	2081.2030	-0.0019	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0347	2226.0274	2226.0415	-0.0141	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0430	2242.0357	2242.0364	-0.0007	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3030	2618.2957	2618.3160	-0.0203	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.3936	2746.3863	2746.4110	-0.0246	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 756.3921, 795.3989, 805.4335, 808.3868, 812.4179, 828.4940, 959.4940, 1167.5803, 1281.2028, 1320.5917, 1399.7314, 1560.6963, 1586.7666, 1691.0289, 1714.8617, 2185.0300, 2273.1587, 2281.8374, 2620.3003, 2748.3792, 3153.4365, 3211.4670

5. gi|1168391 **Mass:** 71701 **Score:** 277 **Expect:** 1.7e-025 **Queries matched:** 28

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3958	739.3885	739.3765	0.0120	115 - 121		0	WGPAGPR
816.4457	815.4384	815.4249	0.0135	472 - 477		1	KEQQQR
855.5270	854.5197	854.5086	0.0111	146 - 152		1	KIRPEGR
896.4477	895.4404	895.4260	0.0144	278 - 284		0	HDNQNLR
1005.5445	1004.5372	1004.5264	0.0108	138 - 145		0	RPSHQQPR
1019.4675	1018.4602	1018.4468	0.0134	124 - 130		1	EREEDWR
1128.6503	1127.6430	1127.6298	0.0132	461 - 471		0	GTGNLELVAVR
1141.5558	1140.5485	1140.5352	0.0133	172 - 180		0	NNPFYFPSR
1184.6049	1183.5976	1183.5846	0.0130	205 - 213		0	QFQNLQNHR
1258.6267	1257.6194	1257.6101	0.0093	255 - 265		0	SFNLDEGHALR
1287.6078	1286.6005	1286.5891	0.0114	308 - 318		0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	172 - 181		1	NNPFYFPSRR
1343.6807	1342.6734	1342.6703	0.0031	440 - 451		0	EGALMLPHFNSK
1376.6738	1375.6665	1375.6619	0.0046	560 - 572		0	DLAFPGSGEQVEK
1379.7811	1378.7738	1378.7608	0.0130	266 - 277		0	IPSGFISYILNR
1386.7233	1385.7160	1385.7051	0.0109	254 - 265		1	KSFNLDEGHALR
1568.7139	1567.7066	1567.7015	0.0052	153 - 166		0	EGEQEWGTPGSHVR
1572.7555	1571.7482	1571.7426	0.0056	335 - 348		0	VLLEENAGGEQEER
1643.7926	1642.7853	1642.7798	0.0056	387 - 401		0	GSEEEGDITNPINLR

1738.8445	1737.8372	1737.8321	0.0051	319 - 333	0	NTLEAAFNAEFNEIR
1771.8853	1770.8780	1770.8747	0.0033	386 - 401	1	KGSEEEGDITNPINLR
1817.9626	1816.9553	1816.9570	-0.0017	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9393	1893.9320	1893.9332	-0.0012	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2083	2081.2010	2081.2030	-0.0019	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0347	2226.0274	2226.0415	-0.0141	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0430	2242.0357	2242.0364	-0.0007	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3030	2618.2957	2618.3160	-0.0203	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.3936	2746.3863	2746.4110	-0.0246	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 756.3921, 795.3989, 805.4335, 808.3868, 812.4179, 828.4940, 959.4940, 1167.5803, 1281.2028, 1320.5917, 1399.7314, 1560.6963, 1586.7666, 1691.0289, 1714.8617, 2185.0300, 2273.1587, 2281.8374, 2620.3003, 2748.3792, 3153.4365, 3211.4670

6. gi|602436 **Mass:** 71701 **Score:** 277 **Expect:** 1.7e-025 **Queries matched:** 28

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3958	739.3885	739.3765	0.0120	115 - 121		0	WGPAGPR
816.4457	815.4384	815.4249	0.0135	472 - 477		1	KEQQQR
855.5270	854.5197	854.5086	0.0111	146 - 152		1	KIRPEGR
896.4477	895.4404	895.4260	0.0144	278 - 284		0	HDNQNLR
1005.5445	1004.5372	1004.5264	0.0108	138 - 145		0	RPSHQQPR
1019.4675	1018.4602	1018.4468	0.0134	124 - 130		1	EREEDWR
1128.6503	1127.6430	1127.6298	0.0132	461 - 471		0	GTGNLELVAVR
1141.5558	1140.5485	1140.5352	0.0133	172 - 180		0	NNPFYFPSR
1184.6049	1183.5976	1183.5846	0.0130	205 - 213		0	QFQNLQNHR
1258.6267	1257.6194	1257.6101	0.0093	255 - 265		0	SFNLDEGHALR
1287.6078	1286.6005	1286.5891	0.0114	308 - 318		0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	172 - 181		1	NNPFYFPSRR
1343.6807	1342.6734	1342.6703	0.0031	440 - 451		0	EGALMLPHFNSK
1376.6738	1375.6665	1375.6619	0.0046	560 - 572		0	DLAFPGSGEQVEK
1379.7811	1378.7738	1378.7608	0.0130	266 - 277		0	IPSGFISYILNR
1386.7233	1385.7160	1385.7051	0.0109	254 - 265		1	KSFNLDEGHALR
1568.7139	1567.7066	1567.7015	0.0052	153 - 166		0	EGEQEWGTPGSHVR
1572.7555	1571.7482	1571.7426	0.0056	335 - 348		0	VLLEENAGGEQEER
1643.7926	1642.7853	1642.7798	0.0056	387 - 401		0	GSEEEGDITNPINLR
1738.8445	1737.8372	1737.8321	0.0051	319 - 333		0	NTLEAAFNAEFNEIR
1771.8853	1770.8780	1770.8747	0.0033	386 - 401		1	KGSEEEGDITNPINLR
1817.9626	1816.9553	1816.9570	-0.0017	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9393	1893.9320	1893.9332	-0.0012	319 - 334		1	NTLEAAFNAEFNEIRR
2082.2083	2081.2010	2081.2030	-0.0019	452 - 471		1	AMVIVVVNKGTGNLELVAVR

2227.0347	2226.0274	2226.0415	-0.0141	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0430	2242.0357	2242.0364	-0.0007	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3030	2618.2957	2618.3160	-0.0203	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.3936	2746.3863	2746.4110	-0.0246	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 756.3921, 795.3989, 805.4335, 808.3868, 812.4179, 828.4940, 959.4940, 1167.5803, 1281.2028, 1320.5917, 1399.7314, 1560.6963, 1586.7666, 1691.0289, 1714.8617, 2185.0300, 2273.1587, 2281.8374, 2620.3003, 2748.3792, 3153.4365, 3211.4670

7. gi|46560476 **Mass:** 48122 **Score:** 193 **Expect:** 4.4e-017 **Queries matched:** 19

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4457	815.4384	815.4249	0.0135	274 -	279	1	KEQQQR
896.4477	895.4404	895.4260	0.0144	81 -	87	0	HDNQNLR
1128.6503	1127.6430	1127.6298	0.0132	263 -	273	0	GTGNLELVAVR
1184.6049	1183.5976	1183.5846	0.0130	8 -	16	0	QFQNLQNHR
1258.6267	1257.6194	1257.6101	0.0093	58 -	68	0	SFNLDEGHALR
1287.6078	1286.6005	1286.5891	0.0114	111 -	121	0	DQSSYLQGFSR
1343.6807	1342.6734	1342.6703	0.0031	242 -	253	0	EGALMLPHFNSK
1376.6738	1375.6665	1375.6619	0.0046	362 -	374	0	DLAFPGSGEQVEK
1379.7811	1378.7738	1378.7608	0.0130	69 -	80	0	IPSGFISYILNR
1386.7233	1385.7160	1385.7051	0.0109	57 -	68	1	KSFNLDEGHALR
1572.7555	1571.7482	1571.7426	0.0056	138 -	151	0	VLLEENAGGEQEER
1738.8445	1737.8372	1737.8321	0.0051	122 -	136	0	NTLEAAFNAEFNEIR
1817.9626	1816.9553	1816.9570	-0.0017	343 -	358	1	IFLAGDKDNVIDQIEK
1894.9393	1893.9320	1893.9332	-0.0012	122 -	137	1	NTLEAAFNAEFNEIRR
2082.2083	2081.2010	2081.2030	-0.0019	254 -	273	1	AMVIVVVNKGTGNLELVAVR
2227.0347	2226.0274	2226.0415	-0.0141	91 -	110	0	ISMPVNTPGQFEDFFPASSR
2243.0430	2242.0357	2242.0364	-0.0007	91 -	110	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.3030	2618.2957	2618.3160	-0.0203	32 -	56	0	HADADNILVIQQGQATVTVANGNNR
2747.3936	2746.3863	2746.4110	-0.0246	32 -	57	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3958, 756.3921, 795.3989, 805.4335, 808.3868, 812.4179, 828.4940, 855.5270, 959.4940, 1005.5445, 1019.4675, 1141.5558, 1167.5803, 1281.2028, 1297.6560, 1320.5917, 1399.7314, 1560.6963, 1568.7139, 1586.7666, 1643.7926, 1691.0289, 1714.8617, 1771.8853, 2185.0300, 2273.1587, 2281.8374, 2620.3003, 2748.3792, 3153.4365, 3211.4670

8. gi|46560472 **Mass:** 34169 **Score:** 100 **Expect:** 8.7e-008 **Queries matched:** 11

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4457	815.4384	815.4249	0.0135	153 -	158	1	KEQQQR
1128.6503	1127.6430	1127.6298	0.0132	142 -	152	0	GTGNLELVAVR
1320.5917	1319.5844	1319.5741	0.0103	83 -	94	0	DGEPDLSNNFGR

1343.6807	1342.6734	1342.6703	0.0031	121 - 132	0	EGALMLPHFNSK
1376.6738	1375.6665	1375.6619	0.0046	244 - 256	0	DLAFPGSGEQVEK
1572.7555	1571.7482	1571.7426	0.0056	18 - 31	0	VLLEENAGGEQEER
1586.7666	1585.7593	1585.7583	0.0010	69 - 82	0	GSEEEDITNPINLR
1714.8617	1713.8544	1713.8533	0.0012	68 - 82	1	KGSEEEDITNPINLR
1817.9626	1816.9553	1816.9570	-0.0017	225 - 240	1	IFLAGDKDNVIDQIEK
2082.2083	2081.2010	2081.2030	-0.0019	133 - 152	1	AMVIVVVNKGTGNLELVAVR
2281.8374	2280.8301	2280.8414	-0.0112	162 - 179	0	EQEWEEEEEDEEEEGSNR

No match to: 740.3958, 756.3921, 795.3989, 805.4335, 808.3868, 812.4179, 828.4940, 855.5270, 896.4477, 959.4940, 1005.5445, 1019.4675, 1141.5558, 1167.5803, 1184.6049, 1258.6267, 1281.2028, 1287.6078, 1297.6560, 1379.7811, 1386.7233, 1399.7314, 1560.6963, 1568.7139, 1643.7926, 1691.0289, 1738.8445, 1771.8853, 1894.9393, 2185.0300, 2227.0347, 2243.0430, 2273.1587, 2619.3030, 2620.3003, 2747.3936, 2748.3792, 3153.4365, 3211.4670

9. gi|46560474 **Mass:** 33641 **Score:** 75 **Expect:** 3e-005 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4457	815.4384	815.4249	0.0135	152 - 157		1	KEQQQR
1128.6503	1127.6430	1127.6298	0.0132	141 - 151		0	GTGNLELVAVR
1343.6807	1342.6734	1342.6703	0.0031	120 - 131		0	EGALMLPHFNSK
1376.6738	1375.6665	1375.6619	0.0046	240 - 252		0	DLAFPGSGEQVEK
1572.7555	1571.7482	1571.7426	0.0056	15 - 28		0	VLLEENAGGEQEER
1643.7926	1642.7853	1642.7798	0.0056	67 - 81		0	GSEEEGDITNPINLR
1771.8853	1770.8780	1770.8747	0.0033	66 - 81		1	KGSEEEGDITNPINLR
1817.9626	1816.9553	1816.9570	-0.0017	221 - 236		1	IFLAGDKDNVIDQIEK
2082.2083	2081.2010	2081.2030	-0.0019	132 - 151		1	AMVIVVVNKGTGNLELVAVR

No match to: 740.3958, 756.3921, 795.3989, 805.4335, 808.3868, 812.4179, 828.4940, 855.5270, 896.4477, 959.4940, 1005.5445, 1019.4675, 1141.5558, 1167.5803, 1184.6049, 1258.6267, 1281.2028, 1287.6078, 1297.6560, 1320.5917, 1379.7811, 1386.7233, 1399.7314, 1560.6963, 1568.7139, 1586.7666, 1691.0289, 1714.8617, 1738.8445, 1894.9393, 2185.0300, 2227.0347, 2243.0430, 2273.1587, 2281.8374, 2619.3030, 2620.3003, 2747.3936, 2748.3792, 3153.4365, 3211.4670

10. gi|62177652 **Mass:** 10056 **Score:** 19 **Expect:** 11 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1379.7811	1378.7738	1378.7496	0.0243	77 - 89		1	EVVKYSGGLPFAL
1894.9393	1893.9320	1893.9009	0.0312	7 - 23		0	QLEYLGGEQAWFGPGSR

No match to: 740.3958, 756.3921, 795.3989, 805.4335, 808.3868, 812.4179, 816.4457, 828.4940, 855.5270, 896.4477, 959.4940, 1005.5445, 1019.4675, 1128.6503, 1141.5558, 1167.5803, 1184.6049, 1258.6267, 1281.2028, 1287.6078, 1297.6560, 1320.5917, 1343.6807, 1376.6738, 1386.7233, 1399.7314, 1560.6963, 1568.7139, 1572.7555, 1586.7666, 1643.7926, 1691.0289, 1714.8617, 1738.8445, 1771.8853, 1817.9626, 2082.2083, 2185.0300, 2227.0347, 2243.0430, 2273.1587, 2281.8374, 2619.3030, 2620.3003, 2747.3936, 2748.3792, 3153.4365, 3211.4670

Search Parameters

Type of search	**: Peptide Mass Fingerprint**
Enzyme	**: Trypsin**
Fixed modifications	**: Carbamidomethyl (C)**
Variable modifications	**: Oxidation (M)**
Mass values	**: MONOISOTOPIC**
Protein Mass	**: Unrestricted**
Peptide Mass Tolerance	**: ± 20 ppm**
Peptide Charge State	**: 1+**
Max Missed Cleavages	**: 1**
Number of queries	**: 50**

Protein View

Match to: **gi|46560478** Score: **349** Expect: **1.1e-032**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **32**
Sequence Coverage: **53%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
109 - 115	812.4179	811.4106	811.3976	0.0130	0	WGPAEPR	
118 - 124	1019.4675	1018.4602	1018.4468	0.0134	1	EREEDWR	
132 - 139	1005.5445	1004.5372	1004.5264	0.0108	0	RPSHQQPR	
140 - 146	855.5270	854.5197	854.5086	0.0111	1	KIRPEGR	
147 - 160	1560.6963	1559.6890	1559.6851	0.0039	0	EGEQEWGTPGSEVR	
166 - 174	1141.5558	1140.5485	1140.5352	0.0133	0	NNPFYFPSR	
166 - 175	1297.6560	1296.6487	1296.6363	0.0124	1	NNPFYFPSRR	
197 - 207	1399.7314	1398.7241	1398.7116	0.0125	1	SKQFQNLQNHR	
199 - 207	1184.6049	1183.5976	1183.5846	0.0130	0	QFQNLQNHR	
208 - 222	1691.0289	1690.0216	1690.0141	0.0076	0	IVQIEARPNTLVLPK	
223 - 247	2619.3030	2618.2957	2618.3160	-0.0203	0	HADADNILVIQQGQATVTVANGNNR	
223 - 248	2747.3936	2746.3863	2746.4110	-0.0246	1	HADADNILVIQQGQATVTVANGNNRK	
248 - 259	1386.7233	1385.7160	1385.7051	0.0109	1	KSFNLDEGHALR	
249 - 259	1258.6267	1257.6194	1257.6101	0.0093	0	SFNLDEGHALR	
260 - 271	1379.7811	1378.7738	1378.7608	0.0130	0	IPSGFISYILNR	
272 - 278	896.4477	895.4404	895.4260	0.0144	0	HDNQNLR	
282 - 301	2227.0347	2226.0274	2226.0415	-0.0141	0	ISMPVNTPGQFEDFFPASSR	
282 - 301	2243.0430	2242.0357	2242.0364	-0.0007	0	ISMPVNTPGQFEDFFPASSR	Oxidation (M)
302 - 312	1287.6078	1286.6005	1286.5891	0.0114	0	DQSSYLQGFSR	
313 - 327	1738.8445	1737.8372	1737.8321	0.0051	0	NTLEAAFNAEFNEIR	
313 - 328	1894.9393	1893.9320	1893.9332	-0.0012	1	NTLEAAFNAEFNEIRR	
329 - 342	1572.7555	1571.7482	1571.7426	0.0056	0	VLLEENAGGEQEER	
379 - 393	1714.8617	1713.8544	1713.8533	0.0012	1	KGSEEEDITNPINLR	
380 - 393	1586.7666	1585.7593	1585.7583	0.0010	0	GSEEEDITNPINLR	
394 - 405	1320.5917	1319.5844	1319.5741	0.0103	0	DGEPDLSNNFGR	
432 - 443	1343.6807	1342.6734	1342.6703	0.0031	0	EGALMLPHFNSK	
444 - 463	2082.2083	2081.2010	2081.2030	-0.0019	1	AMVIVVVNKGTGNLELVAVR	
453 - 463	1128.6503	1127.6430	1127.6298	0.0132	0	GTGNLELVAVR	
464 - 469	816.4457	815.4384	815.4249	0.0135	1	KEQQQR	
473 - 490	2281.8374	2280.8301	2280.8414	-0.0112	0	EQEWEEEEEDEEEEGSNR	
536 - 551	1817.9626	1816.9553	1816.9570	-0.0017	1	IFLAGDKDNVIDQIEK	
555 - 567	1376.6738	1375.6665	1375.6619	0.0046	0	DLAFPGSGEQVEK	

No match to: 740.3958, 756.3921, 795.3989, 805.4335, 808.3868, 828.4940, 959.4940, 1167.5803, 1281.2028, 1568.7139, 1643.7926, 1771.8853, 2185.0300, 2273.1587, 2620.3003, 2748.3792, 3153.4365, 3211.4670

Spot 7

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:30:57 GMT**
Top Score : **345 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	345	conarachin [Arachis hypogaea]
2.	gi|620025	70639	339	Ara h I
3.	gi|1168390	70639	339	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	272	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	272	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	272	Ara h I
7.	gi|46560476	48122	177	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	85	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	61	conarachin [Arachis hypogaea]
10.	gi|62177652	10056	19	resistance protein PRG [Arachis hypogaea]

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 345 **Expect:** 2.8e-032 **Queries matched:** 32
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3604	807.3531	807.3623	-0.0092	180	186	0	YGNQNGR
812.4002	811.3929	811.3976	-0.0047	109	115	0	WGPAEPR
816.4263	815.4190	815.4249	-0.0059	464	469	1	KEQQQR
855.5049	854.4976	854.5086	-0.0110	140	146	1	KIRPEGR
896.4215	895.4142	895.4260	-0.0118	272	278	0	HDNQNLR
1005.5208	1004.5135	1004.5264	-0.0129	132	139	0	RPSHQQPR
1019.4337	1018.4264	1018.4468	-0.0204	118	124	1	EREEDWR
1128.6249	1127.6176	1127.6298	-0.0122	453	463	0	GTGNLELVAVR
1141.5353	1140.5280	1140.5352	-0.0072	166	174	0	NNPFYFPSR
1184.5823	1183.5750	1183.5846	-0.0096	199	207	0	QFQNLQNHR
1258.6033	1257.5960	1257.6101	-0.0141	249	259	0	SFNLDEGHALR

1287.5873	1286.5800	1286.5891	-0.0091	302 - 312	0	DQSSYLQGFSR
1297.6335	1296.6262	1296.6363	-0.0101	166 - 175	1	NNPFYFPSRR
1320.5737	1319.5664	1319.5741	-0.0077	394 - 405	0	DGEPDLSNNFGR
1343.6594	1342.6521	1342.6703	-0.0182	432 - 443	0	EGALMLPHFNSK
1379.7606	1378.7533	1378.7608	-0.0075	260 - 271	0	IPSGFISYILNR
1386.7046	1385.6973	1385.7051	-0.0078	248 - 259	1	KSFNLDEGHALR
1399.7046	1398.6973	1398.7116	-0.0143	197 - 207	1	SKQFQNLQNHR
1560.6766	1559.6693	1559.6851	-0.0158	147 - 160	0	EGEQEWGTPGSEVR
1572.7310	1571.7237	1571.7426	-0.0189	329 - 342	0	VLLEENAGGEQEER
1586.7445	1585.7372	1585.7583	-0.0211	380 - 393	0	GSEEEDITNPINLR
1691.0051	1689.9978	1690.0141	-0.0162	208 - 222	0	IVQIEARPNTLVLPK
1714.8430	1713.8357	1713.8533	-0.0175	379 - 393	1	KGSEEEDITNPINLR
1728.8392	1727.8319	1727.8437	-0.0118	328 - 342	1	RVLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	313 - 327	0	NTLEAAFNAEFNEIR
1817.9440	1816.9367	1816.9570	-0.0203	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9214	1893.9141	1893.9332	-0.0191	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0222	2226.0149	2226.0415	-0.0266	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0330	2242.0257	2242.0364	-0.0107	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8306	2280.8233	2280.8414	-0.0180	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.2815	2618.2742	2618.3160	-0.0418	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3762	2746.3689	2746.4110	-0.0420	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3738, 756.3693, 772.3622, 828.4694, 959.4727, 1167.5520, 1281.1781, 1304.5845, 1449.6284, 1568.6945, 1643.7769, 1771.8672, 1830.8497, 2181.0925, 2273.1367, 2332.0447, 2620.2827, 2748.3699

2. gi|620025 **Mass:** 70639 **Score:** 339 **Expect:** 1.1e-031 **Queries matched:** 32

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3604	807.3531	807.3623	-0.0092	180	186	0	YGNQNGR
812.4002	811.3929	811.3976	-0.0047	109	115	0	WGPAEPR
816.4263	815.4190	815.4249	-0.0059	464	469	1	KEQQQR
855.5049	854.4976	854.5086	-0.0110	140	146	1	KIRPEGR
896.4215	895.4142	895.4260	-0.0118	272	278	0	HDNQNLR
1005.5208	1004.5135	1004.5264	-0.0129	132	139	0	RPSHQQPR
1019.4337	1018.4264	1018.4468	-0.0204	118	124	1	EREEDWR
1128.6249	1127.6176	1127.6298	-0.0122	453	463	0	GTGNLELVAVR
1141.5353	1140.5280	1140.5352	-0.0072	166	174	0	NNPFYFPSR
1184.5823	1183.5750	1183.5846	-0.0096	199	207	0	QFQNLQNHR
1258.6033	1257.5960	1257.6101	-0.0141	249	259	0	SFNLDEGHALR
1287.5873	1286.5800	1286.5891	-0.0091	302	312	0	DQSSYLQGFSR
1297.6335	1296.6262	1296.6363	-0.0101	166	175	1	NNPFYFPSRR

1320.5737	1319.5664	1319.5741	-0.0077	394 - 405	0	DGEPDLSNNFGR
1343.6594	1342.6521	1342.6703	-0.0182	432 - 443	0	EGALMLPHFNSK
1379.7606	1378.7533	1378.7608	-0.0075	260 - 271	0	IPSGFISYILNR
1386.7046	1385.6973	1385.7051	-0.0078	248 - 259	1	KSFNLDEGHALR
1399.7046	1398.6973	1398.7116	-0.0143	197 - 207	1	SKQFQNLQNHR
1560.6766	1559.6693	1559.6851	-0.0158	147 - 160	0	EGEQEWGTPGSEVR
1572.7310	1571.7237	1571.7426	-0.0189	329 - 342	0	VLLEENAGGEQEER
1586.7445	1585.7372	1585.7583	-0.0211	380 - 393	0	GSEEEDITNPINLR
1691.0051	1689.9978	1690.0141	-0.0162	208 - 222	0	IVQIEARPNTLVLPK
1714.8430	1713.8357	1713.8533	-0.0175	379 - 393	1	KGSEEEDITNPINLR
1728.8392	1727.8319	1727.8437	-0.0118	328 - 342	1	RVLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	313 - 327	0	NTLEAAFNAEFNEIR
1817.9440	1816.9367	1816.9570	-0.0203	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9214	1893.9141	1893.9332	-0.0191	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0222	2226.0149	2226.0415	-0.0266	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0330	2242.0257	2242.0364	-0.0107	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8306	2280.8233	2280.8414	-0.0180	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.2815	2618.2742	2618.3160	-0.0418	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3762	2746.3689	2746.4110	-0.0420	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3738, 756.3693, 772.3622, 828.4694, 959.4727, 1167.5520, 1281.1781, 1304.5845, 1449.6284, 1568.6945, 1643.7769, 1771.8672, 1830.8497, 2181.0925, 2273.1367, 2332.0447, 2620.2827, 2748.3699

3. gi|1168390 **Mass:** 70639 **Score:** 339 **Expect:** 1.1e-031 **Queries matched:** 32

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3604	807.3531	807.3623	-0.0092	180 - 186		0	YGNQNGR
812.4002	811.3929	811.3976	-0.0047	109 - 115		0	WGPAEPR
816.4263	815.4190	815.4249	-0.0059	464 - 469		1	KEQQQR
855.5049	854.4976	854.5086	-0.0110	140 - 146		1	KIRPEGR
896.4215	895.4142	895.4260	-0.0118	272 - 278		0	HDNQNLR
1005.5208	1004.5135	1004.5264	-0.0129	132 - 139		0	RPSHQQPR
1019.4337	1018.4264	1018.4468	-0.0204	118 - 124		1	EREEDWR
1128.6249	1127.6176	1127.6298	-0.0122	453 - 463		0	GTGNLELVAVR
1141.5353	1140.5280	1140.5352	-0.0072	166 - 174		0	NNPFYFPSR
1184.5823	1183.5750	1183.5846	-0.0096	199 - 207		0	QFQNLQNHR
1258.6033	1257.5960	1257.6101	-0.0141	249 - 259		0	SFNLDEGHALR
1287.5873	1286.5800	1286.5891	-0.0091	302 - 312		0	DQSSYLQGFSR
1297.6335	1296.6262	1296.6363	-0.0101	166 - 175		1	NNPFYFPSRR
1320.5737	1319.5664	1319.5741	-0.0077	394 - 405		0	DGEPDLSNNFGR
1343.6594	1342.6521	1342.6703	-0.0182	432 - 443		0	EGALMLPHFNSK

1379.7606	1378.7533	1378.7608	-0.0075	260 - 271	0	IPSGFISYILNR
1386.7046	1385.6973	1385.7051	-0.0078	248 - 259	1	KSFNLDEGHALR
1399.7046	1398.6973	1398.7116	-0.0143	197 - 207	1	SKQFQNLQNHR
1560.6766	1559.6693	1559.6851	-0.0158	147 - 160	0	EGEQEWGTPGSEVR
1572.7310	1571.7237	1571.7426	-0.0189	329 - 342	0	VLLEENAGGEQEER
1586.7445	1585.7372	1585.7583	-0.0211	380 - 393	0	GSEEEDITNPINLR
1691.0051	1689.9978	1690.0141	-0.0162	208 - 222	0	IVQIEARPNTLVLPK
1714.8430	1713.8357	1713.8533	-0.0175	379 - 393	1	KGSEEEDITNPINLR
1728.8392	1727.8319	1727.8437	-0.0118	328 - 342	1	RVLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	313 - 327	0	NTLEAAFNAEFNEIR
1817.9440	1816.9367	1816.9570	-0.0203	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9214	1893.9141	1893.9332	-0.0191	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0222	2226.0149	2226.0415	-0.0266	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0330	2242.0257	2242.0364	-0.0107	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8306	2280.8233	2280.8414	-0.0180	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.2815	2618.2742	2618.3160	-0.0418	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3762	2746.3689	2746.4110	-0.0420	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3738, 756.3693, 772.3622, 828.4694, 959.4727, 1167.5520, 1281.1781, 1304.5845, 1449.6284, 1568.6945, 1643.7769, 1771.8672, 1830.8497, 2181.0925, 2273.1367, 2332.0447, 2620.2827, 2748.3699

4. gi|16612200 **Mass:** 71701 **Score:** 272 **Expect:** 5.5e-025 **Queries matched:** 28

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3738	739.3665	739.3765	-0.0100	115 - 121		0	WGPAGPR
808.3604	807.3531	807.3623	-0.0092	186 - 192		0	YGNQNGR
816.4263	815.4190	815.4249	-0.0059	472 - 477		1	KEQQQR
855.5049	854.4976	854.5086	-0.0110	146 - 152		1	KIRPEGR
896.4215	895.4142	895.4260	-0.0118	278 - 284		0	HDNQNLR
1005.5208	1004.5135	1004.5264	-0.0129	138 - 145		0	RPSHQQPR
1019.4337	1018.4264	1018.4468	-0.0204	124 - 130		1	EREEDWR
1128.6249	1127.6176	1127.6298	-0.0122	461 - 471		0	GTGNLELVAVR
1141.5353	1140.5280	1140.5352	-0.0072	172 - 180		0	NNPFYFPSR
1184.5823	1183.5750	1183.5846	-0.0096	205 - 213		0	QFQNLQNHR
1258.6033	1257.5960	1257.6101	-0.0141	255 - 265		0	SFNLDEGHALR
1287.5873	1286.5800	1286.5891	-0.0091	308 - 318		0	DQSSYLQGFSR
1297.6335	1296.6262	1296.6363	-0.0101	172 - 181		1	NNPFYFPSRR
1343.6594	1342.6521	1342.6703	-0.0182	440 - 451		0	EGALMLPHFNSK
1379.7606	1378.7533	1378.7608	-0.0075	266 - 277		0	IPSGFISYILNR
1386.7046	1385.6973	1385.7051	-0.0078	254 - 265		1	KSFNLDEGHALR
1568.6945	1567.6872	1567.7015	-0.0142	153 - 166		0	EGEQEWGTPGSHVR

1572.7310	1571.7237	1571.7426	-0.0189	335 - 348	0	VLLEENAGGEQEER
1643.7769	1642.7696	1642.7798	-0.0101	387 - 401	0	GSEEEGDITNPINLR
1728.8392	1727.8319	1727.8437	-0.0118	334 - 348	1	RVLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	319 - 333	0	NTLEAAFNAEFNEIR
1771.8672	1770.8599	1770.8747	-0.0148	386 - 401	1	KGSEEEGDITNPINLR
1817.9440	1816.9367	1816.9570	-0.0203	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9214	1893.9141	1893.9332	-0.0191	319 - 334	1	NTLEAAFNAEFNEIRR
2227.0222	2226.0149	2226.0415	-0.0266	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0330	2242.0257	2242.0364	-0.0107	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2815	2618.2742	2618.3160	-0.0418	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.3762	2746.3689	2746.4110	-0.0420	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 756.3693, 772.3622, 812.4002, 828.4694, 959.4727, 1167.5520, 1281.1781, 1304.5845, 1320.5737, 1399.7046, 1449.6284, 1560.6766, 1586.7445, 1691.0051, 1714.8430, 1830.8497, 2181.0925, 2273.1367, 2281.8306, 2332.0447, 2620.2827, 2748.3699

5. gi|1168391 **Mass:** 71701 **Score:** 272 **Expect:** 5.5e-025 **Queries matched:** 28

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3738	739.3665	739.3765	-0.0100	115 - 121		0	WGPAGPR
808.3604	807.3531	807.3623	-0.0092	186 - 192		0	YGNQNGR
816.4263	815.4190	815.4249	-0.0059	472 - 477		1	KEQQQR
855.5049	854.4976	854.5086	-0.0110	146 - 152		1	KIRPEGR
896.4215	895.4142	895.4260	-0.0118	278 - 284		0	HDNQNLR
1005.5208	1004.5135	1004.5264	-0.0129	138 - 145		0	RPSHQQPR
1019.4337	1018.4264	1018.4468	-0.0204	124 - 130		1	EREEDWR
1128.6249	1127.6176	1127.6298	-0.0122	461 - 471		0	GTGNLELVAVR
1141.5353	1140.5280	1140.5352	-0.0072	172 - 180		0	NNPFYFPSR
1184.5823	1183.5750	1183.5846	-0.0096	205 - 213		0	QFQNLQNHR
1258.6033	1257.5960	1257.6101	-0.0141	255 - 265		0	SFNLDEGHALR
1287.5873	1286.5800	1286.5891	-0.0091	308 - 318		0	DQSSYLQGFSR
1297.6335	1296.6262	1296.6363	-0.0101	172 - 181		1	NNPFYFPSRR
1343.6594	1342.6521	1342.6703	-0.0182	440 - 451		0	EGALMLPHFNSK
1379.7606	1378.7533	1378.7608	-0.0075	266 - 277		0	IPSGFISYILNR
1386.7046	1385.6973	1385.7051	-0.0078	254 - 265		1	KSFNLDEGHALR
1568.6945	1567.6872	1567.7015	-0.0142	153 - 166		0	EGEQEWGTPGSHVR
1572.7310	1571.7237	1571.7426	-0.0189	335 - 348		0	VLLEENAGGEQEER
1643.7769	1642.7696	1642.7798	-0.0101	387 - 401		0	GSEEEGDITNPINLR
1728.8392	1727.8319	1727.8437	-0.0118	334 - 348		1	RVLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	319 - 333		0	NTLEAAFNAEFNEIR
1771.8672	1770.8599	1770.8747	-0.0148	386 - 401		1	KGSEEEGDITNPINLR

1817.9440	1816.9367	1816.9570	-0.0203	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9214	1893.9141	1893.9332	-0.0191	319 - 334	1	NTLEAAFNAEFNEIRR
2227.0222	2226.0149	2226.0415	-0.0266	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0330	2242.0257	2242.0364	-0.0107	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2815	2618.2742	2618.3160	-0.0418	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.3762	2746.3689	2746.4110	-0.0420	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 756.3693, 772.3622, 812.4002, 828.4694, 959.4727, 1167.5520, 1281.1781, 1304.5845, 1320.5737, 1399.7046, 1449.6284, 1560.6766, 1586.7445, 1691.0051, 1714.8430, 1830.8497, 2181.0925, 2273.1367, 2281.8306, 2332.0447, 2620.2827, 2748.3699

6. gi|602436 **Mass:** 71701 **Score:** 272 **Expect:** 5.5e-025 **Queries matched:** 28

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3738	739.3665	739.3765	-0.0100	115 - 121		0	WGPAGPR
808.3604	807.3531	807.3623	-0.0092	186 - 192		0	YGNQNGR
816.4263	815.4190	815.4249	-0.0059	472 - 477		1	KEQQQR
855.5049	854.4976	854.5086	-0.0110	146 - 152		1	KIRPEGR
896.4215	895.4142	895.4260	-0.0118	278 - 284		0	HDNQNLR
1005.5208	1004.5135	1004.5264	-0.0129	138 - 145		0	RPSHQQPR
1019.4337	1018.4264	1018.4468	-0.0204	124 - 130		1	EREEDWR
1128.6249	1127.6176	1127.6298	-0.0122	461 - 471		0	GTGNLELVAVR
1141.5353	1140.5280	1140.5352	-0.0072	172 - 180		0	NNPFYFPSR
1184.5823	1183.5750	1183.5846	-0.0096	205 - 213		0	QFQNLQNHR
1258.6033	1257.5960	1257.6101	-0.0141	255 - 265		0	SFNLDEGHALR
1287.5873	1286.5800	1286.5891	-0.0091	308 - 318		0	DQSSYLQGFSR
1297.6335	1296.6262	1296.6363	-0.0101	172 - 181		1	NNPFYFPSRR
1343.6594	1342.6521	1342.6703	-0.0182	440 - 451		0	EGALMLPHFNSK
1379.7606	1378.7533	1378.7608	-0.0075	266 - 277		0	IPSGFISYILNR
1386.7046	1385.6973	1385.7051	-0.0078	254 - 265		1	KSFNLDEGHALR
1568.6945	1567.6872	1567.7015	-0.0142	153 - 166		0	EGEQEWGTPGSHVR
1572.7310	1571.7237	1571.7426	-0.0189	335 - 348		0	VLLEENAGGEQEER
1643.7769	1642.7696	1642.7798	-0.0101	387 - 401		0	GSEEEGDITNPINLR
1728.8392	1727.8319	1727.8437	-0.0118	334 - 348		1	RVLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	319 - 333		0	NTLEAAFNAEFNEIR
1771.8672	1770.8599	1770.8747	-0.0148	386 - 401		1	KGSEEEGDITNPINLR
1817.9440	1816.9367	1816.9570	-0.0203	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9214	1893.9141	1893.9332	-0.0191	319 - 334		1	NTLEAAFNAEFNEIRR
2227.0222	2226.0149	2226.0415	-0.0266	288 - 307		0	ISMPVNTPGQFEDFFPASSR
2243.0330	2242.0257	2242.0364	-0.0107	288 - 307		0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2815	2618.2742	2618.3160	-0.0418	229 - 253		0	HADADNILVIQQGQATVTVANGNNR

2747.3762	2746.3689	2746.4110	-0.0420	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 756.3693, 772.3622, 812.4002, 828.4694, 959.4727, 1167.5520, 1281.1781, 1304.5845, 1320.5737, 1399.7046, 1449.6284, 1560.6766, 1586.7445, 1691.0051, 1714.8430, 1830.8497, 2181.0925, 2273.1367, 2281.8306, 2332.0447, 2620.2827, 2748.3699

7. gi|46560476 **Mass:** 48122 **Score:** 177 **Expect:** 1.7e-015 **Queries matched:** 18

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4263	815.4190	815.4249	-0.0059	274 -	279	1	KEQQQR
896.4215	895.4142	895.4260	-0.0118	81 -	87	0	HDNQNLR
1128.6249	1127.6176	1127.6298	-0.0122	263 -	273	0	GTGNLELVAVR
1184.5823	1183.5750	1183.5846	-0.0096	8 -	16	0	QFQNLQNHR
1258.6033	1257.5960	1257.6101	-0.0141	58 -	68	0	SFNLDEGHALR
1287.5873	1286.5800	1286.5891	-0.0091	111 -	121	0	DQSSYLQGFSR
1343.6594	1342.6521	1342.6703	-0.0182	242 -	253	0	EGALMLPHFNSK
1379.7606	1378.7533	1378.7608	-0.0075	69 -	80	0	IPSGFISYILNR
1386.7046	1385.6973	1385.7051	-0.0078	57 -	68	1	KSFNLDEGHALR
1572.7310	1571.7237	1571.7426	-0.0189	138 -	151	0	VLLEENAGGEQEER
1728.8392	1727.8319	1727.8437	-0.0118	137 -	151	1	RVLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	122 -	136	0	NTLEAAFNAEFNEIR
1817.9440	1816.9367	1816.9570	-0.0203	343 -	358	1	IFLAGDKDNVIDQIEK
1894.9214	1893.9141	1893.9332	-0.0191	122 -	137	1	NTLEAAFNAEFNEIRR
2227.0222	2226.0149	2226.0415	-0.0266	91 -	110	0	ISMPVNTPGQFEDFFPASSR
2243.0330	2242.0257	2242.0364	-0.0107	91 -	110	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2815	2618.2742	2618.3160	-0.0418	32 -	56	0	HADADNILVIQQGQATVTVANGNNR
2747.3762	2746.3689	2746.4110	-0.0420	32 -	57	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 740.3738, 756.3693, 772.3622, 808.3604, 812.4002, 828.4694, 855.5049, 959.4727, 1005.5208, 1019.4337, 1141.5353, 1167.5520, 1281.1781, 1297.6335, 1304.5845, 1320.5737, 1399.7046, 1449.6284, 1560.6766, 1568.6945, 1586.7445, 1643.7769, 1691.0051, 1714.8430, 1771.8672, 1830.8497, 2181.0925, 2273.1367, 2281.8306, 2332.0447, 2620.2827, 2748.3699

8. gi|46560472 **Mass:** 34169 **Score:** 85 **Expect:** 2.6e-006 **Queries matched:** 10

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4263	815.4190	815.4249	-0.0059	153 -	158	1	KEQQQR
1128.6249	1127.6176	1127.6298	-0.0122	142 -	152	0	GTGNLELVAVR
1320.5737	1319.5664	1319.5741	-0.0077	83 -	94	0	DGEPDLSNNFGR
1343.6594	1342.6521	1342.6703	-0.0182	121 -	132	0	EGALMLPHFNSK
1572.7310	1571.7237	1571.7426	-0.0189	18 -	31	0	VLLEENAGGEQEER
1586.7445	1585.7372	1585.7583	-0.0211	69 -	82	0	GSEEEDITNPINLR
1714.8430	1713.8357	1713.8533	-0.0175	68 -	82	1	KGSEEEDITNPINLR

1728.8392	1727.8319	1727.8437	-0.0118	17 - 31	1	RVLLEENAGGEQEER
1817.9440	1816.9367	1816.9570	-0.0203	225 - 240	1	IFLAGDKDNVIDQIEK
2281.8306	2280.8233	2280.8414	-0.0180	162 - 179	0	EQEWEEEEEDEEEEGSNR

No match to: 740.3738, 756.3693, 772.3622, 808.3604, 812.4002, 828.4694, 855.5049, 896.4215, 959.4727, 1005.5208, 1019.4337, 1141.5353, 1167.5520, 1184.5823, 1258.6033, 1281.1781, 1287.5873, 1297.6335, 1304.5845, 1379.7606, 1386.7046, 1399.7046, 1449.6284, 1560.6766, 1568.6945, 1643.7769, 1691.0051, 1738.8246, 1771.8672, 1830.8497, 1894.9214, 2181.0925, 2227.0222, 2243.0330, 2273.1367, 2332.0447, 2619.2815, 2620.2827, 2747.3762, 2748.3699

9. gi|46560474 **Mass:** 33641 **Score:** 61 **Expect:** 0.00063 **Queries matched:** 8

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4263	815.4190	815.4249	-0.0059	152 -	157	1	KEQQQR
1128.6249	1127.6176	1127.6298	-0.0122	141 -	151	0	GTGNLELVAVR
1343.6594	1342.6521	1342.6703	-0.0182	120 -	131	0	EGALMLPHFNSK
1572.7310	1571.7237	1571.7426	-0.0189	15 -	28	0	VLLEENAGGEQEER
1643.7769	1642.7696	1642.7798	-0.0101	67 -	81	0	GSEEEGDITNPINLR
1728.8392	1727.8319	1727.8437	-0.0118	14 -	28	1	RVLLEENAGGEQEER
1771.8672	1770.8599	1770.8747	-0.0148	66 -	81	1	KGSEEEGDITNPINLR
1817.9440	1816.9367	1816.9570	-0.0203	221 -	236	1	IFLAGDKDNVIDQIEK

No match to: 740.3738, 756.3693, 772.3622, 808.3604, 812.4002, 828.4694, 855.5049, 896.4215, 959.4727, 1005.5208, 1019.4337, 1141.5353, 1167.5520, 1184.5823, 1258.6033, 1281.1781, 1287.5873, 1297.6335, 1304.5845, 1320.5737, 1379.7606, 1386.7046, 1399.7046, 1449.6284, 1560.6766, 1568.6945, 1586.7445, 1691.0051, 1714.8430, 1738.8246, 1830.8497, 1894.9214, 2181.0925, 2227.0222, 2243.0330, 2273.1367, 2281.8306, 2332.0447, 2619.2815, 2620.2827, 2747.3762, 2748.3699

10. gi|62177652 **Mass:** 10056 **Score:** 19 **Expect:** 11 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1379.7606	1378.7533	1378.7496	0.0038	77 -	89	1	EVVKYSGGLPFAL
1894.9214	1893.9141	1893.9009	0.0133	7 -	23	0	QLEYLGGEQAWFGPGSR

No match to: 740.3738, 756.3693, 772.3622, 808.3604, 812.4002, 816.4263, 828.4694, 855.5049, 896.4215, 959.4727, 1005.5208, 1019.4337, 1128.6249, 1141.5353, 1167.5520, 1184.5823, 1258.6033, 1281.1781, 1287.5873, 1297.6335, 1304.5845, 1320.5737, 1343.6594, 1386.7046, 1399.7046, 1449.6284, 1560.6766, 1568.6945, 1572.7310, 1586.7445, 1643.7769, 1691.0051, 1714.8430, 1728.8392, 1738.8246, 1771.8672, 1817.9440, 1830.8497, 2181.0925, 2227.0222, 2243.0330, 2273.1367, 2281.8306, 2332.0447, 2619.2815, 2620.2827, 2747.3762, 2748.3699

Search Parameters

Type of search	**: Peptide Mass Fingerprint**
Enzyme	**: Trypsin**
Fixed modifications	**: Carbamidomethyl (C)**
Variable modifications	**: Oxidation (M)**
Mass values	**: MONOISOTOPIC**
Protein Mass	**: Unrestricted**
Peptide Mass Tolerance	**: ± 20 ppm**
Peptide Charge State	**: 1+**
Max Missed Cleavages	**: 1**
Number of queries	**: 50**

Protein View

Match to: **gi|46560478** Score: **345** Expect: **2.8e-032**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **32**
Sequence Coverage: **50%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
109 - 115	812.4002	811.3929	811.3976	-0.0047	0	WGPAEPR	
118 - 124	1019.4337	1018.4264	1018.4468	-0.0204	1	EREEDWR	
132 - 139	1005.5208	1004.5135	1004.5264	-0.0129	0	RPSHQQPR	
140 - 146	855.5049	854.4976	854.5086	-0.0110	1	KIRPEGR	
147 - 160	1560.6766	1559.6693	1559.6851	-0.0158	0	EGEQEWGTPGSEVR	
166 - 174	1141.5353	1140.5280	1140.5352	-0.0072	0	NNPFYFPSR	
166 - 175	1297.6335	1296.6262	1296.6363	-0.0101	1	NNPFYFPSRR	
180 - 186	808.3604	807.3531	807.3623	-0.0092	0	YGNQNGR	
197 - 207	1399.7046	1398.6973	1398.7116	-0.0143	1	SKQFQNLQNHR	
199 - 207	1184.5823	1183.5750	1183.5846	-0.0096	0	QFQNLQNHR	
208 - 222	1691.0051	1689.9978	1690.0141	-0.0162	0	IVQIEARPNTLVLPK	
223 - 247	2619.2815	2618.2742	2618.3160	-0.0418	0	HADADNILVIQQGQATVTVANGNNR	
223 - 248	2747.3762	2746.3689	2746.4110	-0.0420	1	HADADNILVIQQGQATVTVANGNNRK	
248 - 259	1386.7046	1385.6973	1385.7051	-0.0078	1	KSFNLDEGHALR	
249 - 259	1258.6033	1257.5960	1257.6101	-0.0141	0	SFNLDEGHALR	
260 - 271	1379.7606	1378.7533	1378.7608	-0.0075	0	IPSGFISYILNR	
272 - 278	896.4215	895.4142	895.4260	-0.0118	0	HDNQNLR	
282 - 301	2227.0222	2226.0149	2226.0415	-0.0266	0	ISMPVNTPGQFEDFFPASSR	
282 - 301	2243.0330	2242.0257	2242.0364	-0.0107	0	ISMPVNTPGQFEDFFPASSR	Oxidation (M)
302 - 312	1287.5873	1286.5800	1286.5891	-0.0091	0	DQSSYLQGFSR	
313 - 327	1738.8246	1737.8173	1737.8321	-0.0148	0	NTLEAAFNAEFNEIR	
313 - 328	1894.9214	1893.9141	1893.9332	-0.0191	1	NTLEAAFNAEFNEIRR	
328 - 342	1728.8392	1727.8319	1727.8437	-0.0118	1	RVLLEENAGGEQEER	
329 - 342	1572.7310	1571.7237	1571.7426	-0.0189	0	VLLEENAGGEQEER	
379 - 393	1714.8430	1713.8357	1713.8533	-0.0175	1	KGSEEEDITNPINLR	
380 - 393	1586.7445	1585.7372	1585.7583	-0.0211	0	GSEEEDITNPINLR	
394 - 405	1320.5737	1319.5664	1319.5741	-0.0077	0	DGEPDLSNNFGR	
432 - 443	1343.6594	1342.6521	1342.6703	-0.0182	0	EGALMLPHFNSK	
453 - 463	1128.6249	1127.6176	1127.6298	-0.0122	0	GTGNLELVAVR	
464 - 469	816.4263	815.4190	815.4249	-0.0059	1	KEQQQR	
473 - 490	2281.8306	2280.8233	2280.8414	-0.0180	0	EQEWEEEEEDEEEEGSNR	
536 - 551	1817.9440	1816.9367	1816.9570	-0.0203	1	IFLAGDKDNVIDQIEK	

No match to: 740.3738, 756.3693, 772.3622, 828.4694, 959.4727, 1167.5520, 1281.1781, 1304.5845, 1449.6284, 1568.6945, 1643.7769, 1771.8672, 1830.8497, 2181.0925, 2273.1367, 2332.0447, 2620.2827, 2748.3699

Spot 8

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:31:05 GMT**
Top Score : **339 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	339	conarachin [Arachis hypogaea]
2.	gi|620025	70639	333	Ara h I
3.	gi|1168390	70639	333	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	254	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	254	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	254	Ara h I
7.	gi|46560476	48122	174	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	101	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	76	conarachin [Arachis hypogaea]
10.	gi|62177652	10056	19	resistance protein PRG [Arachis hypogaea]

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 339 **Expect:** 1.1e-031 **Queries matched:** 31
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	180	186	0	YGNQNGR
812.3914	811.3841	811.3976	-0.0135	109	115	0	WGPAEPR
816.4161	815.4088	815.4249	-0.0161	464	469	1	KEQQQR
855.5047	854.4974	854.5086	-0.0112	140	146	1	KIRPEGR
896.4197	895.4124	895.4260	-0.0136	272	278	0	HDNQNLR
1005.5204	1004.5131	1004.5264	-0.0133	132	139	0	RPSHQQPR
1019.4457	1018.4384	1018.4468	-0.0084	118	124	1	EREEDWR
1128.6202	1127.6129	1127.6298	-0.0169	453	463	0	GTGNLELVAVR

1141.5259	1140.5186	1140.5352	-0.0166	166 - 174	0	NNPFYFPSR
1184.5780	1183.5707	1183.5846	-0.0139	199 - 207	0	QFQNLQNHR
1258.6029	1257.5956	1257.6101	-0.0145	249 - 259	0	SFNLDEGHALR
1287.5793	1286.5720	1286.5891	-0.0171	302 - 312	0	DQSSYLQGFSR
1297.6233	1296.6160	1296.6363	-0.0203	166 - 175	1	NNPFYFPSRR
1320.5668	1319.5595	1319.5741	-0.0146	394 - 405	0	DGEPDLSNNFGR
1343.6597	1342.6524	1342.6703	-0.0179	432 - 443	0	EGALMLPHFNSK
1379.7498	1378.7425	1378.7608	-0.0183	260 - 271	0	IPSGFISYILNR
1386.6877	1385.6804	1385.7051	-0.0247	248 - 259	1	KSFNLDEGHALR
1399.6945	1398.6872	1398.7116	-0.0244	197 - 207	1	SKQFQNLQNHR
1560.6650	1559.6577	1559.6851	-0.0274	147 - 160	0	EGEQEWGTPGSEVR
1572.7295	1571.7222	1571.7426	-0.0204	329 - 342	0	VLLEENAGGEQEER
1586.7350	1585.7277	1585.7583	-0.0306	380 - 393	0	GSEEEDITNPINLR
1690.9983	1689.9910	1690.0141	-0.0230	208 - 222	0	IVQIEARPNTLVLPK
1714.8384	1713.8311	1713.8533	-0.0221	379 - 393	1	KGSEEEDITNPINLR
1738.8147	1737.8074	1737.8321	-0.0247	313 - 327	0	NTLEAAFNAEFNEIR
1817.9404	1816.9331	1816.9570	-0.0239	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9078	1893.9005	1893.9332	-0.0327	313 - 328	1	NTLEAAFNAEFNEIRR
2047.9666	2046.9593	2046.9788	-0.0195	415 - 431	0	NPQLQDLDMMLTCVEIK
2082.1921	2081.1848	2081.2030	-0.0181	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0093	2226.0020	2226.0415	-0.0395	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2281.8069	2280.7996	2280.8414	-0.0417	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.2817	2618.2744	2618.3160	-0.0416	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3672, 756.3662, 772.3577, 828.4578, 932.4515, 959.4672, 1167.5564, 1281.1901, 1319.6077, 1568.6832, 1643.7628, 1771.8529, 2181.0483, 2242.9968, 2273.1243, 2620.2778, 2747.3403, 2748.3186, 3153.3911

2. gi|620025 **Mass:** 70639 **Score:** 333 **Expect:** 4.4e-031 **Queries matched:** 31

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	180 - 186		0	YGNQNGR
812.3914	811.3841	811.3976	-0.0135	109 - 115		0	WGPAEPR
816.4161	815.4088	815.4249	-0.0161	464 - 469		1	KEQQQR
855.5047	854.4974	854.5086	-0.0112	140 - 146		1	KIRPEGR
896.4197	895.4124	895.4260	-0.0136	272 - 278		0	HDNQNLR
1005.5204	1004.5131	1004.5264	-0.0133	132 - 139		0	RPSHQQPR
1019.4457	1018.4384	1018.4468	-0.0084	118 - 124		1	EREEDWR
1128.6202	1127.6129	1127.6298	-0.0169	453 - 463		0	GTGNLELVAVR
1141.5259	1140.5186	1140.5352	-0.0166	166 - 174		0	NNPFYFPSR
1184.5780	1183.5707	1183.5846	-0.0139	199 - 207		0	QFQNLQNHR
1258.6029	1257.5956	1257.6101	-0.0145	249 - 259		0	SFNLDEGHALR

1287.5793	1286.5720	1286.5891	-0.0171	302 - 312	0	DQSSYLQGFSR
1297.6233	1296.6160	1296.6363	-0.0203	166 - 175	1	NNPFYFPSRR
1320.5668	1319.5595	1319.5741	-0.0146	394 - 405	0	DGEPDLSNNFGR
1343.6597	1342.6524	1342.6703	-0.0179	432 - 443	0	EGALMLPHFNSK
1379.7498	1378.7425	1378.7608	-0.0183	260 - 271	0	IPSGFISYILNR
1386.6877	1385.6804	1385.7051	-0.0247	248 - 259	1	KSFNLDEGHALR
1399.6945	1398.6872	1398.7116	-0.0244	197 - 207	1	SKQFQNLQNHR
1560.6650	1559.6577	1559.6851	-0.0274	147 - 160	0	EGEQEWGTPGSEVR
1572.7295	1571.7222	1571.7426	-0.0204	329 - 342	0	VLLEENAGGEQEER
1586.7350	1585.7277	1585.7583	-0.0306	380 - 393	0	GSEEEDITNPINLR
1690.9983	1689.9910	1690.0141	-0.0230	208 - 222	0	IVQIEARPNTLVLPK
1714.8384	1713.8311	1713.8533	-0.0221	379 - 393	1	KGSEEEDITNPINLR
1738.8147	1737.8074	1737.8321	-0.0247	313 - 327	0	NTLEAAFNAEFNEIR
1817.9404	1816.9331	1816.9570	-0.0239	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9078	1893.9005	1893.9332	-0.0327	313 - 328	1	NTLEAAFNAEFNEIRR
2047.9666	2046.9593	2046.9788	-0.0195	415 - 431	0	NPQLQDLDMMLTCVEIK
2082.1921	2081.1848	2081.2030	-0.0181	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0093	2226.0020	2226.0415	-0.0395	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2281.8069	2280.7996	2280.8414	-0.0417	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.2817	2618.2744	2618.3160	-0.0416	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3672, 756.3662, 772.3577, 828.4578, 932.4515, 959.4672, 1167.5564, 1281.1901, 1319.6077, 1568.6832, 1643.7628, 1771.8529, 2181.0483, 2242.9968, 2273.1243, 2620.2778, 2747.3403, 2748.3186, 3153.3911

3. gi|1168390 **Mass:** 70639 **Score:** 333 **Expect:** 4.4e-031 **Queries matched:** 31

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	180 - 186		0	YGNQNGR
812.3914	811.3841	811.3976	-0.0135	109 - 115		0	WGPAEPR
816.4161	815.4088	815.4249	-0.0161	464 - 469		1	KEQQQR
855.5047	854.4974	854.5086	-0.0112	140 - 146		1	KIRPEGR
896.4197	895.4124	895.4260	-0.0136	272 - 278		0	HDNQNLR
1005.5204	1004.5131	1004.5264	-0.0133	132 - 139		0	RPSHQQPR
1019.4457	1018.4384	1018.4468	-0.0084	118 - 124		1	EREEDWR
1128.6202	1127.6129	1127.6298	-0.0169	453 - 463		0	GTGNLELVAVR
1141.5259	1140.5186	1140.5352	-0.0166	166 - 174		0	NNPFYFPSR
1184.5780	1183.5707	1183.5846	-0.0139	199 - 207		0	QFQNLQNHR
1258.6029	1257.5956	1257.6101	-0.0145	249 - 259		0	SFNLDEGHALR
1287.5793	1286.5720	1286.5891	-0.0171	302 - 312		0	DQSSYLQGFSR
1297.6233	1296.6160	1296.6363	-0.0203	166 - 175		1	NNPFYFPSRR
1320.5668	1319.5595	1319.5741	-0.0146	394 - 405		0	DGEPDLSNNFGR

1343.6597	1342.6524	1342.6703	-0.0179	432 - 443	0	EGALMLPHFNSK
1379.7498	1378.7425	1378.7608	-0.0183	260 - 271	0	IPSGFISYILNR
1386.6877	1385.6804	1385.7051	-0.0247	248 - 259	1	KSFNLDEGHALR
1399.6945	1398.6872	1398.7116	-0.0244	197 - 207	1	SKQFQNLQNHR
1560.6650	1559.6577	1559.6851	-0.0274	147 - 160	0	EGEQEWGTPGSEVR
1572.7295	1571.7222	1571.7426	-0.0204	329 - 342	0	VLLEENAGGEQEER
1586.7350	1585.7277	1585.7583	-0.0306	380 - 393	0	GSEEEDITNPINLR
1690.9983	1689.9910	1690.0141	-0.0230	208 - 222	0	IVQIEARPNTLVLPK
1714.8384	1713.8311	1713.8533	-0.0221	379 - 393	1	KGSEEEDITNPINLR
1738.8147	1737.8074	1737.8321	-0.0247	313 - 327	0	NTLEAAFNAEFNEIR
1817.9404	1816.9331	1816.9570	-0.0239	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9078	1893.9005	1893.9332	-0.0327	313 - 328	1	NTLEAAFNAEFNEIRR
2047.9666	2046.9593	2046.9788	-0.0195	415 - 431	0	NPQLQDLDMMLTCVEIK
2082.1921	2081.1848	2081.2030	-0.0181	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0093	2226.0020	2226.0415	-0.0395	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2281.8069	2280.7996	2280.8414	-0.0417	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.2817	2618.2744	2618.3160	-0.0416	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3672, 756.3662, 772.3577, 828.4578, 932.4515, 959.4672, 1167.5564, 1281.1901, 1319.6077, 1568.6832, 1643.7628, 1771.8529, 2181.0483, 2242.9968, 2273.1243, 2620.2778, 2747.3403, 2748.3186, 3153.3911

4. gi|16612200 **Mass:** 71701 **Score:** 254 **Expect:** 3.5e-023 **Queries matched:** 26

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	186 - 192		0	YGNQNGR
816.4161	815.4088	815.4249	-0.0161	472 - 477		1	KEQQQR
855.5047	854.4974	854.5086	-0.0112	146 - 152		1	KIRPEGR
896.4197	895.4124	895.4260	-0.0136	278 - 284		0	HDNQNLR
1005.5204	1004.5131	1004.5264	-0.0133	138 - 145		0	RPSHQQPR
1019.4457	1018.4384	1018.4468	-0.0084	124 - 130		1	EREEDWR
1128.6202	1127.6129	1127.6298	-0.0169	461 - 471		0	GTGNLELVAVR
1141.5259	1140.5186	1140.5352	-0.0166	172 - 180		0	NNPFYFPSR
1184.5780	1183.5707	1183.5846	-0.0139	205 - 213		0	QFQNLQNHR
1258.6029	1257.5956	1257.6101	-0.0145	255 - 265		0	SFNLDEGHALR
1287.5793	1286.5720	1286.5891	-0.0171	308 - 318		0	DQSSYLQGFSR
1297.6233	1296.6160	1296.6363	-0.0203	172 - 181		1	NNPFYFPSRR
1343.6597	1342.6524	1342.6703	-0.0179	440 - 451		0	EGALMLPHFNSK
1379.7498	1378.7425	1378.7608	-0.0183	266 - 277		0	IPSGFISYILNR
1386.6877	1385.6804	1385.7051	-0.0247	254 - 265		1	KSFNLDEGHALR
1568.6832	1567.6759	1567.7015	-0.0255	153 - 166		0	EGEQEWGTPGSHVR
1572.7295	1571.7222	1571.7426	-0.0204	335 - 348		0	VLLEENAGGEQEER

1643.7628	1642.7555	1642.7798	-0.0242	387 - 401	0	GSEEEGDITNPINLR
1738.8147	1737.8074	1737.8321	-0.0247	319 - 333	0	NTLEAAFNAEFNEIR
1771.8529	1770.8456	1770.8747	-0.0291	386 - 401	1	KGSEEEGDITNPINLR
1817.9404	1816.9331	1816.9570	-0.0239	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9078	1893.9005	1893.9332	-0.0327	319 - 334	1	NTLEAAFNAEFNEIRR
2047.9666	2046.9593	2046.9788	-0.0195	423 - 439	0	NPQLQDLDMMLTCVEIK
2082.1921	2081.1848	2081.2030	-0.0181	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0093	2226.0020	2226.0415	-0.0395	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2619.2817	2618.2744	2618.3160	-0.0416	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3672, 756.3662, 772.3577, 812.3914, 828.4578, 932.4515, 959.4672, 1167.5564, 1281.1901, 1319.6077, 1320.5668, 1399.6945, 1560.6650, 1586.7350, 1690.9983, 1714.8384, 2181.0483, 2242.9968, 2273.1243, 2281.8069, 2620.2778, 2747.3403, 2748.3186, 3153.3911

5. gi|1168391 **Mass:** 71701 **Score:** 254 **Expect:** 3.5e-023 **Queries matched:** 26

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	186 - 192	0	YGNQNGR
816.4161	815.4088	815.4249	-0.0161	472 - 477	1	KEQQQR
855.5047	854.4974	854.5086	-0.0112	146 - 152	1	KIRPEGR
896.4197	895.4124	895.4260	-0.0136	278 - 284	0	HDNQNLR
1005.5204	1004.5131	1004.5264	-0.0133	138 - 145	0	RPSHQQPR
1019.4457	1018.4384	1018.4468	-0.0084	124 - 130	1	EREEDWR
1128.6202	1127.6129	1127.6298	-0.0169	461 - 471	0	GTGNLELVAVR
1141.5259	1140.5186	1140.5352	-0.0166	172 - 180	0	NNPFYFPSR
1184.5780	1183.5707	1183.5846	-0.0139	205 - 213	0	QFQNLQNHR
1258.6029	1257.5956	1257.6101	-0.0145	255 - 265	0	SFNLDEGHALR
1287.5793	1286.5720	1286.5891	-0.0171	308 - 318	0	DQSSYLQGFSR
1297.6233	1296.6160	1296.6363	-0.0203	172 - 181	1	NNPFYFPSRR
1343.6597	1342.6524	1342.6703	-0.0179	440 - 451	0	EGALMLPHFNSK
1379.7498	1378.7425	1378.7608	-0.0183	266 - 277	0	IPSGFISYILNR
1386.6877	1385.6804	1385.7051	-0.0247	254 - 265	1	KSFNLDEGHALR
1568.6832	1567.6759	1567.7015	-0.0255	153 - 166	0	EGEQEWGTPGSHVR
1572.7295	1571.7222	1571.7426	-0.0204	335 - 348	0	VLLEENAGGEQEER
1643.7628	1642.7555	1642.7798	-0.0242	387 - 401	0	GSEEEGDITNPINLR
1738.8147	1737.8074	1737.8321	-0.0247	319 - 333	0	NTLEAAFNAEFNEIR
1771.8529	1770.8456	1770.8747	-0.0291	386 - 401	1	KGSEEEGDITNPINLR
1817.9404	1816.9331	1816.9570	-0.0239	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9078	1893.9005	1893.9332	-0.0327	319 - 334	1	NTLEAAFNAEFNEIRR
2047.9666	2046.9593	2046.9788	-0.0195	423 - 439	0	NPQLQDLDMMLTCVEIK
2082.1921	2081.1848	2081.2030	-0.0181	452 - 471	1	AMVIVVVNKGTGNLELVAVR

2227.0093	2226.0020	2226.0415	-0.0395	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2619.2817	2618.2744	2618.3160	-0.0416	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3672, 756.3662, 772.3577, 812.3914, 828.4578, 932.4515, 959.4672, 1167.5564, 1281.1901, 1319.6077, 1320.5668, 1399.6945, 1560.6650, 1586.7350, 1690.9983, 1714.8384, 2181.0483, 2242.9968, 2273.1243, 2281.8069, 2620.2778, 2747.3403, 2748.3186, 3153.3911

6. gi|602436 **Mass:** 71701 **Score:** 254 **Expect:** 3.5e-023 **Queries matched:** 26

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	186 -	192	0	YGNQNGR
816.4161	815.4088	815.4249	-0.0161	472 -	477	1	KEQQQR
855.5047	854.4974	854.5086	-0.0112	146 -	152	1	KIRPEGR
896.4197	895.4124	895.4260	-0.0136	278 -	284	0	HDNQNLR
1005.5204	1004.5131	1004.5264	-0.0133	138 -	145	0	RPSHQQPR
1019.4457	1018.4384	1018.4468	-0.0084	124 -	130	1	EREEDWR
1128.6202	1127.6129	1127.6298	-0.0169	461 -	471	0	GTGNLELVAVR
1141.5259	1140.5186	1140.5352	-0.0166	172 -	180	0	NNPFYFPSR
1184.5780	1183.5707	1183.5846	-0.0139	205 -	213	0	QFQNLQNHR
1258.6029	1257.5956	1257.6101	-0.0145	255 -	265	0	SFNLDEGHALR
1287.5793	1286.5720	1286.5891	-0.0171	308 -	318	0	DQSSYLQGFSR
1297.6233	1296.6160	1296.6363	-0.0203	172 -	181	1	NNPFYFPSRR
1343.6597	1342.6524	1342.6703	-0.0179	440 -	451	0	EGALMLPHFNSK
1379.7498	1378.7425	1378.7608	-0.0183	266 -	277	0	IPSGFISYILNR
1386.6877	1385.6804	1385.7051	-0.0247	254 -	265	1	KSFNLDEGHALR
1568.6832	1567.6759	1567.7015	-0.0255	153 -	166	0	EGEQEWGTPGSHVR
1572.7295	1571.7222	1571.7426	-0.0204	335 -	348	0	VLLEENAGGEQEER
1643.7628	1642.7555	1642.7798	-0.0242	387 -	401	0	GSEEEGDITNPINLR
1738.8147	1737.8074	1737.8321	-0.0247	319 -	333	0	NTLEAAFNAEFNEIR
1771.8529	1770.8456	1770.8747	-0.0291	386 -	401	1	KGSEEEGDITNPINLR
1817.9404	1816.9331	1816.9570	-0.0239	541 -	556	1	IFLAGDKDNVIDQIEK
1894.9078	1893.9005	1893.9332	-0.0327	319 -	334	1	NTLEAAFNAEFNEIRR
2047.9666	2046.9593	2046.9788	-0.0195	423 -	439	0	NPQLQDLDMMLTCVEIK
2082.1921	2081.1848	2081.2030	-0.0181	452 -	471	1	AMVIVVVNKGTGNLELVAVR
2227.0093	2226.0020	2226.0415	-0.0395	288 -	307	0	ISMPVNTPGQFEDFFPASSR
2619.2817	2618.2744	2618.3160	-0.0416	229 -	253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3672, 756.3662, 772.3577, 812.3914, 828.4578, 932.4515, 959.4672, 1167.5564, 1281.1901, 1319.6077, 1320.5668, 1399.6945, 1560.6650, 1586.7350, 1690.9983, 1714.8384, 2181.0483, 2242.9968, 2273.1243, 2281.8069, 2620.2778, 2747.3403, 2748.3186, 3153.3911

7. gi|46560476 **Mass:** 48122 **Score:** 174 **Expect:** 3.5e-015 **Queries matched:** 17

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4161	815.4088	815.4249	-0.0161	274 -	279	1	KEQQQR
896.4197	895.4124	895.4260	-0.0136	81 -	87	0	HDNQNLR
1128.6202	1127.6129	1127.6298	-0.0169	263 -	273	0	GTGNLELVAVR
1184.5780	1183.5707	1183.5846	-0.0139	8 -	16	0	QFQNLQNHR
1258.6029	1257.5956	1257.6101	-0.0145	58 -	68	0	SFNLDEGHALR
1287.5793	1286.5720	1286.5891	-0.0171	111 -	121	0	DQSSYLQGFSR
1343.6597	1342.6524	1342.6703	-0.0179	242 -	253	0	EGALMLPHFNSK
1379.7498	1378.7425	1378.7608	-0.0183	69 -	80	0	IPSGFISYILNR
1386.6877	1385.6804	1385.7051	-0.0247	57 -	68	1	KSFNLDEGHALR
1572.7295	1571.7222	1571.7426	-0.0204	138 -	151	0	VLLEENAGGEQEER
1738.8147	1737.8074	1737.8321	-0.0247	122 -	136	0	NTLEAAFNAEFNEIR
1817.9404	1816.9331	1816.9570	-0.0239	343 -	358	1	IFLAGDKDNVIDQIEK
1894.9078	1893.9005	1893.9332	-0.0327	122 -	137	1	NTLEAAFNAEFNEIRR
2047.9666	2046.9593	2046.9788	-0.0195	225 -	241	0	NPQLQDLDMMLTCVEIK
2082.1921	2081.1848	2081.2030	-0.0181	254 -	273	1	AMVIVVVNKGTGNLELVAVR
2227.0093	2226.0020	2226.0415	-0.0395	91 -	110	0	ISMPVNTPGQFEDFFPASSR
2619.2817	2618.2744	2618.3160	-0.0416	32 -	56	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3672, 756.3662, 772.3577, 808.3605, 812.3914, 828.4578, 855.5047, 932.4515, 959.4672, 1005.5204, 1019.4457, 1141.5259, 1167.5564, 1281.1901, 1297.6233, 1319.6077, 1320.5668, 1399.6945, 1560.6650, 1568.6832, 1586.7350, 1643.7628, 1690.9983, 1714.8384, 1771.8529, 2181.0483, 2242.9968, 2273.1243, 2281.8069, 2620.2778, 2747.3403, 2748.3186, 3153.3911

8. gi|46560472 **Mass:** 34169 **Score:** 101 **Expect:** 7e-008 **Queries matched:** 11

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4161	815.4088	815.4249	-0.0161	153 -	158	1	KEQQQR
1128.6202	1127.6129	1127.6298	-0.0169	142 -	152	0	GTGNLELVAVR
1320.5668	1319.5595	1319.5741	-0.0146	83 -	94	0	DGEPDLSNNFGR
1343.6597	1342.6524	1342.6703	-0.0179	121 -	132	0	EGALMLPHFNSK
1572.7295	1571.7222	1571.7426	-0.0204	18 -	31	0	VLLEENAGGEQEER
1586.7350	1585.7277	1585.7583	-0.0306	69 -	82	0	GSEEEDITNPINLR
1714.8384	1713.8311	1713.8533	-0.0221	68 -	82	1	KGSEEEDITNPINLR
1817.9404	1816.9331	1816.9570	-0.0239	225 -	240	1	IFLAGDKDNVIDQIEK
2047.9666	2046.9593	2046.9788	-0.0195	104 -	120	0	NPQLQDLDMMLTCVEIK
2082.1921	2081.1848	2081.2030	-0.0181	133 -	152	1	AMVIVVVNKGTGNLELVAVR
2281.8069	2280.7996	2280.8414	-0.0417	162 -	179	0	EQEWEEEEEDEEEEGSNR

No match to: 740.3672, 756.3662, 772.3577, 808.3605, 812.3914, 828.4578, 855.5047, 896.4197, 932.4515, 959.4672, 1005.5204, 1019.4457, 1141.5259, 1167.5564, 1184.5780, 1258.6029, 1281.1901, 1287.5793, 1297.6233, 1319.6077, 1379.7498, 1386.6877, 1399.6945, 1560.6650, 1568.6832, 1643.7628, 1690.9983, 1738.8147, 1771.8529, 1894.9078, 2181.0483, 2227.0093, 2242.9968, 2273.1243, 2619.2817, 2620.2778, 2747.3403, 2748.3186, 3153.3911

9. gi|46560474 **Mass:** 33641 **Score:** 76 **Expect:** 2.1e-005 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4161	815.4088	815.4249	-0.0161	152	157	1	KEQQQR
1128.6202	1127.6129	1127.6298	-0.0169	141	151	0	GTGNLELVAVR
1343.6597	1342.6524	1342.6703	-0.0179	120	131	0	EGALMLPHFNSK
1572.7295	1571.7222	1571.7426	-0.0204	15	28	0	VLLEENAGGEQEER
1643.7628	1642.7555	1642.7798	-0.0242	67	81	0	GSEEEGDITNPINLR
1771.8529	1770.8456	1770.8747	-0.0291	66	81	1	KGSEEEGDITNPINLR
1817.9404	1816.9331	1816.9570	-0.0239	221	236	1	IFLAGDKDNVIDQIEK
2047.9666	2046.9593	2046.9788	-0.0195	103	119	0	NPQLQDLDMMLTCVEIK
2082.1921	2081.1848	2081.2030	-0.0181	132	151	1	AMVIVVVNKGTGNLELVAVR

No match to: 740.3672, 756.3662, 772.3577, 808.3605, 812.3914, 828.4578, 855.5047, 896.4197, 932.4515, 959.4672, 1005.5204, 1019.4457, 1141.5259, 1167.5564, 1184.5780, 1258.6029, 1281.1901, 1287.5793, 1297.6233, 1319.6077, 1320.5668, 1379.7498, 1386.6877, 1399.6945, 1560.6650, 1568.6832, 1586.7350, 1690.9983, 1714.8384, 1738.8147, 1894.9078, 2181.0483, 2227.0093, 2242.9968, 2273.1243, 2281.8069, 2619.2817, 2620.2778, 2747.3403, 2748.3186, 3153.3911

10. gi|62177652 **Mass:** 10056 **Score:** 19 **Expect:** 11 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1379.7498	1378.7425	1378.7496	-0.0070	77	89	1	EVVKYSGGLPFAL
1894.9078	1893.9005	1893.9009	-0.0003	7	23	0	QLEYLGGEQAWFGPGSR

No match to: 740.3672, 756.3662, 772.3577, 808.3605, 812.3914, 816.4161, 828.4578, 855.5047, 896.4197, 932.4515, 959.4672, 1005.5204, 1019.4457, 1128.6202, 1141.5259, 1167.5564, 1184.5780, 1258.6029, 1281.1901, 1287.5793, 1297.6233, 1319.6077, 1320.5668, 1343.6597, 1386.6877, 1399.6945, 1560.6650, 1568.6832, 1572.7295, 1586.7350, 1643.7628, 1690.9983, 1714.8384, 1738.8147, 1771.8529, 1817.9404, 2047.9666, 2082.1921, 2181.0483, 2227.0093, 2242.9968, 2273.1243, 2281.8069, 2619.2817, 2620.2778, 2747.3403, 2748.3186, 3153.3911

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|46560478** Score: **339** Expect: **1.1e-031**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **31**
Sequence Coverage: **55%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
109 - 115	812.3914	811.3841	811.3976	-0.0135	0	WGPAEPR
118 - 124	1019.4457	1018.4384	1018.4468	-0.0084	1	EREEDWR
132 - 139	1005.5204	1004.5131	1004.5264	-0.0133	0	RPSHQQPR
140 - 146	855.5047	854.4974	854.5086	-0.0112	1	KIRPEGR
147 - 160	1560.6650	1559.6577	1559.6851	-0.0274	0	EGEQEWGTPGSEVR
166 - 174	1141.5259	1140.5186	1140.5352	-0.0166	0	NNPFYFPSR
166 - 175	1297.6233	1296.6160	1296.6363	-0.0203	1	NNPFYFPSRR
180 - 186	808.3605	807.3532	807.3623	-0.0091	0	YGNQNGR
197 - 207	1399.6945	1398.6872	1398.7116	-0.0244	1	SKQFQNLQNHR

199 - 207	1184.5780	1183.5707	1183.5846	-0.0139	0	QFQNLQNHR
208 - 222	1690.9983	1689.9910	1690.0141	-0.0230	0	IVQIEARPNTLVLPK
223 - 247	2619.2817	2618.2744	2618.3160	-0.0416	0	HADADNILVIQQGQATVTVANGNNR
248 - 259	1386.6877	1385.6804	1385.7051	-0.0247	1	KSFNLDEGHALR
249 - 259	1258.6029	1257.5956	1257.6101	-0.0145	0	SFNLDEGHALR
260 - 271	1379.7498	1378.7425	1378.7608	-0.0183	0	IPSGFISYILNR
272 - 278	896.4197	895.4124	895.4260	-0.0136	0	HDNQNLR
282 - 301	2227.0093	2226.0020	2226.0415	-0.0395	0	ISMPVNTPGQFEDFFPASSR
302 - 312	1287.5793	1286.5720	1286.5891	-0.0171	0	DQSSYLQGFSR
313 - 327	1738.8147	1737.8074	1737.8321	-0.0247	0	NTLEAAFNAEFNEIR
313 - 328	1894.9078	1893.9005	1893.9332	-0.0327	1	NTLEAAFNAEFNEIRR
329 - 342	1572.7295	1571.7222	1571.7426	-0.0204	0	VLLEENAGGEQEER
379 - 393	1714.8384	1713.8311	1713.8533	-0.0221	1	KGSEEEDITNPINLR
380 - 393	1586.7350	1585.7277	1585.7583	-0.0306	0	GSEEEDITNPINLR
394 - 405	1320.5668	1319.5595	1319.5741	-0.0146	0	DGEPDLSNNFGR
415 - 431	2047.9666	2046.9593	2046.9788	-0.0195	0	NPQLQDLDMMLTCVEIK
432 - 443	1343.6597	1342.6524	1342.6703	-0.0179	0	EGALMLPHFNSK
444 - 463	2082.1921	2081.1848	2081.2030	-0.0181	1	AMVIVVVNKGTGNLELVAVR
453 - 463	1128.6202	1127.6129	1127.6298	-0.0169	0	GTGNLELVAVR
464 - 469	816.4161	815.4088	815.4249	-0.0161	1	KEQQQR
473 - 490	2281.8069	2280.7996	2280.8414	-0.0417	0	EQEWEEEEEDEEEEGSNR
536 - 551	1817.9404	1816.9331	1816.9570	-0.0239	1	IFLAGDKDNVIDQIEK

No match to: 740.3672, 756.3662, 772.3577, 828.4578, 932.4515, 959.4672, 1167.5564, 1281.1901, 1319.6077, 1568.6832, 1643.7628, 1771.8529, 2181.0483, 2242.9968, 2273.1243, 2620.2778, 2747.3403, 2748.3186, 3153.3911

Spot 9

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:30:39 GMT**
Top Score : **197 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	197	conarachin [Arachis hypogaea]
2.	gi|620025	70639	192	Ara h I
3.	gi|1168390	70639	192	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	136	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	136	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	136	Ara h I
7.	gi|46560476	48122	100	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	47	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	27	conarachin [Arachis hypogaea]
10.	gi|226258	10809	17	ferredoxin I

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 197 **Expect:** 1.7e-017 **Queries matched:** 23
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3640	807.3567	807.3623	-0.0056	180	186	0	YGNQNGR
812.3975	811.3902	811.3976	-0.0074	109	115	0	WGPAEPR
816.4234	815.4161	815.4249	-0.0088	464	469	1	KEQQQR
855.5092	854.5019	854.5086	-0.0067	140	146	1	KIRPEGR
896.4279	895.4206	895.4260	-0.0054	272	278	0	HDNQNLR
1005.5370	1004.5297	1004.5264	0.0033	132	139	0	RPSHQQPR
1019.4550	1018.4477	1018.4468	0.0009	118	124	1	EREEDWR
1128.6448	1127.6375	1127.6298	0.0077	453	463	0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	166	174	0	NNPFYFPSR
1184.6067	1183.5994	1183.5846	0.0148	199	207	0	QFQNLQNHR
1258.6340	1257.6267	1257.6101	0.0166	249	259	0	SFNLDEGHALR

1287.6149	1286.6076	1286.5891	0.0185	302 - 312	0	DQSSYLQGFSR
1297.6643	1296.6570	1296.6363	0.0207	166 - 175	1	NNPFYFPSRR
1320.6034	1319.5961	1319.5741	0.0220	394 - 405	0	DGEPDLSNNFGR
1343.6937	1342.6864	1342.6703	0.0161	432 - 443	0	EGALMLPHFNSK
1376.6875	1375.6802	1375.6619	0.0183	555 - 567	0	DLAFPGSGEQVEK
1379.7911	1378.7838	1378.7608	0.0230	260 - 271	0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	248 - 259	1	KSFNLDEGHALR
1399.7443	1398.7370	1398.7116	0.0254	197 - 207	1	SKQFQNLQNHR
1560.7225	1559.7152	1559.6851	0.0301	147 - 160	0	EGEQEWGTPGSEVR
1572.7808	1571.7735	1571.7426	0.0309	329 - 342	0	VLLEENAGGEQEER
1586.7939	1585.7866	1585.7583	0.0283	380 - 393	0	GSEEEDITNPINLR
2619.4097	2618.4024	2618.3604	0.0420	249 - 271	1	SFNLDEGHALRIPSGFISYILNR

No match to: 740.3716, 756.3707, 772.3691, 828.4669, 959.4812, 1167.5773, 1281.2108, 1449.6696, 1568.7406, 1643.8228, 1663.0510, 1691.0586, 1714.9017, 1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2620.4048, 2748.5005

2. gi|620025 **Mass:** 70639 **Score:** 192 **Expect:** 5.5e-017 **Queries matched:** 23

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3640	807.3567	807.3623	-0.0056	180	186	0	YGNQNGR
812.3975	811.3902	811.3976	-0.0074	109	115	0	WGPAEPR
816.4234	815.4161	815.4249	-0.0088	464	469	1	KEQQQR
855.5092	854.5019	854.5086	-0.0067	140	146	1	KIRPEGR
896.4279	895.4206	895.4260	-0.0054	272	278	0	HDNQNLR
1005.5370	1004.5297	1004.5264	0.0033	132	139	0	RPSHQQPR
1019.4550	1018.4477	1018.4468	0.0009	118	124	1	EREEDWR
1128.6448	1127.6375	1127.6298	0.0077	453	463	0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	166	174	0	NNPFYFPSR
1184.6067	1183.5994	1183.5846	0.0148	199	207	0	QFQNLQNHR
1258.6340	1257.6267	1257.6101	0.0166	249	259	0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	302	312	0	DQSSYLQGFSR
1297.6643	1296.6570	1296.6363	0.0207	166	175	1	NNPFYFPSRR
1320.6034	1319.5961	1319.5741	0.0220	394	405	0	DGEPDLSNNFGR
1343.6937	1342.6864	1342.6703	0.0161	432	443	0	EGALMLPHFNSK
1376.6875	1375.6802	1375.6619	0.0183	555	567	0	DLAFPGSGEQVEK
1379.7911	1378.7838	1378.7608	0.0230	260	271	0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	248	259	1	KSFNLDEGHALR
1399.7443	1398.7370	1398.7116	0.0254	197	207	1	SKQFQNLQNHR
1560.7225	1559.7152	1559.6851	0.0301	147	160	0	EGEQEWGTPGSEVR
1572.7808	1571.7735	1571.7426	0.0309	329	342	0	VLLEENAGGEQEER

1586.7939	1585.7866	1585.7583	0.0283	380 - 393	0	GSEEEDITNPINLR
2619.4097	2618.4024	2618.3604	0.0420	249 - 271	1	SFNLDEGHALRIPSGFISYILNR

No match to: 740.3716, 756.3707, 772.3691, 828.4669, 959.4812, 1167.5773, 1281.2108, 1449.6696, 1568.7406, 1643.8228, 1663.0510, 1691.0586, 1714.9017, 1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2620.4048, 2748.5005

3. gi|1168390 **Mass:** 70639 **Score:** 192 **Expect:** 5.5e-017 **Queries matched:** 23

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3640	807.3567	807.3623	-0.0056	180 - 186		0	YGNQNGR
812.3975	811.3902	811.3976	-0.0074	109 - 115		0	WGPAEPR
816.4234	815.4161	815.4249	-0.0088	464 - 469		1	KEQQQR
855.5092	854.5019	854.5086	-0.0067	140 - 146		1	KIRPEGR
896.4279	895.4206	895.4260	-0.0054	272 - 278		0	HDNQNLR
1005.5370	1004.5297	1004.5264	0.0033	132 - 139		0	RPSHQQPR
1019.4550	1018.4477	1018.4468	0.0009	118 - 124		1	EREEDWR
1128.6448	1127.6375	1127.6298	0.0077	453 - 463		0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	166 - 174		0	NNPFYFPSR
1184.6067	1183.5994	1183.5846	0.0148	199 - 207		0	QFQNLQNHR
1258.6340	1257.6267	1257.6101	0.0166	249 - 259		0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	302 - 312		0	DQSSYLQGFSR
1297.6643	1296.6570	1296.6363	0.0207	166 - 175		1	NNPFYFPSRR
1320.6034	1319.5961	1319.5741	0.0220	394 - 405		0	DGEPDLSNNFGR
1343.6937	1342.6864	1342.6703	0.0161	432 - 443		0	EGALMLPHFNSK
1376.6875	1375.6802	1375.6619	0.0183	555 - 567		0	DLAFPGSGEQVEK
1379.7911	1378.7838	1378.7608	0.0230	260 - 271		0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	248 - 259		1	KSFNLDEGHALR
1399.7443	1398.7370	1398.7116	0.0254	197 - 207		1	SKQFQNLQNHR
1560.7225	1559.7152	1559.6851	0.0301	147 - 160		0	EGEQEWGTPGSEVR
1572.7808	1571.7735	1571.7426	0.0309	329 - 342		0	VLLEENAGGEQEER
1586.7939	1585.7866	1585.7583	0.0283	380 - 393		0	GSEEEDITNPINLR
2619.4097	2618.4024	2618.3604	0.0420	249 - 271		1	SFNLDEGHALRIPSGFISYILNR

No match to: 740.3716, 756.3707, 772.3691, 828.4669, 959.4812, 1167.5773, 1281.2108, 1449.6696, 1568.7406, 1643.8228, 1663.0510, 1691.0586, 1714.9017, 1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2620.4048, 2748.5005

4. gi|16612200 **Mass:** 71701 **Score:** 136 **Expect:** 2.2e-011 **Queries matched:** 19

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3716	739.3643	739.3765	-0.0122	115 - 121		0	WGPAGPR
808.3640	807.3567	807.3623	-0.0056	186 - 192		0	YGNQNGR

816.4234	815.4161	815.4249	-0.0088	472 - 477	1	KEQQQR
855.5092	854.5019	854.5086	-0.0067	146 - 152	1	KIRPEGR
896.4279	895.4206	895.4260	-0.0054	278 - 284	0	HDNQNLR
1005.5370	1004.5297	1004.5264	0.0033	138 - 145	0	RPSHQQPR
1019.4550	1018.4477	1018.4468	0.0009	124 - 130	1	EREEDWR
1128.6448	1127.6375	1127.6298	0.0077	461 - 471	0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	172 - 180	0	NNPFYFPSR
1184.6067	1183.5994	1183.5846	0.0148	205 - 213	0	QFQNLQNHR
1258.6340	1257.6267	1257.6101	0.0166	255 - 265	0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	308 - 318	0	DQSSYLQGFSR
1297.6643	1296.6570	1296.6363	0.0207	172 - 181	1	NNPFYFPSRR
1343.6937	1342.6864	1342.6703	0.0161	440 - 451	0	EGALMLPHFNSK
1376.6875	1375.6802	1375.6619	0.0183	560 - 572	0	DLAFPGSGEQVEK
1379.7911	1378.7838	1378.7608	0.0230	266 - 277	0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	254 - 265	1	KSFNLDEGHALR
1572.7808	1571.7735	1571.7426	0.0309	335 - 348	0	VLLEENAGGEQEER
2619.4097	2618.4024	2618.3604	0.0420	255 - 277	1	SFNLDEGHALRIPSGFISYILNR

No match to: 756.3707, 772.3691, 812.3975, 828.4669, 959.4812, 1167.5773, 1281.2108, 1320.6034, 1399.7443, 1449.6696, 1560.7225, 1568.7406, 1586.7939, 1643.8228, 1663.0510, 1691.0586, 1714.9017, 1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2620.4048, 2748.5005

5. gi|1168391 **Mass:** 71701 **Score:** 136 **Expect:** 2.2e-011 **Queries matched:** 19

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3716	739.3643	739.3765	-0.0122	115 - 121		0	WGPAGPR
808.3640	807.3567	807.3623	-0.0056	186 - 192		0	YGNQNGR
816.4234	815.4161	815.4249	-0.0088	472 - 477		1	KEQQQR
855.5092	854.5019	854.5086	-0.0067	146 - 152		1	KIRPEGR
896.4279	895.4206	895.4260	-0.0054	278 - 284		0	HDNQNLR
1005.5370	1004.5297	1004.5264	0.0033	138 - 145		0	RPSHQQPR
1019.4550	1018.4477	1018.4468	0.0009	124 - 130		1	EREEDWR
1128.6448	1127.6375	1127.6298	0.0077	461 - 471		0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	172 - 180		0	NNPFYFPSR
1184.6067	1183.5994	1183.5846	0.0148	205 - 213		0	QFQNLQNHR
1258.6340	1257.6267	1257.6101	0.0166	255 - 265		0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	308 - 318		0	DQSSYLQGFSR
1297.6643	1296.6570	1296.6363	0.0207	172 - 181		1	NNPFYFPSRR
1343.6937	1342.6864	1342.6703	0.0161	440 - 451		0	EGALMLPHFNSK
1376.6875	1375.6802	1375.6619	0.0183	560 - 572		0	DLAFPGSGEQVEK

1379.7911	1378.7838	1378.7608	0.0230	266 - 277	0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	254 - 265	1	KSFNLDEGHALR
1572.7808	1571.7735	1571.7426	0.0309	335 - 348	0	VLLEENAGGEQEER
2619.4097	2618.4024	2618.3604	0.0420	255 - 277	1	SFNLDEGHALRIPSGFISYILNR

No match to: 756.3707, 772.3691, 812.3975, 828.4669, 959.4812, 1167.5773, 1281.2108, 1320.6034, 1399.7443, 1449.6696, 1560.7225, 1568.7406, 1586.7939, 1643.8228, 1663.0510, 1691.0586, 1714.9017, 1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2620.4048, 2748.5005

6. gi|602436 **Mass:** 71701 **Score:** 136 **Expect:** 2.2e-011 **Queries matched:** 19

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3716	739.3643	739.3765	-0.0122	115 -	121	0	WGPAGPR
808.3640	807.3567	807.3623	-0.0056	186 -	192	0	YGNQNGR
816.4234	815.4161	815.4249	-0.0088	472 -	477	1	KEQQQR
855.5092	854.5019	854.5086	-0.0067	146 -	152	1	KIRPEGR
896.4279	895.4206	895.4260	-0.0054	278 -	284	0	HDNQNLR
1005.5370	1004.5297	1004.5264	0.0033	138 -	145	0	RPSHQQPR
1019.4550	1018.4477	1018.4468	0.0009	124 -	130	1	EREEDWR
1128.6448	1127.6375	1127.6298	0.0077	461 -	471	0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	172 -	180	0	NNPFYFPSR
1184.6067	1183.5994	1183.5846	0.0148	205 -	213	0	QFQNLQNHR
1258.6340	1257.6267	1257.6101	0.0166	255 -	265	0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	308 -	318	0	DQSSYLQGFSR
1297.6643	1296.6570	1296.6363	0.0207	172 -	181	1	NNPFYFPSRR
1343.6937	1342.6864	1342.6703	0.0161	440 -	451	0	EGALMLPHFNSK
1376.6875	1375.6802	1375.6619	0.0183	560 -	572	0	DLAFPGSGEQVEK
1379.7911	1378.7838	1378.7608	0.0230	266 -	277	0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	254 -	265	1	KSFNLDEGHALR
1572.7808	1571.7735	1571.7426	0.0309	335 -	348	0	VLLEENAGGEQEER
2619.4097	2618.4024	2618.3604	0.0420	255 -	277	1	SFNLDEGHALRIPSGFISYILNR

No match to: 756.3707, 772.3691, 812.3975, 828.4669, 959.4812, 1167.5773, 1281.2108, 1320.6034, 1399.7443, 1449.6696, 1560.7225, 1568.7406, 1586.7939, 1643.8228, 1663.0510, 1691.0586, 1714.9017, 1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2620.4048, 2748.5005

7. gi|46560476 **Mass:** 48122 **Score:** 100 **Expect:** 9.4e-008 **Queries matched:** 12

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4234	815.4161	815.4249	-0.0088	274 -	279	1	KEQQQR
896.4279	895.4206	895.4260	-0.0054	81 -	87	0	HDNQNLR

1128.6448	1127.6375	1127.6298	0.0077	263 - 273	0	GTGNLELVAVR
1184.6067	1183.5994	1183.5846	0.0148	8 - 16	0	QFQNLQNHR
1258.6340	1257.6267	1257.6101	0.0166	58 - 68	0	SFNLDEGHALR
1287.6149	1286.6076	1286.5891	0.0185	111 - 121	0	DQSSYLQGFSR
1343.6937	1342.6864	1342.6703	0.0161	242 - 253	0	EGALMLPHFNSK
1376.6875	1375.6802	1375.6619	0.0183	362 - 374	0	DLAFPGSGEQVEK
1379.7911	1378.7838	1378.7608	0.0230	69 - 80	0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	57 - 68	1	KSFNLDEGHALR
1572.7808	1571.7735	1571.7426	0.0309	138 - 151	0	VLLEENAGGEQEER
2619.4097	2618.4024	2618.3604	0.0420	58 - 80	1	SFNLDEGHALRIPSGFISYILNR

No match to: 740.3716, 756.3707, 772.3691, 808.3640, 812.3975, 828.4669, 855.5092, 959.4812, 1005.5370, 1019.4550, 1141.5530, 1167.5773, 1281.2108, 1297.6643, 1320.6034, 1399.7443, 1449.6696, 1560.7225, 1568.7406, 1586.7939, 1643.8228, 1663.0510, 1691.0586, 1714.9017, 1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2620.4048, 2748.5005

8. gi|46560472 **Mass:** 34169 **Score:** 47 **Expect:** 0.017 **Queries matched:** 7

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4234	815.4161	815.4249	-0.0088	153 - 158		1	KEQQQR
1128.6448	1127.6375	1127.6298	0.0077	142 - 152		0	GTGNLELVAVR
1320.6034	1319.5961	1319.5741	0.0220	83 - 94		0	DGEPDLSNNFGR
1343.6937	1342.6864	1342.6703	0.0161	121 - 132		0	EGALMLPHFNSK
1376.6875	1375.6802	1375.6619	0.0183	244 - 256		0	DLAFPGSGEQVEK
1572.7808	1571.7735	1571.7426	0.0309	18 - 31		0	VLLEENAGGEQEER
1586.7939	1585.7866	1585.7583	0.0283	69 - 82		0	GSEEEDITNPINLR

No match to: 740.3716, 756.3707, 772.3691, 808.3640, 812.3975, 828.4669, 855.5092, 896.4279, 959.4812, 1005.5370, 1019.4550, 1141.5530, 1167.5773, 1184.6067, 1258.6340, 1281.2108, 1287.6149, 1297.6643, 1379.7911, 1386.7344, 1399.7443, 1449.6696, 1560.7225, 1568.7406, 1643.8228, 1663.0510, 1691.0586, 1714.9017, 1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2619.4097, 2620.4048, 2748.5005

9. gi|46560474 **Mass:** 33641 **Score:** 27 **Expect:** 1.6 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4234	815.4161	815.4249	-0.0088	152 - 157		1	KEQQQR
1128.6448	1127.6375	1127.6298	0.0077	141 - 151		0	GTGNLELVAVR
1343.6937	1342.6864	1342.6703	0.0161	120 - 131		0	EGALMLPHFNSK
1376.6875	1375.6802	1375.6619	0.0183	240 - 252		0	DLAFPGSGEQVEK
1572.7808	1571.7735	1571.7426	0.0309	15 - 28		0	VLLEENAGGEQEER

No match to: 740.3716, 756.3707, 772.3691, 808.3640, 812.3975, 828.4669, 855.5092, 896.4279, 959.4812, 1005.5370, 1019.4550, 1141.5530, 1167.5773, 1184.6067, 1258.6340, 1281.2108, 1287.6149, 1297.6643, 1320.6034, 1379.7911, 1386.7344, 1399.7443, 1449.6696, 1560.7225, 1568.7406, 1586.7939, 1643.8228, 1663.0510, 1691.0586, 1714.9017,

1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2619.4097, 2620.4048, 2748.5005

10. gi|226258 **Mass:** 10809 **Score:** 17 **Expect:** 20 **Queries matched:** 2

ferredoxin I

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1141.5530	1140.5457	1140.5484	-0.0027	16	-	26	0	GDLAVAMASYK + Oxidation (M)
1297.6643	1296.6570	1296.6496	0.0075	15	-	26	1	RGDLAVAMASYK + Oxidation (M)

No match to: 740.3716, 756.3707, 772.3691, 808.3640, 812.3975, 816.4234, 828.4669, 855.5092, 896.4279, 959.4812, 1005.5370, 1019.4550, 1128.6448, 1167.5773, 1184.6067, 1258.6340, 1281.2108, 1287.6149, 1320.6034, 1343.6937, 1376.6875, 1379.7911, 1386.7344, 1399.7443, 1449.6696, 1560.7225, 1568.7406, 1572.7808, 1586.7939, 1643.8228, 1663.0510, 1691.0586, 1714.9017, 1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2619.4097, 2620.4048, 2748.5005

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|46560478** Score: **197** Expect: **1.7e-017**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **23**
Sequence Coverage: **33%**

Matched peptides shown in **Bold Red**

```
  1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
 51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
109 - 115	812.3975	811.3902	811.3976	-0.0074	0	WGPAEPR
118 - 124	1019.4550	1018.4477	1018.4468	0.0009	1	EREEDWR
132 - 139	1005.5370	1004.5297	1004.5264	0.0033	0	RPSHQQPR
140 - 146	855.5092	854.5019	854.5086	-0.0067	1	KIRPEGR
147 - 160	1560.7225	1559.7152	1559.6851	0.0301	0	EGEQEWGTPGSEVR
166 - 174	1141.5530	1140.5457	1140.5352	0.0105	0	NNPFYFPSR
166 - 175	1297.6643	1296.6570	1296.6363	0.0207	1	NNPFYFPSRR
180 - 186	808.3640	807.3567	807.3623	-0.0056	0	YGNQNGR
197 - 207	1399.7443	1398.7370	1398.7116	0.0254	1	SKQFQNLQNHR
199 - 207	1184.6067	1183.5994	1183.5846	0.0148	0	QFQNLQNHR
248 - 259	1386.7344	1385.7271	1385.7051	0.0220	1	KSFNLDEGHALR
249 - 259	1258.6340	1257.6267	1257.6101	0.0166	0	SFNLDEGHALR
249 - 271	2619.4097	2618.4024	2618.3604	0.0420	1	SFNLDEGHALRIPSGFISYILNR
260 - 271	1379.7911	1378.7838	1378.7608	0.0230	0	IPSGFISYILNR
272 - 278	896.4279	895.4206	895.4260	-0.0054	0	HDNQNLR
302 - 312	1287.6149	1286.6076	1286.5891	0.0185	0	DQSSYLQGFSR
329 - 342	1572.7808	1571.7735	1571.7426	0.0309	0	VLLEENAGGEQEER
380 - 393	1586.7939	1585.7866	1585.7583	0.0283	0	GSEEEDITNPINLR
394 - 405	1320.6034	1319.5961	1319.5741	0.0220	0	DGEPDLSNNFGR
432 - 443	1343.6937	1342.6864	1342.6703	0.0161	0	EGALMLPHFNSK
453 - 463	1128.6448	1127.6375	1127.6298	0.0077	0	GTGNLELVAVR
464 - 469	816.4234	815.4161	815.4249	-0.0088	1	KEQQQR
555 - 567	1376.6875	1375.6802	1375.6619	0.0183	0	DLAFPGSGEQVEK

No match to: 740.3716, 756.3707, 772.3691, 828.4669, 959.4812, 1167.5773, 1281.2108, 1449.6696, 1568.7406, 1643.8228, 1663.0510, 1691.0586, 1714.9017, 1728.8939, 1738.8817, 1771.9254, 1818.0127, 1894.9878, 2163.1216, 2227.1106, 2243.1201, 2273.2356, 2289.2402, 2316.1643, 2332.1643, 2620.4048, 2748.5005

Spot 10

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 09:58:10 GMT**
Top Score : **241 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	241	conarachin [Arachis hypogaea]
2.	gi|620025	70639	236	Ara h I
3.	gi|1168390	70639	236	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	211	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	211	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	211	Ara h I
7.	gi|46560476	48122	164	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	70	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	62	conarachin [Arachis hypogaea]
10.	gi|226258	10809	13	ferredoxin I

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 241 **Expect:** 7e-022 **Queries matched:** 30
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3555	807.3482	807.3623	-0.0141	180	186	0	YGNQNGR
855.5065	854.4992	854.5086	-0.0094	140	146	1	KIRPEGR
896.4250	895.4177	895.4260	-0.0083	272	278	0	HDNQNLR
1005.5303	1004.5230	1004.5264	-0.0034	132	139	0	RPSHQQPR
1061.5851	1060.5778	1060.5777	0.0001	189	196	1	VLQRFDQR
1141.5542	1140.5469	1140.5352	0.0117	166	174	0	NNPFYFPSR
1184.6010	1183.5937	1183.5846	0.0091	199	207	0	QFQNLQNHR
1258.6305	1257.6232	1257.6101	0.0131	249	259	0	SFNLDEGHALR
1287.6105	1286.6032	1286.5891	0.0141	302	312	0	DQSSYLQGFSR
1297.6548	1296.6475	1296.6363	0.0112	166	175	1	NNPFYFPSRR
1320.5963	1319.5890	1319.5741	0.0149	394	405	0	DGEPDLSNNFGR

1359.6830	1358.6757	1358.6652	0.0105	432 - 443	0	EGALMLPHFNSK + Oxidation (M)
1376.6770	1375.6697	1375.6619	0.0078	555 - 567	0	DLAFPGSGEQVEK
1379.7874	1378.7801	1378.7608	0.0193	260 - 271	0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	248 - 259	1	KSFNLDEGHALR
1399.7382	1398.7309	1398.7116	0.0193	197 - 207	1	SKQFQNLQNHR
1572.7632	1571.7559	1571.7426	0.0133	329 - 342	0	VLLEENAGGEQEER
1586.7848	1585.7775	1585.7583	0.0192	380 - 393	0	GSEEEDITNPINLR
1691.0417	1690.0344	1690.0141	0.0204	208 - 222	0	IVQIEARPNTLVLPK
1714.8820	1713.8747	1713.8533	0.0215	379 - 393	1	KGSEEEDITNPINLR
1728.8715	1727.8642	1727.8437	0.0205	328 - 342	1	RVLLEENAGGEQEER
1738.8590	1737.8517	1737.8321	0.0196	313 - 327	0	NTLEAAFNAEFNEIR
1817.9818	1816.9745	1816.9570	0.0175	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9557	1893.9484	1893.9332	0.0152	313 - 328	1	NTLEAAFNAEFNEIRR
1913.9453	1912.9380	1912.9238	0.0143	329 - 345	1	VLLEENAGGEQEERGQR
2082.2163	2081.2090	2081.2030	0.0061	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2098.2126	2097.2053	2097.1979	0.0075	444 - 463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2243.0500	2242.0427	2242.0364	0.0063	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1755	2256.1682	2256.1763	-0.0080	260 - 278	1	IPSGFISYILNRHDNQNLR
2619.3081	2618.3008	2618.3160	-0.0152	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3991, 816.4015, 828.4594, 844.3855, 848.4257, 861.0674, 959.4711, 975.4677, 1018.4672, 1051.4438, 1147.5208, 1167.5798, 1309.6069, 1336.5990, 1404.6747, 1427.7377, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1643.8168, 1689.8256, 1717.8293, 1771.8973, 1814.4458, 1830.8712, 1899.9265, 2036.2551, 2070.0337, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2273.1570, 2285.8369, 2313.8347, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

2. gi|620025 **Mass:** 70639 **Score:** 236 **Expect:** 2.2e-021 **Queries matched:** 30

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3555	807.3482	807.3623	-0.0141	180 - 186	0	YGNQNGR
855.5065	854.4992	854.5086	-0.0094	140 - 146	1	KIRPEGR
896.4250	895.4177	895.4260	-0.0083	272 - 278	0	HDNQNLR
1005.5303	1004.5230	1004.5264	-0.0034	132 - 139	0	RPSHQQPR
1061.5851	1060.5778	1060.5777	0.0001	189 - 196	1	VLQRFDQR
1141.5542	1140.5469	1140.5352	0.0117	166 - 174	0	NNPFYFPSR
1184.6010	1183.5937	1183.5846	0.0091	199 - 207	0	QFQNLQNHR
1258.6305	1257.6232	1257.6101	0.0131	249 - 259	0	SFNLDEGHALR
1287.6105	1286.6032	1286.5891	0.0141	302 - 312	0	DQSSYLQGFSR
1297.6548	1296.6475	1296.6363	0.0112	166 - 175	1	NNPFYFPSRR
1320.5963	1319.5890	1319.5741	0.0149	394 - 405	0	DGEPDLSNNFGR
1359.6830	1358.6757	1358.6652	0.0105	432 - 443	0	EGALMLPHFNSK + Oxidation (M)
1376.6770	1375.6697	1375.6619	0.0078	555 - 567	0	DLAFPGSGEQVEK

1379.7874	1378.7801	1378.7608	0.0193	260 - 271	0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	248 - 259	1	KSFNLDEGHALR
1399.7382	1398.7309	1398.7116	0.0193	197 - 207	1	SKQFQNLQNHR
1572.7632	1571.7559	1571.7426	0.0133	329 - 342	0	VLLEENAGGEQEER
1586.7848	1585.7775	1585.7583	0.0192	380 - 393	0	GSEEEDITNPINLR
1691.0417	1690.0344	1690.0141	0.0204	208 - 222	0	IVQIEARPNTLVLPK
1714.8820	1713.8747	1713.8533	0.0215	379 - 393	1	KGSEEEDITNPINLR
1728.8715	1727.8642	1727.8437	0.0205	328 - 342	1	RVLLEENAGGEQEER
1738.8590	1737.8517	1737.8321	0.0196	313 - 327	0	NTLEAAFNAEFNEIR
1817.9818	1816.9745	1816.9570	0.0175	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9557	1893.9484	1893.9332	0.0152	313 - 328	1	NTLEAAFNAEFNEIRR
1913.9453	1912.9380	1912.9238	0.0143	329 - 345	1	VLLEENAGGEQEERGQR
2082.2163	2081.2090	2081.2030	0.0061	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2098.2126	2097.2053	2097.1979	0.0075	444 - 463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2243.0500	2242.0427	2242.0364	0.0063	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1755	2256.1682	2256.1763	-0.0080	260 - 278	1	IPSGFISYILNRHDNQNLR
2619.3081	2618.3008	2618.3160	-0.0152	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3991, 816.4015, 828.4594, 844.3855, 848.4257, 861.0674, 959.4711, 975.4677, 1018.4672, 1051.4438, 1147.5208, 1167.5798, 1309.6069, 1336.5990, 1404.6747, 1427.7377, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1643.8168, 1689.8256, 1717.8293, 1771.8973, 1814.4458, 1830.8712, 1899.9265, 2036.2551, 2070.0337, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2273.1570, 2285.8369, 2313.8347, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

3. gi|1168390 **Mass:** 70639 **Score:** 236 **Expect:** 2.2e-021 **Queries matched:** 30

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3555	807.3482	807.3623	-0.0141	180 - 186		0	YGNQNGR
855.5065	854.4992	854.5086	-0.0094	140 - 146		1	KIRPEGR
896.4250	895.4177	895.4260	-0.0083	272 - 278		0	HDNQNLR
1005.5303	1004.5230	1004.5264	-0.0034	132 - 139		0	RPSHQQPR
1061.5851	1060.5778	1060.5777	0.0001	189 - 196		1	VLQRFDQR
1141.5542	1140.5469	1140.5352	0.0117	166 - 174		0	NNPFYFPSR
1184.6010	1183.5937	1183.5846	0.0091	199 - 207		0	QFQNLQNHR
1258.6305	1257.6232	1257.6101	0.0131	249 - 259		0	SFNLDEGHALR
1287.6105	1286.6032	1286.5891	0.0141	302 - 312		0	DQSSYLQGFSR
1297.6548	1296.6475	1296.6363	0.0112	166 - 175		1	NNPFYFPSRR
1320.5963	1319.5890	1319.5741	0.0149	394 - 405		0	DGEPDLSNNFGR
1359.6830	1358.6757	1358.6652	0.0105	432 - 443		0	EGALMLPHFNSK + Oxidation (M)
1376.6770	1375.6697	1375.6619	0.0078	555 - 567		0	DLAFPGSGEQVEK
1379.7874	1378.7801	1378.7608	0.0193	260 - 271		0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	248 - 259		1	KSFNLDEGHALR

1399.7382	1398.7309	1398.7116	0.0193	197 - 207	1	SKQFQNLQNHR
1572.7632	1571.7559	1571.7426	0.0133	329 - 342	0	VLLEENAGGEQEER
1586.7848	1585.7775	1585.7583	0.0192	380 - 393	0	GSEEEDITNPINLR
1691.0417	1690.0344	1690.0141	0.0204	208 - 222	0	IVQIEARPNTLVLPK
1714.8820	1713.8747	1713.8533	0.0215	379 - 393	1	KGSEEEDITNPINLR
1728.8715	1727.8642	1727.8437	0.0205	328 - 342	1	RVLLEENAGGEQEER
1738.8590	1737.8517	1737.8321	0.0196	313 - 327	0	NTLEAAFNAEFNEIR
1817.9818	1816.9745	1816.9570	0.0175	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9557	1893.9484	1893.9332	0.0152	313 - 328	1	NTLEAAFNAEFNEIRR
1913.9453	1912.9380	1912.9238	0.0143	329 - 345	1	VLLEENAGGEQEERGQR
2082.2163	2081.2090	2081.2030	0.0061	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2098.2126	2097.2053	2097.1979	0.0075	444 - 463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2243.0500	2242.0427	2242.0364	0.0063	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1755	2256.1682	2256.1763	-0.0080	260 - 278	1	IPSGFISYILNRHDNQNLR
2619.3081	2618.3008	2618.3160	-0.0152	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3991, 816.4015, 828.4594, 844.3855, 848.4257, 861.0674, 959.4711, 975.4677, 1018.4672, 1051.4438, 1147.5208, 1167.5798, 1309.6069, 1336.5990, 1404.6747, 1427.7377, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1643.8168, 1689.8256, 1717.8293, 1771.8973, 1814.4458, 1830.8712, 1899.9265, 2036.2551, 2070.0337, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2273.1570, 2285.8369, 2313.8347, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

4. gi|16612200 **Mass:** 71701 **Score:** 211 **Expect:** 7e-019 **Queries matched:** 28

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3555	807.3482	807.3623	-0.0141	186 - 192		0	YGNQNGR
855.5065	854.4992	854.5086	-0.0094	146 - 152		1	KIRPEGR
896.4250	895.4177	895.4260	-0.0083	278 - 284		0	HDNQNLR
1005.5303	1004.5230	1004.5264	-0.0034	138 - 145		0	RPSHQQPR
1061.5851	1060.5778	1060.5777	0.0001	195 - 202		1	VLQRFDQR
1141.5542	1140.5469	1140.5352	0.0117	172 - 180		0	NNPFYFPSR
1184.6010	1183.5937	1183.5846	0.0091	205 - 213		0	QFQNLQNHR
1258.6305	1257.6232	1257.6101	0.0131	255 - 265		0	SFNLDEGHALR
1287.6105	1286.6032	1286.5891	0.0141	308 - 318		0	DQSSYLQGFSR
1297.6548	1296.6475	1296.6363	0.0112	172 - 181		1	NNPFYFPSRR
1359.6830	1358.6757	1358.6652	0.0105	440 - 451		0	EGALMLPHFNSK + Oxidation (M)
1376.6770	1375.6697	1375.6619	0.0078	560 - 572		0	DLAFPGSGEQVEK
1379.7874	1378.7801	1378.7608	0.0193	266 - 277		0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	254 - 265		1	KSFNLDEGHALR
1427.7377	1426.7304	1426.7177	0.0127	203 - 213		1	SRQFQNLQNHR
1572.7632	1571.7559	1571.7426	0.0133	335 - 348		0	VLLEENAGGEQEER
1643.8168	1642.8095	1642.7798	0.0298	387 - 401		0	GSEEEGDITNPINLR

1728.8715	1727.8642	1727.8437	0.0205	334 - 348	1	RVLLEENAGGEQEER
1738.8590	1737.8517	1737.8321	0.0196	319 - 333	0	NTLEAAFNAEFNEIR
1771.8973	1770.8900	1770.8747	0.0153	386 - 401	1	KGSEEEGDITNPINLR
1817.9818	1816.9745	1816.9570	0.0175	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9557	1893.9484	1893.9332	0.0152	319 - 334	1	NTLEAAFNAEFNEIRR
1913.9453	1912.9380	1912.9238	0.0143	335 - 351	1	VLLEENAGGEQEERGQR
2082.2163	2081.2090	2081.2030	0.0061	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2098.2126	2097.2053	2097.1979	0.0075	452 - 471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2243.0500	2242.0427	2242.0364	0.0063	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1755	2256.1682	2256.1763	-0.0080	266 - 284	1	IPSGFISYILNRHDNQNLR
2619.3081	2618.3008	2618.3160	-0.0152	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3991, 816.4015, 828.4594, 844.3855, 848.4257, 861.0674, 959.4711, 975.4677, 1018.4672, 1051.4438, 1147.5208, 1167.5798, 1309.6069, 1320.5963, 1336.5990, 1399.7382, 1404.6747, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1586.7848, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1689.8256, 1691.0417, 1714.8820, 1717.8293, 1814.4458, 1830.8712, 1899.9265, 2036.2551, 2070.0337, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2273.1570, 2285.8369, 2313.8347, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

5. gi|1168391 **Mass:** 71701 **Score:** 211 **Expect:** 7e-019 **Queries matched:** 28

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3555	807.3482	807.3623	-0.0141	186 - 192		0	YGNQNGR
855.5065	854.4992	854.5086	-0.0094	146 - 152		1	KIRPEGR
896.4250	895.4177	895.4260	-0.0083	278 - 284		0	HDNQNLR
1005.5303	1004.5230	1004.5264	-0.0034	138 - 145		0	RPSHQQPR
1061.5851	1060.5778	1060.5777	0.0001	195 - 202		1	VLQRFDQR
1141.5542	1140.5469	1140.5352	0.0117	172 - 180		0	NNPFYFPSR
1184.6010	1183.5937	1183.5846	0.0091	205 - 213		0	QFQNLQNHR
1258.6305	1257.6232	1257.6101	0.0131	255 - 265		0	SFNLDEGHALR
1287.6105	1286.6032	1286.5891	0.0141	308 - 318		0	DQSSYLQGFSR
1297.6548	1296.6475	1296.6363	0.0112	172 - 181		1	NNPFYFPSRR
1359.6830	1358.6757	1358.6652	0.0105	440 - 451		0	EGALMLPHFNSK + Oxidation (M)
1376.6770	1375.6697	1375.6619	0.0078	560 - 572		0	DLAFPGSGEQVEK
1379.7874	1378.7801	1378.7608	0.0193	266 - 277		0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	254 - 265		1	KSFNLDEGHALR
1427.7377	1426.7304	1426.7177	0.0127	203 - 213		1	SRQFQNLQNHR
1572.7632	1571.7559	1571.7426	0.0133	335 - 348		0	VLLEENAGGEQEER
1643.8168	1642.8095	1642.7798	0.0298	387 - 401		0	GSEEEGDITNPINLR
1728.8715	1727.8642	1727.8437	0.0205	334 - 348		1	RVLLEENAGGEQEER
1738.8590	1737.8517	1737.8321	0.0196	319 - 333		0	NTLEAAFNAEFNEIR
1771.8973	1770.8900	1770.8747	0.0153	386 - 401		1	KGSEEEGDITNPINLR
1817.9818	1816.9745	1816.9570	0.0175	541 - 556		1	IFLAGDKDNVIDQIEK

1894.9557	1893.9484	1893.9332	0.0152	319 - 334	1	NTLEAAFNAEFNEIRR
1913.9453	1912.9380	1912.9238	0.0143	335 - 351	1	VLLEENAGGEQEERGQR
2082.2163	2081.2090	2081.2030	0.0061	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2098.2126	2097.2053	2097.1979	0.0075	452 - 471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2243.0500	2242.0427	2242.0364	0.0063	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1755	2256.1682	2256.1763	-0.0080	266 - 284	1	IPSGFISYILNRHDNQNLR
2619.3081	2618.3008	2618.3160	-0.0152	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3991, 816.4015, 828.4594, 844.3855, 848.4257, 861.0674, 959.4711, 975.4677, 1018.4672, 1051.4438, 1147.5208, 1167.5798, 1309.6069, 1320.5963, 1336.5990, 1399.7382, 1404.6747, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1586.7848, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1689.8256, 1691.0417, 1714.8820, 1717.8293, 1814.4458, 1830.8712, 1899.9265, 2036.2551, 2070.0337, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2273.1570, 2285.8369, 2313.8347, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

6. gi|602436 **Mass:** 71701 **Score:** 211 **Expect:** 7e-019 **Queries matched:** 28

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3555	807.3482	807.3623	-0.0141	186 - 192		0	YGNQNGR
855.5065	854.4992	854.5086	-0.0094	146 - 152		1	KIRPEGR
896.4250	895.4177	895.4260	-0.0083	278 - 284		0	HDNQNLR
1005.5303	1004.5230	1004.5264	-0.0034	138 - 145		0	RPSHQQPR
1061.5851	1060.5778	1060.5777	0.0001	195 - 202		1	VLQRFDQR
1141.5542	1140.5469	1140.5352	0.0117	172 - 180		0	NNPFYFPSR
1184.6010	1183.5937	1183.5846	0.0091	205 - 213		0	QFQNLQNHR
1258.6305	1257.6232	1257.6101	0.0131	255 - 265		0	SFNLDEGHALR
1287.6105	1286.6032	1286.5891	0.0141	308 - 318		0	DQSSYLQGFSR
1297.6548	1296.6475	1296.6363	0.0112	172 - 181		1	NNPFYFPSRR
1359.6830	1358.6757	1358.6652	0.0105	440 - 451		0	EGALMLPHFNSK + Oxidation (M)
1376.6770	1375.6697	1375.6619	0.0078	560 - 572		0	DLAFPGSGEQVEK
1379.7874	1378.7801	1378.7608	0.0193	266 - 277		0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	254 - 265		1	KSFNLDEGHALR
1427.7377	1426.7304	1426.7177	0.0127	203 - 213		1	SRQFQNLQNHR
1572.7632	1571.7559	1571.7426	0.0133	335 - 348		0	VLLEENAGGEQEER
1643.8168	1642.8095	1642.7798	0.0298	387 - 401		0	GSEEEGDITNPINLR
1728.8715	1727.8642	1727.8437	0.0205	334 - 348		1	RVLLEENAGGEQEER
1738.8590	1737.8517	1737.8321	0.0196	319 - 333		0	NTLEAAFNAEFNEIR
1771.8973	1770.8900	1770.8747	0.0153	386 - 401		1	KGSEEEGDITNPINLR
1817.9818	1816.9745	1816.9570	0.0175	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9557	1893.9484	1893.9332	0.0152	319 - 334		1	NTLEAAFNAEFNEIRR
1913.9453	1912.9380	1912.9238	0.0143	335 - 351		1	VLLEENAGGEQEERGQR
2082.2163	2081.2090	2081.2030	0.0061	452 - 471		1	AMVIVVVNKGTGNLELVAVR
2098.2126	2097.2053	2097.1979	0.0075	452 - 471		1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

2243.0500	2242.0427	2242.0364	0.0063	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1755	2256.1682	2256.1763	-0.0080	266 - 284	1	IPSGFISYILNRHDNQNLR
2619.3081	2618.3008	2618.3160	-0.0152	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3991, 816.4015, 828.4594, 844.3855, 848.4257, 861.0674, 959.4711, 975.4677, 1018.4672, 1051.4438, 1147.5208, 1167.5798, 1309.6069, 1320.5963, 1336.5990, 1399.7382, 1404.6747, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1586.7848, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1689.8256, 1691.0417, 1714.8820, 1717.8293, 1814.4458, 1830.8712, 1899.9265, 2036.2551, 2070.0337, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2273.1570, 2285.8369, 2313.8347, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

7. gi|46560476 **Mass:** 48122 **Score:** 164 **Expect:** 3.5e-014 **Queries matched:** 20

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4250	895.4177	895.4260	-0.0083	81 -	87	0	HDNQNLR
1184.6010	1183.5937	1183.5846	0.0091	8 -	16	0	QFQNLQNHR
1258.6305	1257.6232	1257.6101	0.0131	58 -	68	0	SFNLDEGHALR
1287.6105	1286.6032	1286.5891	0.0141	111 -	121	0	DQSSYLQGFSR
1359.6830	1358.6757	1358.6652	0.0105	242 -	253	0	EGALMLPHFNSK + Oxidation (M)
1376.6770	1375.6697	1375.6619	0.0078	362 -	374	0	DLAFPGSGEQVEK
1379.7874	1378.7801	1378.7608	0.0193	69 -	80	0	IPSGFISYILNR
1386.7344	1385.7271	1385.7051	0.0220	57 -	68	1	KSFNLDEGHALR
1427.7377	1426.7304	1426.7177	0.0127	6 -	16	1	SRQFQNLQNHR
1572.7632	1571.7559	1571.7426	0.0133	138 -	151	0	VLLEENAGGEQEER
1728.8715	1727.8642	1727.8437	0.0205	137 -	151	1	RVLLEENAGGEQEER
1738.8590	1737.8517	1737.8321	0.0196	122 -	136	0	NTLEAAFNAEFNEIR
1817.9818	1816.9745	1816.9570	0.0175	343 -	358	1	IFLAGDKDNVIDQIEK
1894.9557	1893.9484	1893.9332	0.0152	122 -	137	1	NTLEAAFNAEFNEIRR
1913.9453	1912.9380	1912.9238	0.0143	138 -	154	1	VLLEENAGGEQEERGQR
2082.2163	2081.2090	2081.2030	0.0061	254 -	273	1	AMVIVVVNKGTGNLELVAVR
2098.2126	2097.2053	2097.1979	0.0075	254 -	273	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2243.0500	2242.0427	2242.0364	0.0063	91 -	110	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2257.1755	2256.1682	2256.1763	-0.0080	69 -	87	1	IPSGFISYILNRHDNQNLR
2619.3081	2618.3008	2618.3160	-0.0152	32 -	56	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3991, 808.3555, 816.4015, 828.4594, 844.3855, 848.4257, 855.5065, 861.0674, 959.4711, 975.4677, 1005.5303, 1018.4672, 1051.4438, 1061.5851, 1141.5542, 1147.5208, 1167.5798, 1297.6548, 1309.6069, 1320.5963, 1336.5990, 1399.7382, 1404.6747, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1586.7848, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1643.8168, 1689.8256, 1691.0417, 1714.8820, 1717.8293, 1771.8973, 1814.4458, 1830.8712, 1899.9265, 2036.2551, 2070.0337, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2273.1570, 2285.8369, 2313.8347, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

8. gi|46560472 **Mass:** 34169 **Score:** 70 **Expect:** 8.4e-005 **Queries matched:** 11

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1320.5963	1319.5890	1319.5741	0.0149	83 - 94	0	DGEPDLSNNFGR
1359.6830	1358.6757	1358.6652	0.0105	121 - 132	0	EGALMLPHFNSK + Oxidation (M)
1376.6770	1375.6697	1375.6619	0.0078	244 - 256	0	DLAFPGSGEQVEK
1572.7632	1571.7559	1571.7426	0.0133	18 - 31	0	VLLEENAGGEQEER
1586.7848	1585.7775	1585.7583	0.0192	69 - 82	0	GSEEEDITNPINLR
1714.8820	1713.8747	1713.8533	0.0215	68 - 82	1	KGSEEEDITNPINLR
1728.8715	1727.8642	1727.8437	0.0205	17 - 31	1	RVLLEENAGGEQEER
1817.9818	1816.9745	1816.9570	0.0175	225 - 240	1	IFLAGDKDNVIDQIEK
1913.9453	1912.9380	1912.9238	0.0143	18 - 34	1	VLLEENAGGEQEERGQR
2082.2163	2081.2090	2081.2030	0.0061	133 - 152	1	AMVIVVVNKGTGNLELVAVR
2098.2126	2097.2053	2097.1979	0.0075	133 - 152	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3991, 808.3555, 816.4015, 828.4594, 844.3855, 848.4257, 855.5065, 861.0674, 896.4250, 959.4711, 975.4677, 1005.5303, 1018.4672, 1051.4438, 1061.5851, 1141.5542, 1147.5208, 1167.5798, 1184.6010, 1258.6305, 1287.6105, 1297.6548, 1309.6069, 1336.5990, 1379.7874, 1386.7344, 1399.7382, 1404.6747, 1427.7377, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1643.8168, 1689.8256, 1691.0417, 1717.8293, 1738.8590, 1771.8973, 1814.4458, 1830.8712, 1894.9557, 1899.9265, 2036.2551, 2070.0337, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2243.0500, 2257.1755, 2273.1570, 2285.8369, 2313.8347, 2619.3081, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

9. gi|46560474 **Mass:** 33641 **Score:** 62 **Expect:** 0.00052 **Queries matched:** 10

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1359.6830	1358.6757	1358.6652	0.0105	120 - 131		0	EGALMLPHFNSK + Oxidation (M)
1376.6770	1375.6697	1375.6619	0.0078	240 - 252		0	DLAFPGSGEQVEK
1572.7632	1571.7559	1571.7426	0.0133	15 - 28		0	VLLEENAGGEQEER
1643.8168	1642.8095	1642.7798	0.0298	67 - 81		0	GSEEEGDITNPINLR
1728.8715	1727.8642	1727.8437	0.0205	14 - 28		1	RVLLEENAGGEQEER
1771.8973	1770.8900	1770.8747	0.0153	66 - 81		1	KGSEEEGDITNPINLR
1817.9818	1816.9745	1816.9570	0.0175	221 - 236		1	IFLAGDKDNVIDQIEK
1913.9453	1912.9380	1912.9238	0.0143	15 - 31		1	VLLEENAGGEQEERGQR
2082.2163	2081.2090	2081.2030	0.0061	132 - 151		1	AMVIVVVNKGTGNLELVAVR
2098.2126	2097.2053	2097.1979	0.0075	132 - 151		1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3991, 808.3555, 816.4015, 828.4594, 844.3855, 848.4257, 855.5065, 861.0674, 896.4250, 959.4711, 975.4677, 1005.5303, 1018.4672, 1051.4438, 1061.5851, 1141.5542, 1147.5208, 1167.5798, 1184.6010, 1258.6305, 1287.6105, 1297.6548, 1309.6069, 1320.5963, 1336.5990, 1379.7874, 1386.7344, 1399.7382, 1404.6747, 1427.7377, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1586.7848, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1689.8256, 1691.0417, 1714.8820, 1717.8293, 1738.8590, 1814.4458, 1830.8712, 1894.9557, 1899.9265, 2036.2551, 2070.0337, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2243.0500, 2257.1755, 2273.1570, 2285.8369, 2313.8347, 2619.3081, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

10. gi|226258 **Mass:** 10809 **Score:** 13 **Expect:** 45 **Queries matched:** 2

ferredoxin I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1141.5542	1140.5469	1140.5484	-0.0015	16 -	26	0	GDLAVAMASYK + Oxidation (M)
1297.6548	1296.6475	1296.6496	-0.0020	15 -	26	1	RGDLAVAMASYK + Oxidation (M)

No match to: 805.3991, 808.3555, 816.4015, 828.4594, 844.3855, 848.4257, 855.5065, 861.0674, 896.4250, 959.4711, 975.4677, 1005.5303, 1018.4672, 1051.4438, 1061.5851, 1147.5208, 1167.5798, 1184.6010, 1258.6305, 1287.6105, 1309.6069, 1320.5963, 1336.5990, 1359.6830, 1376.6770, 1379.7874, 1386.7344, 1399.7382, 1404.6747, 1427.7377, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1572.7632, 1586.7848, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1643.8168, 1689.8256, 1691.0417, 1714.8820, 1717.8293, 1728.8715, 1738.8590, 1771.8973, 1814.4458, 1817.9818, 1830.8712, 1894.9557, 1899.9265, 1913.9453, 2036.2551, 2070.0337, 2082.2163, 2098.2126, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2243.0500, 2257.1755, 2273.1570, 2285.8369, 2313.8347, 2619.3081, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 80

Protein View

Match to: **gi|46560478** Score: **241** Expect: **7e-022**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **80**
Number of mass values matched: **30**
Sequence Coverage: **47%**

Matched peptides shown in **Bold Red**

```
  1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
 51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
132 - 139	1005.5303	1004.5230	1004.5264	-0.0034	0	RPSHQQPR	
140 - 146	855.5065	854.4992	854.5086	-0.0094	1	KIRPEGR	
166 - 174	1141.5542	1140.5469	1140.5352	0.0117	0	NNPFYFPSR	
166 - 175	1297.6548	1296.6475	1296.6363	0.0112	1	NNPFYFPSRR	
180 - 186	808.3555	807.3482	807.3623	-0.0141	0	YGNQNGR	
189 - 196	1061.5851	1060.5778	1060.5777	0.0001	1	VLQRFDQR	
197 - 207	1399.7382	1398.7309	1398.7116	0.0193	1	SKQFQNLQNHR	
199 - 207	1184.6010	1183.5937	1183.5846	0.0091	0	QFQNLQNHR	
208 - 222	1691.0417	1690.0344	1690.0141	0.0204	0	IVQIEARPNTLVLPK	
223 - 247	2619.3081	2618.3008	2618.3160	-0.0152	0	HADADNILVIQQGQATVTVANGNNR	
248 - 259	1386.7344	1385.7271	1385.7051	0.0220	1	KSFNLDEGHALR	
249 - 259	1258.6305	1257.6232	1257.6101	0.0131	0	SFNLDEGHALR	
260 - 271	1379.7874	1378.7801	1378.7608	0.0193	0	IPSGFISYILNR	
260 - 278	2257.1755	2256.1682	2256.1763	-0.0080	1	IPSGFISYILNRHDNQNLR	
272 - 278	896.4250	895.4177	895.4260	-0.0083	0	HDNQNLR	
282 - 301	2243.0500	2242.0427	2242.0364	0.0063	0	ISMPVNTPGQFEDFFPASSR	Oxidation (M)
302 - 312	1287.6105	1286.6032	1286.5891	0.0141	0	DQSSYLQGFSR	
313 - 327	1738.8590	1737.8517	1737.8321	0.0196	0	NTLEAAFNAEFNEIR	
313 - 328	1894.9557	1893.9484	1893.9332	0.0152	1	NTLEAAFNAEFNEIRR	
328 - 342	1728.8715	1727.8642	1727.8437	0.0205	1	RVLLEENAGGEQEER	
329 - 342	1572.7632	1571.7559	1571.7426	0.0133	0	VLLEENAGGEQEER	
329 - 345	1913.9453	1912.9380	1912.9238	0.0143	1	VLLEENAGGEQEERGQR	
379 - 393	1714.8820	1713.8747	1713.8533	0.0215	1	KGSEEEDITNPINLR	
380 - 393	1586.7848	1585.7775	1585.7583	0.0192	0	GSEEEDITNPINLR	
394 - 405	1320.5963	1319.5890	1319.5741	0.0149	0	DGEPDLSNNFGR	
432 - 443	1359.6830	1358.6757	1358.6652	0.0105	0	EGALMLPHFNSK	Oxidation (M)
444 - 463	2082.2163	2081.2090	2081.2030	0.0061	1	AMVIVVVNKGTGNLELVAVR	
444 - 463	2098.2126	2097.2053	2097.1979	0.0075	1	AMVIVVVNKGTGNLELVAVR	Oxidation (M)

536 - 551	**1817.9818**	**1816.9745**	**1816.9570**	**0.0175**	**1**	**IFLAGDKDNVIDQIEK**
555 - 567	**1376.6770**	**1375.6697**	**1375.6619**	**0.0078**	**0**	**DLAFPGSGEQVEK**

No match to: 805.3991, 816.4015, 828.4594, 844.3855, 848.4257, 861.0674, 959.4711, 975.4677, 1018.4672, 1051.4438, 1147.5208, 1167.5798, 1309.6069, 1336.5990, 1404.6747, 1427.7377, 1432.6725, 1500.7466, 1512.7478, 1528.7444, 1564.7172, 1592.7057, 1595.7991, 1600.7220, 1607.7966, 1623.7906, 1643.8168, 1689.8256, 1717.8293, 1771.8973, 1814.4458, 1830.8712, 1899.9265, 2036.2551, 2070.0337, 2116.0862, 2129.1321, 2145.1548, 2167.9617, 2182.0740, 2194.9417, 2273.1570, 2285.8369, 2313.8347, 2662.3877, 2747.3601, 2748.3574, 2974.2075, 2990.1699, 3496.5918

Spot 11

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 09:57:42 GMT**
Top Score : **179 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	179	conarachin [Arachis hypogaea]
2.	gi|620025	70639	175	Ara h I
3.	gi|1168390	70639	175	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	153	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	153	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	153	Ara h I
7.	gi|46560476	48122	108	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	73	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	54	conarachin [Arachis hypogaea]
10.	gi|230338	23975	25	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 179 **Expect:** 1.1e-015 **Queries matched:** 25
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	272	278	0	HDNQNLR
1005.5253	1004.5180	1004.5264	-0.0084	132	139	0	RPSHQQPR
1019.4594	1018.4521	1018.4468	0.0053	118	124	1	EREEDWR
1061.5924	1060.5851	1060.5777	0.0074	189	196	1	VLQRFDQR
1115.5376	1114.5303	1114.5155	0.0148	120	127	1	EEDWRQPR
1141.5533	1140.5460	1140.5352	0.0108	166	174	0	NNPFYFPSR
1184.6090	1183.6017	1183.5846	0.0171	199	207	0	QFQNLQNHR
1287.6183	1286.6110	1286.5891	0.0219	302	312	0	DQSSYLQGFSR
1297.6653	1296.6580	1296.6363	0.0217	166	175	1	NNPFYFPSRR
1320.6073	1319.6000	1319.5741	0.0259	394	405	0	DGEPDLSNNFGR

1359.6918	1358.6845	1358.6652	0.0193	432 - 443	0	EGALMLPHFNSK + Oxidation (M)
1399.7468	1398.7395	1398.7116	0.0279	197 - 207	1	SKQFQNLQNHR
1400.7289	1399.7216	1399.7307	-0.0090	543 - 554	1	DNVIDQIEKQAK
1572.7758	1571.7685	1571.7426	0.0259	329 - 342	0	VLLEENAGGEQEER
1586.7965	1585.7892	1585.7583	0.0309	380 - 393	0	GSEEEDITNPINLR
1591.8119	1590.8046	1590.7763	0.0283	128 - 139	1	EDWRRPSHQQPR
1714.8901	1713.8828	1713.8533	0.0296	379 - 393	1	KGSEEEDITNPINLR
1728.8792	1727.8719	1727.8437	0.0282	328 - 342	1	RVLLEENAGGEQEER
1730.9023	1729.8950	1729.9250	-0.0299	555 - 570	1	DLAFPGSGEQVEKLIK
1738.8728	1737.8655	1737.8321	0.0334	313 - 327	0	NTLEAAFNAEFNEIR
1817.9792	1816.9719	1816.9570	0.0149	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9624	1893.9551	1893.9332	0.0219	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2161	2081.2088	2081.2030	0.0059	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2098.2087	2097.2014	2097.1979	0.0036	444 - 463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2619.2798	2618.2725	2618.3160	-0.0435	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 906.4893, 959.4706, 975.4730, 1046.6005, 1080.5361, 1111.5687, 1145.0728, 1145.5825, 1167.5784, 1258.6431, 1376.6992, 1379.7988, 1424.7450, 1427.7507, 1440.7399, 1496.7666, 1512.7646, 1560.7281, 1568.7423, 1623.8060, 1685.8398, 1691.0596, 1771.9128, 1830.8895, 1899.9254, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2273.1538, 2282.8325, 2311.1272, 2508.3032, 2515.3044, 2530.2915, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

2. gi|620025 **Mass:** 70639 **Score:** 175 **Expect:** 2.8e-015 **Queries matched:** 25

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	272 - 278		0	HDNQNLR
1005.5253	1004.5180	1004.5264	-0.0084	132 - 139		0	RPSHQQPR
1019.4594	1018.4521	1018.4468	0.0053	118 - 124		1	EREEDWR
1061.5924	1060.5851	1060.5777	0.0074	189 - 196		1	VLQRFDQR
1115.5376	1114.5303	1114.5155	0.0148	120 - 127		1	EEDWRQPR
1141.5533	1140.5460	1140.5352	0.0108	166 - 174		0	NNPFYFPSR
1184.6090	1183.6017	1183.5846	0.0171	199 - 207		0	QFQNLQNHR
1287.6183	1286.6110	1286.5891	0.0219	302 - 312		0	DQSSYLQGFSR
1297.6653	1296.6580	1296.6363	0.0217	166 - 175		1	NNPFYFPSRR
1320.6073	1319.6000	1319.5741	0.0259	394 - 405		0	DGEPDLSNNFGR
1359.6918	1358.6845	1358.6652	0.0193	432 - 443		0	EGALMLPHFNSK + Oxidation (M)
1399.7468	1398.7395	1398.7116	0.0279	197 - 207		1	SKQFQNLQNHR
1400.7289	1399.7216	1399.7307	-0.0090	543 - 554		1	DNVIDQIEKQAK
1572.7758	1571.7685	1571.7426	0.0259	329 - 342		0	VLLEENAGGEQEER
1586.7965	1585.7892	1585.7583	0.0309	380 - 393		0	GSEEEDITNPINLR
1591.8119	1590.8046	1590.7763	0.0283	128 - 139		1	EDWRRPSHQQPR
1714.8901	1713.8828	1713.8533	0.0296	379 - 393		1	KGSEEEDITNPINLR

1728.8792	1727.8719	1727.8437	0.0282	328 - 342	1	RVLLEENAGGEQEER
1730.9023	1729.8950	1729.9250	-0.0299	555 - 570	1	DLAFPGSGEQVEKLIK
1738.8728	1737.8655	1737.8321	0.0334	313 - 327	0	NTLEAAFNAEFNEIR
1817.9792	1816.9719	1816.9570	0.0149	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9624	1893.9551	1893.9332	0.0219	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2161	2081.2088	2081.2030	0.0059	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2098.2087	2097.2014	2097.1979	0.0036	444 - 463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2619.2798	2618.2725	2618.3160	-0.0435	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 906.4893, 959.4706, 975.4730, 1046.6005, 1080.5361, 1111.5687, 1145.0728, 1145.5825, 1167.5784, 1258.6431, 1376.6992, 1379.7988, 1424.7450, 1427.7507, 1440.7399, 1496.7666, 1512.7646, 1560.7281, 1568.7423, 1623.8060, 1685.8398, 1691.0596, 1771.9128, 1830.8895, 1899.9254, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2273.1538, 2282.8325, 2311.1272, 2508.3032, 2515.3044, 2530.2915, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

3. gi|1168390 **Mass:** 70639 **Score:** 175 **Expect:** 2.8e-015 **Queries matched:** 25

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	272 - 278		0	HDNQNLR
1005.5253	1004.5180	1004.5264	-0.0084	132 - 139		0	RPSHQQPR
1019.4594	1018.4521	1018.4468	0.0053	118 - 124		1	EREEDWR
1061.5924	1060.5851	1060.5777	0.0074	189 - 196		1	VLQRFDQR
1115.5376	1114.5303	1114.5155	0.0148	120 - 127		1	EEDWRQPR
1141.5533	1140.5460	1140.5352	0.0108	166 - 174		0	NNPFYFPSR
1184.6090	1183.6017	1183.5846	0.0171	199 - 207		0	QFQNLQNHR
1287.6183	1286.6110	1286.5891	0.0219	302 - 312		0	DQSSYLQGFSR
1297.6653	1296.6580	1296.6363	0.0217	166 - 175		1	NNPFYFPSRR
1320.6073	1319.6000	1319.5741	0.0259	394 - 405		0	DGEPDLSNNFGR
1359.6918	1358.6845	1358.6652	0.0193	432 - 443		0	EGALMLPHFNSK + Oxidation (M)
1399.7468	1398.7395	1398.7116	0.0279	197 - 207		1	SKQFQNLQNHR
1400.7289	1399.7216	1399.7307	-0.0090	543 - 554		1	DNVIDQIEKQAK
1572.7758	1571.7685	1571.7426	0.0259	329 - 342		0	VLLEENAGGEQEER
1586.7965	1585.7892	1585.7583	0.0309	380 - 393		0	GSEEEDITNPINLR
1591.8119	1590.8046	1590.7763	0.0283	128 - 139		1	EDWRRPSHQQPR
1714.8901	1713.8828	1713.8533	0.0296	379 - 393		1	KGSEEEDITNPINLR
1728.8792	1727.8719	1727.8437	0.0282	328 - 342		1	RVLLEENAGGEQEER
1730.9023	1729.8950	1729.9250	-0.0299	555 - 570		1	DLAFPGSGEQVEKLIK
1738.8728	1737.8655	1737.8321	0.0334	313 - 327		0	NTLEAAFNAEFNEIR
1817.9792	1816.9719	1816.9570	0.0149	536 - 551		1	IFLAGDKDNVIDQIEK
1894.9624	1893.9551	1893.9332	0.0219	313 - 328		1	NTLEAAFNAEFNEIRR
2082.2161	2081.2088	2081.2030	0.0059	444 - 463		1	AMVIVVVNKGTGNLELVAVR
2098.2087	2097.2014	2097.1979	0.0036	444 - 463		1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

2619.2798	2618.2725	2618.3160	-0.0435	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 906.4893, 959.4706, 975.4730, 1046.6005, 1080.5361, 1111.5687, 1145.0728, 1145.5825, 1167.5784, 1258.6431, 1376.6992, 1379.7988, 1424.7450, 1427.7507, 1440.7399, 1496.7666, 1512.7646, 1560.7281, 1568.7423, 1623.8060, 1685.8398, 1691.0596, 1771.9128, 1830.8895, 1899.9254, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2273.1538, 2282.8325, 2311.1272, 2508.3032, 2515.3044, 2530.2915, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

4. gi|16612200 **Mass:** 71701 **Score:** 153 **Expect:** 4.4e-013 **Queries matched:** 23

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	278	284	0	HDNQNLR
1005.5253	1004.5180	1004.5264	-0.0084	138	145	0	RPSHQQPR
1019.4594	1018.4521	1018.4468	0.0053	124	130	1	EREEDWR
1061.5924	1060.5851	1060.5777	0.0074	195	202	1	VLQRFDQR
1115.5376	1114.5303	1114.5155	0.0148	126	133	1	EEDWRQPR
1141.5533	1140.5460	1140.5352	0.0108	172	180	0	NNPFYFPSR
1184.6090	1183.6017	1183.5846	0.0171	205	213	0	QFQNLQNHR
1287.6183	1286.6110	1286.5891	0.0219	308	318	0	DQSSYLQGFSR
1297.6653	1296.6580	1296.6363	0.0217	172	181	1	NNPFYFPSRR
1359.6918	1358.6845	1358.6652	0.0193	440	451	0	EGALMLPHFNSK + Oxidation (M)
1400.7289	1399.7216	1399.7307	-0.0090	548	559	1	DNVIDQIEKQAK
1427.7507	1426.7434	1426.7177	0.0257	203	213	1	SRQFQNLQNHR
1572.7758	1571.7685	1571.7426	0.0259	335	348	0	VLLEENAGGEQEER
1591.8119	1590.8046	1590.7763	0.0283	134	145	1	EDWRRPSHQQPR
1728.8792	1727.8719	1727.8437	0.0282	334	348	1	RVLLEENAGGEQEER
1730.9023	1729.8950	1729.9250	-0.0299	560	575	1	DLAFPGSGEQVEKLIK
1738.8728	1737.8655	1737.8321	0.0334	319	333	0	NTLEAAFNAEFNEIR
1771.9128	1770.9055	1770.8747	0.0308	386	401	1	KGSEEEGDITNPINLR
1817.9792	1816.9719	1816.9570	0.0149	541	556	1	IFLAGDKDNVIDQIEK
1894.9624	1893.9551	1893.9332	0.0219	319	334	1	NTLEAAFNAEFNEIRR
2082.2161	2081.2088	2081.2030	0.0059	452	471	1	AMVIVVVNKGTGNLELVAVR
2098.2087	2097.2014	2097.1979	0.0036	452	471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2619.2798	2618.2725	2618.3160	-0.0435	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 906.4893, 959.4706, 975.4730, 1046.6005, 1080.5361, 1111.5687, 1145.0728, 1145.5825, 1167.5784, 1258.6431, 1320.6073, 1376.6992, 1379.7988, 1399.7468, 1424.7450, 1440.7399, 1496.7666, 1512.7646, 1560.7281, 1568.7423, 1586.7965, 1623.8060, 1685.8398, 1691.0596, 1714.8901, 1830.8895, 1899.9254, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2273.1538, 2282.8325, 2311.1272, 2508.3032, 2515.3044, 2530.2915, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

5. gi|1168391 **Mass:** 71701 **Score:** 153 **Expect:** 4.4e-013 **Queries matched:** 23

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

896.4271	895.4198	895.4260	-0.0062	278 - 284	0	HDNQNLR
1005.5253	1004.5180	1004.5264	-0.0084	138 - 145	0	RPSHQQPR
1019.4594	1018.4521	1018.4468	0.0053	124 - 130	1	EREEDWR
1061.5924	1060.5851	1060.5777	0.0074	195 - 202	1	VLQRFDQR
1115.5376	1114.5303	1114.5155	0.0148	126 - 133	1	EEDWRQPR
1141.5533	1140.5460	1140.5352	0.0108	172 - 180	0	NNPFYFPSR
1184.6090	1183.6017	1183.5846	0.0171	205 - 213	0	QFQNLQNHR
1287.6183	1286.6110	1286.5891	0.0219	308 - 318	0	DQSSYLQGFSR
1297.6653	1296.6580	1296.6363	0.0217	172 - 181	1	NNPFYFPSRR
1359.6918	1358.6845	1358.6652	0.0193	440 - 451	0	EGALMLPHFNSK + Oxidation (M)
1400.7289	1399.7216	1399.7307	-0.0090	548 - 559	1	DNVIDQIEKQAK
1427.7507	1426.7434	1426.7177	0.0257	203 - 213	1	SRQFQNLQNHR
1572.7758	1571.7685	1571.7426	0.0259	335 - 348	0	VLLEENAGGEQEER
1591.8119	1590.8046	1590.7763	0.0283	134 - 145	1	EDWRRPSHQQPR
1728.8792	1727.8719	1727.8437	0.0282	334 - 348	1	RVLLEENAGGEQEER
1730.9023	1729.8950	1729.9250	-0.0299	560 - 575	1	DLAFPGSGEQVEKLIK
1738.8728	1737.8655	1737.8321	0.0334	319 - 333	0	NTLEAAFNAEFNEIR
1771.9128	1770.9055	1770.8747	0.0308	386 - 401	1	KGSEEEGDITNPINLR
1817.9792	1816.9719	1816.9570	0.0149	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9624	1893.9551	1893.9332	0.0219	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2161	2081.2088	2081.2030	0.0059	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2098.2087	2097.2014	2097.1979	0.0036	452 - 471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2619.2798	2618.2725	2618.3160	-0.0435	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 906.4893, 959.4706, 975.4730, 1046.6005, 1080.5361, 1111.5687, 1145.0728, 1145.5825, 1167.5784, 1258.6431, 1320.6073, 1376.6992, 1379.7988, 1399.7468, 1424.7450, 1440.7399, 1496.7666, 1512.7646, 1560.7281, 1568.7423, 1586.7965, 1623.8060, 1685.8398, 1691.0596, 1714.8901, 1830.8895, 1899.9254, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2273.1538, 2282.8325, 2311.1272, 2508.3032, 2515.3044, 2530.2915, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

6. gi|602436 **Mass:** 71701 **Score:** 153 **Expect:** 4.4e-013 **Queries matched:** 23

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	278 - 284		0	HDNQNLR
1005.5253	1004.5180	1004.5264	-0.0084	138 - 145		0	RPSHQQPR
1019.4594	1018.4521	1018.4468	0.0053	124 - 130		1	EREEDWR
1061.5924	1060.5851	1060.5777	0.0074	195 - 202		1	VLQRFDQR
1115.5376	1114.5303	1114.5155	0.0148	126 - 133		1	EEDWRQPR
1141.5533	1140.5460	1140.5352	0.0108	172 - 180		0	NNPFYFPSR
1184.6090	1183.6017	1183.5846	0.0171	205 - 213		0	QFQNLQNHR
1287.6183	1286.6110	1286.5891	0.0219	308 - 318		0	DQSSYLQGFSR
1297.6653	1296.6580	1296.6363	0.0217	172 - 181		1	NNPFYFPSRR

1359.6918	1358.6845	1358.6652	0.0193	440 - 451	0	EGALMLPHFNSK + Oxidation (M)
1400.7289	1399.7216	1399.7307	-0.0090	548 - 559	1	DNVIDQIEKQAK
1427.7507	1426.7434	1426.7177	0.0257	203 - 213	1	SRQFQNLQNHR
1572.7758	1571.7685	1571.7426	0.0259	335 - 348	0	VLLEENAGGEQEER
1591.8119	1590.8046	1590.7763	0.0283	134 - 145	1	EDWRRPSHQQPR
1728.8792	1727.8719	1727.8437	0.0282	334 - 348	1	RVLLEENAGGEQEER
1730.9023	1729.8950	1729.9250	-0.0299	560 - 575	1	DLAFPGSGEQVEKLIK
1738.8728	1737.8655	1737.8321	0.0334	319 - 333	0	NTLEAAFNAEFNEIR
1771.9128	1770.9055	1770.8747	0.0308	386 - 401	1	KGSEEEGDITNPINLR
1817.9792	1816.9719	1816.9570	0.0149	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9624	1893.9551	1893.9332	0.0219	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2161	2081.2088	2081.2030	0.0059	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2098.2087	2097.2014	2097.1979	0.0036	452 - 471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2619.2798	2618.2725	2618.3160	-0.0435	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 906.4893, 959.4706, 975.4730, 1046.6005, 1080.5361, 1111.5687, 1145.0728, 1145.5825, 1167.5784, 1258.6431, 1320.6073, 1376.6992, 1379.7988, 1399.7468, 1424.7450, 1440.7399, 1496.7666, 1512.7646, 1560.7281, 1568.7423, 1586.7965, 1623.8060, 1685.8398, 1691.0596, 1714.8901, 1830.8895, 1899.9254, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2273.1538, 2282.8325, 2311.1272, 2508.3032, 2515.3044, 2530.2915, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

7. gi|46560476 **Mass:** 48122 **Score:** 108 **Expect:** 1.4e-008 **Queries matched:** 15

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	81 -	87	0	HDNQNLR
1184.6090	1183.6017	1183.5846	0.0171	8 -	16	0	QFQNLQNHR
1287.6183	1286.6110	1286.5891	0.0219	111 -	121	0	DQSSYLQGFSR
1359.6918	1358.6845	1358.6652	0.0193	242 -	253	0	EGALMLPHFNSK + Oxidation (M)
1400.7289	1399.7216	1399.7307	-0.0090	350 -	361	1	DNVIDQIEKQAK
1427.7507	1426.7434	1426.7177	0.0257	6 -	16	1	SRQFQNLQNHR
1572.7758	1571.7685	1571.7426	0.0259	138 -	151	0	VLLEENAGGEQEER
1728.8792	1727.8719	1727.8437	0.0282	137 -	151	1	RVLLEENAGGEQEER
1730.9023	1729.8950	1729.9250	-0.0299	362 -	377	1	DLAFPGSGEQVEKLIK
1738.8728	1737.8655	1737.8321	0.0334	122 -	136	0	NTLEAAFNAEFNEIR
1817.9792	1816.9719	1816.9570	0.0149	343 -	358	1	IFLAGDKDNVIDQIEK
1894.9624	1893.9551	1893.9332	0.0219	122 -	137	1	NTLEAAFNAEFNEIRR
2082.2161	2081.2088	2081.2030	0.0059	254 -	273	1	AMVIVVVNKGTGNLELVAVR
2098.2087	2097.2014	2097.1979	0.0036	254 -	273	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2619.2798	2618.2725	2618.3160	-0.0435	32 -	56	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 906.4893, 959.4706, 975.4730, 1005.5253, 1019.4594, 1046.6005, 1061.5924, 1080.5361, 1111.5687, 1115.5376, 1141.5533, 1145.0728, 1145.5825, 1167.5784, 1258.6431, 1297.6653, 1320.6073, 1376.6992, 1379.7988, 1399.7468, 1424.7450, 1440.7399, 1496.7666, 1512.7646, 1560.7281,

1568.7423, 1586.7965, 1591.8119, 1623.8060, 1685.8398, 1691.0596, 1714.8901, 1771.9128, 1830.8895, 1899.9254, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2273.1538, 2282.8325, 2311.1272, 2508.3032, 2515.3044, 2530.2915, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

8. gi|46560472 **Mass:** 34169 **Score:** 73 **Expect:** 4.6e-005 **Queries matched:** 11

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1320.6073	1319.6000	1319.5741	0.0259	83	94	0	DGEPDLSNNFGR
1359.6918	1358.6845	1358.6652	0.0193	121	132	0	EGALMLPHFNSK + Oxidation (M)
1400.7289	1399.7216	1399.7307	-0.0090	232	243	1	DNVIDQIEKQAK
1572.7758	1571.7685	1571.7426	0.0259	18	31	0	VLLEENAGGEQEER
1586.7965	1585.7892	1585.7583	0.0309	69	82	0	GSEEEDITNPINLR
1714.8901	1713.8828	1713.8533	0.0296	68	82	1	KGSEEEDITNPINLR
1728.8792	1727.8719	1727.8437	0.0282	17	31	1	RVLLEENAGGEQEER
1730.9023	1729.8950	1729.9250	-0.0299	244	259	1	DLAFPGSGEQVEKLIK
1817.9792	1816.9719	1816.9570	0.0149	225	240	1	IFLAGDKDNVIDQIEK
2082.2161	2081.2088	2081.2030	0.0059	133	152	1	AMVIVVVNKGTGNLELVAVR
2098.2087	2097.2014	2097.1979	0.0036	133	152	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 896.4271, 906.4893, 959.4706, 975.4730, 1005.5253, 1019.4594, 1046.6005, 1061.5924, 1080.5361, 1111.5687, 1115.5376, 1141.5533, 1145.0728, 1145.5825, 1167.5784, 1184.6090, 1258.6431, 1287.6183, 1297.6653, 1376.6992, 1379.7988, 1399.7468, 1424.7450, 1427.7507, 1440.7399, 1496.7666, 1512.7646, 1560.7281, 1568.7423, 1591.8119, 1623.8060, 1685.8398, 1691.0596, 1738.8728, 1771.9128, 1830.8895, 1894.9624, 1899.9254, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2273.1538, 2282.8325, 2311.1272, 2508.3032, 2515.3044, 2530.2915, 2619.2798, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

9. gi|46560474 **Mass:** 33641 **Score:** 54 **Expect:** 0.0033 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1359.6918	1358.6845	1358.6652	0.0193	120	131	0	EGALMLPHFNSK + Oxidation (M)
1400.7289	1399.7216	1399.7307	-0.0090	228	239	1	DNVIDQIEKQAK
1572.7758	1571.7685	1571.7426	0.0259	15	28	0	VLLEENAGGEQEER
1728.8792	1727.8719	1727.8437	0.0282	14	28	1	RVLLEENAGGEQEER
1730.9023	1729.8950	1729.9250	-0.0299	240	255	1	DLAFPGSGEQVEKLIK
1771.9128	1770.9055	1770.8747	0.0308	66	81	1	KGSEEEGDITNPINLR
1817.9792	1816.9719	1816.9570	0.0149	221	236	1	IFLAGDKDNVIDQIEK
2082.2161	2081.2088	2081.2030	0.0059	132	151	1	AMVIVVVNKGTGNLELVAVR
2098.2087	2097.2014	2097.1979	0.0036	132	151	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 896.4271, 906.4893, 959.4706, 975.4730, 1005.5253, 1019.4594, 1046.6005, 1061.5924, 1080.5361, 1111.5687, 1115.5376, 1141.5533, 1145.0728, 1145.5825, 1167.5784, 1184.6090, 1258.6431, 1287.6183, 1297.6653, 1320.6073, 1376.6992, 1379.7988, 1399.7468, 1424.7450, 1427.7507, 1440.7399, 1496.7666, 1512.7646, 1560.7281, 1568.7423, 1586.7965, 1591.8119, 1623.8060, 1685.8398, 1691.0596, 1714.8901, 1738.8728, 1830.8895, 1894.9624, 1899.9254, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2273.1538, 2282.8325, 2311.1272,

2508.3032, 2515.3044, 2530.2915, 2619.2798, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

10. gi|230338 **Mass:** 23975 **Score:** 25 **Expect:** 2.5 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
906.4893	905.4820	905.4970	-0.0150	201	208	0	NKPGVYTK
1046.6005	1045.5932	1045.5880	0.0053	90	99	1	LKSAASLNSR
2273.1538	2272.1465	2272.1521	-0.0056	70	89	0	SIVHPSYNSNTLNNDIMLIK
2530.2915	2529.2842	2529.3260	-0.0418	70	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 896.4271, 959.4706, 975.4730, 1005.5253, 1019.4594, 1061.5924, 1080.5361, 1111.5687, 1115.5376, 1141.5533, 1145.0728, 1145.5825, 1167.5784, 1184.6090, 1258.6431, 1287.6183, 1297.6653, 1320.6073, 1359.6918, 1376.6992, 1379.7988, 1399.7468, 1400.7289, 1424.7450, 1427.7507, 1440.7399, 1496.7666, 1512.7646, 1560.7281, 1568.7423, 1572.7758, 1586.7965, 1591.8119, 1623.8060, 1685.8398, 1691.0596, 1714.8901, 1728.8792, 1730.9023, 1738.8728, 1771.9128, 1817.9792, 1830.8895, 1894.9624, 1899.9254, 2082.2161, 2098.2087, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2282.8325, 2311.1272, 2508.3032, 2515.3044, 2619.2798, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 74

Protein View

Match to: **gi|46560478** Score: **179** Expect: **1.1e-015**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **74**
Number of mass values matched: **25**
Sequence Coverage: **37%**

Matched peptides shown in **Bold Red**

```
    1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
   51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
  101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
  151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
  201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
  251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
  301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
  351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
  401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
  451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
  501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
  551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
118 - 124	1019.4594	1018.4521	1018.4468	0.0053	1	EREEDWR	
120 - 127	1115.5376	1114.5303	1114.5155	0.0148	1	EEDWRQPR	
128 - 139	1591.8119	1590.8046	1590.7763	0.0283	1	EDWRRPSHQQPR	
132 - 139	1005.5253	1004.5180	1004.5264	-0.0084	0	RPSHQQPR	
166 - 174	1141.5533	1140.5460	1140.5352	0.0108	0	NNPFYFPSR	
166 - 175	1297.6653	1296.6580	1296.6363	0.0217	1	NNPFYFPSRR	
189 - 196	1061.5924	1060.5851	1060.5777	0.0074	1	VLQRFDQR	
197 - 207	1399.7468	1398.7395	1398.7116	0.0279	1	SKQFQNLQNHR	
199 - 207	1184.6090	1183.6017	1183.5846	0.0171	0	QFQNLQNHR	
223 - 247	2619.2798	2618.2725	2618.3160	-0.0435	0	HADADNILVIQQGQATVTVANGNNR	
272 - 278	896.4271	895.4198	895.4260	-0.0062	0	HDNQNLR	
302 - 312	1287.6183	1286.6110	1286.5891	0.0219	0	DQSSYLQGFSR	
313 - 327	1738.8728	1737.8655	1737.8321	0.0334	0	NTLEAAFNAEFNEIR	
313 - 328	1894.9624	1893.9551	1893.9332	0.0219	1	NTLEAAFNAEFNEIRR	
328 - 342	1728.8792	1727.8719	1727.8437	0.0282	1	RVLLEENAGGEQEER	
329 - 342	1572.7758	1571.7685	1571.7426	0.0259	0	VLLEENAGGEQEER	
379 - 393	1714.8901	1713.8828	1713.8533	0.0296	1	KGSEEEDITNPINLR	
380 - 393	1586.7965	1585.7892	1585.7583	0.0309	0	GSEEEDITNPINLR	
394 - 405	1320.6073	1319.6000	1319.5741	0.0259	0	DGEPDLSNNFGR	
432 - 443	1359.6918	1358.6845	1358.6652	0.0193	0	EGALMLPHFNSK	Oxidation (M)
444 - 463	2082.2161	2081.2088	2081.2030	0.0059	1	AMVIVVVNKGTGNLELVAVR	
444 - 463	2098.2087	2097.2014	2097.1979	0.0036	1	AMVIVVVNKGTGNLELVAVR	Oxidation (M)

536 - 551	**1817.9792**	**1816.9719**	**1816.9570**	**0.0149**	**1**	**IFLAGDKDNVIDQIEK**
543 - 554	**1400.7289**	**1399.7216**	**1399.7307**	**-0.0090**	**1**	**DNVIDQIEKQAK**
555 - 570	**1730.9023**	**1729.8950**	**1729.9250**	**-0.0299**	**1**	**DLAFPGSGEQVEKLIK**

No match to: 805.3870, 808.3477, 812.3688, 816.4055, 855.4879, 861.0534, 877.0198, 906.4893, 959.4706, 975.4730, 1046.6005, 1080.5361, 1111.5687, 1145.0728, 1145.5825, 1167.5784, 1258.6431, 1376.6992, 1379.7988, 1424.7450, 1427.7507, 1440.7399, 1496.7666, 1512.7646, 1560.7281, 1568.7423, 1623.8060, 1685.8398, 1691.0596, 1771.9128, 1830.8895, 1899.9254, 2129.1318, 2185.0337, 2244.0498, 2258.1719, 2273.1538, 2282.8325, 2311.1272, 2508.3032, 2515.3044, 2530.2915, 2748.3296, 2974.1399, 3154.2988, 3212.2610, 3228.3057, 3301.4534, 3317.5032

Spot 12

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 09:57:10 GMT**
Top Score : **126 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	126	conarachin [Arachis hypogaea]
2.	gi|620025	70639	123	Ara h I
3.	gi|1168390	70639	123	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	119	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	119	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	119	Ara h I
7.	gi|46560476	48122	78	conarachin [Arachis hypogaea]
8.	gi|22135348	25768	41	trypsin inhibitor [Arachis hypogaea]
9.	gi|46560472	34169	35	conarachin [Arachis hypogaea]
10.	gi|46560474	33641	28	conarachin [Arachis hypogaea]

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 126 **Expect:** 2.2e-010 **Queries matched:** 20
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4160	895.4087	895.4260	-0.0173	272	278	0	HDNQNLR
1005.5273	1004.5200	1004.5264	-0.0064	132	139	0	RPSHQQPR
1061.5854	1060.5781	1060.5777	0.0004	189	196	1	VLQRFDQR
1141.5505	1140.5432	1140.5352	0.0080	166	174	0	NNPFYFPSR
1184.6040	1183.5967	1183.5846	0.0121	199	207	0	QFQNLQNHR
1258.6388	1257.6315	1257.6101	0.0214	249	259	0	SFNLDEGHALR
1287.6157	1286.6084	1286.5891	0.0193	302	312	0	DQSSYLQGFSR
1297.6606	1296.6533	1296.6363	0.0170	166	175	1	NNPFYFPSRR
1379.7853	1378.7780	1378.7608	0.0172	260	271	0	IPSGFISYILNR

1399.7443	1398.7370	1398.7116	0.0254	197 - 207	1	SKQFQNLQNHR
1572.7727	1571.7654	1571.7426	0.0228	329 - 342	0	VLLEENAGGEQEER
1586.7910	1585.7837	1585.7583	0.0254	380 - 393	0	GSEEEDITNPINLR
1591.8118	1590.8045	1590.7763	0.0282	128 - 139	1	EDWRRPSHQQPR
1691.0487	1690.0414	1690.0141	0.0274	208 - 222	0	IVQIEARPNTLVLPK
1714.8923	1713.8850	1713.8533	0.0318	379 - 393	1	KGSEEEDITNPINLR
1728.8778	1727.8705	1727.8437	0.0268	328 - 342	1	RVLLEENAGGEQEER
1738.8684	1737.8611	1737.8321	0.0290	313 - 327	0	NTLEAAFNAEFNEIR
1817.9805	1816.9732	1816.9570	0.0162	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9601	1893.9528	1893.9332	0.0196	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2256	2081.2183	2081.2030	0.0154	444 - 463	1	AMVIVVVNKGTGNLELVAVR

No match to: 805.3861, 808.3455, 809.3467, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 906.4804, 928.4681, 959.4717, 975.4710, 1020.4769, 1027.5079, 1046.5984, 1066.0745, 1080.5227, 1083.5629, 1167.5706, 1175.5624, 1269.7792, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1427.7483, 1496.7629, 1534.6993, 1541.8055, 1560.7286, 1568.7362, 1644.8359, 1685.8359, 1730.8953, 1771.9049, 1830.8779, 1899.9296, 2038.9731, 2051.0515, 2072.9661, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113, 2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

2. gi|620025 **Mass:** 70639 **Score:** 123 **Expect:** 4.4e-010 **Queries matched:** 20

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4160	895.4087	895.4260	-0.0173	272 - 278		0	HDNQNLR
1005.5273	1004.5200	1004.5264	-0.0064	132 - 139		0	RPSHQQPR
1061.5854	1060.5781	1060.5777	0.0004	189 - 196		1	VLQRFDQR
1141.5505	1140.5432	1140.5352	0.0080	166 - 174		0	NNPFYFPSR
1184.6040	1183.5967	1183.5846	0.0121	199 - 207		0	QFQNLQNHR
1258.6388	1257.6315	1257.6101	0.0214	249 - 259		0	SFNLDEGHALR
1287.6157	1286.6084	1286.5891	0.0193	302 - 312		0	DQSSYLQGFSR
1297.6606	1296.6533	1296.6363	0.0170	166 - 175		1	NNPFYFPSRR
1379.7853	1378.7780	1378.7608	0.0172	260 - 271		0	IPSGFISYILNR
1399.7443	1398.7370	1398.7116	0.0254	197 - 207		1	SKQFQNLQNHR
1572.7727	1571.7654	1571.7426	0.0228	329 - 342		0	VLLEENAGGEQEER
1586.7910	1585.7837	1585.7583	0.0254	380 - 393		0	GSEEEDITNPINLR
1591.8118	1590.8045	1590.7763	0.0282	128 - 139		1	EDWRRPSHQQPR
1691.0487	1690.0414	1690.0141	0.0274	208 - 222		0	IVQIEARPNTLVLPK
1714.8923	1713.8850	1713.8533	0.0318	379 - 393		1	KGSEEEDITNPINLR
1728.8778	1727.8705	1727.8437	0.0268	328 - 342		1	RVLLEENAGGEQEER
1738.8684	1737.8611	1737.8321	0.0290	313 - 327		0	NTLEAAFNAEFNEIR
1817.9805	1816.9732	1816.9570	0.0162	536 - 551		1	IFLAGDKDNVIDQIEK
1894.9601	1893.9528	1893.9332	0.0196	313 - 328		1	NTLEAAFNAEFNEIRR
2082.2256	2081.2183	2081.2030	0.0154	444 - 463		1	AMVIVVVNKGTGNLELVAVR

No match to: 805.3861, 808.3455, 809.3467, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 906.4804, 928.4681, 959.4717, 975.4710, 1020.4769, 1027.5079, 1046.5984, 1066.0745, 1080.5227, 1083.5629, 1167.5706, 1175.5624, 1269.7792, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1427.7483, 1496.7629, 1534.6993, 1541.8055, 1560.7286, 1568.7362, 1644.8359, 1685.8359, 1730.8953, 1771.9049, 1830.8779, 1899.9296, 2038.9731, 2051.0515, 2072.9661, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113, 2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

3. gi|1168390 **Mass:** 70639 **Score:** 123 **Expect:** 4.4e-010 **Queries matched:** 20

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4160	895.4087	895.4260	-0.0173	272	278	0	HDNQNLR
1005.5273	1004.5200	1004.5264	-0.0064	132	139	0	RPSHQQPR
1061.5854	1060.5781	1060.5777	0.0004	189	196	1	VLQRFDQR
1141.5505	1140.5432	1140.5352	0.0080	166	174	0	NNPFYFPSR
1184.6040	1183.5967	1183.5846	0.0121	199	207	0	QFQNLQNHR
1258.6388	1257.6315	1257.6101	0.0214	249	259	0	SFNLDEGHALR
1287.6157	1286.6084	1286.5891	0.0193	302	312	0	DQSSYLQGFSR
1297.6606	1296.6533	1296.6363	0.0170	166	175	1	NNPFYFPSRR
1379.7853	1378.7780	1378.7608	0.0172	260	271	0	IPSGFISYILNR
1399.7443	1398.7370	1398.7116	0.0254	197	207	1	SKQFQNLQNHR
1572.7727	1571.7654	1571.7426	0.0228	329	342	0	VLLEENAGGEQEER
1586.7910	1585.7837	1585.7583	0.0254	380	393	0	GSEEEDITNPINLR
1591.8118	1590.8045	1590.7763	0.0282	128	139	1	EDWRRPSHQQPR
1691.0487	1690.0414	1690.0141	0.0274	208	222	0	IVQIEARPNTLVLPK
1714.8923	1713.8850	1713.8533	0.0318	379	393	1	KGSEEEDITNPINLR
1728.8778	1727.8705	1727.8437	0.0268	328	342	1	RVLLEENAGGEQEER
1738.8684	1737.8611	1737.8321	0.0290	313	327	0	NTLEAAFNAEFNEIR
1817.9805	1816.9732	1816.9570	0.0162	536	551	1	IFLAGDKDNVIDQIEK
1894.9601	1893.9528	1893.9332	0.0196	313	328	1	NTLEAAFNAEFNEIRR
2082.2256	2081.2183	2081.2030	0.0154	444	463	1	AMVIVVVNKGTGNLELVAVR

No match to: 805.3861, 808.3455, 809.3467, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 906.4804, 928.4681, 959.4717, 975.4710, 1020.4769, 1027.5079, 1046.5984, 1066.0745, 1080.5227, 1083.5629, 1167.5706, 1175.5624, 1269.7792, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1427.7483, 1496.7629, 1534.6993, 1541.8055, 1560.7286, 1568.7362, 1644.8359, 1685.8359, 1730.8953, 1771.9049, 1830.8779, 1899.9296, 2038.9731, 2051.0515, 2072.9661, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113, 2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

4. gi|16612200 **Mass:** 71701 **Score:** 119 **Expect:** 1.1e-009 **Queries matched:** 20

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3467	808.3394	808.3537	-0.0143	71	76	0	CVYDPR
896.4160	895.4087	895.4260	-0.0173	278	284	0	HDNQNLR

1005.5273	1004.5200	1004.5264	-0.0064	138 - 145	0	RPSHQQPR
1061.5854	1060.5781	1060.5777	0.0004	195 - 202	1	VLQRFDQR
1141.5505	1140.5432	1140.5352	0.0080	172 - 180	0	NNPFYFPSR
1184.6040	1183.5967	1183.5846	0.0121	205 - 213	0	QFQNLQNHR
1258.6388	1257.6315	1257.6101	0.0214	255 - 265	0	SFNLDEGHALR
1287.6157	1286.6084	1286.5891	0.0193	308 - 318	0	DQSSYLQGFSR
1297.6606	1296.6533	1296.6363	0.0170	172 - 181	1	NNPFYFPSRR
1379.7853	1378.7780	1378.7608	0.0172	266 - 277	0	IPSGFISYILNR
1427.7483	1426.7410	1426.7177	0.0233	203 - 213	1	SRQFQNLQNHR
1568.7362	1567.7289	1567.7015	0.0275	153 - 166	0	EGEQEWGTPGSHVR
1572.7727	1571.7654	1571.7426	0.0228	335 - 348	0	VLLEENAGGEQEER
1591.8118	1590.8045	1590.7763	0.0282	134 - 145	1	EDWRRPSHQQPR
1728.8778	1727.8705	1727.8437	0.0268	334 - 348	1	RVLLEENAGGEQEER
1738.8684	1737.8611	1737.8321	0.0290	319 - 333	0	NTLEAAFNAEFNEIR
1771.9049	1770.8976	1770.8747	0.0229	386 - 401	1	KGSEEEGDITNPINLR
1817.9805	1816.9732	1816.9570	0.0162	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9601	1893.9528	1893.9332	0.0196	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2256	2081.2183	2081.2030	0.0154	452 - 471	1	AMVIVVVNKGTGNLELVAVR

No match to: 805.3861, 808.3455, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 906.4804, 928.4681, 959.4717, 975.4710, 1020.4769, 1027.5079, 1046.5984, 1066.0745, 1080.5227, 1083.5629, 1167.5706, 1175.5624, 1269.7792, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1399.7443, 1496.7629, 1534.6993, 1541.8055, 1560.7286, 1586.7910, 1644.8359, 1685.8359, 1691.0487, 1714.8923, 1730.8953, 1830.8779, 1899.9296, 2038.9731, 2051.0515, 2072.9661, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113, 2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

5. gi|1168391 **Mass:** 71701 **Score:** 119 **Expect:** 1.1e-009 **Queries matched:** 20

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3467	808.3394	808.3537	-0.0143	71	76	0	CVYDPR
896.4160	895.4087	895.4260	-0.0173	278	284	0	HDNQNLR
1005.5273	1004.5200	1004.5264	-0.0064	138	145	0	RPSHQQPR
1061.5854	1060.5781	1060.5777	0.0004	195	202	1	VLQRFDQR
1141.5505	1140.5432	1140.5352	0.0080	172	180	0	NNPFYFPSR
1184.6040	1183.5967	1183.5846	0.0121	205	213	0	QFQNLQNHR
1258.6388	1257.6315	1257.6101	0.0214	255	265	0	SFNLDEGHALR
1287.6157	1286.6084	1286.5891	0.0193	308	318	0	DQSSYLQGFSR
1297.6606	1296.6533	1296.6363	0.0170	172	181	1	NNPFYFPSRR
1379.7853	1378.7780	1378.7608	0.0172	266	277	0	IPSGFISYILNR
1427.7483	1426.7410	1426.7177	0.0233	203	213	1	SRQFQNLQNHR
1568.7362	1567.7289	1567.7015	0.0275	153	166	0	EGEQEWGTPGSHVR
1572.7727	1571.7654	1571.7426	0.0228	335	348	0	VLLEENAGGEQEER

1591.8118	1590.8045	1590.7763	0.0282	134 - 145	1	EDWRRPSHQQPR
1728.8778	1727.8705	1727.8437	0.0268	334 - 348	1	RVLLEENAGGEQEER
1738.8684	1737.8611	1737.8321	0.0290	319 - 333	0	NTLEAAFNAEFNEIR
1771.9049	1770.8976	1770.8747	0.0229	386 - 401	1	KGSEEEGDITNPINLR
1817.9805	1816.9732	1816.9570	0.0162	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9601	1893.9528	1893.9332	0.0196	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2256	2081.2183	2081.2030	0.0154	452 - 471	1	AMVIVVVNKGTGNLELVAVR

No match to: 805.3861, 808.3455, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 906.4804, 928.4681, 959.4717, 975.4710, 1020.4769, 1027.5079, 1046.5984, 1066.0745, 1080.5227, 1083.5629, 1167.5706, 1175.5624, 1269.7792, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1399.7443, 1496.7629, 1534.6993, 1541.8055, 1560.7286, 1586.7910, 1644.8359, 1685.8359, 1691.0487, 1714.8923, 1730.8953, 1830.8779, 1899.9296, 2038.9731, 2051.0515, 2072.9661, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113, 2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

6. gi|602436 **Mass:** 71701 **Score:** 119 **Expect:** 1.1e-009 **Queries matched:** 20

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3467	808.3394	808.3537	-0.0143	71 -	76	0	CVYDPR
896.4160	895.4087	895.4260	-0.0173	278 -	284	0	HDNQNLR
1005.5273	1004.5200	1004.5264	-0.0064	138 -	145	0	RPSHQQPR
1061.5854	1060.5781	1060.5777	0.0004	195 -	202	1	VLQRFDQR
1141.5505	1140.5432	1140.5352	0.0080	172 -	180	0	NNPFYFPSR
1184.6040	1183.5967	1183.5846	0.0121	205 -	213	0	QFQNLQNHR
1258.6388	1257.6315	1257.6101	0.0214	255 -	265	0	SFNLDEGHALR
1287.6157	1286.6084	1286.5891	0.0193	308 -	318	0	DQSSYLQGFSR
1297.6606	1296.6533	1296.6363	0.0170	172 -	181	1	NNPFYFPSRR
1379.7853	1378.7780	1378.7608	0.0172	266 -	277	0	IPSGFISYILNR
1427.7483	1426.7410	1426.7177	0.0233	203 -	213	1	SRQFQNLQNHR
1568.7362	1567.7289	1567.7015	0.0275	153 -	166	0	EGEQEWGTPGSHVR
1572.7727	1571.7654	1571.7426	0.0228	335 -	348	0	VLLEENAGGEQEER
1591.8118	1590.8045	1590.7763	0.0282	134 -	145	1	EDWRRPSHQQPR
1728.8778	1727.8705	1727.8437	0.0268	334 -	348	1	RVLLEENAGGEQEER
1738.8684	1737.8611	1737.8321	0.0290	319 -	333	0	NTLEAAFNAEFNEIR
1771.9049	1770.8976	1770.8747	0.0229	386 -	401	1	KGSEEEGDITNPINLR
1817.9805	1816.9732	1816.9570	0.0162	541 -	556	1	IFLAGDKDNVIDQIEK
1894.9601	1893.9528	1893.9332	0.0196	319 -	334	1	NTLEAAFNAEFNEIRR
2082.2256	2081.2183	2081.2030	0.0154	452 -	471	1	AMVIVVVNKGTGNLELVAVR

No match to: 805.3861, 808.3455, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 906.4804, 928.4681, 959.4717, 975.4710, 1020.4769, 1027.5079, 1046.5984, 1066.0745, 1080.5227, 1083.5629, 1167.5706, 1175.5624, 1269.7792, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1399.7443, 1496.7629, 1534.6993, 1541.8055, 1560.7286, 1586.7910, 1644.8359, 1685.8359, 1691.0487, 1714.8923, 1730.8953, 1830.8779, 1899.9296, 2038.9731, 2051.0515, 2072.9661, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113,

2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

7. gi|46560476 **Mass:** 48122 **Score:** 78 **Expect:** 1.3e-005 **Queries matched:** 12

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4160	895.4087	895.4260	-0.0173	81	87	0	HDNQNLR
1184.6040	1183.5967	1183.5846	0.0121	8	16	0	QFQNLQNHR
1258.6388	1257.6315	1257.6101	0.0214	58	68	0	SFNLDEGHALR
1287.6157	1286.6084	1286.5891	0.0193	111	121	0	DQSSYLQGFSR
1379.7853	1378.7780	1378.7608	0.0172	69	80	0	IPSGFISYILNR
1427.7483	1426.7410	1426.7177	0.0233	6	16	1	SRQFQNLQNHR
1572.7727	1571.7654	1571.7426	0.0228	138	151	0	VLLEENAGGEQEER
1728.8778	1727.8705	1727.8437	0.0268	137	151	1	RVLLEENAGGEQEER
1738.8684	1737.8611	1737.8321	0.0290	122	136	0	NTLEAAFNAEFNEIR
1817.9805	1816.9732	1816.9570	0.0162	343	358	1	IFLAGDKDNVIDQIEK
1894.9601	1893.9528	1893.9332	0.0196	122	137	1	NTLEAAFNAEFNEIRR
2082.2256	2081.2183	2081.2030	0.0154	254	273	1	AMVIVVVNKGTGNLELVAVR

No match to: 805.3861, 808.3455, 809.3467, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 906.4804, 928.4681, 959.4717, 975.4710, 1005.5273, 1020.4769, 1027.5079, 1046.5984, 1061.5854, 1066.0745, 1080.5227, 1083.5629, 1141.5505, 1167.5706, 1175.5624, 1269.7792, 1297.6606, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1399.7443, 1496.7629, 1534.6993, 1541.8055, 1560.7286, 1568.7362, 1586.7910, 1591.8118, 1644.8359, 1685.8359, 1691.0487, 1714.8923, 1730.8953, 1771.9049, 1830.8779, 1899.9296, 2038.9731, 2051.0515, 2072.9661, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113, 2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

8. gi|22135348 **Mass:** 25768 **Score:** 41 **Expect:** 0.078 **Queries matched:** 6

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5273	1004.5200	1004.5264	-0.0064	124	131	0	HQSQRPPR
1083.5629	1082.5556	1082.5581	-0.0024	39	47	0	LNAQRPDNR
1534.6993	1533.6920	1533.6630	0.0290	27	38	0	QQPEENACQFQR
1730.8953	1729.8880	1729.8648	0.0233	197	210	1	RFNLAGNHEQEFLR
2051.0515	2050.0442	2050.0384	0.0058	84	100	0	RPFYSNAPQEIFIQQGR
2072.9661	2071.9588	2071.9420	0.0169	132	148	1	RFQGQDQSQQQQDSHQK

No match to: 805.3861, 808.3455, 809.3467, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 896.4160, 906.4804, 928.4681, 959.4717, 975.4710, 1020.4769, 1027.5079, 1046.5984, 1061.5854, 1066.0745, 1080.5227, 1141.5505, 1167.5706, 1175.5624, 1184.6040, 1258.6388, 1269.7792, 1287.6157, 1297.6606, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1379.7853, 1399.7443, 1427.7483, 1496.7629, 1541.8055, 1560.7286, 1568.7362, 1572.7727, 1586.7910, 1591.8118, 1644.8359, 1685.8359, 1691.0487, 1714.8923, 1728.8778, 1738.8684, 1771.9049, 1817.9805, 1830.8779, 1894.9601, 1899.9296, 2038.9731, 2082.2256, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113, 2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

9. gi|46560472 **Mass:** 34169 **Score:** 35 **Expect:** 0.3 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1572.7727	1571.7654	1571.7426	0.0228	18	31	0	VLLEENAGGEQEER
1586.7910	1585.7837	1585.7583	0.0254	69	82	0	GSEEEDITNPINLR
1714.8923	1713.8850	1713.8533	0.0318	68	82	1	KGSEEEDITNPINLR
1728.8778	1727.8705	1727.8437	0.0268	17	31	1	RVLLEENAGGEQEER
1817.9805	1816.9732	1816.9570	0.0162	225	240	1	IFLAGDKDNVIDQIEK
2082.2256	2081.2183	2081.2030	0.0154	133	152	1	AMVIVVVNKGTGNLELVAVR

No match to: 805.3861, 808.3455, 809.3467, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 896.4160, 906.4804, 928.4681, 959.4717, 975.4710, 1005.5273, 1020.4769, 1027.5079, 1046.5984, 1061.5854, 1066.0745, 1080.5227, 1083.5629, 1141.5505, 1167.5706, 1175.5624, 1184.6040, 1258.6388, 1269.7792, 1287.6157, 1297.6606, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1379.7853, 1399.7443, 1427.7483, 1496.7629, 1534.6993, 1541.8055, 1560.7286, 1568.7362, 1591.8118, 1644.8359, 1685.8359, 1691.0487, 1730.8953, 1738.8684, 1771.9049, 1830.8779, 1894.9601, 1899.9296, 2038.9731, 2051.0515, 2072.9661, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113, 2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

10. gi|46560474 **Mass:** 33641 **Score:** 28 **Expect:** 1.4 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1572.7727	1571.7654	1571.7426	0.0228	15	28	0	VLLEENAGGEQEER
1728.8778	1727.8705	1727.8437	0.0268	14	28	1	RVLLEENAGGEQEER
1771.9049	1770.8976	1770.8747	0.0229	66	81	1	KGSEEEGDITNPINLR
1817.9805	1816.9732	1816.9570	0.0162	221	236	1	IFLAGDKDNVIDQIEK
2082.2256	2081.2183	2081.2030	0.0154	132	151	1	AMVIVVVNKGTGNLELVAVR

No match to: 805.3861, 808.3455, 809.3467, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 896.4160, 906.4804, 928.4681, 959.4717, 975.4710, 1005.5273, 1020.4769, 1027.5079, 1046.5984, 1061.5854, 1066.0745, 1080.5227, 1083.5629, 1141.5505, 1167.5706, 1175.5624, 1184.6040, 1258.6388, 1269.7792, 1287.6157, 1297.6606, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1379.7853, 1399.7443, 1427.7483, 1496.7629, 1534.6993, 1541.8055, 1560.7286, 1568.7362, 1586.7910, 1591.8118, 1644.8359, 1685.8359, 1691.0487, 1714.8923, 1730.8953, 1738.8684, 1830.8779, 1894.9601, 1899.9296, 2038.9731, 2051.0515, 2072.9661, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113, 2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1

Number of queries : 79

Protein View

Match to: **gi|46560478** Score: **126** Expect: **2.2e-010**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **79**
Number of mass values matched: **20**
Sequence Coverage: **30%**

Matched peptides shown in **Bold Red**

```
    1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
   51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
  101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
  151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
  201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
  251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
  301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
  351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
  401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
  451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
  501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
  551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
128 - 139	1591.8118	1590.8045	1590.7763	0.0282	1	EDWRRPSHQQPR
132 - 139	1005.5273	1004.5200	1004.5264	-0.0064	0	RPSHQQPR
166 - 174	1141.5505	1140.5432	1140.5352	0.0080	0	NNPFYFPSR
166 - 175	1297.6606	1296.6533	1296.6363	0.0170	1	NNPFYFPSRR
189 - 196	1061.5854	1060.5781	1060.5777	0.0004	1	VLQRFDQR
197 - 207	1399.7443	1398.7370	1398.7116	0.0254	1	SKQFQNLQNHR

199 - 207	1184.6040	1183.5967	1183.5846	0.0121	0	QFQNLQNHR
208 - 222	1691.0487	1690.0414	1690.0141	0.0274	0	IVQIEARPNTLVLPK
249 - 259	1258.6388	1257.6315	1257.6101	0.0214	0	SFNLDEGHALR
260 - 271	1379.7853	1378.7780	1378.7608	0.0172	0	IPSGFISYILNR
272 - 278	896.4160	895.4087	895.4260	-0.0173	0	HDNQNLR
302 - 312	1287.6157	1286.6084	1286.5891	0.0193	0	DQSSYLQGFSR
313 - 327	1738.8684	1737.8611	1737.8321	0.0290	0	NTLEAAFNAEFNEIR
313 - 328	1894.9601	1893.9528	1893.9332	0.0196	1	NTLEAAFNAEFNEIRR
328 - 342	1728.8778	1727.8705	1727.8437	0.0268	1	RVLLEENAGGEQEER
329 - 342	1572.7727	1571.7654	1571.7426	0.0228	0	VLLEENAGGEQEER
379 - 393	1714.8923	1713.8850	1713.8533	0.0318	1	KGSEEEDITNPINLR
380 - 393	1586.7910	1585.7837	1585.7583	0.0254	0	GSEEEDITNPINLR
444 - 463	2082.2256	2081.2183	2081.2030	0.0154	1	AMVIVVVNKGTGNLELVAVR
536 - 551	1817.9805	1816.9732	1816.9570	0.0162	1	IFLAGDKDNVIDQIEK

No match to: 805.3861, 808.3455, 809.3467, 812.3750, 816.3994, 827.3696, 828.4224, 855.0284, 855.4889, 861.0511, 877.0193, 906.4804, 928.4681, 959.4717, 975.4710, 1020.4769, 1027.5079, 1046.5984, 1066.0745, 1080.5227, 1083.5629, 1167.5706, 1175.5624, 1269.7792, 1306.6750, 1319.6482, 1320.6088, 1360.6942, 1376.6978, 1377.7217, 1427.7483, 1496.7629, 1534.6993, 1541.8055, 1560.7286, 1568.7362, 1644.8359, 1685.8359, 1730.8953, 1771.9049, 1830.8779, 1899.9296, 2038.9731, 2051.0515, 2072.9661, 2185.0361, 2202.0134, 2273.1528, 2295.1384, 2311.1306, 2327.1260, 2333.1213, 2507.2957, 2515.3113, 2530.2954, 2749.3364, 2974.1563, 3154.3176, 3212.3486

Spot 13

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:30:52 GMT**
Top Score : **289 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	289	conarachin [Arachis hypogaea]
2.	gi|620025	70639	284	Ara h I
3.	gi|1168390	70639	284	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	233	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	233	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	233	Ara h I
7.	gi|46560476	48122	144	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	73	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	50	conarachin [Arachis hypogaea]
10.	gi|62177652	10056	19	resistance protein PRG [Arachis hypogaea]

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 289 **Expect:** 1.1e-026 **Queries matched:** 29
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
812.4169	811.4096	811.3976	0.0120	109	115	0	WGPAEPR
816.4437	815.4364	815.4249	0.0115	464	469	1	KEQQQR
855.5226	854.5153	854.5086	0.0067	140	146	1	KIRPEGR
896.4459	895.4386	895.4260	0.0126	272	278	0	HDNQNLR
1005.5432	1004.5359	1004.5264	0.0095	132	139	0	RPSHQQPR
1019.4650	1018.4577	1018.4468	0.0109	118	124	1	EREEDWR
1128.6471	1127.6398	1127.6298	0.0100	453	463	0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	166	174	0	NNPFYFPSR

1184.6008	1183.5935	1183.5846	0.0089	199 - 207	0	QFQNLQNHR
1258.6270	1257.6197	1257.6101	0.0096	249 - 259	0	SFNLDEGHALR
1287.6040	1286.5967	1286.5891	0.0076	302 - 312	0	DQSSYLQGFSR
1297.6521	1296.6448	1296.6363	0.0085	166 - 175	1	NNPFYFPSRR
1320.5890	1319.5817	1319.5741	0.0076	394 - 405	0	DGEPDLSNNFGR
1343.6791	1342.6718	1342.6703	0.0015	432 - 443	0	EGALMLPHFNSK
1379.7761	1378.7688	1378.7608	0.0080	260 - 271	0	IPSGFISYILNR
1386.7208	1385.7135	1385.7051	0.0084	248 - 259	1	KSFNLDEGHALR
1399.7262	1398.7189	1398.7116	0.0073	197 - 207	1	SKQFQNLQNHR
1560.6971	1559.6898	1559.6851	0.0047	147 - 160	0	EGEQEWGTPGSEVR
1572.7520	1571.7447	1571.7426	0.0021	329 - 342	0	VLLEENAGGEQEER
1586.7656	1585.7583	1585.7583	0.0000	380 - 393	0	GSEEEDITNPINLR
1691.0262	1690.0189	1690.0141	0.0049	208 - 222	0	IVQIEARPNTLVLPK
1714.8612	1713.8539	1713.8533	0.0007	379 - 393	1	KGSEEEDITNPINLR
1738.8401	1737.8328	1737.8321	0.0007	313 - 327	0	NTLEAAFNAEFNEIR
1817.9658	1816.9585	1816.9570	0.0015	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9305	1893.9232	1893.9332	-0.0100	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0332	2226.0259	2226.0415	-0.0156	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0415	2242.0342	2242.0364	-0.0022	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8416	2280.8343	2280.8414	-0.0070	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.2966	2618.2893	2618.3160	-0.0267	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3970, 756.3916, 772.3854, 808.3914, 828.4969, 959.4957, 1111.5713, 1167.5775, 1568.7104, 1643.7893, 1771.8806, 2185.0183, 2193.0002, 2273.1597, 2295.1399, 2332.0640, 2612.1736, 2620.2971, 2748.3928, 3153.4465, 3211.4810

2. gi|620025 **Mass:** 70639 **Score:** 284 **Expect:** 3.5e-026 **Queries matched:** 29

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
812.4169	811.4096	811.3976	0.0120	109 - 115		0	WGPAEPR
816.4437	815.4364	815.4249	0.0115	464 - 469		1	KEQQQR
855.5226	854.5153	854.5086	0.0067	140 - 146		1	KIRPEGR
896.4459	895.4386	895.4260	0.0126	272 - 278		0	HDNQNLR
1005.5432	1004.5359	1004.5264	0.0095	132 - 139		0	RPSHQQPR
1019.4650	1018.4577	1018.4468	0.0109	118 - 124		1	EREEDWR
1128.6471	1127.6398	1127.6298	0.0100	453 - 463		0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	166 - 174		0	NNPFYFPSR
1184.6008	1183.5935	1183.5846	0.0089	199 - 207		0	QFQNLQNHR
1258.6270	1257.6197	1257.6101	0.0096	249 - 259		0	SFNLDEGHALR
1287.6040	1286.5967	1286.5891	0.0076	302 - 312		0	DQSSYLQGFSR
1297.6521	1296.6448	1296.6363	0.0085	166 - 175		1	NNPFYFPSRR

1320.5890	1319.5817	1319.5741	0.0076	394 - 405	0	DGEPDLSNNFGR
1343.6791	1342.6718	1342.6703	0.0015	432 - 443	0	EGALMLPHFNSK
1379.7761	1378.7688	1378.7608	0.0080	260 - 271	0	IPSGFISYILNR
1386.7208	1385.7135	1385.7051	0.0084	248 - 259	1	KSFNLDEGHALR
1399.7262	1398.7189	1398.7116	0.0073	197 - 207	1	SKQFQNLQNHR
1560.6971	1559.6898	1559.6851	0.0047	147 - 160	0	EGEQEWGTPGSEVR
1572.7520	1571.7447	1571.7426	0.0021	329 - 342	0	VLLEENAGGEQEER
1586.7656	1585.7583	1585.7583	0.0000	380 - 393	0	GSEEEDITNPINLR
1691.0262	1690.0189	1690.0141	0.0049	208 - 222	0	IVQIEARPNTLVLPK
1714.8612	1713.8539	1713.8533	0.0007	379 - 393	1	KGSEEEDITNPINLR
1738.8401	1737.8328	1737.8321	0.0007	313 - 327	0	NTLEAAFNAEFNEIR
1817.9658	1816.9585	1816.9570	0.0015	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9305	1893.9232	1893.9332	-0.0100	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0332	2226.0259	2226.0415	-0.0156	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0415	2242.0342	2242.0364	-0.0022	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8416	2280.8343	2280.8414	-0.0070	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.2966	2618.2893	2618.3160	-0.0267	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3970, 756.3916, 772.3854, 808.3914, 828.4969, 959.4957, 1111.5713, 1167.5775, 1568.7104, 1643.7893, 1771.8806, 2185.0183, 2193.0002, 2273.1597, 2295.1399, 2332.0640, 2612.1736, 2620.2971, 2748.3928, 3153.4465, 3211.4810

3. gi|1168390 **Mass:** 70639 **Score:** 284 **Expect:** 3.5e-026 **Queries matched:** 29

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
812.4169	811.4096	811.3976	0.0120	109	115	0	WGPAEPR
816.4437	815.4364	815.4249	0.0115	464	469	1	KEQQQR
855.5226	854.5153	854.5086	0.0067	140	146	1	KIRPEGR
896.4459	895.4386	895.4260	0.0126	272	278	0	HDNQNLR
1005.5432	1004.5359	1004.5264	0.0095	132	139	0	RPSHQQPR
1019.4650	1018.4577	1018.4468	0.0109	118	124	1	EREEDWR
1128.6471	1127.6398	1127.6298	0.0100	453	463	0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	166	174	0	NNPFYFPSR
1184.6008	1183.5935	1183.5846	0.0089	199	207	0	QFQNLQNHR
1258.6270	1257.6197	1257.6101	0.0096	249	259	0	SFNLDEGHALR
1287.6040	1286.5967	1286.5891	0.0076	302	312	0	DQSSYLQGFSR
1297.6521	1296.6448	1296.6363	0.0085	166	175	1	NNPFYFPSRR
1320.5890	1319.5817	1319.5741	0.0076	394	405	0	DGEPDLSNNFGR
1343.6791	1342.6718	1342.6703	0.0015	432	443	0	EGALMLPHFNSK
1379.7761	1378.7688	1378.7608	0.0080	260	271	0	IPSGFISYILNR
1386.7208	1385.7135	1385.7051	0.0084	248	259	1	KSFNLDEGHALR

1399.7262	1398.7189	1398.7116	0.0073	197 - 207	1	SKQFQNLQNHR
1560.6971	1559.6898	1559.6851	0.0047	147 - 160	0	EGEQEWGTPGSEVR
1572.7520	1571.7447	1571.7426	0.0021	329 - 342	0	VLLEENAGGEQEER
1586.7656	1585.7583	1585.7583	0.0000	380 - 393	0	GSEEEDITNPINLR
1691.0262	1690.0189	1690.0141	0.0049	208 - 222	0	IVQIEARPNTLVLPK
1714.8612	1713.8539	1713.8533	0.0007	379 - 393	1	KGSEEEDITNPINLR
1738.8401	1737.8328	1737.8321	0.0007	313 - 327	0	NTLEAAFNAEFNEIR
1817.9658	1816.9585	1816.9570	0.0015	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9305	1893.9232	1893.9332	-0.0100	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0332	2226.0259	2226.0415	-0.0156	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0415	2242.0342	2242.0364	-0.0022	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2281.8416	2280.8343	2280.8414	-0.0070	473 - 490	0	EQEWEEEEEDEEEEGSNR
2619.2966	2618.2893	2618.3160	-0.0267	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3970, 756.3916, 772.3854, 808.3914, 828.4969, 959.4957, 1111.5713, 1167.5775, 1568.7104, 1643.7893, 1771.8806, 2185.0183, 2193.0002, 2273.1597, 2295.1399, 2332.0640, 2612.1736, 2620.2971, 2748.3928, 3153.4465, 3211.4810

4. gi|16612200 **Mass:** 71701 **Score:** 233 **Expect:** 4.4e-021 **Queries matched:** 26

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3970	739.3897	739.3765	0.0132	115 - 121		0	WGPAGPR
808.3914	807.3841	807.3987	-0.0146	199 - 204		1	FDQRSR
816.4437	815.4364	815.4249	0.0115	472 - 477		1	KEQQQR
855.5226	854.5153	854.5086	0.0067	146 - 152		1	KIRPEGR
896.4459	895.4386	895.4260	0.0126	278 - 284		0	HDNQNLR
1005.5432	1004.5359	1004.5264	0.0095	138 - 145		0	RPSHQQPR
1019.4650	1018.4577	1018.4468	0.0109	124 - 130		1	EREEDWR
1128.6471	1127.6398	1127.6298	0.0100	461 - 471		0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	172 - 180		0	NNPFYFPSR
1184.6008	1183.5935	1183.5846	0.0089	205 - 213		0	QFQNLQNHR
1258.6270	1257.6197	1257.6101	0.0096	255 - 265		0	SFNLDEGHALR
1287.6040	1286.5967	1286.5891	0.0076	308 - 318		0	DQSSYLQGFSR
1297.6521	1296.6448	1296.6363	0.0085	172 - 181		1	NNPFYFPSRR
1343.6791	1342.6718	1342.6703	0.0015	440 - 451		0	EGALMLPHFNSK
1379.7761	1378.7688	1378.7608	0.0080	266 - 277		0	IPSGFISYILNR
1386.7208	1385.7135	1385.7051	0.0084	254 - 265		1	KSFNLDEGHALR
1568.7104	1567.7031	1567.7015	0.0017	153 - 166		0	EGEQEWGTPGSHVR
1572.7520	1571.7447	1571.7426	0.0021	335 - 348		0	VLLEENAGGEQEER
1643.7893	1642.7820	1642.7798	0.0023	387 - 401		0	GSEEEGDITNPINLR
1738.8401	1737.8328	1737.8321	0.0007	319 - 333		0	NTLEAAFNAEFNEIR

1771.8806	1770.8733	1770.8747	-0.0014	386 - 401	1	KGSEEEGDITNPINLR
1817.9658	1816.9585	1816.9570	0.0015	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9305	1893.9232	1893.9332	-0.0100	319 - 334	1	NTLEAAFNAEFNEIRR
2227.0332	2226.0259	2226.0415	-0.0156	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0415	2242.0342	2242.0364	-0.0022	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2966	2618.2893	2618.3160	-0.0267	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 756.3916, 772.3854, 812.4169, 828.4969, 959.4957, 1111.5713, 1167.5775, 1320.5890, 1399.7262, 1560.6971, 1586.7656, 1691.0262, 1714.8612, 2185.0183, 2193.0002, 2273.1597, 2281.8416, 2295.1399, 2332.0640, 2612.1736, 2620.2971, 2748.3928, 3153.4465, 3211.4810

5. gi|1168391 **Mass:** 71701 **Score:** 233 **Expect:** 4.4e-021 **Queries matched:** 26

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3970	739.3897	739.3765	0.0132	115 - 121		0	WGPAGPR
808.3914	807.3841	807.3987	-0.0146	199 - 204		1	FDQRSR
816.4437	815.4364	815.4249	0.0115	472 - 477		1	KEQQQR
855.5226	854.5153	854.5086	0.0067	146 - 152		1	KIRPEGR
896.4459	895.4386	895.4260	0.0126	278 - 284		0	HDNQNLR
1005.5432	1004.5359	1004.5264	0.0095	138 - 145		0	RPSHQQPR
1019.4650	1018.4577	1018.4468	0.0109	124 - 130		1	EREEDWR
1128.6471	1127.6398	1127.6298	0.0100	461 - 471		0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	172 - 180		0	NNPFYFPSR
1184.6008	1183.5935	1183.5846	0.0089	205 - 213		0	QFQNLQNHR
1258.6270	1257.6197	1257.6101	0.0096	255 - 265		0	SFNLDEGHALR
1287.6040	1286.5967	1286.5891	0.0076	308 - 318		0	DQSSYLQGFSR
1297.6521	1296.6448	1296.6363	0.0085	172 - 181		1	NNPFYFPSRR
1343.6791	1342.6718	1342.6703	0.0015	440 - 451		0	EGALMLPHFNSK
1379.7761	1378.7688	1378.7608	0.0080	266 - 277		0	IPSGFISYILNR
1386.7208	1385.7135	1385.7051	0.0084	254 - 265		1	KSFNLDEGHALR
1568.7104	1567.7031	1567.7015	0.0017	153 - 166		0	EGEQEWGTPGSHVR
1572.7520	1571.7447	1571.7426	0.0021	335 - 348		0	VLLEENAGGEQEER
1643.7893	1642.7820	1642.7798	0.0023	387 - 401		0	GSEEEGDITNPINLR
1738.8401	1737.8328	1737.8321	0.0007	319 - 333		0	NTLEAAFNAEFNEIR
1771.8806	1770.8733	1770.8747	-0.0014	386 - 401		1	KGSEEEGDITNPINLR
1817.9658	1816.9585	1816.9570	0.0015	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9305	1893.9232	1893.9332	-0.0100	319 - 334		1	NTLEAAFNAEFNEIRR
2227.0332	2226.0259	2226.0415	-0.0156	288 - 307		0	ISMPVNTPGQFEDFFPASSR
2243.0415	2242.0342	2242.0364	-0.0022	288 - 307		0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2966	2618.2893	2618.3160	-0.0267	229 - 253		0	HADADNILVIQQGQATVTVANGNNR

No match to: 756.3916, 772.3854, 812.4169, 828.4969, 959.4957, 1111.5713, 1167.5775, 1320.5890, 1399.7262, 1560.6971, 1586.7656, 1691.0262, 1714.8612, 2185.0183, 2193.0002, 2273.1597, 2281.8416, 2295.1399, 2332.0640,

2612.1736, 2620.2971, 2748.3928, 3153.4465, 3211.4810

6. gi|602436 **Mass:** 71701 **Score:** 233 **Expect:** 4.4e-021 **Queries matched:** 26

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3970	739.3897	739.3765	0.0132	115 -	121	0	WGPAGPR
808.3914	807.3841	807.3987	-0.0146	199 -	204	1	FDQRSR
816.4437	815.4364	815.4249	0.0115	472 -	477	1	KEQQQR
855.5226	854.5153	854.5086	0.0067	146 -	152	1	KIRPEGR
896.4459	895.4386	895.4260	0.0126	278 -	284	0	HDNQNLR
1005.5432	1004.5359	1004.5264	0.0095	138 -	145	0	RPSHQQPR
1019.4650	1018.4577	1018.4468	0.0109	124 -	130	1	EREEDWR
1128.6471	1127.6398	1127.6298	0.0100	461 -	471	0	GTGNLELVAVR
1141.5530	1140.5457	1140.5352	0.0105	172 -	180	0	NNPFYFPSR
1184.6008	1183.5935	1183.5846	0.0089	205 -	213	0	QFQNLQNHR
1258.6270	1257.6197	1257.6101	0.0096	255 -	265	0	SFNLDEGHALR
1287.6040	1286.5967	1286.5891	0.0076	308 -	318	0	DQSSYLQGFSR
1297.6521	1296.6448	1296.6363	0.0085	172 -	181	1	NNPFYFPSRR
1343.6791	1342.6718	1342.6703	0.0015	440 -	451	0	EGALMLPHFNSK
1379.7761	1378.7688	1378.7608	0.0080	266 -	277	0	IPSGFISYILNR
1386.7208	1385.7135	1385.7051	0.0084	254 -	265	1	KSFNLDEGHALR
1568.7104	1567.7031	1567.7015	0.0017	153 -	166	0	EGEQEWGTPGSHVR
1572.7520	1571.7447	1571.7426	0.0021	335 -	348	0	VLLEENAGGEQEER
1643.7893	1642.7820	1642.7798	0.0023	387 -	401	0	GSEEEGDITNPINLR
1738.8401	1737.8328	1737.8321	0.0007	319 -	333	0	NTLEAAFNAEFNEIR
1771.8806	1770.8733	1770.8747	-0.0014	386 -	401	1	KGSEEEGDITNPINLR
1817.9658	1816.9585	1816.9570	0.0015	541 -	556	1	IFLAGDKDNVIDQIEK
1894.9305	1893.9232	1893.9332	-0.0100	319 -	334	1	NTLEAAFNAEFNEIRR
2227.0332	2226.0259	2226.0415	-0.0156	288 -	307	0	ISMPVNTPGQFEDFFPASSR
2243.0415	2242.0342	2242.0364	-0.0022	288 -	307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2966	2618.2893	2618.3160	-0.0267	229 -	253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 756.3916, 772.3854, 812.4169, 828.4969, 959.4957, 1111.5713, 1167.5775, 1320.5890, 1399.7262, 1560.6971, 1586.7656, 1691.0262, 1714.8612, 2185.0183, 2193.0002, 2273.1597, 2281.8416, 2295.1399, 2332.0640, 2612.1736, 2620.2971, 2748.3928, 3153.4465, 3211.4810

7. gi|46560476 **Mass:** 48122 **Score:** 144 **Expect:** 3.5e-012 **Queries matched:** 16

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4437	815.4364	815.4249	0.0115	274 -	279	1	KEQQQR
896.4459	895.4386	895.4260	0.0126	81 -	87	0	HDNQNLR
1128.6471	1127.6398	1127.6298	0.0100	263 -	273	0	GTGNLELVAVR

1184.6008	1183.5935	1183.5846	0.0089	8 - 16	0	QFQNLQNHR
1258.6270	1257.6197	1257.6101	0.0096	58 - 68	0	SFNLDEGHALR
1287.6040	1286.5967	1286.5891	0.0076	111 - 121	0	DQSSYLQGFSR
1343.6791	1342.6718	1342.6703	0.0015	242 - 253	0	EGALMLPHFNSK
1379.7761	1378.7688	1378.7608	0.0080	69 - 80	0	IPSGFISYILNR
1386.7208	1385.7135	1385.7051	0.0084	57 - 68	1	KSFNLDEGHALR
1572.7520	1571.7447	1571.7426	0.0021	138 - 151	0	VLLEENAGGEQEER
1738.8401	1737.8328	1737.8321	0.0007	122 - 136	0	NTLEAAFNAEFNEIR
1817.9658	1816.9585	1816.9570	0.0015	343 - 358	1	IFLAGDKDNVIDQIEK
1894.9305	1893.9232	1893.9332	-0.0100	122 - 137	1	NTLEAAFNAEFNEIRR
2227.0332	2226.0259	2226.0415	-0.0156	91 - 110	0	ISMPVNTPGQFEDFFPASSR
2243.0415	2242.0342	2242.0364	-0.0022	91 - 110	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2966	2618.2893	2618.3160	-0.0267	32 - 56	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3970, 756.3916, 772.3854, 808.3914, 812.4169, 828.4969, 855.5226, 959.4957, 1005.5432, 1019.4650, 1111.5713, 1141.5530, 1167.5775, 1297.6521, 1320.5890, 1399.7262, 1560.6971, 1568.7104, 1586.7656, 1643.7893, 1691.0262, 1714.8612, 1771.8806, 2185.0183, 2193.0002, 2273.1597, 2281.8416, 2295.1399, 2332.0640, 2612.1736, 2620.2971, 2748.3928, 3153.4465, 3211.4810

8. gi|46560472 **Mass:** 34169 **Score:** 73 **Expect:** 4.9e-005 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4437	815.4364	815.4249	0.0115	153 - 158		1	KEQQQR
1128.6471	1127.6398	1127.6298	0.0100	142 - 152		0	GTGNLELVAVR
1320.5890	1319.5817	1319.5741	0.0076	83 - 94		0	DGEPDLSNNFGR
1343.6791	1342.6718	1342.6703	0.0015	121 - 132		0	EGALMLPHFNSK
1572.7520	1571.7447	1571.7426	0.0021	18 - 31		0	VLLEENAGGEQEER
1586.7656	1585.7583	1585.7583	0.0000	69 - 82		0	GSEEEDITNPINLR
1714.8612	1713.8539	1713.8533	0.0007	68 - 82		1	KGSEEEDITNPINLR
1817.9658	1816.9585	1816.9570	0.0015	225 - 240		1	IFLAGDKDNVIDQIEK
2281.8416	2280.8343	2280.8414	-0.0070	162 - 179		0	EQEWEEEEEDEEEEGSNR

No match to: 740.3970, 756.3916, 772.3854, 808.3914, 812.4169, 828.4969, 855.5226, 896.4459, 959.4957, 1005.5432, 1019.4650, 1111.5713, 1141.5530, 1167.5775, 1184.6008, 1258.6270, 1287.6040, 1297.6521, 1379.7761, 1386.7208, 1399.7262, 1560.6971, 1568.7104, 1643.7893, 1691.0262, 1738.8401, 1771.8806, 1894.9305, 2185.0183, 2193.0002, 2227.0332, 2243.0415, 2273.1597, 2295.1399, 2332.0640, 2612.1736, 2619.2966, 2620.2971, 2748.3928, 3153.4465, 3211.4810

9. gi|46560474 **Mass:** 33641 **Score:** 50 **Expect:** 0.0094 **Queries matched:** 7

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4437	815.4364	815.4249	0.0115	152 - 157		1	KEQQQR
1128.6471	1127.6398	1127.6298	0.0100	141 - 151		0	GTGNLELVAVR

1343.6791	1342.6718	1342.6703	0.0015	120 - 131	0	EGALMLPHFNSK
1572.7520	1571.7447	1571.7426	0.0021	15 - 28	0	VLLEENAGGEQEER
1643.7893	1642.7820	1642.7798	0.0023	67 - 81	0	GSEEEGDITNPINLR
1771.8806	1770.8733	1770.8747	-0.0014	66 - 81	1	KGSEEEGDITNPINLR
1817.9658	1816.9585	1816.9570	0.0015	221 - 236	1	IFLAGDKDNVIDQIEK

No match to: 740.3970, 756.3916, 772.3854, 808.3914, 812.4169, 828.4969, 855.5226, 896.4459, 959.4957, 1005.5432, 1019.4650, 1111.5713, 1141.5530, 1167.5775, 1184.6008, 1258.6270, 1287.6040, 1297.6521, 1320.5890, 1379.7761, 1386.7208, 1399.7262, 1560.6971, 1568.7104, 1586.7656, 1691.0262, 1714.8612, 1738.8401, 1894.9305, 2185.0183, 2193.0002, 2227.0332, 2243.0415, 2273.1597, 2281.8416, 2295.1399, 2332.0640, 2612.1736, 2619.2966, 2620.2971, 2748.3928, 3153.4465, 3211.4810

10. gi|62177652 **Mass:** 10056 **Score:** 19 **Expect:** 11 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1379.7761	1378.7688	1378.7496	0.0193	77 -	89	1	EVVKYSGGLPFAL
1894.9305	1893.9232	1893.9009	0.0224	7 -	23	0	QLEYLGGEQAWFGPGSR

No match to: 740.3970, 756.3916, 772.3854, 808.3914, 812.4169, 816.4437, 828.4969, 855.5226, 896.4459, 959.4957, 1005.5432, 1019.4650, 1111.5713, 1128.6471, 1141.5530, 1167.5775, 1184.6008, 1258.6270, 1287.6040, 1297.6521, 1320.5890, 1343.6791, 1386.7208, 1399.7262, 1560.6971, 1568.7104, 1572.7520, 1586.7656, 1643.7893, 1691.0262, 1714.8612, 1738.8401, 1771.8806, 1817.9658, 2185.0183, 2193.0002, 2227.0332, 2243.0415, 2273.1597, 2281.8416, 2295.1399, 2332.0640, 2612.1736, 2619.2966, 2620.2971, 2748.3928, 3153.4465, 3211.4810

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|46560478** Score: **289** Expect: **1.1e-026**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **29**
Sequence Coverage: **49%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
109 - 115	812.4169	811.4096	811.3976	0.0120	0	WGPAEPR
118 - 124	1019.4650	1018.4577	1018.4468	0.0109	1	EREEDWR
132 - 139	1005.5432	1004.5359	1004.5264	0.0095	0	RPSHQQPR
140 - 146	855.5226	854.5153	854.5086	0.0067	1	KIRPEGR
147 - 160	1560.6971	1559.6898	1559.6851	0.0047	0	EGEQEWGTPGSEVR
166 - 174	1141.5530	1140.5457	1140.5352	0.0105	0	NNPFYFPSR
166 - 175	1297.6521	1296.6448	1296.6363	0.0085	1	NNPFYFPSRR
197 - 207	1399.7262	1398.7189	1398.7116	0.0073	1	SKQFQNLQNHR
199 - 207	1184.6008	1183.5935	1183.5846	0.0089	0	QFQNLQNHR

208 - 222	1691.0262	1690.0189	1690.0141	0.0049	0	IVQIEARPNTLVLPK
223 - 247	2619.2966	2618.2893	2618.3160	-0.0267	0	HADADNILVIQQGQATVTVANGNNR
248 - 259	1386.7208	1385.7135	1385.7051	0.0084	1	KSFNLDEGHALR
249 - 259	1258.6270	1257.6197	1257.6101	0.0096	0	SFNLDEGHALR
260 - 271	1379.7761	1378.7688	1378.7608	0.0080	0	IPSGFISYILNR
272 - 278	896.4459	895.4386	895.4260	0.0126	0	HDNQNLR
282 - 301	2227.0332	2226.0259	2226.0415	-0.0156	0	ISMPVNTPGQFEDFFPASSR
282 - 301	2243.0415	2242.0342	2242.0364	-0.0022	0	ISMPVNTPGQFEDFFPASSR Oxidation (M)
302 - 312	1287.6040	1286.5967	1286.5891	0.0076	0	DQSSYLQGFSR
313 - 327	1738.8401	1737.8328	1737.8321	0.0007	0	NTLEAAFNAEFNEIR
313 - 328	1894.9305	1893.9232	1893.9332	-0.0100	1	NTLEAAFNAEFNEIRR
329 - 342	1572.7520	1571.7447	1571.7426	0.0021	0	VLLEENAGGEQEER
379 - 393	1714.8612	1713.8539	1713.8533	0.0007	1	KGSEEEDITNPINLR
380 - 393	1586.7656	1585.7583	1585.7583	0.0000	0	GSEEEDITNPINLR
394 - 405	1320.5890	1319.5817	1319.5741	0.0076	0	DGEPDLSNNFGR
432 - 443	1343.6791	1342.6718	1342.6703	0.0015	0	EGALMLPHFNSK
453 - 463	1128.6471	1127.6398	1127.6298	0.0100	0	GTGNLELVAVR
464 - 469	816.4437	815.4364	815.4249	0.0115	1	KEQQQR
473 - 490	2281.8416	2280.8343	2280.8414	-0.0070	0	EQEWEEEEEDEEEEGSNR
536 - 551	1817.9658	1816.9585	1816.9570	0.0015	1	IFLAGDKDNVIDQIEK

No match to: 740.3970, 756.3916, 772.3854, 808.3914, 828.4969, 959.4957, 1111.5713, 1167.5775, 1568.7104, 1643.7893, 1771.8806, 2185.0183, 2193.0002, 2273.1597, 2295.1399, 2332.0640, 2612.1736, 2620.2971, 2748.3928, 3153.4465, 3211.4810

Spot 14

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:30:43 GMT**
Top Score : **265 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	265	conarachin [Arachis hypogaea]
2.	gi|620025	70639	260	Ara h I
3.	gi|1168390	70639	260	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	219	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	219	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	219	Ara h I
7.	gi|46560476	48122	156	conarachin [Arachis hypogaea]
8.	gi|46560474	33641	75	conarachin [Arachis hypogaea]
9.	gi|46560472	34169	73	conarachin [Arachis hypogaea]
10.	gi|226258	10809	17	ferredoxin I

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 265 **Expect:** 2.8e-024 **Queries matched:** 27
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	180	186	0	YGNQNGR
812.3922	811.3849	811.3976	-0.0127	109	115	0	WGPAEPR
816.4219	815.4146	815.4249	-0.0103	464	469	1	KEQQQR
896.4248	895.4175	895.4260	-0.0085	272	278	0	HDNQNLR
1005.5332	1004.5259	1004.5264	-0.0005	132	139	0	RPSHQQPR
1019.4574	1018.4501	1018.4468	0.0033	118	124	1	EREEDWR
1128.6459	1127.6386	1127.6298	0.0088	453	463	0	GTGNLELVAVR
1141.5515	1140.5442	1140.5352	0.0090	166	174	0	NNPFYFPSR
1184.6061	1183.5988	1183.5846	0.0142	199	207	0	QFQNLQNHR

1258.6304	1257.6231	1257.6101	0.0130	249 - 259	0	SFNLDEGHALR
1287.6119	1286.6046	1286.5891	0.0155	302 - 312	0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	166 - 175	1	NNPFYFPSRR
1320.6030	1319.5957	1319.5741	0.0216	394 - 405	0	DGEPDLSNNFGR
1343.6904	1342.6831	1342.6703	0.0128	432 - 443	0	EGALMLPHFNSK
1376.6954	1375.6881	1375.6619	0.0262	555 - 567	0	DLAFPGSGEQVEK
1379.7858	1378.7785	1378.7608	0.0177	260 - 271	0	IPSGFISYILNR
1386.7295	1385.7222	1385.7051	0.0171	248 - 259	1	KSFNLDEGHALR
1399.7382	1398.7309	1398.7116	0.0193	197 - 207	1	SKQFQNLQNHR
1560.7083	1559.7010	1559.6851	0.0159	147 - 160	0	EGEQEWGTPGSEVR
1572.7620	1571.7547	1571.7426	0.0121	329 - 342	0	VLLEENAGGEQEER
1586.7837	1585.7764	1585.7583	0.0181	380 - 393	0	GSEEEDITNPINLR
1691.0385	1690.0312	1690.0141	0.0172	208 - 222	0	IVQIEARPNTLVLPK
1738.8491	1737.8418	1737.8321	0.0097	313 - 327	0	NTLEAAFNAEFNEIR
1817.9683	1816.9610	1816.9570	0.0040	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9403	1893.9330	1893.9332	-0.0002	313 - 328	1	NTLEAAFNAEFNEIRR
2082.1934	2081.1861	2081.2030	-0.0168	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0374	2226.0301	2226.0415	-0.0114	282 - 301	0	ISMPVNTPGQFEDFFPASSR

No match to: 740.3641, 756.3600, 828.4744, 906.4890, 959.4813, 1111.5616, 1167.5778, 1449.6564, 1568.7242, 1643.7987, 1756.8502, 1771.8864, 1774.8645, 2185.0251, 2192.9919, 2201.0010, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

2. gi|620025 **Mass:** 70639 **Score:** 260 **Expect:** 8.7e-024 **Queries matched:** 27

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	180	186	0	YGNQNGR
812.3922	811.3849	811.3976	-0.0127	109	115	0	WGPAEPR
816.4219	815.4146	815.4249	-0.0103	464	469	1	KEQQQR
896.4248	895.4175	895.4260	-0.0085	272	278	0	HDNQNLR
1005.5332	1004.5259	1004.5264	-0.0005	132	139	0	RPSHQQPR
1019.4574	1018.4501	1018.4468	0.0033	118	124	1	EREEDWR
1128.6459	1127.6386	1127.6298	0.0088	453	463	0	GTGNLELVAVR
1141.5515	1140.5442	1140.5352	0.0090	166	174	0	NNPFYFPSR
1184.6061	1183.5988	1183.5846	0.0142	199	207	0	QFQNLQNHR
1258.6304	1257.6231	1257.6101	0.0130	249	259	0	SFNLDEGHALR
1287.6119	1286.6046	1286.5891	0.0155	302	312	0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	166	175	1	NNPFYFPSRR
1320.6030	1319.5957	1319.5741	0.0216	394	405	0	DGEPDLSNNFGR
1343.6904	1342.6831	1342.6703	0.0128	432	443	0	EGALMLPHFNSK
1376.6954	1375.6881	1375.6619	0.0262	555	567	0	DLAFPGSGEQVEK

1379.7858	1378.7785	1378.7608	0.0177	260 - 271	0	IPSGFISYILNR
1386.7295	1385.7222	1385.7051	0.0171	248 - 259	1	KSFNLDEGHALR
1399.7382	1398.7309	1398.7116	0.0193	197 - 207	1	SKQFQNLQNHR
1560.7083	1559.7010	1559.6851	0.0159	147 - 160	0	EGEQEWGTPGSEVR
1572.7620	1571.7547	1571.7426	0.0121	329 - 342	0	VLLEENAGGEQEER
1586.7837	1585.7764	1585.7583	0.0181	380 - 393	0	GSEEEDITNPINLR
1691.0385	1690.0312	1690.0141	0.0172	208 - 222	0	IVQIEARPNTLVLPK
1738.8491	1737.8418	1737.8321	0.0097	313 - 327	0	NTLEAAFNAEFNEIR
1817.9683	1816.9610	1816.9570	0.0040	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9403	1893.9330	1893.9332	-0.0002	313 - 328	1	NTLEAAFNAEFNEIRR
2082.1934	2081.1861	2081.2030	-0.0168	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0374	2226.0301	2226.0415	-0.0114	282 - 301	0	ISMPVNTPGQFEDFFPASSR

No match to: 740.3641, 756.3600, 828.4744, 906.4890, 959.4813, 1111.5616, 1167.5778, 1449.6564, 1568.7242, 1643.7987, 1756.8502, 1771.8864, 1774.8645, 2185.0251, 2192.9919, 2201.0010, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

3. gi|1168390 **Mass:** 70639 **Score:** 260 **Expect:** 8.7e-024 **Queries matched:** 27

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	180 - 186		0	YGNQNGR
812.3922	811.3849	811.3976	-0.0127	109 - 115		0	WGPAEPR
816.4219	815.4146	815.4249	-0.0103	464 - 469		1	KEQQQR
896.4248	895.4175	895.4260	-0.0085	272 - 278		0	HDNQNLR
1005.5332	1004.5259	1004.5264	-0.0005	132 - 139		0	RPSHQQPR
1019.4574	1018.4501	1018.4468	0.0033	118 - 124		1	EREEDWR
1128.6459	1127.6386	1127.6298	0.0088	453 - 463		0	GTGNLELVAVR
1141.5515	1140.5442	1140.5352	0.0090	166 - 174		0	NNPFYFPSR
1184.6061	1183.5988	1183.5846	0.0142	199 - 207		0	QFQNLQNHR
1258.6304	1257.6231	1257.6101	0.0130	249 - 259		0	SFNLDEGHALR
1287.6119	1286.6046	1286.5891	0.0155	302 - 312		0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	166 - 175		1	NNPFYFPSRR
1320.6030	1319.5957	1319.5741	0.0216	394 - 405		0	DGEPDLSNNFGR
1343.6904	1342.6831	1342.6703	0.0128	432 - 443		0	EGALMLPHFNSK
1376.6954	1375.6881	1375.6619	0.0262	555 - 567		0	DLAFPGSGEQVEK
1379.7858	1378.7785	1378.7608	0.0177	260 - 271		0	IPSGFISYILNR
1386.7295	1385.7222	1385.7051	0.0171	248 - 259		1	KSFNLDEGHALR
1399.7382	1398.7309	1398.7116	0.0193	197 - 207		1	SKQFQNLQNHR
1560.7083	1559.7010	1559.6851	0.0159	147 - 160		0	EGEQEWGTPGSEVR
1572.7620	1571.7547	1571.7426	0.0121	329 - 342		0	VLLEENAGGEQEER
1586.7837	1585.7764	1585.7583	0.0181	380 - 393		0	GSEEEDITNPINLR

1691.0385	1690.0312	1690.0141	0.0172	208 - 222	0	IVQIEARPNTLVLPK
1738.8491	1737.8418	1737.8321	0.0097	313 - 327	0	NTLEAAFNAEFNEIR
1817.9683	1816.9610	1816.9570	0.0040	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9403	1893.9330	1893.9332	-0.0002	313 - 328	1	NTLEAAFNAEFNEIRR
2082.1934	2081.1861	2081.2030	-0.0168	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0374	2226.0301	2226.0415	-0.0114	282 - 301	0	ISMPVNTPGQFEDFFPASSR

No match to: 740.3641, 756.3600, 828.4744, 906.4890, 959.4813, 1111.5616, 1167.5778, 1449.6564, 1568.7242, 1643.7987, 1756.8502, 1771.8864, 1774.8645, 2185.0251, 2192.9919, 2201.0010, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

4. gi|16612200 **Mass:** 71701 **Score:** 219 **Expect:** 1.1e-019 **Queries matched:** 24

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	186 - 192	0	YGNQNGR
816.4219	815.4146	815.4249	-0.0103	472 - 477	1	KEQQQR
896.4248	895.4175	895.4260	-0.0085	278 - 284	0	HDNQNLR
1005.5332	1004.5259	1004.5264	-0.0005	138 - 145	0	RPSHQQPR
1019.4574	1018.4501	1018.4468	0.0033	124 - 130	1	EREEDWR
1128.6459	1127.6386	1127.6298	0.0088	461 - 471	0	GTGNLELVAVR
1141.5515	1140.5442	1140.5352	0.0090	172 - 180	0	NNPFYFPSR
1184.6061	1183.5988	1183.5846	0.0142	205 - 213	0	QFQNLQNHR
1258.6304	1257.6231	1257.6101	0.0130	255 - 265	0	SFNLDEGHALR
1287.6119	1286.6046	1286.5891	0.0155	308 - 318	0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	172 - 181	1	NNPFYFPSRR
1343.6904	1342.6831	1342.6703	0.0128	440 - 451	0	EGALMLPHFNSK
1376.6954	1375.6881	1375.6619	0.0262	560 - 572	0	DLAFPGSGEQVEK
1379.7858	1378.7785	1378.7608	0.0177	266 - 277	0	IPSGFISYILNR
1386.7295	1385.7222	1385.7051	0.0171	254 - 265	1	KSFNLDEGHALR
1568.7242	1567.7169	1567.7015	0.0155	153 - 166	0	EGEQEWGTPGSHVR
1572.7620	1571.7547	1571.7426	0.0121	335 - 348	0	VLLEENAGGEQEER
1643.7987	1642.7914	1642.7798	0.0117	387 - 401	0	GSEEEGDITNPINLR
1738.8491	1737.8418	1737.8321	0.0097	319 - 333	0	NTLEAAFNAEFNEIR
1771.8864	1770.8791	1770.8747	0.0044	386 - 401	1	KGSEEEGDITNPINLR
1817.9683	1816.9610	1816.9570	0.0040	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9403	1893.9330	1893.9332	-0.0002	319 - 334	1	NTLEAAFNAEFNEIRR
2082.1934	2081.1861	2081.2030	-0.0168	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0374	2226.0301	2226.0415	-0.0114	288 - 307	0	ISMPVNTPGQFEDFFPASSR

No match to: 740.3641, 756.3600, 812.3922, 828.4744, 906.4890, 959.4813, 1111.5616, 1167.5778, 1320.6030, 1399.7382, 1449.6564, 1560.7083, 1586.7837, 1691.0385, 1756.8502, 1774.8645, 2185.0251, 2192.9919, 2201.0010, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

5. gi|1168391 **Mass:** 71701 **Score:** 219 **Expect:** 1.1e-019 **Queries matched:** 24

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	186	192	0	YGNQNGR
816.4219	815.4146	815.4249	-0.0103	472	477	1	KEQQQR
896.4248	895.4175	895.4260	-0.0085	278	284	0	HDNQNLR
1005.5332	1004.5259	1004.5264	-0.0005	138	145	0	RPSHQQPR
1019.4574	1018.4501	1018.4468	0.0033	124	130	1	EREEDWR
1128.6459	1127.6386	1127.6298	0.0088	461	471	0	GTGNLELVAVR
1141.5515	1140.5442	1140.5352	0.0090	172	180	0	NNPFYFPSR
1184.6061	1183.5988	1183.5846	0.0142	205	213	0	QFQNLQNHR
1258.6304	1257.6231	1257.6101	0.0130	255	265	0	SFNLDEGHALR
1287.6119	1286.6046	1286.5891	0.0155	308	318	0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	172	181	1	NNPFYFPSRR
1343.6904	1342.6831	1342.6703	0.0128	440	451	0	EGALMLPHFNSK
1376.6954	1375.6881	1375.6619	0.0262	560	572	0	DLAFPGSGEQVEK
1379.7858	1378.7785	1378.7608	0.0177	266	277	0	IPSGFISYILNR
1386.7295	1385.7222	1385.7051	0.0171	254	265	1	KSFNLDEGHALR
1568.7242	1567.7169	1567.7015	0.0155	153	166	0	EGEQEWGTPGSHVR
1572.7620	1571.7547	1571.7426	0.0121	335	348	0	VLLEENAGGEQEER
1643.7987	1642.7914	1642.7798	0.0117	387	401	0	GSEEEGDITNPINLR
1738.8491	1737.8418	1737.8321	0.0097	319	333	0	NTLEAAFNAEFNEIR
1771.8864	1770.8791	1770.8747	0.0044	386	401	1	KGSEEEGDITNPINLR
1817.9683	1816.9610	1816.9570	0.0040	541	556	1	IFLAGDKDNVIDQIEK
1894.9403	1893.9330	1893.9332	-0.0002	319	334	1	NTLEAAFNAEFNEIRR
2082.1934	2081.1861	2081.2030	-0.0168	452	471	1	AMVIVVVNKGTGNLELVAVR
2227.0374	2226.0301	2226.0415	-0.0114	288	307	0	ISMPVNTPGQFEDFFPASSR

No match to: 740.3641, 756.3600, 812.3922, 828.4744, 906.4890, 959.4813, 1111.5616, 1167.5778, 1320.6030, 1399.7382, 1449.6564, 1560.7083, 1586.7837, 1691.0385, 1756.8502, 1774.8645, 2185.0251, 2192.9919, 2201.0010, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

6. gi|602436 **Mass:** 71701 **Score:** 219 **Expect:** 1.1e-019 **Queries matched:** 24

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3605	807.3532	807.3623	-0.0091	186	192	0	YGNQNGR
816.4219	815.4146	815.4249	-0.0103	472	477	1	KEQQQR
896.4248	895.4175	895.4260	-0.0085	278	284	0	HDNQNLR
1005.5332	1004.5259	1004.5264	-0.0005	138	145	0	RPSHQQPR
1019.4574	1018.4501	1018.4468	0.0033	124	130	1	EREEDWR
1128.6459	1127.6386	1127.6298	0.0088	461	471	0	GTGNLELVAVR

1141.5515	1140.5442	1140.5352	0.0090	172 - 180	0	NNPFYFPSR
1184.6061	1183.5988	1183.5846	0.0142	205 - 213	0	QFQNLQNHR
1258.6304	1257.6231	1257.6101	0.0130	255 - 265	0	SFNLDEGHALR
1287.6119	1286.6046	1286.5891	0.0155	308 - 318	0	DQSSYLQGFSR
1297.6560	1296.6487	1296.6363	0.0124	172 - 181	1	NNPFYFPSRR
1343.6904	1342.6831	1342.6703	0.0128	440 - 451	0	EGALMLPHFNSK
1376.6954	1375.6881	1375.6619	0.0262	560 - 572	0	DLAFPGSGEQVEK
1379.7858	1378.7785	1378.7608	0.0177	266 - 277	0	IPSGFISYILNR
1386.7295	1385.7222	1385.7051	0.0171	254 - 265	1	KSFNLDEGHALR
1568.7242	1567.7169	1567.7015	0.0155	153 - 166	0	EGEQEWGTPGSHVR
1572.7620	1571.7547	1571.7426	0.0121	335 - 348	0	VLLEENAGGEQEER
1643.7987	1642.7914	1642.7798	0.0117	387 - 401	0	GSEEEGDITNPINLR
1738.8491	1737.8418	1737.8321	0.0097	319 - 333	0	NTLEAAFNAEFNEIR
1771.8864	1770.8791	1770.8747	0.0044	386 - 401	1	KGSEEEGDITNPINLR
1817.9683	1816.9610	1816.9570	0.0040	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9403	1893.9330	1893.9332	-0.0002	319 - 334	1	NTLEAAFNAEFNEIRR
2082.1934	2081.1861	2081.2030	-0.0168	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0374	2226.0301	2226.0415	-0.0114	288 - 307	0	ISMPVNTPGQFEDFFPASSR

No match to: 740.3641, 756.3600, 812.3922, 828.4744, 906.4890, 959.4813, 1111.5616, 1167.5778, 1320.6030, 1399.7382, 1449.6564, 1560.7083, 1586.7837, 1691.0385, 1756.8502, 1774.8645, 2185.0251, 2192.9919, 2201.0010, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

7. gi|46560476 **Mass:** 48122 **Score:** 156 **Expect:** 2.2e-013 **Queries matched:** 16

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4219	815.4146	815.4249	-0.0103	274	279	1	KEQQQR
896.4248	895.4175	895.4260	-0.0085	81	87	0	HDNQNLR
1128.6459	1127.6386	1127.6298	0.0088	263	273	0	GTGNLELVAVR
1184.6061	1183.5988	1183.5846	0.0142	8	16	0	QFQNLQNHR
1258.6304	1257.6231	1257.6101	0.0130	58	68	0	SFNLDEGHALR
1287.6119	1286.6046	1286.5891	0.0155	111	121	0	DQSSYLQGFSR
1343.6904	1342.6831	1342.6703	0.0128	242	253	0	EGALMLPHFNSK
1376.6954	1375.6881	1375.6619	0.0262	362	374	0	DLAFPGSGEQVEK
1379.7858	1378.7785	1378.7608	0.0177	69	80	0	IPSGFISYILNR
1386.7295	1385.7222	1385.7051	0.0171	57	68	1	KSFNLDEGHALR
1572.7620	1571.7547	1571.7426	0.0121	138	151	0	VLLEENAGGEQEER
1738.8491	1737.8418	1737.8321	0.0097	122	136	0	NTLEAAFNAEFNEIR
1817.9683	1816.9610	1816.9570	0.0040	343	358	1	IFLAGDKDNVIDQIEK
1894.9403	1893.9330	1893.9332	-0.0002	122	137	1	NTLEAAFNAEFNEIRR
2082.1934	2081.1861	2081.2030	-0.0168	254	273	1	AMVIVVVNKGTGNLELVAVR

2227.0374	2226.0301	2226.0415	-0.0114	91 - 110	0	ISMPVNTPGQFEDFFPASSR

No match to: 740.3641, 756.3600, 808.3605, 812.3922, 828.4744, 906.4890, 959.4813, 1005.5332, 1019.4574, 1111.5616, 1141.5515, 1167.5778, 1297.6560, 1320.6030, 1399.7382, 1449.6564, 1560.7083, 1568.7242, 1586.7837, 1643.7987, 1691.0385, 1756.8502, 1771.8864, 1774.8645, 2185.0251, 2192.9919, 2201.0010, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

8. gi|46560474 **Mass:** 33641 **Score:** 75 **Expect:** 3e-005 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4219	815.4146	815.4249	-0.0103	152 -	157	1	KEQQQR
1128.6459	1127.6386	1127.6298	0.0088	141 -	151	0	GTGNLELVAVR
1343.6904	1342.6831	1342.6703	0.0128	120 -	131	0	EGALMLPHFNSK
1376.6954	1375.6881	1375.6619	0.0262	240 -	252	0	DLAFPGSGEQVEK
1572.7620	1571.7547	1571.7426	0.0121	15 -	28	0	VLLEENAGGEQEER
1643.7987	1642.7914	1642.7798	0.0117	67 -	81	0	GSEEEGDITNPINLR
1771.8864	1770.8791	1770.8747	0.0044	66 -	81	1	KGSEEEGDITNPINLR
1817.9683	1816.9610	1816.9570	0.0040	221 -	236	1	IFLAGDKDNVIDQIEK
2082.1934	2081.1861	2081.2030	-0.0168	132 -	151	1	AMVIVVVNKGTGNLELVAVR

No match to: 740.3641, 756.3600, 808.3605, 812.3922, 828.4744, 896.4248, 906.4890, 959.4813, 1005.5332, 1019.4574, 1111.5616, 1141.5515, 1167.5778, 1184.6061, 1258.6304, 1287.6119, 1297.6560, 1320.6030, 1379.7858, 1386.7295, 1399.7382, 1449.6564, 1560.7083, 1568.7242, 1586.7837, 1691.0385, 1738.8491, 1756.8502, 1774.8645, 1894.9403, 2185.0251, 2192.9919, 2201.0010, 2227.0374, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

9. gi|46560472 **Mass:** 34169 **Score:** 73 **Expect:** 4.4e-005 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4219	815.4146	815.4249	-0.0103	153 -	158	1	KEQQQR
1128.6459	1127.6386	1127.6298	0.0088	142 -	152	0	GTGNLELVAVR
1320.6030	1319.5957	1319.5741	0.0216	83 -	94	0	DGEPDLSNNFGR
1343.6904	1342.6831	1342.6703	0.0128	121 -	132	0	EGALMLPHFNSK
1376.6954	1375.6881	1375.6619	0.0262	244 -	256	0	DLAFPGSGEQVEK
1572.7620	1571.7547	1571.7426	0.0121	18 -	31	0	VLLEENAGGEQEER
1586.7837	1585.7764	1585.7583	0.0181	69 -	82	0	GSEEEDITNPINLR
1817.9683	1816.9610	1816.9570	0.0040	225 -	240	1	IFLAGDKDNVIDQIEK
2082.1934	2081.1861	2081.2030	-0.0168	133 -	152	1	AMVIVVVNKGTGNLELVAVR

No match to: 740.3641, 756.3600, 808.3605, 812.3922, 828.4744, 896.4248, 906.4890, 959.4813, 1005.5332, 1019.4574, 1111.5616, 1141.5515, 1167.5778, 1184.6061, 1258.6304, 1287.6119, 1297.6560, 1379.7858, 1386.7295, 1399.7382, 1449.6564, 1560.7083, 1568.7242, 1643.7987, 1691.0385, 1738.8491, 1756.8502, 1771.8864, 1774.8645, 1894.9403, 2185.0251, 2192.9919, 2201.0010, 2227.0374, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

10. gi|226258 **Mass:** 10809 **Score:** 17 **Expect:** 20 **Queries matched:** 2

ferredoxin I

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1141.5515	1140.5442	1140.5484	-0.0042	16	-	26	0	GDLAVAMASYK + Oxidation (M)
1297.6560	1296.6487	1296.6496	-0.0008	15	-	26	1	RGDLAVAMASYK + Oxidation (M)

No match to: 740.3641, 756.3600, 808.3605, 812.3922, 816.4219, 828.4744, 896.4248, 906.4890, 959.4813, 1005.5332, 1019.4574, 1111.5616, 1128.6459, 1167.5778, 1184.6061, 1258.6304, 1287.6119, 1320.6030, 1343.6904, 1376.6954, 1379.7858, 1386.7295, 1399.7382, 1449.6564, 1560.7083, 1568.7242, 1572.7620, 1586.7837, 1643.7987, 1691.0385, 1738.8491, 1756.8502, 1771.8864, 1774.8645, 1817.9683, 1894.9403, 2082.1934, 2185.0251, 2192.9919, 2201.0010, 2227.0374, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 5

Protein View

Match to: **gi|46560478** Score: **265** Expect: **2.8e-024**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **27**
Sequence Coverage: **45%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
```

```
201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
109 - 115	812.3922	811.3849	811.3976	-0.0127	0	WGPAEPR
118 - 124	1019.4574	1018.4501	1018.4468	0.0033	1	EREEDWR
132 - 139	1005.5332	1004.5259	1004.5264	-0.0005	0	RPSHQQPR
147 - 160	1560.7083	1559.7010	1559.6851	0.0159	0	EGEQEWGTPGSEVR
166 - 174	1141.5515	1140.5442	1140.5352	0.0090	0	NNPFYFPSR
166 - 175	1297.6560	1296.6487	1296.6363	0.0124	1	NNPFYFPSRR
180 - 186	808.3605	807.3532	807.3623	-0.0091	0	YGNQNGR
197 - 207	1399.7382	1398.7309	1398.7116	0.0193	1	SKQFQNLQNHR
199 - 207	1184.6061	1183.5988	1183.5846	0.0142	0	QFQNLQNHR
208 - 222	1691.0385	1690.0312	1690.0141	0.0172	0	IVQIEARPNTLVLPK
248 - 259	1386.7295	1385.7222	1385.7051	0.0171	1	KSFNLDEGHALR
249 - 259	1258.6304	1257.6231	1257.6101	0.0130	0	SFNLDEGHALR
260 - 271	1379.7858	1378.7785	1378.7608	0.0177	0	IPSGFISYILNR
272 - 278	896.4248	895.4175	895.4260	-0.0085	0	HDNQNLR
282 - 301	2227.0374	2226.0301	2226.0415	-0.0114	0	ISMPVNTPGQFEDFFPASSR
302 - 312	1287.6119	1286.6046	1286.5891	0.0155	0	DQSSYLQGFSR
313 - 327	1738.8491	1737.8418	1737.8321	0.0097	0	NTLEAAFNAEFNEIR
313 - 328	1894.9403	1893.9330	1893.9332	-0.0002	1	NTLEAAFNAEFNEIRR
329 - 342	1572.7620	1571.7547	1571.7426	0.0121	0	VLLEENAGGEQEER
380 - 393	1586.7837	1585.7764	1585.7583	0.0181	0	GSEEEDITNPINLR
394 - 405	1320.6030	1319.5957	1319.5741	0.0216	0	DGEPDLSNNFGR
432 - 443	1343.6904	1342.6831	1342.6703	0.0128	0	EGALMLPHFNSK
444 - 463	2082.1934	2081.1861	2081.2030	-0.0168	1	AMVIVVVNKGTGNLELVAVR
453 - 463	1128.6459	1127.6386	1127.6298	0.0088	0	GTGNLELVAVR
464 - 469	816.4219	815.4146	815.4249	-0.0103	1	KEQQQR
536 - 551	1817.9683	1816.9610	1816.9570	0.0040	1	IFLAGDKDNVIDQIEK
555 - 567	1376.6954	1375.6881	1375.6619	0.0262	0	DLAFPGSGEQVEK

No match to: 740.3641, 756.3600, 828.4744, 906.4890, 959.4813, 1111.5616, 1167.5778, 1449.6564, 1568.7242, 1643.7987, 1756.8502, 1771.8864, 1774.8645, 2185.0251, 2192.9919, 2201.0010, 2273.1597, 2295.1399, 2612.1416, 2619.2620, 2748.3369, 3153.3318, 3211.3672

Spot 15

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 4 May 2007 at 11:30:48 GMT
Top Score : 206 for gi|46560478, conarachin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	206	conarachin [Arachis hypogaea]
2.	gi|16612200	71701	203	major allergen Arah1 [Arachis hypogaea]
3.	gi|1168391	71701	203	Allergen Ara h 1, clone P41B precursor (Ara h I)
4.	gi|602436	71701	203	Ara h I
5.	gi|620025	70639	201	Ara h I
6.	gi|1168390	70639	201	Allergen Ara h 1, clone P17 precursor (Ara h I)
7.	gi|46560476	48122	117	conarachin [Arachis hypogaea]
8.	gi|46560474	33641	42	conarachin [Arachis hypogaea]
9.	gi|46560472	34169	39	conarachin [Arachis hypogaea]
10.	gi|62177652	10056	19	resistance protein PRG [Arachis hypogaea]

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 206 **Expect:** 2.2e-018 **Queries matched:** 23
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3777	807.3704	807.3623	0.0081	180	186	0	YGNQNGR
812.4006	811.3933	811.3976	-0.0043	109	115	0	WGPAEPR
855.5176	854.5103	854.5086	0.0017	140	146	1	KIRPEGR
896.4360	895.4287	895.4260	0.0027	272	278	0	HDNQNLR
1005.5390	1004.5317	1004.5264	0.0053	132	139	0	RPSHQQPR
1019.4731	1018.4658	1018.4468	0.0190	118	124	1	EREEDWR
1128.6423	1127.6350	1127.6298	0.0052	453	463	0	GTGNLELVAVR
1141.5519	1140.5446	1140.5352	0.0094	166	174	0	NNPFYFPSR
1184.6041	1183.5968	1183.5846	0.0122	199	207	0	QFQNLQNHR
1258.6292	1257.6219	1257.6101	0.0118	249	259	0	SFNLDEGHALR
1287.6121	1286.6048	1286.5891	0.0157	302	312	0	DQSSYLQGFSR

1297.6549	1296.6476	1296.6363	0.0113	166 - 175	1	NNPFYFPSRR
1320.5964	1319.5891	1319.5741	0.0150	394 - 405	0	DGEPDLSNNFGR
1343.6876	1342.6803	1342.6703	0.0100	432 - 443	0	EGALMLPHFNSK
1379.7799	1378.7726	1378.7608	0.0118	260 - 271	0	IPSGFISYILNR
1560.7048	1559.6975	1559.6851	0.0124	147 - 160	0	EGEQEWGTPGSEVR
1572.7579	1571.7506	1571.7426	0.0080	329 - 342	0	VLLEENAGGEQEER
1586.7701	1585.7628	1585.7583	0.0045	380 - 393	0	GSEEEDITNPINLR
1738.8466	1737.8393	1737.8321	0.0072	313 - 327	0	NTLEAAFNAEFNEIR
1817.9814	1816.9741	1816.9570	0.0171	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9453	1893.9380	1893.9332	0.0048	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0461	2226.0388	2226.0415	-0.0027	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2619.2749	2618.2676	2618.3160	-0.0484	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3815, 756.3749, 1080.5404, 1111.5596, 1167.5770, 1375.7365, 1568.7214, 1643.8082, 1756.8466, 1771.8901, 1774.8644, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

2. gi|16612200 **Mass:** 71701 **Score:** 203 **Expect:** 4.4e-018 **Queries matched:** 23

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3815	739.3742	739.3765	-0.0023	115 - 121		0	WGPAGPR
808.3777	807.3704	807.3623	0.0081	186 - 192		0	YGNQNGR
855.5176	854.5103	854.5086	0.0017	146 - 152		1	KIRPEGR
896.4360	895.4287	895.4260	0.0027	278 - 284		0	HDNQNLR
1005.5390	1004.5317	1004.5264	0.0053	138 - 145		0	RPSHQQPR
1019.4731	1018.4658	1018.4468	0.0190	124 - 130		1	EREEDWR
1128.6423	1127.6350	1127.6298	0.0052	461 - 471		0	GTGNLELVAVR
1141.5519	1140.5446	1140.5352	0.0094	172 - 180		0	NNPFYFPSR
1184.6041	1183.5968	1183.5846	0.0122	205 - 213		0	QFQNLQNHR
1258.6292	1257.6219	1257.6101	0.0118	255 - 265		0	SFNLDEGHALR
1287.6121	1286.6048	1286.5891	0.0157	308 - 318		0	DQSSYLQGFSR
1297.6549	1296.6476	1296.6363	0.0113	172 - 181		1	NNPFYFPSRR
1343.6876	1342.6803	1342.6703	0.0100	440 - 451		0	EGALMLPHFNSK
1379.7799	1378.7726	1378.7608	0.0118	266 - 277		0	IPSGFISYILNR
1568.7214	1567.7141	1567.7015	0.0127	153 - 166		0	EGEQEWGTPGSHVR
1572.7579	1571.7506	1571.7426	0.0080	335 - 348		0	VLLEENAGGEQEER
1643.8082	1642.8009	1642.7798	0.0212	387 - 401		0	GSEEEGDITNPINLR
1738.8466	1737.8393	1737.8321	0.0072	319 - 333		0	NTLEAAFNAEFNEIR
1771.8901	1770.8828	1770.8747	0.0081	386 - 401		1	KGSEEEGDITNPINLR
1817.9814	1816.9741	1816.9570	0.0171	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9453	1893.9380	1893.9332	0.0048	319 - 334		1	NTLEAAFNAEFNEIRR

2227.0461	2226.0388	2226.0415	-0.0027	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2619.2749	2618.2676	2618.3160	-0.0484	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 756.3749, 812.4006, 1080.5404, 1111.5596, 1167.5770, 1320.5964, 1375.7365, 1560.7048, 1586.7701, 1756.8466, 1774.8644, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

3. gi|1168391 **Mass:** 71701 **Score:** 203 **Expect:** 4.4e-018 **Queries matched:** 23

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3815	739.3742	739.3765	-0.0023	115 -	121	0	WGPAGPR
808.3777	807.3704	807.3623	0.0081	186 -	192	0	YGNQNGR
855.5176	854.5103	854.5086	0.0017	146 -	152	1	KIRPEGR
896.4360	895.4287	895.4260	0.0027	278 -	284	0	HDNQNLR
1005.5390	1004.5317	1004.5264	0.0053	138 -	145	0	RPSHQQPR
1019.4731	1018.4658	1018.4468	0.0190	124 -	130	1	EREEDWR
1128.6423	1127.6350	1127.6298	0.0052	461 -	471	0	GTGNLELVAVR
1141.5519	1140.5446	1140.5352	0.0094	172 -	180	0	NNPFYFPSR
1184.6041	1183.5968	1183.5846	0.0122	205 -	213	0	QFQNLQNHR
1258.6292	1257.6219	1257.6101	0.0118	255 -	265	0	SFNLDEGHALR
1287.6121	1286.6048	1286.5891	0.0157	308 -	318	0	DQSSYLQGFSR
1297.6549	1296.6476	1296.6363	0.0113	172 -	181	1	NNPFYFPSRR
1343.6876	1342.6803	1342.6703	0.0100	440 -	451	0	EGALMLPHFNSK
1379.7799	1378.7726	1378.7608	0.0118	266 -	277	0	IPSGFISYILNR
1568.7214	1567.7141	1567.7015	0.0127	153 -	166	0	EGEQEWGTPGSHVR
1572.7579	1571.7506	1571.7426	0.0080	335 -	348	0	VLLEENAGGEQEER
1643.8082	1642.8009	1642.7798	0.0212	387 -	401	0	GSEEEGDITNPINLR
1738.8466	1737.8393	1737.8321	0.0072	319 -	333	0	NTLEAAFNAEFNEIR
1771.8901	1770.8828	1770.8747	0.0081	386 -	401	1	KGSEEEGDITNPINLR
1817.9814	1816.9741	1816.9570	0.0171	541 -	556	1	IFLAGDKDNVIDQIEK
1894.9453	1893.9380	1893.9332	0.0048	319 -	334	1	NTLEAAFNAEFNEIRR
2227.0461	2226.0388	2226.0415	-0.0027	288 -	307	0	ISMPVNTPGQFEDFFPASSR
2619.2749	2618.2676	2618.3160	-0.0484	229 -	253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 756.3749, 812.4006, 1080.5404, 1111.5596, 1167.5770, 1320.5964, 1375.7365, 1560.7048, 1586.7701, 1756.8466, 1774.8644, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

4. gi|602436 **Mass:** 71701 **Score:** 203 **Expect:** 4.4e-018 **Queries matched:** 23

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
740.3815	739.3742	739.3765	-0.0023	115 -	121	0	WGPAGPR
808.3777	807.3704	807.3623	0.0081	186 -	192	0	YGNQNGR

855.5176	854.5103	854.5086	0.0017	146 - 152	1	KIRPEGR
896.4360	895.4287	895.4260	0.0027	278 - 284	0	HDNQNLR
1005.5390	1004.5317	1004.5264	0.0053	138 - 145	0	RPSHQQPR
1019.4731	1018.4658	1018.4468	0.0190	124 - 130	1	EREEDWR
1128.6423	1127.6350	1127.6298	0.0052	461 - 471	0	GTGNLELVAVR
1141.5519	1140.5446	1140.5352	0.0094	172 - 180	0	NNPFYFPSR
1184.6041	1183.5968	1183.5846	0.0122	205 - 213	0	QFQNLQNHR
1258.6292	1257.6219	1257.6101	0.0118	255 - 265	0	SFNLDEGHALR
1287.6121	1286.6048	1286.5891	0.0157	308 - 318	0	DQSSYLQGFSR
1297.6549	1296.6476	1296.6363	0.0113	172 - 181	1	NNPFYFPSRR
1343.6876	1342.6803	1342.6703	0.0100	440 - 451	0	EGALMLPHFNSK
1379.7799	1378.7726	1378.7608	0.0118	266 - 277	0	IPSGFISYILNR
1568.7214	1567.7141	1567.7015	0.0127	153 - 166	0	EGEQEWGTPGSHVR
1572.7579	1571.7506	1571.7426	0.0080	335 - 348	0	VLLEENAGGEQEER
1643.8082	1642.8009	1642.7798	0.0212	387 - 401	0	GSEEEGDITNPINLR
1738.8466	1737.8393	1737.8321	0.0072	319 - 333	0	NTLEAAFNAEFNEIR
1771.8901	1770.8828	1770.8747	0.0081	386 - 401	1	KGSEEEGDITNPINLR
1817.9814	1816.9741	1816.9570	0.0171	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9453	1893.9380	1893.9332	0.0048	319 - 334	1	NTLEAAFNAEFNEIRR
2227.0461	2226.0388	2226.0415	-0.0027	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2619.2749	2618.2676	2618.3160	-0.0484	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 756.3749, 812.4006, 1080.5404, 1111.5596, 1167.5770, 1320.5964, 1375.7365, 1560.7048, 1586.7701, 1756.8466, 1774.8644, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

5. gi|620025 **Mass:** 70639 **Score:** 201 **Expect:** 7e-018 **Queries matched:** 23

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3777	807.3704	807.3623	0.0081	180 - 186		0	YGNQNGR
812.4006	811.3933	811.3976	-0.0043	109 - 115		0	WGPAEPR
855.5176	854.5103	854.5086	0.0017	140 - 146		1	KIRPEGR
896.4360	895.4287	895.4260	0.0027	272 - 278		0	HDNQNLR
1005.5390	1004.5317	1004.5264	0.0053	132 - 139		0	RPSHQQPR
1019.4731	1018.4658	1018.4468	0.0190	118 - 124		1	EREEDWR
1128.6423	1127.6350	1127.6298	0.0052	453 - 463		0	GTGNLELVAVR
1141.5519	1140.5446	1140.5352	0.0094	166 - 174		0	NNPFYFPSR
1184.6041	1183.5968	1183.5846	0.0122	199 - 207		0	QFQNLQNHR
1258.6292	1257.6219	1257.6101	0.0118	249 - 259		0	SFNLDEGHALR
1287.6121	1286.6048	1286.5891	0.0157	302 - 312		0	DQSSYLQGFSR
1297.6549	1296.6476	1296.6363	0.0113	166 - 175		1	NNPFYFPSRR

1320.5964	1319.5891	1319.5741	0.0150	394 - 405	0	DGEPDLSNNFGR
1343.6876	1342.6803	1342.6703	0.0100	432 - 443	0	EGALMLPHFNSK
1379.7799	1378.7726	1378.7608	0.0118	260 - 271	0	IPSGFISYILNR
1560.7048	1559.6975	1559.6851	0.0124	147 - 160	0	EGEQEWGTPGSEVR
1572.7579	1571.7506	1571.7426	0.0080	329 - 342	0	VLLEENAGGEQEER
1586.7701	1585.7628	1585.7583	0.0045	380 - 393	0	GSEEEDITNPINLR
1738.8466	1737.8393	1737.8321	0.0072	313 - 327	0	NTLEAAFNAEFNEIR
1817.9814	1816.9741	1816.9570	0.0171	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9453	1893.9380	1893.9332	0.0048	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0461	2226.0388	2226.0415	-0.0027	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2619.2749	2618.2676	2618.3160	-0.0484	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3815, 756.3749, 1080.5404, 1111.5596, 1167.5770, 1375.7365, 1568.7214, 1643.8082, 1756.8466, 1771.8901, 1774.8644, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

6. gi|1168390 **Mass:** 70639 **Score:** 201 **Expect:** 7e-018 **Queries matched:** 23

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
808.3777	807.3704	807.3623	0.0081	180 - 186		0	YGNQNGR
812.4006	811.3933	811.3976	-0.0043	109 - 115		0	WGPAEPR
855.5176	854.5103	854.5086	0.0017	140 - 146		1	KIRPEGR
896.4360	895.4287	895.4260	0.0027	272 - 278		0	HDNQNLR
1005.5390	1004.5317	1004.5264	0.0053	132 - 139		0	RPSHQQPR
1019.4731	1018.4658	1018.4468	0.0190	118 - 124		1	EREEDWR
1128.6423	1127.6350	1127.6298	0.0052	453 - 463		0	GTGNLELVAVR
1141.5519	1140.5446	1140.5352	0.0094	166 - 174		0	NNPFYFPSR
1184.6041	1183.5968	1183.5846	0.0122	199 - 207		0	QFQNLQNHR
1258.6292	1257.6219	1257.6101	0.0118	249 - 259		0	SFNLDEGHALR
1287.6121	1286.6048	1286.5891	0.0157	302 - 312		0	DQSSYLQGFSR
1297.6549	1296.6476	1296.6363	0.0113	166 - 175		1	NNPFYFPSRR
1320.5964	1319.5891	1319.5741	0.0150	394 - 405		0	DGEPDLSNNFGR
1343.6876	1342.6803	1342.6703	0.0100	432 - 443		0	EGALMLPHFNSK
1379.7799	1378.7726	1378.7608	0.0118	260 - 271		0	IPSGFISYILNR
1560.7048	1559.6975	1559.6851	0.0124	147 - 160		0	EGEQEWGTPGSEVR
1572.7579	1571.7506	1571.7426	0.0080	329 - 342		0	VLLEENAGGEQEER
1586.7701	1585.7628	1585.7583	0.0045	380 - 393		0	GSEEEDITNPINLR
1738.8466	1737.8393	1737.8321	0.0072	313 - 327		0	NTLEAAFNAEFNEIR
1817.9814	1816.9741	1816.9570	0.0171	536 - 551		1	IFLAGDKDNVIDQIEK
1894.9453	1893.9380	1893.9332	0.0048	313 - 328		1	NTLEAAFNAEFNEIRR
2227.0461	2226.0388	2226.0415	-0.0027	282 - 301		0	ISMPVNTPGQFEDFFPASSR

2619.2749	2618.2676	2618.3160	-0.0484	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3815, 756.3749, 1080.5404, 1111.5596, 1167.5770, 1375.7365, 1568.7214, 1643.8082, 1756.8466, 1771.8901, 1774.8644, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

7. gi|46560476 **Mass:** 48122 **Score:** 117 **Expect:** 1.7e-009 **Queries matched:** 13

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4360	895.4287	895.4260	0.0027	81 -	87	0	HDNQNLR
1128.6423	1127.6350	1127.6298	0.0052	263 -	273	0	GTGNLELVAVR
1184.6041	1183.5968	1183.5846	0.0122	8 -	16	0	QFQNLQNHR
1258.6292	1257.6219	1257.6101	0.0118	58 -	68	0	SFNLDEGHALR
1287.6121	1286.6048	1286.5891	0.0157	111 -	121	0	DQSSYLQGFSR
1343.6876	1342.6803	1342.6703	0.0100	242 -	253	0	EGALMLPHFNSK
1379.7799	1378.7726	1378.7608	0.0118	69 -	80	0	IPSGFISYILNR
1572.7579	1571.7506	1571.7426	0.0080	138 -	151	0	VLLEENAGGEQEER
1738.8466	1737.8393	1737.8321	0.0072	122 -	136	0	NTLEAAFNAEFNEIR
1817.9814	1816.9741	1816.9570	0.0171	343 -	358	1	IFLAGDKDNVIDQIEK
1894.9453	1893.9380	1893.9332	0.0048	122 -	137	1	NTLEAAFNAEFNEIRR
2227.0461	2226.0388	2226.0415	-0.0027	91 -	110	0	ISMPVNTPGQFEDFFPASSR
2619.2749	2618.2676	2618.3160	-0.0484	32 -	56	0	HADADNILVIQQGQATVTVANGNNR

No match to: 740.3815, 756.3749, 808.3777, 812.4006, 855.5176, 1005.5390, 1019.4731, 1080.5404, 1111.5596, 1141.5519, 1167.5770, 1297.6549, 1320.5964, 1375.7365, 1560.7048, 1568.7214, 1586.7701, 1643.8082, 1756.8466, 1771.8901, 1774.8644, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

8. gi|46560474 **Mass:** 33641 **Score:** 42 **Expect:** 0.062 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6423	1127.6350	1127.6298	0.0052	141 -	151	0	GTGNLELVAVR
1343.6876	1342.6803	1342.6703	0.0100	120 -	131	0	EGALMLPHFNSK
1572.7579	1571.7506	1571.7426	0.0080	15 -	28	0	VLLEENAGGEQEER
1643.8082	1642.8009	1642.7798	0.0212	67 -	81	0	GSEEEGDITNPINLR
1771.8901	1770.8828	1770.8747	0.0081	66 -	81	1	KGSEEEGDITNPINLR
1817.9814	1816.9741	1816.9570	0.0171	221 -	236	1	IFLAGDKDNVIDQIEK

No match to: 740.3815, 756.3749, 808.3777, 812.4006, 855.5176, 896.4360, 1005.5390, 1019.4731, 1080.5404, 1111.5596, 1141.5519, 1167.5770, 1184.6041, 1258.6292, 1287.6121, 1297.6549, 1320.5964, 1375.7365, 1379.7799, 1560.7048, 1568.7214, 1586.7701, 1738.8466, 1756.8466, 1774.8644, 1894.9453, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2227.0461, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2619.2749, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

9. gi|46560472 **Mass:** 34169 **Score:** 39 **Expect:** 0.1 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6423	1127.6350	1127.6298	0.0052	142	152	0	GTGNLELVAVR
1320.5964	1319.5891	1319.5741	0.0150	83	94	0	DGEPDLSNNFGR
1343.6876	1342.6803	1342.6703	0.0100	121	132	0	EGALMLPHFNSK
1572.7579	1571.7506	1571.7426	0.0080	18	31	0	VLLEENAGGEQEER
1586.7701	1585.7628	1585.7583	0.0045	69	82	0	GSEEEDITNPINLR
1817.9814	1816.9741	1816.9570	0.0171	225	240	1	IFLAGDKDNVIDQIEK

No match to: 740.3815, 756.3749, 808.3777, 812.4006, 855.5176, 896.4360, 1005.5390, 1019.4731, 1080.5404, 1111.5596, 1141.5519, 1167.5770, 1184.6041, 1258.6292, 1287.6121, 1297.6549, 1375.7365, 1379.7799, 1560.7048, 1568.7214, 1643.8082, 1738.8466, 1756.8466, 1771.8901, 1774.8644, 1894.9453, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2227.0461, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2619.2749, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

10. gi|62177652 **Mass:** 10056 **Score:** 19 **Expect:** 11 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1379.7799	1378.7726	1378.7496	0.0231	77	89	1	EVVKYSGGLPFAL
1894.9453	1893.9380	1893.9009	0.0372	7	23	0	QLEYLGGEQAWFGPGSR

No match to: 740.3815, 756.3749, 808.3777, 812.4006, 855.5176, 896.4360, 1005.5390, 1019.4731, 1080.5404, 1111.5596, 1128.6423, 1141.5519, 1167.5770, 1184.6041, 1258.6292, 1287.6121, 1297.6549, 1320.5964, 1343.6876, 1375.7365, 1560.7048, 1568.7214, 1572.7579, 1586.7701, 1643.8082, 1738.8466, 1756.8466, 1771.8901, 1774.8644, 1817.9814, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2227.0461, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2619.2749, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|46560478** Score: **206** Expect: **2.2e-018**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **23**
Sequence Coverage: **43%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
109 - 115	812.4006	811.3933	811.3976	-0.0043	0	WGPAEPR
118 - 124	1019.4731	1018.4658	1018.4468	0.0190	1	EREEDWR
132 - 139	1005.5390	1004.5317	1004.5264	0.0053	0	RPSHQQPR
140 - 146	855.5176	854.5103	854.5086	0.0017	1	KIRPEGR
147 - 160	1560.7048	1559.6975	1559.6851	0.0124	0	EGEQEWGTPGSEVR
166 - 174	1141.5519	1140.5446	1140.5352	0.0094	0	NNPFYFPSR
166 - 175	1297.6549	1296.6476	1296.6363	0.0113	1	NNPFYFPSRR
180 - 186	808.3777	807.3704	807.3623	0.0081	0	YGNQNGR
199 - 207	1184.6041	1183.5968	1183.5846	0.0122	0	QFQNLQNHR
223 - 247	2619.2749	2618.2676	2618.3160	-0.0484	0	HADADNILVIQQGQATVTVANGNNR
249 - 259	1258.6292	1257.6219	1257.6101	0.0118	0	SFNLDEGHALR
260 - 271	1379.7799	1378.7726	1378.7608	0.0118	0	IPSGFISYILNR
272 - 278	896.4360	895.4287	895.4260	0.0027	0	HDNQNLR

282 - 301	2227.0461	2226.0388	2226.0415	-0.0027	0	ISMPVNTPGQFEDFFPASSR
302 - 312	1287.6121	1286.6048	1286.5891	0.0157	0	DQSSYLQGFSR
313 - 327	1738.8466	1737.8393	1737.8321	0.0072	0	NTLEAAFNAEFNEIR
313 - 328	1894.9453	1893.9380	1893.9332	0.0048	1	NTLEAAFNAEFNEIRR
329 - 342	1572.7579	1571.7506	1571.7426	0.0080	0	VLLEENAGGEQEER
380 - 393	1586.7701	1585.7628	1585.7583	0.0045	0	GSEEEDITNPINLR
394 - 405	1320.5964	1319.5891	1319.5741	0.0150	0	DGEPDLSNNFGR
432 - 443	1343.6876	1342.6803	1342.6703	0.0100	0	EGALMLPHFNSK
453 - 463	1128.6423	1127.6350	1127.6298	0.0052	0	GTGNLELVAVR
536 - 551	1817.9814	1816.9741	1816.9570	0.0171	1	IFLAGDKDNVIDQIEK

No match to: 740.3815, 756.3749, 1080.5404, 1111.5596, 1167.5770, 1375.7365, 1568.7214, 1643.8082, 1756.8466, 1771.8901, 1774.8644, 2146.5845, 2185.0310, 2192.9988, 2201.0046, 2256.6917, 2273.1587, 2295.1426, 2311.1211, 2332.0723, 2612.1514, 2748.3745, 2926.3096, 3136.3982, 3153.4116, 3211.4299, 3300.6743

Spot 16

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:32:03 GMT**
Top Score : **54 for gi|16612200, major allergen Arah1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|16612200	71701	54	major allergen Arah1 [Arachis hypogaea]
2.	gi|1168391	71701	54	Allergen Ara h 1, clone P41B precursor (Ara h I)
3.	gi|602436	71701	54	Ara h I
4.	gi|46560476	48122	50	conarachin [Arachis hypogaea]
5.	gi|46560478	66934	43	conarachin [Arachis hypogaea]
6.	gi|620025	70639	42	Ara h I
7.	gi|1168390	70639	42	Allergen Ara h 1, clone P17 precursor (Ara h I)
8.	gi|230338	23975	25	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
9.	gi|62177652	10056	20	resistance protein PRG [Arachis hypogaea]
10.	gi|62361235	16047	15	resistance protein PLTR [Arachis hypogaea]

Results List

1. gi|16612200 **Mass:** 71701 **Score:** 54 **Expect:** 0.0034 **Queries matched:** 9
major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5830	1183.5757	1183.5846	-0.0089	205	213	0	QFQNLQNHR
1258.6074	1257.6001	1257.6101	-0.0100	255	265	0	SFNLDEGHALR
1287.6085	1286.6012	1286.5891	0.0121	308	318	0	DQSSYLQGFSR
1297.6479	1296.6406	1296.6363	0.0043	172	181	1	NNPFYFPSRR
1379.7893	1378.7820	1378.7608	0.0212	266	277	0	IPSGFISYILNR
1572.7356	1571.7283	1571.7426	-0.0143	335	348	0	VLLEENAGGEQEER
1738.8674	1737.8601	1737.8321	0.0280	319	333	0	NTLEAAFNAEFNEIR
1771.8800	1770.8727	1770.8747	-0.0020	386	401	1	KGSEEEGDITNPINLR
1894.9478	1893.9405	1893.9332	0.0073	319	334	1	NTLEAAFNAEFNEIRR

No match to: 805.4424, 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1046.5890, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 2146.5923, 2162.0281, 2185.0403, 2273.1626, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2514.3855, 2530.3003, 2612.1467, 3136.4341, 3211.5200, 3300.7344, 3316.7712

2. gi|1168391 **Mass:** 71701 **Score:** 54 **Expect:** 0.0034 **Queries matched:** 9

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5830	1183.5757	1183.5846	-0.0089	205	213	0	QFQNLQNHR
1258.6074	1257.6001	1257.6101	-0.0100	255	265	0	SFNLDEGHALR
1287.6085	1286.6012	1286.5891	0.0121	308	318	0	DQSSYLQGFSR
1297.6479	1296.6406	1296.6363	0.0043	172	181	1	NNPFYFPSRR
1379.7893	1378.7820	1378.7608	0.0212	266	277	0	IPSGFISYILNR
1572.7356	1571.7283	1571.7426	-0.0143	335	348	0	VLLEENAGGEQEER
1738.8674	1737.8601	1737.8321	0.0280	319	333	0	NTLEAAFNAEFNEIR
1771.8800	1770.8727	1770.8747	-0.0020	386	401	1	KGSEEEGDITNPINLR
1894.9478	1893.9405	1893.9332	0.0073	319	334	1	NTLEAAFNAEFNEIRR

No match to: 805.4424, 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1046.5890, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 2146.5923, 2162.0281, 2185.0403, 2273.1626, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2514.3855, 2530.3003, 2612.1467, 3136.4341, 3211.5200, 3300.7344, 3316.7712

3. gi|602436 **Mass:** 71701 **Score:** 54 **Expect:** 0.0034 **Queries matched:** 9

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5830	1183.5757	1183.5846	-0.0089	205	213	0	QFQNLQNHR
1258.6074	1257.6001	1257.6101	-0.0100	255	265	0	SFNLDEGHALR
1287.6085	1286.6012	1286.5891	0.0121	308	318	0	DQSSYLQGFSR
1297.6479	1296.6406	1296.6363	0.0043	172	181	1	NNPFYFPSRR
1379.7893	1378.7820	1378.7608	0.0212	266	277	0	IPSGFISYILNR
1572.7356	1571.7283	1571.7426	-0.0143	335	348	0	VLLEENAGGEQEER
1738.8674	1737.8601	1737.8321	0.0280	319	333	0	NTLEAAFNAEFNEIR
1771.8800	1770.8727	1770.8747	-0.0020	386	401	1	KGSEEEGDITNPINLR
1894.9478	1893.9405	1893.9332	0.0073	319	334	1	NTLEAAFNAEFNEIRR

No match to: 805.4424, 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1046.5890, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 2146.5923, 2162.0281, 2185.0403, 2273.1626, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2514.3855, 2530.3003, 2612.1467, 3136.4341,

3211.5200, 3300.7344, 3316.7712

4. gi|46560476 **Mass:** 48122 **Score:** 50 **Expect:** 0.0094 **Queries matched:** 7

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5830	1183.5757	1183.5846	-0.0089	8	16	0	QFQNLQNHR
1258.6074	1257.6001	1257.6101	-0.0100	58	68	0	SFNLDEGHALR
1287.6085	1286.6012	1286.5891	0.0121	111	121	0	DQSSYLQGFSR
1379.7893	1378.7820	1378.7608	0.0212	69	80	0	IPSGFISYILNR
1572.7356	1571.7283	1571.7426	-0.0143	138	151	0	VLLEENAGGEQEER
1738.8674	1737.8601	1737.8321	0.0280	122	136	0	NTLEAAFNAEFNEIR
1894.9478	1893.9405	1893.9332	0.0073	122	137	1	NTLEAAFNAEFNEIRR

No match to: 805.4424, 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1046.5890, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 1297.6479, 1771.8800, 2146.5923, 2162.0281, 2185.0403, 2273.1626, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2514.3855, 2530.3003, 2612.1467, 3136.4341, 3211.5200, 3300.7344, 3316.7712

5. gi|46560478 **Mass:** 66934 **Score:** 43 **Expect:** 0.043 **Queries matched:** 8

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5830	1183.5757	1183.5846	-0.0089	199	207	0	QFQNLQNHR
1258.6074	1257.6001	1257.6101	-0.0100	249	259	0	SFNLDEGHALR
1287.6085	1286.6012	1286.5891	0.0121	302	312	0	DQSSYLQGFSR
1297.6479	1296.6406	1296.6363	0.0043	166	175	1	NNPFYFPSRR
1379.7893	1378.7820	1378.7608	0.0212	260	271	0	IPSGFISYILNR
1572.7356	1571.7283	1571.7426	-0.0143	329	342	0	VLLEENAGGEQEER
1738.8674	1737.8601	1737.8321	0.0280	313	327	0	NTLEAAFNAEFNEIR
1894.9478	1893.9405	1893.9332	0.0073	313	328	1	NTLEAAFNAEFNEIRR

No match to: 805.4424, 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1046.5890, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 1771.8800, 2146.5923, 2162.0281, 2185.0403, 2273.1626, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2514.3855, 2530.3003, 2612.1467, 3136.4341, 3211.5200, 3300.7344, 3316.7712

6. gi|620025 **Mass:** 70639 **Score:** 42 **Expect:** 0.061 **Queries matched:** 8

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1184.5830	1183.5757	1183.5846	-0.0089	199 - 207	0	QFQNLQNHR
1258.6074	1257.6001	1257.6101	-0.0100	249 - 259	0	SFNLDEGHALR
1287.6085	1286.6012	1286.5891	0.0121	302 - 312	0	DQSSYLQGFSR
1297.6479	1296.6406	1296.6363	0.0043	166 - 175	1	NNPFYFPSRR
1379.7893	1378.7820	1378.7608	0.0212	260 - 271	0	IPSGFISYILNR
1572.7356	1571.7283	1571.7426	-0.0143	329 - 342	0	VLLEENAGGEQEER
1738.8674	1737.8601	1737.8321	0.0280	313 - 327	0	NTLEAAFNAEFNEIR
1894.9478	1893.9405	1893.9332	0.0073	313 - 328	1	NTLEAAFNAEFNEIRR

No match to: 805.4424, 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1046.5890, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 1771.8800, 2146.5923, 2162.0281, 2185.0403, 2273.1626, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2514.3855, 2530.3003, 2612.1467, 3136.4341, 3211.5200, 3300.7344, 3316.7712

7. gi|1168390 **Mass:** 70639 **Score:** 42 **Expect:** 0.061 **Queries matched:** 8

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5830	1183.5757	1183.5846	-0.0089	199 - 207		0	QFQNLQNHR
1258.6074	1257.6001	1257.6101	-0.0100	249 - 259		0	SFNLDEGHALR
1287.6085	1286.6012	1286.5891	0.0121	302 - 312		0	DQSSYLQGFSR
1297.6479	1296.6406	1296.6363	0.0043	166 - 175		1	NNPFYFPSRR
1379.7893	1378.7820	1378.7608	0.0212	260 - 271		0	IPSGFISYILNR
1572.7356	1571.7283	1571.7426	-0.0143	329 - 342		0	VLLEENAGGEQEER
1738.8674	1737.8601	1737.8321	0.0280	313 - 327		0	NTLEAAFNAEFNEIR
1894.9478	1893.9405	1893.9332	0.0073	313 - 328		1	NTLEAAFNAEFNEIRR

No match to: 805.4424, 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1046.5890, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 1771.8800, 2146.5923, 2162.0281, 2185.0403, 2273.1626, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2514.3855, 2530.3003, 2612.1467, 3136.4341, 3211.5200, 3300.7344, 3316.7712

8. gi|230338 **Mass:** 23975 **Score:** 25 **Expect:** 2.7 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.5890	1045.5817	1045.5880	-0.0062	90 -	99	1	LKSAASLNSR
2273.1626	2272.1553	2272.1521	0.0032	70 -	89	0	SIVHPSYNSNTLNNDIMLIK
2514.3855	2513.3782	2513.3311	0.0471	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK
2530.3003	2529.2930	2529.3260	-0.0330	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4424, 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 1184.5830, 1258.6074, 1287.6085, 1297.6479, 1379.7893, 1572.7356, 1738.8674, 1771.8800, 1894.9478, 2146.5923, 2162.0281, 2185.0403, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2612.1467, 3136.4341, 3211.5200, 3300.7344, 3316.7712

9. gi|62177652 **Mass:** 10056 **Score:** 20 **Expect:** 8 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1379.7893	1378.7820	1378.7496	0.0325	77	-	89	1	EVVKYSGGLPFAL
1894.9478	1893.9405	1893.9009	0.0397	7	-	23	0	QLEYLGGEQAWFGPGSR

No match to: 805.4424, 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1046.5890, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 1184.5830, 1258.6074, 1287.6085, 1297.6479, 1572.7356, 1738.8674, 1771.8800, 2146.5923, 2162.0281, 2185.0403, 2273.1626, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2514.3855, 2530.3003, 2612.1467, 3136.4341, 3211.5200, 3300.7344, 3316.7712

10. gi|62361235 **Mass:** 16047 **Score:** 15 **Expect:** 30 **Queries matched:** 2

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
805.4424	804.4351	804.4163	0.0188	1	-	9	0	SIGMGGVGK
2185.0403	2184.0330	2184.0785	-0.0455	90	-	108	1	LEQLRMIAGGLDWFGYGSR + Oxidation (M)

No match to: 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1046.5890, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 1184.5830, 1258.6074, 1287.6085, 1297.6479, 1379.7893, 1572.7356, 1738.8674, 1771.8800, 1894.9478, 2146.5923, 2162.0281, 2273.1626, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2514.3855, 2530.3003, 2612.1467, 3136.4341, 3211.5200, 3300.7344, 3316.7712

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 42

Protein View

Match to: **gi|16612200** Score: **54** Expect: **0.0034**
major allergen Arah1 [Arachis hypogaea]

Nominal mass (M_r): **71701**; Calculated pI value: **6.62**
NCBI BLAST search of gi|16612200 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **42**
Number of mass values matched: **9**
Sequence Coverage: **15%**

Matched peptides shown in **Bold Red**

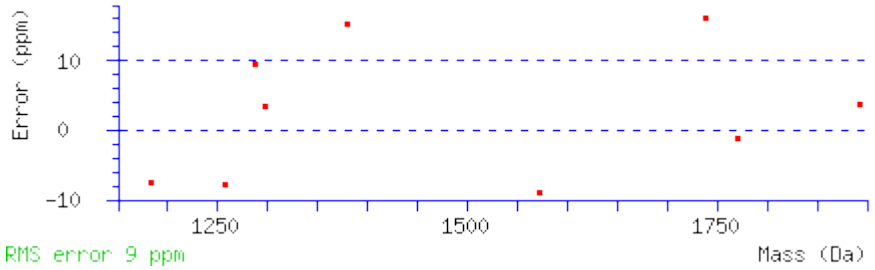
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     1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP
    51 DDLKQKACES RCTKLEYDPR CVYDPRGHTG TTNQRSPPGE RTRGRQPGDY
   101 DDDRRQPRRE EGGRWGPAGP RERERREEDWR QPREDWRRPS HQQPRKIRPE
   151 GREGEQEWGT PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD
   201 QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ GQATVTVANG
   251 NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED
   301 FFPASSRDQS SYLQGFSRNT LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ
   351 RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
   401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS
   451 KAMVIVVVNK GTGNLELVAV RKEQQQRGRR EEEEDEDEEE EGSNREVRRY
   501 TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV
   551 IDQIEKQAKD LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE
   601 SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
172 - 181	1297.6479	1296.6406	1296.6363	0.0043	1	NNPFYFPSRR
205 - 213	1184.5830	1183.5757	1183.5846	-0.0089	0	QFQNLQNHR
255 - 265	1258.6074	1257.6001	1257.6101	-0.0100	0	SFNLDEGHALR
266 - 277	1379.7893	1378.7820	1378.7608	0.0212	0	IPSGFISYILNR
308 - 318	1287.6085	1286.6012	1286.5891	0.0121	0	DQSSYLQGFSR
319 - 333	1738.8674	1737.8601	1737.8321	0.0280	0	NTLEAAFNAEFNEIR
319 - 334	1894.9478	1893.9405	1893.9332	0.0073	1	NTLEAAFNAEFNEIRR
335 - 348	1572.7356	1571.7283	1571.7426	-0.0143	0	VLLEENAGGEQEER

386 - 401 1771.8800 1770.8727 1770.8747 -0.0020 1 KGSEEEGDITNPINLR

No match to: 805.4424, 845.0993, 855.0521, 861.0754, 877.0596, 881.2827, 1046.5890, 1050.0945, 1066.0677, 1111.5665, 1137.0883, 1137.5769, 1143.5614, 1145.0673, 1145.5697, 1167.5801, 2146.5923, 2162.0281, 2185.0403, 2273.1626, 2295.1387, 2305.1853, 2311.1455, 2313.1367, 2334.1504, 2351.1182, 2514.3855, 2530.3003, 2612.1467, 3136.4341, 3211.5200, 3300.7344, 3316.7712



Spot 17

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:35:38 GMT
Top Score : 108 for gi|16612200, major allergen Arah1 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|16612200	71701	108	major allergen Arah1 [Arachis hypogaea]
2.	gi|1168391	71701	108	Allergen Ara h 1, clone P41B precursor (Ara h I)
3.	gi|602436	71701	108	Ara h I
4.	gi|46560478	66934	97	conarachin [Arachis hypogaea]
5.	gi|620025	70639	95	Ara h I
6.	gi|1168390	70639	95	Allergen Ara h 1, clone P17 precursor (Ara h I)
7.	gi|46560476	48122	78	conarachin [Arachis hypogaea]
8.	gi|62177385	14731	25	resistance protein Cre [Arachis hypogaea]
9.	gi|46560474	33641	23	conarachin [Arachis hypogaea]
10.	gi|46560472	34169	22	conarachin [Arachis hypogaea]

Results List

1. gi|16612200 **Mass:** 71701 **Score:** 108 **Expect:** 1.4e-008 **Queries matched:** 15
major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5231	1004.5158	1004.5264	-0.0106	138	145	0	RPSHQQPR
1141.5486	1140.5413	1140.5352	0.0061	172	180	0	NNPFYFPSR
1184.6028	1183.5955	1183.5846	0.0109	205	213	0	QFQNLQNHR
1258.5948	1257.5875	1257.6101	-0.0226	255	265	0	SFNLDEGHALR
1287.5936	1286.5863	1286.5891	-0.0028	308	318	0	DQSSYLQGFSR
1297.6406	1296.6333	1296.6363	-0.0030	172	181	1	NNPFYFPSRR
1376.6606	1375.6533	1375.6619	-0.0086	560	572	0	DLAFPGSGEQVEK
1427.7129	1426.7056	1426.7177	-0.0121	203	213	1	SRQFQNLQNHR
1568.6865	1567.6792	1567.7015	-0.0222	153	166	0	EGEQEWGTPGSHVR

1572.7402	1571.7329	1571.7426	-0.0097	335 - 348	0	VLLEENAGGEQEER
1728.8256	1727.8183	1727.8437	-0.0254	334 - 348	1	RVLLEENAGGEQEER
1738.8058	1737.7985	1737.8321	-0.0336	319 - 333	0	NTLEAAFNAEFNEIR
1771.8815	1770.8742	1770.8747	-0.0005	386 - 401	1	KGSEEEGDITNPINLR
1894.9221	1893.9148	1893.9332	-0.0184	319 - 334	1	NTLEAAFNAEFNEIRR
2619.3320	2618.3247	2618.3160	0.0087	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1050.0919, 1066.0786, 1080.5289, 1082.0463, 1111.5627, 1137.0779, 1137.5735, 1145.0774, 1145.5640, 1167.5822, 1320.5846, 1399.7168, 1730.8546, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2295.1538, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 3136.5237, 3211.5962, 3300.8435, 3317.8713

2. gi|1168391 **Mass:** 71701 **Score:** 108 **Expect:** 1.4e-008 **Queries matched:** 15

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5231	1004.5158	1004.5264	-0.0106	138 - 145		0	RPSHQQPR
1141.5486	1140.5413	1140.5352	0.0061	172 - 180		0	NNPFYFPSR
1184.6028	1183.5955	1183.5846	0.0109	205 - 213		0	QFQNLQNHR
1258.5948	1257.5875	1257.6101	-0.0226	255 - 265		0	SFNLDEGHALR
1287.5936	1286.5863	1286.5891	-0.0028	308 - 318		0	DQSSYLQGFSR
1297.6406	1296.6333	1296.6363	-0.0030	172 - 181		1	NNPFYFPSRR
1376.6606	1375.6533	1375.6619	-0.0086	560 - 572		0	DLAFPGSGEQVEK
1427.7129	1426.7056	1426.7177	-0.0121	203 - 213		1	SRQFQNLQNHR
1568.6865	1567.6792	1567.7015	-0.0222	153 - 166		0	EGEQEWGTPGSHVR
1572.7402	1571.7329	1571.7426	-0.0097	335 - 348		0	VLLEENAGGEQEER
1728.8256	1727.8183	1727.8437	-0.0254	334 - 348		1	RVLLEENAGGEQEER
1738.8058	1737.7985	1737.8321	-0.0336	319 - 333		0	NTLEAAFNAEFNEIR
1771.8815	1770.8742	1770.8747	-0.0005	386 - 401		1	KGSEEEGDITNPINLR
1894.9221	1893.9148	1893.9332	-0.0184	319 - 334		1	NTLEAAFNAEFNEIRR
2619.3320	2618.3247	2618.3160	0.0087	229 - 253		0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1050.0919, 1066.0786, 1080.5289, 1082.0463, 1111.5627, 1137.0779, 1137.5735, 1145.0774, 1145.5640, 1167.5822, 1320.5846, 1399.7168, 1730.8546, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2295.1538, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 3136.5237, 3211.5962, 3300.8435, 3317.8713

3. gi|602436 **Mass:** 71701 **Score:** 108 **Expect:** 1.4e-008 **Queries matched:** 15

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1005.5231	1004.5158	1004.5264	-0.0106	138 - 145	0	RPSHQQPR
1141.5486	1140.5413	1140.5352	0.0061	172 - 180	0	NNPFYFPSR
1184.6028	1183.5955	1183.5846	0.0109	205 - 213	0	QFQNLQNHR
1258.5948	1257.5875	1257.6101	-0.0226	255 - 265	0	SFNLDEGHALR
1287.5936	1286.5863	1286.5891	-0.0028	308 - 318	0	DQSSYLQGFSR
1297.6406	1296.6333	1296.6363	-0.0030	172 - 181	1	NNPFYFPSRR
1376.6606	1375.6533	1375.6619	-0.0086	560 - 572	0	DLAFPGSGEQVEK
1427.7129	1426.7056	1426.7177	-0.0121	203 - 213	1	SRQFQNLQNHR
1568.6865	1567.6792	1567.7015	-0.0222	153 - 166	0	EGEQEWGTPGSHVR
1572.7402	1571.7329	1571.7426	-0.0097	335 - 348	0	VLLEENAGGEQEER
1728.8256	1727.8183	1727.8437	-0.0254	334 - 348	1	RVLLEENAGGEQEER
1738.8058	1737.7985	1737.8321	-0.0336	319 - 333	0	NTLEAAFNAEFNEIR
1771.8815	1770.8742	1770.8747	-0.0005	386 - 401	1	KGSEEEGDITNPINLR
1894.9221	1893.9148	1893.9332	-0.0184	319 - 334	1	NTLEAAFNAEFNEIRR
2619.3320	2618.3247	2618.3160	0.0087	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1050.0919, 1066.0786, 1080.5289, 1082.0463, 1111.5627, 1137.0779, 1137.5735, 1145.0774, 1145.5640, 1167.5822, 1320.5846, 1399.7168, 1730.8546, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2295.1538, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 3136.5237, 3211.5962, 3300.8435, 3317.8713

4. gi|46560478 **Mass:** 66934 **Score:** 97 **Expect:** 1.7e-007 **Queries matched:** 14

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5231	1004.5158	1004.5264	-0.0106	132 - 139		0	RPSHQQPR
1141.5486	1140.5413	1140.5352	0.0061	166 - 174		0	NNPFYFPSR
1184.6028	1183.5955	1183.5846	0.0109	199 - 207		0	QFQNLQNHR
1258.5948	1257.5875	1257.6101	-0.0226	249 - 259		0	SFNLDEGHALR
1287.5936	1286.5863	1286.5891	-0.0028	302 - 312		0	DQSSYLQGFSR
1297.6406	1296.6333	1296.6363	-0.0030	166 - 175		1	NNPFYFPSRR
1320.5846	1319.5773	1319.5741	0.0032	394 - 405		0	DGEPDLSNNFGR
1376.6606	1375.6533	1375.6619	-0.0086	555 - 567		0	DLAFPGSGEQVEK
1399.7168	1398.7095	1398.7116	-0.0021	197 - 207		1	SKQFQNLQNHR
1572.7402	1571.7329	1571.7426	-0.0097	329 - 342		0	VLLEENAGGEQEER
1728.8256	1727.8183	1727.8437	-0.0254	328 - 342		1	RVLLEENAGGEQEER
1738.8058	1737.7985	1737.8321	-0.0336	313 - 327		0	NTLEAAFNAEFNEIR
1894.9221	1893.9148	1893.9332	-0.0184	313 - 328		1	NTLEAAFNAEFNEIRR
2619.3320	2618.3247	2618.3160	0.0087	223 - 247		0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1050.0919, 1066.0786, 1080.5289, 1082.0463,

1111.5627, 1137.0779, 1137.5735, 1145.0774, 1145.5640, 1167.5822, 1427.7129, 1568.6865, 1730.8546, 1771.8815, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2295.1538, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 3136.5237, 3211.5962, 3300.8435, 3317.8713

5. gi|620025 **Mass:** 70639 **Score:** 95 **Expect:** 3e-007 **Queries matched:** 14

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5231	1004.5158	1004.5264	-0.0106	132	139	0	RPSHQQPR
1141.5486	1140.5413	1140.5352	0.0061	166	174	0	NNPFYFPSR
1184.6028	1183.5955	1183.5846	0.0109	199	207	0	QFQNLQNHR
1258.5948	1257.5875	1257.6101	-0.0226	249	259	0	SFNLDEGHALR
1287.5936	1286.5863	1286.5891	-0.0028	302	312	0	DQSSYLQGFSR
1297.6406	1296.6333	1296.6363	-0.0030	166	175	1	NNPFYFPSRR
1320.5846	1319.5773	1319.5741	0.0032	394	405	0	DGEPDLSNNFGR
1376.6606	1375.6533	1375.6619	-0.0086	555	567	0	DLAFPGSGEQVEK
1399.7168	1398.7095	1398.7116	-0.0021	197	207	1	SKQFQNLQNHR
1572.7402	1571.7329	1571.7426	-0.0097	329	342	0	VLLEENAGGEQEER
1728.8256	1727.8183	1727.8437	-0.0254	328	342	1	RVLLEENAGGEQEER
1738.8058	1737.7985	1737.8321	-0.0336	313	327	0	NTLEAAFNAEFNEIR
1894.9221	1893.9148	1893.9332	-0.0184	313	328	1	NTLEAAFNAEFNEIRR
2619.3320	2618.3247	2618.3160	0.0087	223	247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1050.0919, 1066.0786, 1080.5289, 1082.0463, 1111.5627, 1137.0779, 1137.5735, 1145.0774, 1145.5640, 1167.5822, 1427.7129, 1568.6865, 1730.8546, 1771.8815, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2295.1538, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 3136.5237, 3211.5962, 3300.8435, 3317.8713

6. gi|1168390 **Mass:** 70639 **Score:** 95 **Expect:** 3e-007 **Queries matched:** 14

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5231	1004.5158	1004.5264	-0.0106	132	139	0	RPSHQQPR
1141.5486	1140.5413	1140.5352	0.0061	166	174	0	NNPFYFPSR
1184.6028	1183.5955	1183.5846	0.0109	199	207	0	QFQNLQNHR
1258.5948	1257.5875	1257.6101	-0.0226	249	259	0	SFNLDEGHALR
1287.5936	1286.5863	1286.5891	-0.0028	302	312	0	DQSSYLQGFSR
1297.6406	1296.6333	1296.6363	-0.0030	166	175	1	NNPFYFPSRR
1320.5846	1319.5773	1319.5741	0.0032	394	405	0	DGEPDLSNNFGR
1376.6606	1375.6533	1375.6619	-0.0086	555	567	0	DLAFPGSGEQVEK
1399.7168	1398.7095	1398.7116	-0.0021	197	207	1	SKQFQNLQNHR

1572.7402	1571.7329	1571.7426	-0.0097	329 - 342	0	VLLEENAGGEQEER
1728.8256	1727.8183	1727.8437	-0.0254	328 - 342	1	RVLLEENAGGEQEER
1738.8058	1737.7985	1737.8321	-0.0336	313 - 327	0	NTLEAAFNAEFNEIR
1894.9221	1893.9148	1893.9332	-0.0184	313 - 328	1	NTLEAAFNAEFNEIRR
2619.3320	2618.3247	2618.3160	0.0087	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1050.0919, 1066.0786, 1080.5289, 1082.0463, 1111.5627, 1137.0779, 1137.5735, 1145.0774, 1145.5640, 1167.5822, 1427.7129, 1568.6865, 1730.8546, 1771.8815, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2295.1538, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 3136.5237, 3211.5962, 3300.8435, 3317.8713

7. gi|46560476 **Mass:** 48122 **Score:** 78 **Expect:** 1.4e-005 **Queries matched:** 10

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.6028	1183.5955	1183.5846	0.0109	8 -	16	0	QFQNLQNHR
1258.5948	1257.5875	1257.6101	-0.0226	58 -	68	0	SFNLDEGHALR
1287.5936	1286.5863	1286.5891	-0.0028	111 -	121	0	DQSSYLQGFSR
1376.6606	1375.6533	1375.6619	-0.0086	362 -	374	0	DLAFPGSGEQVEK
1427.7129	1426.7056	1426.7177	-0.0121	6 -	16	1	SRQFQNLQNHR
1572.7402	1571.7329	1571.7426	-0.0097	138 -	151	0	VLLEENAGGEQEER
1728.8256	1727.8183	1727.8437	-0.0254	137 -	151	1	RVLLEENAGGEQEER
1738.8058	1737.7985	1737.8321	-0.0336	122 -	136	0	NTLEAAFNAEFNEIR
1894.9221	1893.9148	1893.9332	-0.0184	122 -	137	1	NTLEAAFNAEFNEIRR
2619.3320	2618.3247	2618.3160	0.0087	32 -	56	0	HADADNILVIQQGQATVTVANGNNR

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1005.5231, 1050.0919, 1066.0786, 1080.5289, 1082.0463, 1111.5627, 1137.0779, 1137.5735, 1141.5486, 1145.0774, 1145.5640, 1167.5822, 1297.6406, 1320.5846, 1399.7168, 1568.6865, 1730.8546, 1771.8815, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2295.1538, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 3136.5237, 3211.5962, 3300.8435, 3317.8713

8. gi|62177385 **Mass:** 14731 **Score:** 25 **Expect:** 3 **Queries matched:** 3

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1427.7129	1426.7056	1426.6986	0.0070	71 -	82	1	RNCPPELESIGR
1730.8546	1729.8473	1729.8787	-0.0314	1 -	14	1	NLILDDVWDSKAWR
2295.1538	2294.1465	2294.1147	0.0319	15 -	34	1	TIKNCFPENNNGGMILVTTR + Oxidation (M)

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1005.5231, 1050.0919, 1066.0786, 1080.5289, 1082.0463, 1111.5627, 1137.0779, 1137.5735, 1141.5486, 1145.0774, 1145.5640, 1167.5822, 1184.6028, 1258.5948,

1287.5936, 1297.6406, 1320.5846, 1376.6606, 1399.7168, 1568.6865, 1572.7402, 1728.8256, 1738.8058, 1771.8815, 1894.9221, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 2619.3320, 3136.5237, 3211.5962, 3300.8435, 3317.8713

9. gi|46560474 **Mass:** 33641 **Score:** 23 **Expect:** 4.2 **Queries matched:** 4

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1376.6606	1375.6533	1375.6619	-0.0086	240	-	252	0	DLAFPGSGEQVEK
1572.7402	1571.7329	1571.7426	-0.0097	15	-	28	0	VLLEENAGGEQEER
1728.8256	1727.8183	1727.8437	-0.0254	14	-	28	1	RVLLEENAGGEQEER
1771.8815	1770.8742	1770.8747	-0.0005	66	-	81	1	KGSEEEGDITNPINLR

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1005.5231, 1050.0919, 1066.0786, 1080.5289, 1082.0463, 1111.5627, 1137.0779, 1137.5735, 1141.5486, 1145.0774, 1145.5640, 1167.5822, 1184.6028, 1258.5948, 1287.5936, 1297.6406, 1320.5846, 1399.7168, 1427.7129, 1568.6865, 1730.8546, 1738.8058, 1894.9221, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2295.1538, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 2619.3320, 3136.5237, 3211.5962, 3300.8435, 3317.8713

10. gi|46560472 **Mass:** 34169 **Score:** 22 **Expect:** 6.1 **Queries matched:** 4

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1320.5846	1319.5773	1319.5741	0.0032	83	-	94	0	DGEPDLSNNFGR
1376.6606	1375.6533	1375.6619	-0.0086	244	-	256	0	DLAFPGSGEQVEK
1572.7402	1571.7329	1571.7426	-0.0097	18	-	31	0	VLLEENAGGEQEER
1728.8256	1727.8183	1727.8437	-0.0254	17	-	31	1	RVLLEENAGGEQEER

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1005.5231, 1050.0919, 1066.0786, 1080.5289, 1082.0463, 1111.5627, 1137.0779, 1137.5735, 1141.5486, 1145.0774, 1145.5640, 1167.5822, 1184.6028, 1258.5948, 1287.5936, 1297.6406, 1399.7168, 1427.7129, 1568.6865, 1730.8546, 1738.8058, 1771.8815, 1894.9221, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2295.1538, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 2619.3320, 3136.5237, 3211.5962, 3300.8435, 3317.8713

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm

Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 52

Protein View

Match to: **gi|16612200** Score: **108** Expect: **1.4e-008**
major allergen Arah1 [Arachis hypogaea]

Nominal mass (M_r): **71701**; Calculated pI value: **6.62**
NCBI BLAST search of gi|16612200 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **52**
Number of mass values matched: **15**
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP
    51 DDLKQKACES RCTKLEYDPR CVYDPRGHTG TTNQRSPPGE RTRGRQPGDY
   101 DDDRRQPRRE EGGRWGPAGP RERERREEDWR QPREDWRRPS HQQPRKIRPE
   151 GREGEQEWGT PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD
   201 QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ GQATVTVANG
   251 NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED
   301 FFPASSRDQS SYLQGFSRNT LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ
   351 RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
   401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS
   451 KAMVIVVVNK GTGNLELVAV RKEQQQRGRR EEEEDEDEEE EGSNREVRRY
   501 TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV
   551 IDQIEKQAKD LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE
   601 SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
138 - 145	1005.5231	1004.5158	1004.5264	-0.0106	0	RPSHQQPR
153 - 166	1568.6865	1567.6792	1567.7015	-0.0222	0	EGEQEWGTPGSHVR
172 - 180	1141.5486	1140.5413	1140.5352	0.0061	0	NNPFYFPSR
172 - 181	1297.6406	1296.6333	1296.6363	-0.0030	1	NNPFYFPSRR

203 - 213	1427.7129	1426.7056	1426.7177	-0.0121	1	SRQFQNLQNHR
205 - 213	1184.6028	1183.5955	1183.5846	0.0109	0	QFQNLQNHR
229 - 253	2619.3320	2618.3247	2618.3160	0.0087	0	HADADNILVIQQGQATVTVANGNNR
255 - 265	1258.5948	1257.5875	1257.6101	-0.0226	0	SFNLDEGHALR
308 - 318	1287.5936	1286.5863	1286.5891	-0.0028	0	DQSSYLQGFSR
319 - 333	1738.8058	1737.7985	1737.8321	-0.0336	0	NTLEAAFNAEFNEIR
319 - 334	1894.9221	1893.9148	1893.9332	-0.0184	1	NTLEAAFNAEFNEIRR
334 - 348	1728.8256	1727.8183	1727.8437	-0.0254	1	RVLLEENAGGEQEER
335 - 348	1572.7402	1571.7329	1571.7426	-0.0097	0	VLLEENAGGEQEER
386 - 401	1771.8815	1770.8742	1770.8747	-0.0005	1	KGSEEEGDITNPINLR
560 - 572	1376.6606	1375.6533	1375.6619	-0.0086	0	DLAFPGSGEQVEK

No match to: 805.4908, 839.0915, 845.1010, 855.0726, 861.0858, 877.0534, 1050.0919, 1066.0786, 1080.5289, 1082.0463, 1111.5627, 1137.0779, 1137.5735, 1145.0774, 1145.5640, 1167.5822, 1320.5846, 1399.7168, 1730.8546, 2050.9824, 2145.0637, 2146.6072, 2185.0347, 2227.1348, 2273.1616, 2295.1538, 2311.1382, 2334.1309, 2337.0779, 2351.1091, 2514.3606, 2530.3140, 2612.2312, 3136.5237, 3211.5962, 3300.8435, 3317.8713

Spot 18

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 4 May 2007 at 11:31:09 GMT
Top Score : 301 for gi|16612200, major allergen Arah1 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|16612200	71701	301	major allergen Arah1 [Arachis hypogaea]
2.	gi|1168391	71701	301	Allergen Ara h 1, clone P41B precursor (Ara h I)
3.	gi|602436	71701	301	Ara h I
4.	gi|46560478	66934	273	conarachin [Arachis hypogaea]
5.	gi|620025	70639	268	Ara h I
6.	gi|1168390	70639	268	Allergen Ara h 1, clone P17 precursor (Ara h I)
7.	gi|46560476	48122	192	conarachin [Arachis hypogaea]
8.	gi|46560474	33641	73	conarachin [Arachis hypogaea]
9.	gi|46560472	34169	50	conarachin [Arachis hypogaea]
10.	gi|62177652	10056	19	resistance protein PRG [Arachis hypogaea]

Results List

1. gi|16612200 **Mass:** 71701 **Score:** 301 **Expect:** 7e-028 **Queries matched:** 30
major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
727.4120	726.4047	726.4136	-0.0089	147	152	0	IRPEGR
740.3809	739.3736	739.3765	-0.0029	115	121	0	WGPAGPR
808.3682	807.3609	807.3623	-0.0014	186	192	0	YGNQNGR
816.4279	815.4206	815.4249	-0.0043	472	477	1	KEQQQR
855.5059	854.4986	854.5086	-0.0100	146	152	1	KIRPEGR
896.4286	895.4213	895.4260	-0.0047	278	284	0	HDNQNLR
972.5761	971.5688	971.5837	-0.0149	452	460	0	AMVIVVVNK
1005.5266	1004.5193	1004.5264	-0.0071	138	145	0	RPSHQQPR
1019.4446	1018.4373	1018.4468	-0.0095	124	130	1	EREEDWR
1128.6295	1127.6222	1127.6298	-0.0076	461	471	0	GTGNLELVAVR

1141.5363	1140.5290	1140.5352	-0.0062	172 - 180	0	NNPFYFPSR
1184.5852	1183.5779	1183.5846	-0.0067	205 - 213	0	QFQNLQNHR
1258.6086	1257.6013	1257.6101	-0.0088	255 - 265	0	SFNLDEGHALR
1287.5880	1286.5807	1286.5891	-0.0084	308 - 318	0	DQSSYLQGFSR
1297.6375	1296.6302	1296.6363	-0.0061	172 - 181	1	NNPFYFPSRR
1343.6626	1342.6553	1342.6703	-0.0150	440 - 451	0	EGALMLPHFNSK
1379.7607	1378.7534	1378.7608	-0.0074	266 - 277	0	IPSGFISYILNR
1386.7021	1385.6948	1385.7051	-0.0103	254 - 265	1	KSFNLDEGHALR
1568.6929	1567.6856	1567.7015	-0.0158	153 - 166	0	EGEQEWGTPGSHVR
1572.7305	1571.7232	1571.7426	-0.0194	335 - 348	0	VLLEENAGGEQEER
1643.7693	1642.7620	1642.7798	-0.0177	387 - 401	0	GSEEEGDITNPINLR
1738.8247	1737.8174	1737.8321	-0.0147	319 - 333	0	NTLEAAFNAEFNEIR
1771.8617	1770.8544	1770.8747	-0.0203	386 - 401	1	KGSEEEGDITNPINLR
1817.9468	1816.9395	1816.9570	-0.0175	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9192	1893.9119	1893.9332	-0.0213	319 - 334	1	NTLEAAFNAEFNEIRR
2082.1760	2081.1687	2081.2030	-0.0342	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0173	2226.0100	2226.0415	-0.0315	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0244	2242.0171	2242.0364	-0.0193	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2808	2618.2735	2618.3160	-0.0425	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.3794	2746.3721	2746.4110	-0.0388	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 723.3585, 756.3761, 772.3698, 812.4009, 932.4545, 1167.5571, 1206.5665, 1281.1873, 1319.6185, 1560.6783, 1760.8031, 2181.0642, 2184.9985, 2249.0046, 2273.1487, 2295.1162, 2316.0474, 2332.0483, 2620.2803, 2748.3638

2. gi|1168391 **Mass:** 71701 **Score:** 301 **Expect:** 7e-028 **Queries matched:** 30

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
727.4120	726.4047	726.4136	-0.0089	147 - 152		0	IRPEGR
740.3809	739.3736	739.3765	-0.0029	115 - 121		0	WGPAGPR
808.3682	807.3609	807.3623	-0.0014	186 - 192		0	YGNQNGR
816.4279	815.4206	815.4249	-0.0043	472 - 477		1	KEQQQR
855.5059	854.4986	854.5086	-0.0100	146 - 152		1	KIRPEGR
896.4286	895.4213	895.4260	-0.0047	278 - 284		0	HDNQNLR
972.5761	971.5688	971.5837	-0.0149	452 - 460		0	AMVIVVVNK
1005.5266	1004.5193	1004.5264	-0.0071	138 - 145		0	RPSHQQPR
1019.4446	1018.4373	1018.4468	-0.0095	124 - 130		1	EREEDWR
1128.6295	1127.6222	1127.6298	-0.0076	461 - 471		0	GTGNLELVAVR
1141.5363	1140.5290	1140.5352	-0.0062	172 - 180		0	NNPFYFPSR
1184.5852	1183.5779	1183.5846	-0.0067	205 - 213		0	QFQNLQNHR
1258.6086	1257.6013	1257.6101	-0.0088	255 - 265		0	SFNLDEGHALR

1287.5880	1286.5807	1286.5891	-0.0084	308 - 318	0	DQSSYLQGFSR
1297.6375	1296.6302	1296.6363	-0.0061	172 - 181	1	NNPFYFPSRR
1343.6626	1342.6553	1342.6703	-0.0150	440 - 451	0	EGALMLPHFNSK
1379.7607	1378.7534	1378.7608	-0.0074	266 - 277	0	IPSGFISYILNR
1386.7021	1385.6948	1385.7051	-0.0103	254 - 265	1	KSFNLDEGHALR
1568.6929	1567.6856	1567.7015	-0.0158	153 - 166	0	EGEQEWGTPGSHVR
1572.7305	1571.7232	1571.7426	-0.0194	335 - 348	0	VLLEENAGGEQEER
1643.7693	1642.7620	1642.7798	-0.0177	387 - 401	0	GSEEEGDITNPINLR
1738.8247	1737.8174	1737.8321	-0.0147	319 - 333	0	NTLEAAFNAEFNEIR
1771.8617	1770.8544	1770.8747	-0.0203	386 - 401	1	KGSEEEGDITNPINLR
1817.9468	1816.9395	1816.9570	-0.0175	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9192	1893.9119	1893.9332	-0.0213	319 - 334	1	NTLEAAFNAEFNEIRR
2082.1760	2081.1687	2081.2030	-0.0342	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0173	2226.0100	2226.0415	-0.0315	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0244	2242.0171	2242.0364	-0.0193	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2808	2618.2735	2618.3160	-0.0425	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.3794	2746.3721	2746.4110	-0.0388	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 723.3585, 756.3761, 772.3698, 812.4009, 932.4545, 1167.5571, 1206.5665, 1281.1873, 1319.6185, 1560.6783, 1760.8031, 2181.0642, 2184.9985, 2249.0046, 2273.1487, 2295.1162, 2316.0474, 2332.0483, 2620.2803, 2748.3638

3. gi|602436 **Mass:** 71701 **Score:** 301 **Expect:** 7e-028 **Queries matched:** 30

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
727.4120	726.4047	726.4136	-0.0089	147 - 152		0	IRPEGR
740.3809	739.3736	739.3765	-0.0029	115 - 121		0	WGPAGPR
808.3682	807.3609	807.3623	-0.0014	186 - 192		0	YGNQNGR
816.4279	815.4206	815.4249	-0.0043	472 - 477		1	KEQQQR
855.5059	854.4986	854.5086	-0.0100	146 - 152		1	KIRPEGR
896.4286	895.4213	895.4260	-0.0047	278 - 284		0	HDNQNLR
972.5761	971.5688	971.5837	-0.0149	452 - 460		0	AMVIVVVNK
1005.5266	1004.5193	1004.5264	-0.0071	138 - 145		0	RPSHQQPR
1019.4446	1018.4373	1018.4468	-0.0095	124 - 130		1	EREEDWR
1128.6295	1127.6222	1127.6298	-0.0076	461 - 471		0	GTGNLELVAVR
1141.5363	1140.5290	1140.5352	-0.0062	172 - 180		0	NNPFYFPSR
1184.5852	1183.5779	1183.5846	-0.0067	205 - 213		0	QFQNLQNHR
1258.6086	1257.6013	1257.6101	-0.0088	255 - 265		0	SFNLDEGHALR
1287.5880	1286.5807	1286.5891	-0.0084	308 - 318		0	DQSSYLQGFSR
1297.6375	1296.6302	1296.6363	-0.0061	172 - 181		1	NNPFYFPSRR
1343.6626	1342.6553	1342.6703	-0.0150	440 - 451		0	EGALMLPHFNSK

1379.7607	1378.7534	1378.7608	-0.0074	266 - 277	0	IPSGFISYILNR
1386.7021	1385.6948	1385.7051	-0.0103	254 - 265	1	KSFNLDEGHALR
1568.6929	1567.6856	1567.7015	-0.0158	153 - 166	0	EGEQEWGTPGSHVR
1572.7305	1571.7232	1571.7426	-0.0194	335 - 348	0	VLLEENAGGEQEER
1643.7693	1642.7620	1642.7798	-0.0177	387 - 401	0	GSEEEGDITNPINLR
1738.8247	1737.8174	1737.8321	-0.0147	319 - 333	0	NTLEAAFNAEFNEIR
1771.8617	1770.8544	1770.8747	-0.0203	386 - 401	1	KGSEEEGDITNPINLR
1817.9468	1816.9395	1816.9570	-0.0175	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9192	1893.9119	1893.9332	-0.0213	319 - 334	1	NTLEAAFNAEFNEIRR
2082.1760	2081.1687	2081.2030	-0.0342	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0173	2226.0100	2226.0415	-0.0315	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0244	2242.0171	2242.0364	-0.0193	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2808	2618.2735	2618.3160	-0.0425	229 - 253	0	HADADNILVIQQGQATVTVANGNNR
2747.3794	2746.3721	2746.4110	-0.0388	229 - 254	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 723.3585, 756.3761, 772.3698, 812.4009, 932.4545, 1167.5571, 1206.5665, 1281.1873, 1319.6185, 1560.6783, 1760.8031, 2181.0642, 2184.9985, 2249.0046, 2273.1487, 2295.1162, 2316.0474, 2332.0483, 2620.2803, 2748.3638

4. gi|46560478 **Mass:** 66934 **Score:** 273 **Expect:** 4.4e-025 **Queries matched:** 28

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
727.4120	726.4047	726.4136	-0.0089	141 - 146		0	IRPEGR
808.3682	807.3609	807.3623	-0.0014	180 - 186		0	YGNQNGR
812.4009	811.3936	811.3976	-0.0040	109 - 115		0	WGPAEPR
816.4279	815.4206	815.4249	-0.0043	464 - 469		1	KEQQQR
855.5059	854.4986	854.5086	-0.0100	140 - 146		1	KIRPEGR
896.4286	895.4213	895.4260	-0.0047	272 - 278		0	HDNQNLR
972.5761	971.5688	971.5837	-0.0149	444 - 452		0	AMVIVVVNK
1005.5266	1004.5193	1004.5264	-0.0071	132 - 139		0	RPSHQQPR
1019.4446	1018.4373	1018.4468	-0.0095	118 - 124		1	EREEDWR
1128.6295	1127.6222	1127.6298	-0.0076	453 - 463		0	GTGNLELVAVR
1141.5363	1140.5290	1140.5352	-0.0062	166 - 174		0	NNPFYFPSR
1184.5852	1183.5779	1183.5846	-0.0067	199 - 207		0	QFQNLQNHR
1258.6086	1257.6013	1257.6101	-0.0088	249 - 259		0	SFNLDEGHALR
1287.5880	1286.5807	1286.5891	-0.0084	302 - 312		0	DQSSYLQGFSR
1297.6375	1296.6302	1296.6363	-0.0061	166 - 175		1	NNPFYFPSRR
1343.6626	1342.6553	1342.6703	-0.0150	432 - 443		0	EGALMLPHFNSK
1379.7607	1378.7534	1378.7608	-0.0074	260 - 271		0	IPSGFISYILNR
1386.7021	1385.6948	1385.7051	-0.0103	248 - 259		1	KSFNLDEGHALR
1560.6783	1559.6710	1559.6851	-0.0141	147 - 160		0	EGEQEWGTPGSEVR

1572.7305	1571.7232	1571.7426	-0.0194	329 - 342	0	VLLEENAGGEQEER
1738.8247	1737.8174	1737.8321	-0.0147	313 - 327	0	NTLEAAFNAEFNEIR
1817.9468	1816.9395	1816.9570	-0.0175	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9192	1893.9119	1893.9332	-0.0213	313 - 328	1	NTLEAAFNAEFNEIRR
2082.1760	2081.1687	2081.2030	-0.0342	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0173	2226.0100	2226.0415	-0.0315	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0244	2242.0171	2242.0364	-0.0193	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2808	2618.2735	2618.3160	-0.0425	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3794	2746.3721	2746.4110	-0.0388	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 723.3585, 740.3809, 756.3761, 772.3698, 932.4545, 1167.5571, 1206.5665, 1281.1873, 1319.6185, 1568.6929, 1643.7693, 1760.8031, 1771.8617, 2181.0642, 2184.9985, 2249.0046, 2273.1487, 2295.1162, 2316.0474, 2332.0483, 2620.2803, 2748.3638

5. gi|620025 **Mass:** 70639 **Score:** 268 **Expect:** 1.4e-024 **Queries matched:** 28

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
727.4120	726.4047	726.4136	-0.0089	141 - 146		0	IRPEGR
808.3682	807.3609	807.3623	-0.0014	180 - 186		0	YGNQNGR
812.4009	811.3936	811.3976	-0.0040	109 - 115		0	WGPAEPR
816.4279	815.4206	815.4249	-0.0043	464 - 469		1	KEQQQR
855.5059	854.4986	854.5086	-0.0100	140 - 146		1	KIRPEGR
896.4286	895.4213	895.4260	-0.0047	272 - 278		0	HDNQNLR
972.5761	971.5688	971.5837	-0.0149	444 - 452		0	AMVIVVVNK
1005.5266	1004.5193	1004.5264	-0.0071	132 - 139		0	RPSHQQPR
1019.4446	1018.4373	1018.4468	-0.0095	118 - 124		1	EREEDWR
1128.6295	1127.6222	1127.6298	-0.0076	453 - 463		0	GTGNLELVAVR
1141.5363	1140.5290	1140.5352	-0.0062	166 - 174		0	NNPFYFPSR
1184.5852	1183.5779	1183.5846	-0.0067	199 - 207		0	QFQNLQNHR
1258.6086	1257.6013	1257.6101	-0.0088	249 - 259		0	SFNLDEGHALR
1287.5880	1286.5807	1286.5891	-0.0084	302 - 312		0	DQSSYLQGFSR
1297.6375	1296.6302	1296.6363	-0.0061	166 - 175		1	NNPFYFPSRR
1343.6626	1342.6553	1342.6703	-0.0150	432 - 443		0	EGALMLPHFNSK
1379.7607	1378.7534	1378.7608	-0.0074	260 - 271		0	IPSGFISYILNR
1386.7021	1385.6948	1385.7051	-0.0103	248 - 259		1	KSFNLDEGHALR
1560.6783	1559.6710	1559.6851	-0.0141	147 - 160		0	EGEQEWGTPGSEVR
1572.7305	1571.7232	1571.7426	-0.0194	329 - 342		0	VLLEENAGGEQEER
1738.8247	1737.8174	1737.8321	-0.0147	313 - 327		0	NTLEAAFNAEFNEIR
1817.9468	1816.9395	1816.9570	-0.0175	536 - 551		1	IFLAGDKDNVIDQIEK
1894.9192	1893.9119	1893.9332	-0.0213	313 - 328		1	NTLEAAFNAEFNEIRR
2082.1760	2081.1687	2081.2030	-0.0342	444 - 463		1	AMVIVVVNKGTGNLELVAVR

2227.0173	2226.0100	2226.0415	-0.0315	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0244	2242.0171	2242.0364	-0.0193	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2808	2618.2735	2618.3160	-0.0425	223 - 247	0	HADADNILVIQQGQATVTVANGNNR
2747.3794	2746.3721	2746.4110	-0.0388	223 - 248	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 723.3585, 740.3809, 756.3761, 772.3698, 932.4545, 1167.5571, 1206.5665, 1281.1873, 1319.6185, 1568.6929, 1643.7693, 1760.8031, 1771.8617, 2181.0642, 2184.9985, 2249.0046, 2273.1487, 2295.1162, 2316.0474, 2332.0483, 2620.2803, 2748.3638

6. gi|1168390 **Mass:** 70639 **Score:** 268 **Expect:** 1.4e-024 **Queries matched:** 28

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
727.4120	726.4047	726.4136	-0.0089	141 - 146		0	IRPEGR
808.3682	807.3609	807.3623	-0.0014	180 - 186		0	YGNQNGR
812.4009	811.3936	811.3976	-0.0040	109 - 115		0	WGPAEPR
816.4279	815.4206	815.4249	-0.0043	464 - 469		1	KEQQQR
855.5059	854.4986	854.5086	-0.0100	140 - 146		1	KIRPEGR
896.4286	895.4213	895.4260	-0.0047	272 - 278		0	HDNQNLR
972.5761	971.5688	971.5837	-0.0149	444 - 452		0	AMVIVVVNK
1005.5266	1004.5193	1004.5264	-0.0071	132 - 139		0	RPSHQQPR
1019.4446	1018.4373	1018.4468	-0.0095	118 - 124		1	EREEDWR
1128.6295	1127.6222	1127.6298	-0.0076	453 - 463		0	GTGNLELVAVR
1141.5363	1140.5290	1140.5352	-0.0062	166 - 174		0	NNPFYFPSR
1184.5852	1183.5779	1183.5846	-0.0067	199 - 207		0	QFQNLQNHR
1258.6086	1257.6013	1257.6101	-0.0088	249 - 259		0	SFNLDEGHALR
1287.5880	1286.5807	1286.5891	-0.0084	302 - 312		0	DQSSYLQGFSR
1297.6375	1296.6302	1296.6363	-0.0061	166 - 175		1	NNPFYFPSRR
1343.6626	1342.6553	1342.6703	-0.0150	432 - 443		0	EGALMLPHFNSK
1379.7607	1378.7534	1378.7608	-0.0074	260 - 271		0	IPSGFISYILNR
1386.7021	1385.6948	1385.7051	-0.0103	248 - 259		1	KSFNLDEGHALR
1560.6783	1559.6710	1559.6851	-0.0141	147 - 160		0	EGEQEWGTPGSEVR
1572.7305	1571.7232	1571.7426	-0.0194	329 - 342		0	VLLEENAGGEQEER
1738.8247	1737.8174	1737.8321	-0.0147	313 - 327		0	NTLEAAFNAEFNEIR
1817.9468	1816.9395	1816.9570	-0.0175	536 - 551		1	IFLAGDKDNVIDQIEK
1894.9192	1893.9119	1893.9332	-0.0213	313 - 328		1	NTLEAAFNAEFNEIRR
2082.1760	2081.1687	2081.2030	-0.0342	444 - 463		1	AMVIVVVNKGTGNLELVAVR
2227.0173	2226.0100	2226.0415	-0.0315	282 - 301		0	ISMPVNTPGQFEDFFPASSR
2243.0244	2242.0171	2242.0364	-0.0193	282 - 301		0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2808	2618.2735	2618.3160	-0.0425	223 - 247		0	HADADNILVIQQGQATVTVANGNNR
2747.3794	2746.3721	2746.4110	-0.0388	223 - 248		1	HADADNILVIQQGQATVTVANGNNRK

No match to: 723.3585, 740.3809, 756.3761, 772.3698, 932.4545, 1167.5571, 1206.5665, 1281.1873, 1319.6185, 1568.6929, 1643.7693, 1760.8031, 1771.8617, 2181.0642, 2184.9985, 2249.0046, 2273.1487, 2295.1162, 2316.0474,

2332.0483, 2620.2803, 2748.3638

7. gi|46560476 **Mass:** 48122 **Score:** 192 **Expect:** 5.5e-017 **Queries matched:** 19

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4279	815.4206	815.4249	-0.0043	274	279	1	KEQQQR
896.4286	895.4213	895.4260	-0.0047	81	87	0	HDNQNLR
972.5761	971.5688	971.5837	-0.0149	254	262	0	AMVIVVVNK
1128.6295	1127.6222	1127.6298	-0.0076	263	273	0	GTGNLELVAVR
1184.5852	1183.5779	1183.5846	-0.0067	8	16	0	QFQNLQNHR
1258.6086	1257.6013	1257.6101	-0.0088	58	68	0	SFNLDEGHALR
1287.5880	1286.5807	1286.5891	-0.0084	111	121	0	DQSSYLQGFSR
1343.6626	1342.6553	1342.6703	-0.0150	242	253	0	EGALMLPHFNSK
1379.7607	1378.7534	1378.7608	-0.0074	69	80	0	IPSGFISYILNR
1386.7021	1385.6948	1385.7051	-0.0103	57	68	1	KSFNLDEGHALR
1572.7305	1571.7232	1571.7426	-0.0194	138	151	0	VLLEENAGGEQEER
1738.8247	1737.8174	1737.8321	-0.0147	122	136	0	NTLEAAFNAEFNEIR
1817.9468	1816.9395	1816.9570	-0.0175	343	358	1	IFLAGDKDNVIDQIEK
1894.9192	1893.9119	1893.9332	-0.0213	122	137	1	NTLEAAFNAEFNEIRR
2082.1760	2081.1687	2081.2030	-0.0342	254	273	1	AMVIVVVNKGTGNLELVAVR
2227.0173	2226.0100	2226.0415	-0.0315	91	110	0	ISMPVNTPGQFEDFFPASSR
2243.0244	2242.0171	2242.0364	-0.0193	91	110	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2808	2618.2735	2618.3160	-0.0425	32	56	0	HADADNILVIQQGQATVTVANGNNR
2747.3794	2746.3721	2746.4110	-0.0388	32	57	1	HADADNILVIQQGQATVTVANGNNRK

No match to: 723.3585, 727.4120, 740.3809, 756.3761, 772.3698, 808.3682, 812.4009, 855.5059, 932.4545, 1005.5266, 1019.4446, 1141.5363, 1167.5571, 1206.5665, 1281.1873, 1297.6375, 1319.6185, 1560.6783, 1568.6929, 1643.7693, 1760.8031, 1771.8617, 2181.0642, 2184.9985, 2249.0046, 2273.1487, 2295.1162, 2316.0474, 2332.0483, 2620.2803, 2748.3638

8. gi|46560474 **Mass:** 33641 **Score:** 73 **Expect:** 4.1e-005 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4279	815.4206	815.4249	-0.0043	152	157	1	KEQQQR
972.5761	971.5688	971.5837	-0.0149	132	140	0	AMVIVVVNK
1128.6295	1127.6222	1127.6298	-0.0076	141	151	0	GTGNLELVAVR
1343.6626	1342.6553	1342.6703	-0.0150	120	131	0	EGALMLPHFNSK
1572.7305	1571.7232	1571.7426	-0.0194	15	28	0	VLLEENAGGEQEER
1643.7693	1642.7620	1642.7798	-0.0177	67	81	0	GSEEEGDITNPINLR
1771.8617	1770.8544	1770.8747	-0.0203	66	81	1	KGSEEEGDITNPINLR
1817.9468	1816.9395	1816.9570	-0.0175	221	236	1	IFLAGDKDNVIDQIEK
2082.1760	2081.1687	2081.2030	-0.0342	132	151	1	AMVIVVVNKGTGNLELVAVR

No match to: 723.3585, 727.4120, 740.3809, 756.3761, 772.3698, 808.3682, 812.4009, 855.5059, 896.4286, 932.4545, 1005.5266, 1019.4446, 1141.5363, 1167.5571, 1184.5852, 1206.5665, 1258.6086, 1281.1873, 1287.5880, 1297.6375, 1319.6185, 1379.7607, 1386.7021, 1560.6783, 1568.6929, 1738.8247, 1760.8031, 1894.9192, 2181.0642, 2184.9985, 2227.0173, 2243.0244, 2249.0046, 2273.1487, 2295.1162, 2316.0474, 2332.0483, 2619.2808, 2620.2803, 2747.3794, 2748.3638

9. gi|46560472 **Mass:** 34169 **Score:** 50 **Expect:** 0.0092 **Queries matched:** 7

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4279	815.4206	815.4249	-0.0043	153	158	1	KEQQQR
972.5761	971.5688	971.5837	-0.0149	133	141	0	AMVIVVVNK
1128.6295	1127.6222	1127.6298	-0.0076	142	152	0	GTGNLELVAVR
1343.6626	1342.6553	1342.6703	-0.0150	121	132	0	EGALMLPHFNSK
1572.7305	1571.7232	1571.7426	-0.0194	18	31	0	VLLEENAGGEQEER
1817.9468	1816.9395	1816.9570	-0.0175	225	240	1	IFLAGDKDNVIDQIEK
2082.1760	2081.1687	2081.2030	-0.0342	133	152	1	AMVIVVVNKGTGNLELVAVR

No match to: 723.3585, 727.4120, 740.3809, 756.3761, 772.3698, 808.3682, 812.4009, 855.5059, 896.4286, 932.4545, 1005.5266, 1019.4446, 1141.5363, 1167.5571, 1184.5852, 1206.5665, 1258.6086, 1281.1873, 1287.5880, 1297.6375, 1319.6185, 1379.7607, 1386.7021, 1560.6783, 1568.6929, 1643.7693, 1738.8247, 1760.8031, 1771.8617, 1894.9192, 2181.0642, 2184.9985, 2227.0173, 2243.0244, 2249.0046, 2273.1487, 2295.1162, 2316.0474, 2332.0483, 2619.2808, 2620.2803, 2747.3794, 2748.3638

10. gi|62177652 **Mass:** 10056 **Score:** 19 **Expect:** 11 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1379.7607	1378.7534	1378.7496	0.0039	77	89	1	EVVKYSGGLPFAL
1894.9192	1893.9119	1893.9009	0.0111	7	23	0	QLEYLGGEQAWFGPGSR

No match to: 723.3585, 727.4120, 740.3809, 756.3761, 772.3698, 808.3682, 812.4009, 816.4279, 855.5059, 896.4286, 932.4545, 972.5761, 1005.5266, 1019.4446, 1128.6295, 1141.5363, 1167.5571, 1184.5852, 1206.5665, 1258.6086, 1281.1873, 1287.5880, 1297.6375, 1319.6185, 1343.6626, 1386.7021, 1560.6783, 1568.6929, 1572.7305, 1643.7693, 1738.8247, 1760.8031, 1771.8617, 1817.9468, 2082.1760, 2181.0642, 2184.9985, 2227.0173, 2243.0244, 2249.0046, 2273.1487, 2295.1162, 2316.0474, 2332.0483, 2619.2808, 2620.2803, 2747.3794, 2748.3638

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+

Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|16612200** Score: **301** Expect: **7e-028**
major allergen Arah1 [Arachis hypogaea]

Nominal mass (M_r): **71701**; Calculated pI value: **6.62**
NCBI BLAST search of gi|16612200 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **30**
Sequence Coverage: **40%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP
    51 DDLKQKACES RCTKLEYDPR CVYDPRGHTG TTNQRSPPGE RTRGRQPGDY
   101 DDDRRQPRRE EGGRWGPAGP RERERREEDWR QPREDWRRPS HQQPRKIRPE
   151 GREGEQEWGT PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD
   201 QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ GQATVTVANG
   251 NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED
   301 FFPASSRDQS SYLQGFSRNT LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ
   351 RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
   401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS
   451 KAMVIVVVNK GTGNLELVAV RKEQQQRGRR EEEEDEDEEE EGSNREVRRY
   501 TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV
   551 IDQIEKQAKD LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE
   601 SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
115 - 121	740.3809	739.3736	739.3765	-0.0029	0	WGPAGPR
124 - 130	1019.4446	1018.4373	1018.4468	-0.0095	1	EREEDWR
138 - 145	1005.5266	1004.5193	1004.5264	-0.0071	0	RPSHQQPR
146 - 152	855.5059	854.4986	854.5086	-0.0100	1	KIRPEGR

147 - 152	727.4120	726.4047	726.4136	-0.0089	0	IRPEGR
153 - 166	1568.6929	1567.6856	1567.7015	-0.0158	0	EGEQEWGTPGSHVR
172 - 180	1141.5363	1140.5290	1140.5352	-0.0062	0	NNPFYFPSR
172 - 181	1297.6375	1296.6302	1296.6363	-0.0061	1	NNPFYFPSRR
186 - 192	808.3682	807.3609	807.3623	-0.0014	0	YGNQNGR
205 - 213	1184.5852	1183.5779	1183.5846	-0.0067	0	QFQNLQNHR
229 - 253	2619.2808	2618.2735	2618.3160	-0.0425	0	HADADNILVIQQGQATVTVANGNNR
229 - 254	2747.3794	2746.3721	2746.4110	-0.0388	1	HADADNILVIQQGQATVTVANGNNRK
254 - 265	1386.7021	1385.6948	1385.7051	-0.0103	1	KSFNLDEGHALR
255 - 265	1258.6086	1257.6013	1257.6101	-0.0088	0	SFNLDEGHALR
266 - 277	1379.7607	1378.7534	1378.7608	-0.0074	0	IPSGFISYILNR
278 - 284	896.4286	895.4213	895.4260	-0.0047	0	HDNQNLR
288 - 307	2227.0173	2226.0100	2226.0415	-0.0315	0	ISMPVNTPGQFEDFFPASSR
288 - 307	2243.0244	2242.0171	2242.0364	-0.0193	0	ISMPVNTPGQFEDFFPASSR Oxidation (M)
308 - 318	1287.5880	1286.5807	1286.5891	-0.0084	0	DQSSYLQGFSR
319 - 333	1738.8247	1737.8174	1737.8321	-0.0147	0	NTLEAAFNAEFNEIR
319 - 334	1894.9192	1893.9119	1893.9332	-0.0213	1	NTLEAAFNAEFNEIRR
335 - 348	1572.7305	1571.7232	1571.7426	-0.0194	0	VLLEENAGGEQEER
386 - 401	1771.8617	1770.8544	1770.8747	-0.0203	1	KGSEEEGDITNPINLR
387 - 401	1643.7693	1642.7620	1642.7798	-0.0177	0	GSEEEGDITNPINLR
440 - 451	1343.6626	1342.6553	1342.6703	-0.0150	0	EGALMLPHFNSK
452 - 460	972.5761	971.5688	971.5837	-0.0149	0	AMVIVVVNK
452 - 471	2082.1760	2081.1687	2081.2030	-0.0342	1	AMVIVVVNKGTGNLELVAVR
461 - 471	1128.6295	1127.6222	1127.6298	-0.0076	0	GTGNLELVAVR
472 - 477	816.4279	815.4206	815.4249	-0.0043	1	KEQQQR
541 - 556	1817.9468	1816.9395	1816.9570	-0.0175	1	IFLAGDKDNVIDQIEK

No match to: 723.3585, 756.3761, 772.3698, 812.4009, 932.4545, 1167.5571, 1206.5665, 1281.1873, 1319.6185, 1560.6783, 1760.8031, 2181.0642, 2184.9985, 2249.0046, 2273.1487, 2295.1162, 2316.0474, 2332.0483, 2620.2803, 2748.3638

Spot 19

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:33:17 GMT
Top Score : 44 for gi|46560476, conarachin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560476	48122	43	conarachin [Arachis hypogaea]
2.	gi|16612200	71701	43	major allergen Arah1 [Arachis hypogaea]
3.	gi|1168391	71701	43	Allergen Ara h 1, clone P41B precursor (Ara h I)
4.	gi|602436	71701	43	Ara h I
5.	gi|46560478	66934	36	conarachin [Arachis hypogaea]
6.	gi|620025	70639	34	Ara h I
7.	gi|1168390	70639	34	Allergen Ara h 1, clone P17 precursor (Ara h I)
8.	gi|230338	23975	19	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
9.	gi|40738310	112681	14	1a protein [Cucumber mosaic virus]
10.	gi|115187491	12957	14	aux/IAA protein [Arachis hypogaea]

Results List

1. gi|46560476 **Mass:** 48122 **Score:** 43 **Expect:** 0.038 **Queries matched:** 8
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5923	1183.5850	1183.5846	0.0004	8	16	0	QFQNLQNHR
1287.6112	1286.6039	1286.5891	0.0148	111	121	0	DQSSYLQGFSR
1376.6974	1375.6901	1375.6619	0.0282	362	374	0	DLAFPGSGEQVEK
1379.7346	1378.7273	1378.7608	-0.0335	69	80	0	IPSGFISYILNR
1572.7456	1571.7383	1571.7426	-0.0043	138	151	0	VLLEENAGGEQEER
1738.8181	1737.8108	1737.8321	-0.0213	122	136	0	NTLEAAFNAEFNEIR
1817.9653	1816.9580	1816.9570	0.0010	343	358	1	IFLAGDKDNVIDQIEK

1894.9684	1893.9611	1893.9332	0.0279	122 - 137	1	NTLEAAFNAEFNEIRR

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1046.6002, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1209.5676, 1277.1021, 1297.6343, 1300.6149, 1309.6343, 1431.6971, 1456.7368, 1458.7396, 1547.7474, 1568.7085, 1606.7209, 1729.8398, 1756.8262, 1770.8704, 1774.8431, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2273.1602, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2456.1919, 2461.1924, 2514.3459, 2530.3186, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549

2. gi|16612200 **Mass:** 71701 **Score:** 43 **Expect:** 0.044 **Queries matched:** 10

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5923	1183.5850	1183.5846	0.0004	205 -	213	0	QFQNLQNHR
1287.6112	1286.6039	1286.5891	0.0148	308 -	318	0	DQSSYLQGFSR
1297.6343	1296.6270	1296.6363	-0.0093	172 -	181	1	NNPFYFPSRR
1376.6974	1375.6901	1375.6619	0.0282	560 -	572	0	DLAFPGSGEQVEK
1379.7346	1378.7273	1378.7608	-0.0335	266 -	277	0	IPSGFISYILNR
1568.7085	1567.7012	1567.7015	-0.0002	153 -	166	0	EGEQEWGTPGSHVR
1572.7456	1571.7383	1571.7426	-0.0043	335 -	348	0	VLLEENAGGEQEER
1738.8181	1737.8108	1737.8321	-0.0213	319 -	333	0	NTLEAAFNAEFNEIR
1817.9653	1816.9580	1816.9570	0.0010	541 -	556	1	IFLAGDKDNVIDQIEK
1894.9684	1893.9611	1893.9332	0.0279	319 -	334	1	NTLEAAFNAEFNEIRR

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1046.6002, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1209.5676, 1277.1021, 1300.6149, 1309.6343, 1431.6971, 1456.7368, 1458.7396, 1547.7474, 1606.7209, 1729.8398, 1756.8262, 1770.8704, 1774.8431, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2273.1602, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2456.1919, 2461.1924, 2514.3459, 2530.3186, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549

3. gi|1168391 **Mass:** 71701 **Score:** 43 **Expect:** 0.044 **Queries matched:** 10

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5923	1183.5850	1183.5846	0.0004	205 -	213	0	QFQNLQNHR
1287.6112	1286.6039	1286.5891	0.0148	308 -	318	0	DQSSYLQGFSR
1297.6343	1296.6270	1296.6363	-0.0093	172 -	181	1	NNPFYFPSRR
1376.6974	1375.6901	1375.6619	0.0282	560 -	572	0	DLAFPGSGEQVEK
1379.7346	1378.7273	1378.7608	-0.0335	266 -	277	0	IPSGFISYILNR

1568.7085	1567.7012	1567.7015	-0.0002	153 - 166	0	EGEQEWGTPGSHVR
1572.7456	1571.7383	1571.7426	-0.0043	335 - 348	0	VLLEENAGGEQEER
1738.8181	1737.8108	1737.8321	-0.0213	319 - 333	0	NTLEAAFNAEFNEIR
1817.9653	1816.9580	1816.9570	0.0010	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9684	1893.9611	1893.9332	0.0279	319 - 334	1	NTLEAAFNAEFNEIRR

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1046.6002, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1209.5676, 1277.1021, 1300.6149, 1309.6343, 1431.6971, 1456.7368, 1458.7396, 1547.7474, 1606.7209, 1729.8398, 1756.8262, 1770.8704, 1774.8431, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2273.1602, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2456.1919, 2461.1924, 2514.3459, 2530.3186, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549

4. gi|602436 **Mass:** 71701 **Score:** 43 **Expect:** 0.044 **Queries matched:** 10

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5923	1183.5850	1183.5846	0.0004	205 - 213		0	QFQNLQNHR
1287.6112	1286.6039	1286.5891	0.0148	308 - 318		0	DQSSYLQGFSR
1297.6343	1296.6270	1296.6363	-0.0093	172 - 181		1	NNPFYFPSRR
1376.6974	1375.6901	1375.6619	0.0282	560 - 572		0	DLAFPGSGEQVEK
1379.7346	1378.7273	1378.7608	-0.0335	266 - 277		0	IPSGFISYILNR
1568.7085	1567.7012	1567.7015	-0.0002	153 - 166		0	EGEQEWGTPGSHVR
1572.7456	1571.7383	1571.7426	-0.0043	335 - 348		0	VLLEENAGGEQEER
1738.8181	1737.8108	1737.8321	-0.0213	319 - 333		0	NTLEAAFNAEFNEIR
1817.9653	1816.9580	1816.9570	0.0010	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9684	1893.9611	1893.9332	0.0279	319 - 334		1	NTLEAAFNAEFNEIRR

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1046.6002, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1209.5676, 1277.1021, 1300.6149, 1309.6343, 1431.6971, 1456.7368, 1458.7396, 1547.7474, 1606.7209, 1729.8398, 1756.8262, 1770.8704, 1774.8431, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2273.1602, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2456.1919, 2461.1924, 2514.3459, 2530.3186, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549

5. gi|46560478 **Mass:** 66934 **Score:** 36 **Expect:** 0.25 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5923	1183.5850	1183.5846	0.0004	199 - 207		0	QFQNLQNHR

1287.6112	1286.6039	1286.5891	0.0148	302 - 312	0	DQSSYLQGFSR
1297.6343	1296.6270	1296.6363	-0.0093	166 - 175	1	NNPFYFPSRR
1376.6974	1375.6901	1375.6619	0.0282	555 - 567	0	DLAFPGSGEQVEK
1379.7346	1378.7273	1378.7608	-0.0335	260 - 271	0	IPSGFISYILNR
1572.7456	1571.7383	1571.7426	-0.0043	329 - 342	0	VLLEENAGGEQEER
1738.8181	1737.8108	1737.8321	-0.0213	313 - 327	0	NTLEAAFNAEFNEIR
1817.9653	1816.9580	1816.9570	0.0010	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9684	1893.9611	1893.9332	0.0279	313 - 328	1	NTLEAAFNAEFNEIRR

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1046.6002, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1209.5676, 1277.1021, 1300.6149, 1309.6343, 1431.6971, 1456.7368, 1458.7396, 1547.7474, 1568.7085, 1606.7209, 1729.8398, 1756.8262, 1770.8704, 1774.8431, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2273.1602, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2456.1919, 2461.1924, 2514.3459, 2530.3186, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549

6. gi|620025 **Mass:** 70639 **Score:** 34 **Expect:** 0.33 **Queries matched:** 9

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5923	1183.5850	1183.5846	0.0004	199 - 207		0	QFQNLQNHR
1287.6112	1286.6039	1286.5891	0.0148	302 - 312		0	DQSSYLQGFSR
1297.6343	1296.6270	1296.6363	-0.0093	166 - 175		1	NNPFYFPSRR
1376.6974	1375.6901	1375.6619	0.0282	555 - 567		0	DLAFPGSGEQVEK
1379.7346	1378.7273	1378.7608	-0.0335	260 - 271		0	IPSGFISYILNR
1572.7456	1571.7383	1571.7426	-0.0043	329 - 342		0	VLLEENAGGEQEER
1738.8181	1737.8108	1737.8321	-0.0213	313 - 327		0	NTLEAAFNAEFNEIR
1817.9653	1816.9580	1816.9570	0.0010	536 - 551		1	IFLAGDKDNVIDQIEK
1894.9684	1893.9611	1893.9332	0.0279	313 - 328		1	NTLEAAFNAEFNEIRR

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1046.6002, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1209.5676, 1277.1021, 1300.6149, 1309.6343, 1431.6971, 1456.7368, 1458.7396, 1547.7474, 1568.7085, 1606.7209, 1729.8398, 1756.8262, 1770.8704, 1774.8431, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2273.1602, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2456.1919, 2461.1924, 2514.3459, 2530.3186, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549

7. gi|1168390 **Mass:** 70639 **Score:** 34 **Expect:** 0.33 **Queries matched:** 9

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5923	1183.5850	1183.5846	0.0004	199 -	207	0	QFQNLQNHR
1287.6112	1286.6039	1286.5891	0.0148	302 -	312	0	DQSSYLQGFSR
1297.6343	1296.6270	1296.6363	-0.0093	166 -	175	1	NNPFYFPSRR
1376.6974	1375.6901	1375.6619	0.0282	555 -	567	0	DLAFPGSGEQVEK
1379.7346	1378.7273	1378.7608	-0.0335	260 -	271	0	IPSGFISYILNR
1572.7456	1571.7383	1571.7426	-0.0043	329 -	342	0	VLLEENAGGEQEER
1738.8181	1737.8108	1737.8321	-0.0213	313 -	327	0	NTLEAAFNAEFNEIR
1817.9653	1816.9580	1816.9570	0.0010	536 -	551	1	IFLAGDKDNVIDQIEK
1894.9684	1893.9611	1893.9332	0.0279	313 -	328	1	NTLEAAFNAEFNEIRR

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1046.6002, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1209.5676, 1277.1021, 1300.6149, 1309.6343, 1431.6971, 1456.7368, 1458.7396, 1547.7474, 1568.7085, 1606.7209, 1729.8398, 1756.8262, 1770.8704, 1774.8431, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2273.1602, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2456.1919, 2461.1924, 2514.3459, 2530.3186, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549

8. gi|230338 **Mass:** 23975 **Score:** 19 **Expect:** 12 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.6002	1045.5929	1045.5880	0.0050	90 -	99	1	LKSAASLNSR
2273.1602	2272.1529	2272.1521	0.0008	70 -	89	0	SIVHPSYNSNTLNNDIMLIK
2514.3459	2513.3386	2513.3311	0.0075	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK
2530.3186	2529.3113	2529.3260	-0.0147	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1184.5923, 1209.5676, 1277.1021, 1287.6112, 1297.6343, 1300.6149, 1309.6343, 1376.6974, 1379.7346, 1431.6971, 1456.7368, 1458.7396, 1547.7474, 1568.7085, 1572.7456, 1606.7209, 1729.8398, 1738.8181, 1756.8262, 1770.8704, 1774.8431, 1817.9653, 1894.9684, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2456.1919, 2461.1924, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549

9. gi|40738310 **Mass:** 112681 **Score:** 14 **Expect:** 36 **Queries matched:** 4

1a protein [Cucumber mosaic virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2273.1602	2272.1529	2272.1958	-0.0429	780 -	799	0	VLVDEVVLLHFGQLCAVMSK + Oxidation (M)
2456.1919	2455.1846	2455.2230	-0.0384	237 -	259	1	SAFSEAEDVTPLSGKLNSTIFSR

2461.1924	2460.1851	2460.2113	-0.0262	632 - 652	0	FVFDTYFTVDPLVNVHFSTGR
2514.3459	2513.3386	2513.3749	-0.0362	780 - 801	1	VLVDEVVLLHFGQLCAVMSKLK + Oxidation (M)

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1046.6002, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1184.5923, 1209.5676, 1277.1021, 1287.6112, 1297.6343, 1300.6149, 1309.6343, 1376.6974, 1379.7346, 1431.6971, 1456.7368, 1458.7396, 1547.7474, 1568.7085, 1572.7456, 1606.7209, 1729.8398, 1738.8181, 1756.8262, 1770.8704, 1774.8431, 1817.9653, 1894.9684, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2530.3186, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549

10. gi|115187491 **Mass:** 12957 **Score:** 14 **Expect:** 39 **Queries matched:** 2

aux/IAA protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1458.7396	1457.7323	1457.7110	0.0214	20 -	34	0	LGLPGGSNDGESSLR
1774.8431	1773.8358	1773.8243	0.0115	6 -	19	1	DKYSMINFEETELR

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1046.6002, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1184.5923, 1209.5676, 1277.1021, 1287.6112, 1297.6343, 1300.6149, 1309.6343, 1376.6974, 1379.7346, 1431.6971, 1456.7368, 1547.7474, 1568.7085, 1572.7456, 1606.7209, 1729.8398, 1738.8181, 1756.8262, 1770.8704, 1817.9653, 1894.9684, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2273.1602, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2456.1919, 2461.1924, 2514.3459, 2530.3186, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 72

Protein View

Match to: **gi|46560476** Score: **43** Expect: **0.038**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **48122**; Calculated pI value: **5.43**
NCBI BLAST search of gi|46560476 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **72**
Number of mass values matched: **8**
Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

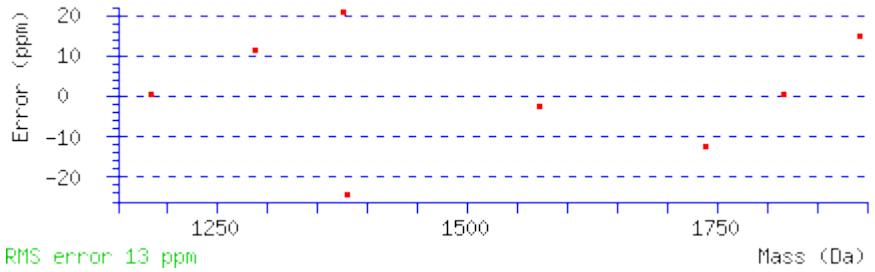
```
     1 GFDQRSRQFQ NLQNHRIVQI EAKPNTLVLP KHADADNILV IQQGQATVTV
    51 ANGNNRKSFN LDEGHALRIP SGFISYILNR HDNQNLRVAK ISMPVNTPGQ
   101 FEDFFPASSR DQSSYLQGFS RNTLEAAFNA EFNEIRRVLL EENAGGEQEE
   151 RGQRRWSTRS SENNEGVIVK VSKEHVEELT KHAKSVSKKG SEEGDITNPI
   201 NLREGEPDLS NNFGKLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF
   251 NSKAMVIVVV NKGTGNLELV AVRKEQQQRG RREEEEDEDE EEEGSNREVR
   301 RYTARLKEGD VFIMPAAHPV AINASSELHL LGFGINAENN HRIFLAGDKD
   351 NVIDQIEKQA KDLAFPGSGE QVEKLIKNQK ESHFVSARPQ SQSQSPSSPE
   401 KESPEKEDQE EENQGGKGPL LSILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
8 - 16	1184.5923	1183.5850	1183.5846	0.0004	0	QFQNLQNHR
69 - 80	1379.7346	1378.7273	1378.7608	-0.0335	0	IPSGFISYILNR
111 - 121	1287.6112	1286.6039	1286.5891	0.0148	0	DQSSYLQGFSR
122 - 136	1738.8181	1737.8108	1737.8321	-0.0213	0	NTLEAAFNAEFNEIR
122 - 137	1894.9684	1893.9611	1893.9332	0.0279	1	NTLEAAFNAEFNEIRR
138 - 151	1572.7456	1571.7383	1571.7426	-0.0043	0	VLLEENAGGEQEER
343 - 358	1817.9653	1816.9580	1816.9570	0.0010	1	IFLAGDKDNVIDQIEK
362 - 374	1376.6974	1375.6901	1375.6619	0.0282	0	DLAFPGSGEQVEK

No match to: 805.4598, 827.3997, 839.0997, 845.1149, 855.0673, 861.0899, 877.0602, 1046.6002, 1066.0756, 1079.5249, 1080.5260, 1082.0466, 1111.5613, 1137.0792, 1137.5746, 1145.0732, 1145.5663, 1167.5570, 1175.5492, 1209.5676, 1277.1021, 1297.6343, 1300.6149, 1309.6343, 1431.6971, 1456.7368, 1458.7396, 1547.7474, 1568.7085, 1606.7209, 1729.8398, 1756.8262,

1770.8704, 1774.8431, 1918.8846, 2145.0544, 2146.5916, 2162.0413, 2185.0349, 2207.0291, 2225.0234, 2227.1274, 2273.1602, 2295.1467, 2305.1458, 2311.1384, 2333.1240, 2335.1018, 2336.1003, 2338.0896, 2351.0894, 2353.1067, 2456.1919, 2461.1924, 2514.3459, 2530.3186, 2612.1863, 2926.3145, 3136.4419, 3211.5083, 3233.4868, 3300.7568, 3316.7505, 3614.7549



Spot 20

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:33:11 GMT**
Top Score : **85 for gi|16612200, major allergen Arah1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|16612200	71701	85	major allergen Arah1 [Arachis hypogaea]
2.	gi|1168391	71701	85	Allergen Ara h 1, clone P41B precursor (Ara h I)
3.	gi|602436	71701	85	Ara h I
4.	gi|46560476	48122	60	conarachin [Arachis hypogaea]
5.	gi|46560478	66934	57	conarachin [Arachis hypogaea]
6.	gi|620025	70639	55	Ara h I
7.	gi|1168390	70639	55	Allergen Ara h 1, clone P17 precursor (Ara h I)
8.	gi|46560474	33641	29	conarachin [Arachis hypogaea]
9.	gi|230338	23975	21	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
10.	gi|115187491	12957	17	aux/IAA protein [Arachis hypogaea]

Results List

1. gi|16612200 **Mass:** 71701 **Score:** 85 **Expect:** 3e-006 **Queries matched:** 14
major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1061.6105	1060.6032	1060.5777	0.0255	195 -	202	1	VLQRFDQR
1141.5464	1140.5391	1140.5352	0.0039	172 -	180	0	NNPFYFPSR
1175.5609	1174.5536	1174.5829	-0.0293	357 -	367	0	SSENNEGVIVK
1184.5892	1183.5819	1183.5846	-0.0027	205 -	213	0	QFQNLQNHR
1258.6282	1257.6209	1257.6101	0.0108	255 -	265	0	SFNLDEGHALR
1287.5957	1286.5884	1286.5891	-0.0007	308 -	318	0	DQSSYLQGFSR
1297.6431	1296.6358	1296.6363	-0.0005	172 -	181	1	NNPFYFPSRR

1376.6796	1375.6723	1375.6619	0.0104	560 - 572	0	DLAFPGSGEQVEK
1568.7120	1567.7047	1567.7015	0.0033	153 - 166	0	EGEQEWGTPGSHVR
1572.7527	1571.7454	1571.7426	0.0028	335 - 348	0	VLLEENAGGEQEER
1728.8541	1727.8468	1727.8437	0.0031	334 - 348	1	RVLLEENAGGEQEER
1738.8419	1737.8346	1737.8321	0.0025	319 - 333	0	NTLEAAFNAEFNEIR
1771.8719	1770.8646	1770.8747	-0.0101	386 - 401	1	KGSEEEGDITNPINLR
1894.9297	1893.9224	1893.9332	-0.0108	319 - 334	1	NTLEAAFNAEFNEIRR

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1046.6082, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1145.0781, 1145.5732, 1167.5807, 1296.5975, 1400.6614, 1434.7024, 1606.7410, 1643.8302, 1651.3890, 1651.8542, 1774.8475, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2273.1602, 2295.1396, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2514.3438, 2530.3162, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

2. gi|1168391 **Mass:** 71701 **Score:** 85 **Expect:** 3e-006 **Queries matched:** 14

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
1061.6105	1060.6032	1060.5777	0.0255	195 - 202	1	VLQRFDQR
1141.5464	1140.5391	1140.5352	0.0039	172 - 180	0	NNPFYFPSR
1175.5609	1174.5536	1174.5829	-0.0293	357 - 367	0	SSENNEGVIVK
1184.5892	1183.5819	1183.5846	-0.0027	205 - 213	0	QFQNLQNHR
1258.6282	1257.6209	1257.6101	0.0108	255 - 265	0	SFNLDEGHALR
1287.5957	1286.5884	1286.5891	-0.0007	308 - 318	0	DQSSYLQGFSR
1297.6431	1296.6358	1296.6363	-0.0005	172 - 181	1	NNPFYFPSRR
1376.6796	1375.6723	1375.6619	0.0104	560 - 572	0	DLAFPGSGEQVEK
1568.7120	1567.7047	1567.7015	0.0033	153 - 166	0	EGEQEWGTPGSHVR
1572.7527	1571.7454	1571.7426	0.0028	335 - 348	0	VLLEENAGGEQEER
1728.8541	1727.8468	1727.8437	0.0031	334 - 348	1	RVLLEENAGGEQEER
1738.8419	1737.8346	1737.8321	0.0025	319 - 333	0	NTLEAAFNAEFNEIR
1771.8719	1770.8646	1770.8747	-0.0101	386 - 401	1	KGSEEEGDITNPINLR
1894.9297	1893.9224	1893.9332	-0.0108	319 - 334	1	NTLEAAFNAEFNEIRR

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1046.6082, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1145.0781, 1145.5732, 1167.5807, 1296.5975, 1400.6614, 1434.7024, 1606.7410, 1643.8302, 1651.3890, 1651.8542, 1774.8475, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2273.1602, 2295.1396, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2514.3438, 2530.3162, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

3. gi|602436 **Mass:** 71701 **Score:** 85 **Expect:** 3e-006 **Queries matched:** 14

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1061.6105	1060.6032	1060.5777	0.0255	195	-	202	1	VLQRFDQR
1141.5464	1140.5391	1140.5352	0.0039	172	-	180	0	NNPFYFPSR
1175.5609	1174.5536	1174.5829	-0.0293	357	-	367	0	SSENNEGVIVK
1184.5892	1183.5819	1183.5846	-0.0027	205	-	213	0	QFQNLQNHR
1258.6282	1257.6209	1257.6101	0.0108	255	-	265	0	SFNLDEGHALR
1287.5957	1286.5884	1286.5891	-0.0007	308	-	318	0	DQSSYLQGFSR
1297.6431	1296.6358	1296.6363	-0.0005	172	-	181	1	NNPFYFPSRR
1376.6796	1375.6723	1375.6619	0.0104	560	-	572	0	DLAFPGSGEQVEK
1568.7120	1567.7047	1567.7015	0.0033	153	-	166	0	EGEQEWGTPGSHVR
1572.7527	1571.7454	1571.7426	0.0028	335	-	348	0	VLLEENAGGEQEER
1728.8541	1727.8468	1727.8437	0.0031	334	-	348	1	RVLLEENAGGEQEER
1738.8419	1737.8346	1737.8321	0.0025	319	-	333	0	NTLEAAFNAEFNEIR
1771.8719	1770.8646	1770.8747	-0.0101	386	-	401	1	KGSEEEGDITNPINLR
1894.9297	1893.9224	1893.9332	-0.0108	319	-	334	1	NTLEAAFNAEFNEIRR

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1046.6082, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1145.0781, 1145.5732, 1167.5807, 1296.5975, 1400.6614, 1434.7024, 1606.7410, 1643.8302, 1651.3890, 1651.8542, 1774.8475, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2273.1602, 2295.1396, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2514.3438, 2530.3162, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

4. gi|46560476 **Mass:** 48122 **Score:** 60 **Expect:** 0.00092 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1175.5609	1174.5536	1174.5829	-0.0293	160	-	170	0	SSENNEGVIVK
1184.5892	1183.5819	1183.5846	-0.0027	8	-	16	0	QFQNLQNHR
1258.6282	1257.6209	1257.6101	0.0108	58	-	68	0	SFNLDEGHALR
1287.5957	1286.5884	1286.5891	-0.0007	111	-	121	0	DQSSYLQGFSR
1376.6796	1375.6723	1375.6619	0.0104	362	-	374	0	DLAFPGSGEQVEK
1572.7527	1571.7454	1571.7426	0.0028	138	-	151	0	VLLEENAGGEQEER
1728.8541	1727.8468	1727.8437	0.0031	137	-	151	1	RVLLEENAGGEQEER
1738.8419	1737.8346	1737.8321	0.0025	122	-	136	0	NTLEAAFNAEFNEIR
1894.9297	1893.9224	1893.9332	-0.0108	122	-	137	1	NTLEAAFNAEFNEIRR

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1046.6082, 1061.6105, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1141.5464, 1145.0781, 1145.5732, 1167.5807, 1296.5975, 1297.6431, 1400.6614, 1434.7024, 1568.7120, 1606.7410, 1643.8302, 1651.3890, 1651.8542, 1771.8719, 1774.8475, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2273.1602, 2295.1396, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2514.3438, 2530.3162, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

5. gi|46560478 **Mass:** 66934 **Score:** 57 **Expect:** 0.002 **Queries matched:** 11

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1061.6105	1060.6032	1060.5777	0.0255	189	196	1	VLQRFDQR
1141.5464	1140.5391	1140.5352	0.0039	166	174	0	NNPFYFPSR
1184.5892	1183.5819	1183.5846	-0.0027	199	207	0	QFQNLQNHR
1258.6282	1257.6209	1257.6101	0.0108	249	259	0	SFNLDEGHALR
1287.5957	1286.5884	1286.5891	-0.0007	302	312	0	DQSSYLQGFSR
1297.6431	1296.6358	1296.6363	-0.0005	166	175	1	NNPFYFPSRR
1376.6796	1375.6723	1375.6619	0.0104	555	567	0	DLAFPGSGEQVEK
1572.7527	1571.7454	1571.7426	0.0028	329	342	0	VLLEENAGGEQEER
1728.8541	1727.8468	1727.8437	0.0031	328	342	1	RVLLEENAGGEQEER
1738.8419	1737.8346	1737.8321	0.0025	313	327	0	NTLEAAFNAEFNEIR
1894.9297	1893.9224	1893.9332	-0.0108	313	328	1	NTLEAAFNAEFNEIRR

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1046.6082, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1145.0781, 1145.5732, 1167.5807, 1175.5609, 1296.5975, 1400.6614, 1434.7024, 1568.7120, 1606.7410, 1643.8302, 1651.3890, 1651.8542, 1771.8719, 1774.8475, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2273.1602, 2295.1396, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2514.3438, 2530.3162, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

6. gi|620025 **Mass:** 70639 **Score:** 55 **Expect:** 0.003 **Queries matched:** 11

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1061.6105	1060.6032	1060.5777	0.0255	189	196	1	VLQRFDQR
1141.5464	1140.5391	1140.5352	0.0039	166	174	0	NNPFYFPSR
1184.5892	1183.5819	1183.5846	-0.0027	199	207	0	QFQNLQNHR
1258.6282	1257.6209	1257.6101	0.0108	249	259	0	SFNLDEGHALR
1287.5957	1286.5884	1286.5891	-0.0007	302	312	0	DQSSYLQGFSR
1297.6431	1296.6358	1296.6363	-0.0005	166	175	1	NNPFYFPSRR
1376.6796	1375.6723	1375.6619	0.0104	555	567	0	DLAFPGSGEQVEK
1572.7527	1571.7454	1571.7426	0.0028	329	342	0	VLLEENAGGEQEER
1728.8541	1727.8468	1727.8437	0.0031	328	342	1	RVLLEENAGGEQEER
1738.8419	1737.8346	1737.8321	0.0025	313	327	0	NTLEAAFNAEFNEIR
1894.9297	1893.9224	1893.9332	-0.0108	313	328	1	NTLEAAFNAEFNEIRR

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1046.6082, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1145.0781, 1145.5732, 1167.5807, 1175.5609, 1296.5975, 1400.6614, 1434.7024, 1568.7120,

1606.7410, 1643.8302, 1651.3890, 1651.8542, 1771.8719, 1774.8475, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2273.1602, 2295.1396, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2514.3438, 2530.3162, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

7. gi|1168390 **Mass:** 70639 **Score:** 55 **Expect:** 0.003 **Queries matched:** 11

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1061.6105	1060.6032	1060.5777	0.0255	189	196	1	VLQRFDQR
1141.5464	1140.5391	1140.5352	0.0039	166	174	0	NNPFYFPSR
1184.5892	1183.5819	1183.5846	-0.0027	199	207	0	QFQNLQNHR
1258.6282	1257.6209	1257.6101	0.0108	249	259	0	SFNLDEGHALR
1287.5957	1286.5884	1286.5891	-0.0007	302	312	0	DQSSYLQGFSR
1297.6431	1296.6358	1296.6363	-0.0005	166	175	1	NNPFYFPSRR
1376.6796	1375.6723	1375.6619	0.0104	555	567	0	DLAFPGSGEQVEK
1572.7527	1571.7454	1571.7426	0.0028	329	342	0	VLLEENAGGEQEER
1728.8541	1727.8468	1727.8437	0.0031	328	342	1	RVLLEENAGGEQEER
1738.8419	1737.8346	1737.8321	0.0025	313	327	0	NTLEAAFNAEFNEIR
1894.9297	1893.9224	1893.9332	-0.0108	313	328	1	NTLEAAFNAEFNEIRR

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1046.6082, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1145.0781, 1145.5732, 1167.5807, 1175.5609, 1296.5975, 1400.6614, 1434.7024, 1568.7120, 1606.7410, 1643.8302, 1651.3890, 1651.8542, 1771.8719, 1774.8475, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2273.1602, 2295.1396, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2514.3438, 2530.3162, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

8. gi|46560474 **Mass:** 33641 **Score:** 29 **Expect:** 1.2 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1175.5609	1174.5536	1174.5829	-0.0293	37	47	0	SSENNEGVIVK
1376.6796	1375.6723	1375.6619	0.0104	240	252	0	DLAFPGSGEQVEK
1572.7527	1571.7454	1571.7426	0.0028	15	28	0	VLLEENAGGEQEER
1728.8541	1727.8468	1727.8437	0.0031	14	28	1	RVLLEENAGGEQEER
1771.8719	1770.8646	1770.8747	-0.0101	66	81	1	KGSEEEGDITNPINLR

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1046.6082, 1061.6105, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1141.5464, 1145.0781, 1145.5732, 1167.5807, 1184.5892, 1258.6282, 1287.5957, 1296.5975, 1297.6431, 1400.6614, 1434.7024, 1568.7120, 1606.7410, 1643.8302, 1651.3890, 1651.8542, 1738.8419, 1774.8475, 1894.9297, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2273.1602, 2295.1396, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2514.3438, 2530.3162, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

9. gi|230338 **Mass:** 23975 **Score:** 21 **Expect:** 6.5 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1046.6082	1045.6009	1045.5880	0.0130	90	-	99	1	LKSAASLNSR
2273.1602	2272.1529	2272.1521	0.0008	70	-	89	0	SIVHPSYNSNTLNNDIMLIK
2514.3438	2513.3365	2513.3311	0.0054	70	-	91	1	SIVHPSYNSNTLNNDIMLIKLK
2530.3162	2529.3089	2529.3260	-0.0171	70	-	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1061.6105, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1141.5464, 1145.0781, 1145.5732, 1167.5807, 1175.5609, 1184.5892, 1258.6282, 1287.5957, 1296.5975, 1297.6431, 1376.6796, 1400.6614, 1434.7024, 1568.7120, 1572.7527, 1606.7410, 1643.8302, 1651.3890, 1651.8542, 1728.8541, 1738.8419, 1771.8719, 1774.8475, 1894.9297, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2295.1396, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

10. gi|115187491 **Mass:** 12957 **Score:** 17 **Expect:** 16 **Queries matched:** 2

aux/IAA protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1774.8475	1773.8402	1773.8243	0.0159	6	-	19	1	DKYSMINFEETELR
2295.1396	2294.1323	2294.0808	0.0515	20	-	42	1	LGLPGGSNDGESSLRSTCTTTGK

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1046.6082, 1061.6105, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1141.5464, 1145.0781, 1145.5732, 1167.5807, 1175.5609, 1184.5892, 1258.6282, 1287.5957, 1296.5975, 1297.6431, 1376.6796, 1400.6614, 1434.7024, 1568.7120, 1572.7527, 1606.7410, 1643.8302, 1651.3890, 1651.8542, 1728.8541, 1738.8419, 1771.8719, 1894.9297, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2273.1602, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2514.3438, 2530.3162, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 58

Protein View

Match to: **gi|16612200** Score: **85** Expect: **3e-006**
major allergen Arah1 [Arachis hypogaea]

Nominal mass (M_r): **71701**; Calculated pI value: **6.62**
NCBI BLAST search of gi|16612200 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **58**
Number of mass values matched: **14**
Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP
    51 DDLKQKACES RCTKLEYDPR CVYDPRGHTG TTNQRSPPGE RTRGRQPGDY
   101 DDDRRQPRRE EGGRWGPAGP RERERREEDWR QPREDWRRPS HQQPRKIRPE
   151 GREGEQEWGT PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD
   201 QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ GQATVTVANG
   251 NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED
   301 FFPASSRDQS SYLQGFSRNT LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ
   351 RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
   401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS
   451 KAMVIVVVNK GTGNLELVAV RKEQQQRGRR EEEEDEDEEE EGSNREVRRY
   501 TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV
   551 IDQIEKQAKD LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE
   601 SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
153 - 166	1568.7120	1567.7047	1567.7015	0.0033	0	EGEQEWGTPGSHVR
172 - 180	1141.5464	1140.5391	1140.5352	0.0039	0	NNPFYFPSR
172 - 181	1297.6431	1296.6358	1296.6363	-0.0005	1	NNPFYFPSRR
195 - 202	1061.6105	1060.6032	1060.5777	0.0255	1	VLQRFDQR
205 - 213	1184.5892	1183.5819	1183.5846	-0.0027	0	QFQNLQNHR
255 - 265	1258.6282	1257.6209	1257.6101	0.0108	0	SFNLDEGHALR

308 - 318	1287.5957	1286.5884	1286.5891	-0.0007	0	DQSSYLQGFSR
319 - 333	1738.8419	1737.8346	1737.8321	0.0025	0	NTLEAAFNAEFNEIR
319 - 334	1894.9297	1893.9224	1893.9332	-0.0108	1	NTLEAAFNAEFNEIRR
334 - 348	1728.8541	1727.8468	1727.8437	0.0031	1	RVLLEENAGGEQEER
335 - 348	1572.7527	1571.7454	1571.7426	0.0028	0	VLLEENAGGEQEER
357 - 367	1175.5609	1174.5536	1174.5829	-0.0293	0	SSENNEGVIVK
386 - 401	1771.8719	1770.8646	1770.8747	-0.0101	1	KGSEEEGDITNPINLR
560 - 572	1376.6796	1375.6723	1375.6619	0.0104	0	DLAFPGSGEQVEK

No match to: 805.4508, 855.0532, 861.0752, 877.0568, 917.2953, 1005.5038, 1046.6082, 1066.0730, 1080.5529, 1111.5671, 1137.0775, 1137.5657, 1145.0781, 1145.5732, 1167.5807, 1296.5975, 1400.6614, 1434.7024, 1606.7410, 1643.8302, 1651.3890, 1651.8542, 1774.8475, 1918.8820, 1934.8839, 2147.6067, 2185.0378, 2227.1416, 2273.1602, 2295.1396, 2306.1465, 2311.1328, 2335.0986, 2351.0786, 2353.0901, 2513.2808, 2514.3438, 2530.3162, 2610.2349, 2613.1885, 3136.4265, 3211.5093, 3300.7095, 3317.7395

Spot 21

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:34:19 GMT
Top Score : 103 for gi|16612200, major allergen Arah1 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|16612200	71701	103	major allergen Arah1 [Arachis hypogaea]
2.	gi|1168391	71701	103	Allergen Ara h 1, clone P41B precursor (Ara h I)
3.	gi|602436	71701	103	Ara h I
4.	gi|46560478	66934	83	conarachin [Arachis hypogaea]
5.	gi|620025	70639	81	Ara h I
6.	gi|1168390	70639	81	Allergen Ara h 1, clone P17 precursor (Ara h I)
7.	gi|46560476	48122	69	conarachin [Arachis hypogaea]
8.	gi|46560474	33641	38	conarachin [Arachis hypogaea]
9.	gi|46560472	34169	28	conarachin [Arachis hypogaea]
10.	gi|230338	23975	21	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|16612200 **Mass:** 71701 **Score:** 103 **Expect:** 4.4e-008 **Queries matched:** 16
major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5411	1004.5338	1004.5264	0.0074	138	145	0	RPSHQQPR
1141.5397	1140.5324	1140.5352	-0.0028	172	180	0	NNPFYFPSR
1184.5983	1183.5910	1183.5846	0.0064	205	213	0	QFQNLQNHR
1258.6228	1257.6155	1257.6101	0.0054	255	265	0	SFNLDEGHALR
1287.5995	1286.5922	1286.5891	0.0031	308	318	0	DQSSYLQGFSR
1297.6453	1296.6380	1296.6363	0.0017	172	181	1	NNPFYFPSRR
1376.6873	1375.6800	1375.6619	0.0181	560	572	0	DLAFPGSGEQVEK

1427.7173	1426.7100	1426.7177	-0.0077	203 - 213	1	SRQFQNLQNHR
1568.7148	1567.7075	1567.7015	0.0061	153 - 166	0	EGEQEWGTPGSHVR
1572.7396	1571.7323	1571.7426	-0.0103	335 - 348	0	VLLEENAGGEQEER
1643.7765	1642.7692	1642.7798	-0.0105	387 - 401	0	GSEEEGDITNPINLR
1728.8552	1727.8479	1727.8437	0.0042	334 - 348	1	RVLLEENAGGEQEER
1738.8257	1737.8184	1737.8321	-0.0137	319 - 333	0	NTLEAAFNAEFNEIR
1771.8647	1770.8574	1770.8747	-0.0173	386 - 401	1	KGSEEEGDITNPINLR
1817.9481	1816.9408	1816.9570	-0.0162	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9272	1893.9199	1893.9332	-0.0133	319 - 334	1	NTLEAAFNAEFNEIRR

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1046.5957, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1209.5590, 1320.5980, 1399.7009, 1756.8326, 1774.8629, 1830.8320, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2273.1633, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2514.3450, 2516.3413, 2530.3625, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

2. gi|1168391 **Mass:** 71701 **Score:** 103 **Expect:** 4.4e-008 **Queries matched:** 16

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5411	1004.5338	1004.5264	0.0074	138	145	0	RPSHQQPR
1141.5397	1140.5324	1140.5352	-0.0028	172	180	0	NNPFYFPSR
1184.5983	1183.5910	1183.5846	0.0064	205	213	0	QFQNLQNHR
1258.6228	1257.6155	1257.6101	0.0054	255	265	0	SFNLDEGHALR
1287.5995	1286.5922	1286.5891	0.0031	308	318	0	DQSSYLQGFSR
1297.6453	1296.6380	1296.6363	0.0017	172	181	1	NNPFYFPSRR
1376.6873	1375.6800	1375.6619	0.0181	560	572	0	DLAFPGSGEQVEK
1427.7173	1426.7100	1426.7177	-0.0077	203	213	1	SRQFQNLQNHR
1568.7148	1567.7075	1567.7015	0.0061	153	166	0	EGEQEWGTPGSHVR
1572.7396	1571.7323	1571.7426	-0.0103	335	348	0	VLLEENAGGEQEER
1643.7765	1642.7692	1642.7798	-0.0105	387	401	0	GSEEEGDITNPINLR
1728.8552	1727.8479	1727.8437	0.0042	334	348	1	RVLLEENAGGEQEER
1738.8257	1737.8184	1737.8321	-0.0137	319	333	0	NTLEAAFNAEFNEIR
1771.8647	1770.8574	1770.8747	-0.0173	386	401	1	KGSEEEGDITNPINLR
1817.9481	1816.9408	1816.9570	-0.0162	541	556	1	IFLAGDKDNVIDQIEK
1894.9272	1893.9199	1893.9332	-0.0133	319	334	1	NTLEAAFNAEFNEIRR

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1046.5957, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1209.5590, 1320.5980, 1399.7009, 1756.8326, 1774.8629, 1830.8320, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2273.1633, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2514.3450, 2516.3413,

2530.3625, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

3. gi|602436 **Mass:** 71701 **Score:** 103 **Expect:** 4.4e-008 **Queries matched:** 16

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5411	1004.5338	1004.5264	0.0074	138	145	0	RPSHQQPR
1141.5397	1140.5324	1140.5352	-0.0028	172	180	0	NNPFYFPSR
1184.5983	1183.5910	1183.5846	0.0064	205	213	0	QFQNLQNHR
1258.6228	1257.6155	1257.6101	0.0054	255	265	0	SFNLDEGHALR
1287.5995	1286.5922	1286.5891	0.0031	308	318	0	DQSSYLQGFSR
1297.6453	1296.6380	1296.6363	0.0017	172	181	1	NNPFYFPSRR
1376.6873	1375.6800	1375.6619	0.0181	560	572	0	DLAFPGSGEQVEK
1427.7173	1426.7100	1426.7177	-0.0077	203	213	1	SRQFQNLQNHR
1568.7148	1567.7075	1567.7015	0.0061	153	166	0	EGEQEWGTPGSHVR
1572.7396	1571.7323	1571.7426	-0.0103	335	348	0	VLLEENAGGEQEER
1643.7765	1642.7692	1642.7798	-0.0105	387	401	0	GSEEEGDITNPINLR
1728.8552	1727.8479	1727.8437	0.0042	334	348	1	RVLLEENAGGEQEER
1738.8257	1737.8184	1737.8321	-0.0137	319	333	0	NTLEAAFNAEFNEIR
1771.8647	1770.8574	1770.8747	-0.0173	386	401	1	KGSEEEGDITNPINLR
1817.9481	1816.9408	1816.9570	-0.0162	541	556	1	IFLAGDKDNVIDQIEK
1894.9272	1893.9199	1893.9332	-0.0133	319	334	1	NTLEAAFNAEFNEIRR

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1046.5957, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1209.5590, 1320.5980, 1399.7009, 1756.8326, 1774.8629, 1830.8320, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2273.1633, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2514.3450, 2516.3413, 2530.3625, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

4. gi|46560478 **Mass:** 66934 **Score:** 83 **Expect:** 4.5e-006 **Queries matched:** 14

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5411	1004.5338	1004.5264	0.0074	132	139	0	RPSHQQPR
1141.5397	1140.5324	1140.5352	-0.0028	166	174	0	NNPFYFPSR
1184.5983	1183.5910	1183.5846	0.0064	199	207	0	QFQNLQNHR
1258.6228	1257.6155	1257.6101	0.0054	249	259	0	SFNLDEGHALR
1287.5995	1286.5922	1286.5891	0.0031	302	312	0	DQSSYLQGFSR
1297.6453	1296.6380	1296.6363	0.0017	166	175	1	NNPFYFPSRR
1320.5980	1319.5907	1319.5741	0.0166	394	405	0	DGEPDLSNNFGR
1376.6873	1375.6800	1375.6619	0.0181	555	567	0	DLAFPGSGEQVEK

1399.7009	1398.6936	1398.7116	-0.0180	197 - 207	1	SKQFQNLQNHR
1572.7396	1571.7323	1571.7426	-0.0103	329 - 342	0	VLLEENAGGEQEER
1728.8552	1727.8479	1727.8437	0.0042	328 - 342	1	RVLLEENAGGEQEER
1738.8257	1737.8184	1737.8321	-0.0137	313 - 327	0	NTLEAAFNAEFNEIR
1817.9481	1816.9408	1816.9570	-0.0162	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9272	1893.9199	1893.9332	-0.0133	313 - 328	1	NTLEAAFNAEFNEIRR

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1046.5957, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1209.5590, 1427.7173, 1568.7148, 1643.7765, 1756.8326, 1771.8647, 1774.8629, 1830.8320, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2273.1633, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2514.3450, 2516.3413, 2530.3625, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

5. gi|620025 **Mass:** 70639 **Score:** 81 **Expect:** 7.8e-006 **Queries matched:** 14

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5411	1004.5338	1004.5264	0.0074	132 - 139		0	RPSHQQPR
1141.5397	1140.5324	1140.5352	-0.0028	166 - 174		0	NNPFYFPSR
1184.5983	1183.5910	1183.5846	0.0064	199 - 207		0	QFQNLQNHR
1258.6228	1257.6155	1257.6101	0.0054	249 - 259		0	SFNLDEGHALR
1287.5995	1286.5922	1286.5891	0.0031	302 - 312		0	DQSSYLQGFSR
1297.6453	1296.6380	1296.6363	0.0017	166 - 175		1	NNPFYFPSRR
1320.5980	1319.5907	1319.5741	0.0166	394 - 405		0	DGEPDLSNNFGR
1376.6873	1375.6800	1375.6619	0.0181	555 - 567		0	DLAFPGSGEQVEK
1399.7009	1398.6936	1398.7116	-0.0180	197 - 207		1	SKQFQNLQNHR
1572.7396	1571.7323	1571.7426	-0.0103	329 - 342		0	VLLEENAGGEQEER
1728.8552	1727.8479	1727.8437	0.0042	328 - 342		1	RVLLEENAGGEQEER
1738.8257	1737.8184	1737.8321	-0.0137	313 - 327		0	NTLEAAFNAEFNEIR
1817.9481	1816.9408	1816.9570	-0.0162	536 - 551		1	IFLAGDKDNVIDQIEK
1894.9272	1893.9199	1893.9332	-0.0133	313 - 328		1	NTLEAAFNAEFNEIRR

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1046.5957, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1209.5590, 1427.7173, 1568.7148, 1643.7765, 1756.8326, 1771.8647, 1774.8629, 1830.8320, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2273.1633, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2514.3450, 2516.3413, 2530.3625, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

6. gi|1168390 **Mass:** 70639 **Score:** 81 **Expect:** 7.8e-006 **Queries matched:** 14

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1005.5411	1004.5338	1004.5264	0.0074	132 - 139	0	RPSHQQPR
1141.5397	1140.5324	1140.5352	-0.0028	166 - 174	0	NNPFYFPSR
1184.5983	1183.5910	1183.5846	0.0064	199 - 207	0	QFQNLQNHR
1258.6228	1257.6155	1257.6101	0.0054	249 - 259	0	SFNLDEGHALR
1287.5995	1286.5922	1286.5891	0.0031	302 - 312	0	DQSSYLQGFSR
1297.6453	1296.6380	1296.6363	0.0017	166 - 175	1	NNPFYFPSRR
1320.5980	1319.5907	1319.5741	0.0166	394 - 405	0	DGEPDLSNNFGR
1376.6873	1375.6800	1375.6619	0.0181	555 - 567	0	DLAFPGSGEQVEK
1399.7009	1398.6936	1398.7116	-0.0180	197 - 207	1	SKQFQNLQNHR
1572.7396	1571.7323	1571.7426	-0.0103	329 - 342	0	VLLEENAGGEQEER
1728.8552	1727.8479	1727.8437	0.0042	328 - 342	1	RVLLEENAGGEQEER
1738.8257	1737.8184	1737.8321	-0.0137	313 - 327	0	NTLEAAFNAEFNEIR
1817.9481	1816.9408	1816.9570	-0.0162	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9272	1893.9199	1893.9332	-0.0133	313 - 328	1	NTLEAAFNAEFNEIRR

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1046.5957, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1209.5590, 1427.7173, 1568.7148, 1643.7765, 1756.8326, 1771.8647, 1774.8629, 1830.8320, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2273.1633, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2514.3450, 2516.3413, 2530.3625, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

7. gi|46560476 **Mass:** 48122 **Score:** 69 **Expect:** 0.00012 **Queries matched:** 10

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1184.5983	1183.5910	1183.5846	0.0064	8 -	16	0	QFQNLQNHR
1258.6228	1257.6155	1257.6101	0.0054	58 -	68	0	SFNLDEGHALR
1287.5995	1286.5922	1286.5891	0.0031	111 -	121	0	DQSSYLQGFSR
1376.6873	1375.6800	1375.6619	0.0181	362 -	374	0	DLAFPGSGEQVEK
1427.7173	1426.7100	1426.7177	-0.0077	6 -	16	1	SRQFQNLQNHR
1572.7396	1571.7323	1571.7426	-0.0103	138 -	151	0	VLLEENAGGEQEER
1728.8552	1727.8479	1727.8437	0.0042	137 -	151	1	RVLLEENAGGEQEER
1738.8257	1737.8184	1737.8321	-0.0137	122 -	136	0	NTLEAAFNAEFNEIR
1817.9481	1816.9408	1816.9570	-0.0162	343 -	358	1	IFLAGDKDNVIDQIEK
1894.9272	1893.9199	1893.9332	-0.0133	122 -	137	1	NTLEAAFNAEFNEIRR

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1005.5411, 1046.5957, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1141.5397, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1209.5590, 1297.6453, 1320.5980, 1399.7009, 1568.7148, 1643.7765, 1756.8326, 1771.8647, 1774.8629, 1830.8320, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2273.1633, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2514.3450, 2516.3413, 2530.3625, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

8. gi|46560474 **Mass:** 33641 **Score:** 38 **Expect:** 0.13 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1376.6873	1375.6800	1375.6619	0.0181	240 -	252	0	DLAFPGSGEQVEK
1572.7396	1571.7323	1571.7426	-0.0103	15 -	28	0	VLLEENAGGEQEER
1643.7765	1642.7692	1642.7798	-0.0105	67 -	81	0	GSEEEGDITNPINLR
1728.8552	1727.8479	1727.8437	0.0042	14 -	28	1	RVLLEENAGGEQEER
1771.8647	1770.8574	1770.8747	-0.0173	66 -	81	1	KGSEEEGDITNPINLR
1817.9481	1816.9408	1816.9570	-0.0162	221 -	236	1	IFLAGDKDNVIDQIEK

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1005.5411, 1046.5957, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1141.5397, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1184.5983, 1209.5590, 1258.6228, 1287.5995, 1297.6453, 1320.5980, 1399.7009, 1427.7173, 1568.7148, 1738.8257, 1756.8326, 1774.8629, 1830.8320, 1894.9272, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2273.1633, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2514.3450, 2516.3413, 2530.3625, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

9. gi|46560472 **Mass:** 34169 **Score:** 28 **Expect:** 1.5 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1320.5980	1319.5907	1319.5741	0.0166	83 -	94	0	DGEPDLSNNFGR
1376.6873	1375.6800	1375.6619	0.0181	244 -	256	0	DLAFPGSGEQVEK
1572.7396	1571.7323	1571.7426	-0.0103	18 -	31	0	VLLEENAGGEQEER
1728.8552	1727.8479	1727.8437	0.0042	17 -	31	1	RVLLEENAGGEQEER
1817.9481	1816.9408	1816.9570	-0.0162	225 -	240	1	IFLAGDKDNVIDQIEK

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1005.5411, 1046.5957, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1141.5397, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1184.5983, 1209.5590, 1258.6228, 1287.5995, 1297.6453, 1399.7009, 1427.7173, 1568.7148, 1643.7765, 1738.8257, 1756.8326, 1771.8647, 1774.8629, 1830.8320, 1894.9272, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2273.1633, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2514.3450, 2516.3413, 2530.3625, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

10. gi|230338 **Mass:** 23975 **Score:** 21 **Expect:** 7.4 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.5957	1045.5884	1045.5880	0.0005	90 -	99	1	LKSAASLNSR
2273.1633	2272.1560	2272.1521	0.0039	70 -	89	0	SIVHPSYNSNTLNNDIMLIK

2514.3450	2513.3377	2513.3311	0.0066	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK
2530.3625	2529.3552	2529.3260	0.0292	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1005.5411, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1141.5397, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1184.5983, 1209.5590, 1258.6228, 1287.5995, 1297.6453, 1320.5980, 1376.6873, 1399.7009, 1427.7173, 1568.7148, 1572.7396, 1643.7765, 1728.8552, 1738.8257, 1756.8326, 1771.8647, 1774.8629, 1817.9481, 1830.8320, 1894.9272, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2516.3413, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 61

Protein View

Match to: **gi|16612200** Score: **103** Expect: **4.4e-008**
major allergen Arah1 [Arachis hypogaea]

Nominal mass (M_r): **71701**; Calculated pI value: **6.62**
NCBI BLAST search of gi|16612200 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **61**
Number of mass values matched: **16**
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP

```
  51 DDLKQKACES RCTKLEYDPR CVYDPRGHTG TTNQRSPPGE RTRGRQPGDY
 101 DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE
 151 GREGEQEWGT PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD
 201 QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ GQATVTVANG
 251 NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED
 301 FFPASSRDQS SYLQGFSRNT LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ
 351 RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
 401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS
 451 KAMVIVVVNK GTGNLELVAV RKEQQQRGRR EEEEDEDEEE EGSNREVRRY
 501 TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV
 551 IDQIEKQAKD LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE
 601 SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
138 - 145	1005.5411	1004.5338	1004.5264	0.0074	0	RPSHQQPR
153 - 166	1568.7148	1567.7075	1567.7015	0.0061	0	EGEQEWGTPGSHVR
172 - 180	1141.5397	1140.5324	1140.5352	-0.0028	0	NNPFYFPSR
172 - 181	1297.6453	1296.6380	1296.6363	0.0017	1	NNPFYFPSRR
203 - 213	1427.7173	1426.7100	1426.7177	-0.0077	1	SRQFQNLQNHR
205 - 213	1184.5983	1183.5910	1183.5846	0.0064	0	QFQNLQNHR
255 - 265	1258.6228	1257.6155	1257.6101	0.0054	0	SFNLDEGHALR
308 - 318	1287.5995	1286.5922	1286.5891	0.0031	0	DQSSYLQGFSR
319 - 333	1738.8257	1737.8184	1737.8321	-0.0137	0	NTLEAAFNAEFNEIR
319 - 334	1894.9272	1893.9199	1893.9332	-0.0133	1	NTLEAAFNAEFNEIRR
334 - 348	1728.8552	1727.8479	1727.8437	0.0042	1	RVLLEENAGGEQEER
335 - 348	1572.7396	1571.7323	1571.7426	-0.0103	0	VLLEENAGGEQEER
386 - 401	1771.8647	1770.8574	1770.8747	-0.0173	1	KGSEEEGDITNPINLR
387 - 401	1643.7765	1642.7692	1642.7798	-0.0105	0	GSEEEGDITNPINLR
541 - 556	1817.9481	1816.9408	1816.9570	-0.0162	1	IFLAGDKDNVIDQIEK
560 - 572	1376.6873	1375.6800	1375.6619	0.0181	0	DLAFPGSGEQVEK

No match to: 805.4426, 855.0587, 861.0780, 877.0409, 1046.5957, 1066.0670, 1080.5385, 1111.5625, 1137.0739, 1137.5681, 1145.0735, 1145.5692, 1167.5741, 1174.6351, 1209.5590, 1320.5980, 1399.7009, 1756.8326, 1774.8629, 1830.8320, 1918.8727, 2145.0884, 2146.6086, 2185.0251, 2225.0142, 2272.1563, 2273.1633, 2295.1460, 2305.1492, 2311.1174, 2333.1123, 2335.0876, 2336.0884, 2337.0791, 2351.0796, 2460.2009, 2513.3289, 2514.3450, 2516.3413, 2530.3625, 2612.1880, 3136.4387, 3211.5081, 3300.7295, 3316.8420

Spot 22

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:48:36 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **373 for gi|16612200, major allergen Arah1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|16612200	71701	373	major allergen Arah1 [Arachis hypogaea]
2.	gi|1168391	71701	373	Allergen Ara h 1, clone P41B precursor (Ara h I)
3.	gi|602436	71701	373	Ara h I
4.	gi|46560478	66934	334	conarachin [Arachis hypogaea]
5.	gi|620025	70639	332	Ara h I
6.	gi|1168390	70639	332	Allergen Ara h 1, clone P17 precursor (Ara h I)
7.	gi|46560476	48122	242	conarachin [Arachis hypogaea]
8.	gi|46560474	33641	84	conarachin [Arachis hypogaea]
9.	gi|46560472	34169	70	conarachin [Arachis hypogaea]
10.	gi|62177652	10056	31	resistance protein PRG [Arachis hypogaea]

Results List

1. gi|16612200 **Mass:** 71701 **Score:** 373 **Expect:** 4.4e-035 **Queries matched:** 18
major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1005.5212	1004.5139	1004.5264	-0.0125	138	145	0	---	RPSHQQPR
1141.5282	1140.5209	1140.5352	-0.0143	172	180	0	27	NNPFYFPSR
1141.5282	1140.5209	1140.5352	-0.0143	172	180	0	---	NNPFYFPSR
1184.5801	1183.5728	1183.5846	-0.0118	205	213	0	---	QFQNLQNHR
1258.6058	1257.5985	1257.6101	-0.0116	255	265	0	---	SFNLDEGHALR
1287.5836	1286.5763	1286.5891	-0.0128	308	318	0	---	DQSSYLQGFSR
1297.6268	1296.6195	1296.6363	-0.0168	172	181	1	32	NNPFYFPSRR
1297.6268	1296.6195	1296.6363	-0.0168	172	181	1	---	NNPFYFPSRR
1379.7531	1378.7458	1378.7608	-0.0150	266	277	0	63	IPSGFISYILNR
1379.7531	1378.7458	1378.7608	-0.0150	266	277	0	---	IPSGFISYILNR

1572.7245	1571.7172	1571.7426	-0.0254	335 - 348	0	---	VLLEENAGGEQEER
1572.7245	1571.7172	1571.7426	-0.0254	335 - 348	0	45	VLLEENAGGEQEER
1643.7699	1642.7626	1642.7798	-0.0171	387 - 401	0	---	GSEEEGDITNPINLR
1738.8246	1737.8173	1737.8321	-0.0148	319 - 333	0	---	NTLEAAFNAEFNEIR
1771.8645	1770.8572	1770.8747	-0.0175	386 - 401	1	---	KGSEEEGDITNPINLR
1817.9482	1816.9409	1816.9570	-0.0161	541 - 556	1	---	IFLAGDKDNVIDQIEK
1894.9233	1893.9160	1893.9332	-0.0172	319 - 334	1	---	NTLEAAFNAEFNEIRR
1894.9233	1893.9160	1893.9332	-0.0172	319 - 334	1	41	NTLEAAFNAEFNEIRR

No match to: 1151.7098, 1167.5533, 2333.0603

2. gi|1168391 **Mass:** 71701 **Score:** 373 **Expect:** 4.4e-035 **Queries matched:** 18

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1005.5212	1004.5139	1004.5264	-0.0125	138 - 145		0	---	RPSHQQPR
1141.5282	1140.5209	1140.5352	-0.0143	172 - 180		0	27	NNPFYFPSR
1141.5282	1140.5209	1140.5352	-0.0143	172 - 180		0	---	NNPFYFPSR
1184.5801	1183.5728	1183.5846	-0.0118	205 - 213		0	---	QFQNLQNHR
1258.6058	1257.5985	1257.6101	-0.0116	255 - 265		0	---	SFNLDEGHALR
1287.5836	1286.5763	1286.5891	-0.0128	308 - 318		0	---	DQSSYLQGFSR
1297.6268	1296.6195	1296.6363	-0.0168	172 - 181		1	32	NNPFYFPSRR
1297.6268	1296.6195	1296.6363	-0.0168	172 - 181		1	---	NNPFYFPSRR
1379.7531	1378.7458	1378.7608	-0.0150	266 - 277		0	63	IPSGFISYILNR
1379.7531	1378.7458	1378.7608	-0.0150	266 - 277		0	---	IPSGFISYILNR
1572.7245	1571.7172	1571.7426	-0.0254	335 - 348		0	---	VLLEENAGGEQEER
1572.7245	1571.7172	1571.7426	-0.0254	335 - 348		0	45	VLLEENAGGEQEER
1643.7699	1642.7626	1642.7798	-0.0171	387 - 401		0	---	GSEEEGDITNPINLR
1738.8246	1737.8173	1737.8321	-0.0148	319 - 333		0	---	NTLEAAFNAEFNEIR
1771.8645	1770.8572	1770.8747	-0.0175	386 - 401		1	---	KGSEEEGDITNPINLR
1817.9482	1816.9409	1816.9570	-0.0161	541 - 556		1	---	IFLAGDKDNVIDQIEK
1894.9233	1893.9160	1893.9332	-0.0172	319 - 334		1	---	NTLEAAFNAEFNEIRR
1894.9233	1893.9160	1893.9332	-0.0172	319 - 334		1	41	NTLEAAFNAEFNEIRR

No match to: 1151.7098, 1167.5533, 2333.0603

3. gi|602436 **Mass:** 71701 **Score:** 373 **Expect:** 4.4e-035 **Queries matched:** 18

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1005.5212	1004.5139	1004.5264	-0.0125	138 - 145		0	---	RPSHQQPR
1141.5282	1140.5209	1140.5352	-0.0143	172 - 180		0	27	NNPFYFPSR
1141.5282	1140.5209	1140.5352	-0.0143	172 - 180		0	---	NNPFYFPSR
1184.5801	1183.5728	1183.5846	-0.0118	205 - 213		0	---	QFQNLQNHR

1258.6058	1257.5985	1257.6101	-0.0116	255 - 265	0	---	SFNLDEGHALR
1287.5836	1286.5763	1286.5891	-0.0128	308 - 318	0	---	DQSSYLQGFSR
1297.6268	1296.6195	1296.6363	-0.0168	172 - 181	1	32	NNPFYFPSRR
1297.6268	1296.6195	1296.6363	-0.0168	172 - 181	1	---	NNPFYFPSRR
1379.7531	1378.7458	1378.7608	-0.0150	266 - 277	0	63	IPSGFISYILNR
1379.7531	1378.7458	1378.7608	-0.0150	266 - 277	0	---	IPSGFISYILNR
1572.7245	1571.7172	1571.7426	-0.0254	335 - 348	0	---	VLLEENAGGEQEER
1572.7245	1571.7172	1571.7426	-0.0254	335 - 348	0	45	VLLEENAGGEQEER
1643.7699	1642.7626	1642.7798	-0.0171	387 - 401	0	---	GSEEEGDITNPINLR
1738.8246	1737.8173	1737.8321	-0.0148	319 - 333	0	---	NTLEAAFNAEFNEIR
1771.8645	1770.8572	1770.8747	-0.0175	386 - 401	1	---	KGSEEEGDITNPINLR
1817.9482	1816.9409	1816.9570	-0.0161	541 - 556	1	---	IFLAGDKDNVIDQIEK
1894.9233	1893.9160	1893.9332	-0.0172	319 - 334	1	---	NTLEAAFNAEFNEIRR
1894.9233	1893.9160	1893.9332	-0.0172	319 - 334	1	41	NTLEAAFNAEFNEIRR

No match to: 1151.7098, 1167.5533, 2333.0603

4. gi|46560478 **Mass:** 66934 **Score:** 334 **Expect:** 3.5e-031 **Queries matched:** 16

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1005.5212	1004.5139	1004.5264	-0.0125	132 - 139	0	---	RPSHQQPR
1141.5282	1140.5209	1140.5352	-0.0143	166 - 174	0	27	NNPFYFPSR
1141.5282	1140.5209	1140.5352	-0.0143	166 - 174	0	---	NNPFYFPSR
1184.5801	1183.5728	1183.5846	-0.0118	199 - 207	0	---	QFQNLQNHR
1258.6058	1257.5985	1257.6101	-0.0116	249 - 259	0	---	SFNLDEGHALR
1287.5836	1286.5763	1286.5891	-0.0128	302 - 312	0	---	DQSSYLQGFSR
1297.6268	1296.6195	1296.6363	-0.0168	166 - 175	1	32	NNPFYFPSRR
1297.6268	1296.6195	1296.6363	-0.0168	166 - 175	1	---	NNPFYFPSRR
1379.7531	1378.7458	1378.7608	-0.0150	260 - 271	0	63	IPSGFISYILNR
1379.7531	1378.7458	1378.7608	-0.0150	260 - 271	0	---	IPSGFISYILNR
1572.7245	1571.7172	1571.7426	-0.0254	329 - 342	0	---	VLLEENAGGEQEER
1572.7245	1571.7172	1571.7426	-0.0254	329 - 342	0	45	VLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	313 - 327	0	---	NTLEAAFNAEFNEIR
1817.9482	1816.9409	1816.9570	-0.0161	536 - 551	1	---	IFLAGDKDNVIDQIEK
1894.9233	1893.9160	1893.9332	-0.0172	313 - 328	1	---	NTLEAAFNAEFNEIRR
1894.9233	1893.9160	1893.9332	-0.0172	313 - 328	1	41	NTLEAAFNAEFNEIRR

No match to: 1151.7098, 1167.5533, 1643.7699, 1771.8645, 2333.0603

5. gi|620025 **Mass:** 70639 **Score:** 332 **Expect:** 5.5e-031 **Queries matched:** 16

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1005.5212	1004.5139	1004.5264	-0.0125	132 - 139	0	---	RPSHQQPR
1141.5282	1140.5209	1140.5352	-0.0143	166 - 174	0	27	NNPFYFPSR
1141.5282	1140.5209	1140.5352	-0.0143	166 - 174	0	---	NNPFYFPSR
1184.5801	1183.5728	1183.5846	-0.0118	199 - 207	0	---	QFQNLQNHR
1258.6058	1257.5985	1257.6101	-0.0116	249 - 259	0	---	SFNLDEGHALR
1287.5836	1286.5763	1286.5891	-0.0128	302 - 312	0	---	DQSSYLQGFSR
1297.6268	1296.6195	1296.6363	-0.0168	166 - 175	1	32	NNPFYFPSRR
1297.6268	1296.6195	1296.6363	-0.0168	166 - 175	1	---	NNPFYFPSRR
1379.7531	1378.7458	1378.7608	-0.0150	260 - 271	0	63	IPSGFISYILNR
1379.7531	1378.7458	1378.7608	-0.0150	260 - 271	0	---	IPSGFISYILNR
1572.7245	1571.7172	1571.7426	-0.0254	329 - 342	0	---	VLLEENAGGEQEER
1572.7245	1571.7172	1571.7426	-0.0254	329 - 342	0	45	VLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	313 - 327	0	---	NTLEAAFNAEFNEIR
1817.9482	1816.9409	1816.9570	-0.0161	536 - 551	1	---	IFLAGDKDNVIDQIEK
1894.9233	1893.9160	1893.9332	-0.0172	313 - 328	1	---	NTLEAAFNAEFNEIRR
1894.9233	1893.9160	1893.9332	-0.0172	313 - 328	1	41	NTLEAAFNAEFNEIRR

No match to: 1151.7098, 1167.5533, 1643.7699, 1771.8645, 2333.0603

6. gi|1168390 **Mass:** 70639 **Score:** 332 **Expect:** 5.5e-031 **Queries matched:** 16

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1005.5212	1004.5139	1004.5264	-0.0125	132 - 139		0	---	RPSHQQPR
1141.5282	1140.5209	1140.5352	-0.0143	166 - 174		0	27	NNPFYFPSR
1141.5282	1140.5209	1140.5352	-0.0143	166 - 174		0	---	NNPFYFPSR
1184.5801	1183.5728	1183.5846	-0.0118	199 - 207		0	---	QFQNLQNHR
1258.6058	1257.5985	1257.6101	-0.0116	249 - 259		0	---	SFNLDEGHALR
1287.5836	1286.5763	1286.5891	-0.0128	302 - 312		0	---	DQSSYLQGFSR
1297.6268	1296.6195	1296.6363	-0.0168	166 - 175		1	32	NNPFYFPSRR
1297.6268	1296.6195	1296.6363	-0.0168	166 - 175		1	---	NNPFYFPSRR
1379.7531	1378.7458	1378.7608	-0.0150	260 - 271		0	63	IPSGFISYILNR
1379.7531	1378.7458	1378.7608	-0.0150	260 - 271		0	---	IPSGFISYILNR
1572.7245	1571.7172	1571.7426	-0.0254	329 - 342		0	---	VLLEENAGGEQEER
1572.7245	1571.7172	1571.7426	-0.0254	329 - 342		0	45	VLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	313 - 327		0	---	NTLEAAFNAEFNEIR
1817.9482	1816.9409	1816.9570	-0.0161	536 - 551		1	---	IFLAGDKDNVIDQIEK
1894.9233	1893.9160	1893.9332	-0.0172	313 - 328		1	---	NTLEAAFNAEFNEIRR
1894.9233	1893.9160	1893.9332	-0.0172	313 - 328		1	41	NTLEAAFNAEFNEIRR

No match to: 1151.7098, 1167.5533, 1643.7699, 1771.8645, 2333.0603

7. gi|46560476 **Mass:** 48122 **Score:** 242 **Expect:** 5.5e-022 **Queries matched:** 11

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1184.5801	1183.5728	1183.5846	-0.0118	8	-	16	0	---	QFQNLQNHR
1258.6058	1257.5985	1257.6101	-0.0116	58	-	68	0	---	SFNLDEGHALR
1287.5836	1286.5763	1286.5891	-0.0128	111	-	121	0	---	DQSSYLQGFSR
1379.7531	1378.7458	1378.7608	-0.0150	69	-	80	0	63	IPSGFISYILNR
1379.7531	1378.7458	1378.7608	-0.0150	69	-	80	0	---	IPSGFISYILNR
1572.7245	1571.7172	1571.7426	-0.0254	138	-	151	0	---	VLLEENAGGEQEER
1572.7245	1571.7172	1571.7426	-0.0254	138	-	151	0	45	VLLEENAGGEQEER
1738.8246	1737.8173	1737.8321	-0.0148	122	-	136	0	---	NTLEAAFNAEFNEIR
1817.9482	1816.9409	1816.9570	-0.0161	343	-	358	1	---	IFLAGDKDNVIDQIEK
1894.9233	1893.9160	1893.9332	-0.0172	122	-	137	1	---	NTLEAAFNAEFNEIRR
1894.9233	1893.9160	1893.9332	-0.0172	122	-	137	1	41	NTLEAAFNAEFNEIRR

No match to: 1005.5212, 1141.5282, 1141.5282, 1151.7098, 1167.5533, 1297.6268, 1297.6268, 1643.7699, 1771.8645, 2333.0603

8. gi|46560474 **Mass:** 33641 **Score:** 84 **Expect:** 3.6e-006 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1572.7245	1571.7172	1571.7426	-0.0254	15	-	28	0	---	VLLEENAGGEQEER
1572.7245	1571.7172	1571.7426	-0.0254	15	-	28	0	45	VLLEENAGGEQEER
1643.7699	1642.7626	1642.7798	-0.0171	67	-	81	0	---	GSEEEGDITNPINLR
1771.8645	1770.8572	1770.8747	-0.0175	66	-	81	1	---	KGSEEEGDITNPINLR
1817.9482	1816.9409	1816.9570	-0.0161	221	-	236	1	---	IFLAGDKDNVIDQIEK

No match to: 1005.5212, 1141.5282, 1141.5282, 1151.7098, 1167.5533, 1184.5801, 1258.6058, 1287.5836, 1297.6268, 1297.6268, 1379.7531, 1379.7531, 1738.8246, 1894.9233, 1894.9233, 2333.0603

9. gi|46560472 **Mass:** 34169 **Score:** 70 **Expect:** 8e-005 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1297.6268	1296.6195	1296.7037	-0.0842	50	-	60	1	---	VSKEHVQELTK
1297.6268	1296.6195	1296.7037	-0.0842	50	-	60	1	---	VSKEHVQELTK
1572.7245	1571.7172	1571.7426	-0.0254	18	-	31	0	---	VLLEENAGGEQEER
1572.7245	1571.7172	1571.7426	-0.0254	18	-	31	0	45	VLLEENAGGEQEER
1817.9482	1816.9409	1816.9570	-0.0161	225	-	240	1	---	IFLAGDKDNVIDQIEK

No match to: 1005.5212, 1141.5282, 1141.5282, 1151.7098, 1167.5533, 1184.5801, 1258.6058, 1287.5836, 1379.7531, 1379.7531, 1643.7699, 1738.8246, 1771.8645, 1894.9233, 1894.9233, 2333.0603

10. gi|62177652 **Mass:** 10056 **Score:** 31 **Expect:** 0.71 **Queries matched:** 4

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide

1379.7531	1378.7458	1378.7496	-0.0037	77 -	89	1	5	EVVKYSGGLPFAL
1379.7531	1378.7458	1378.7496	-0.0037	77 -	89	1	---	EVVKYSGGLPFAL
1894.9233	1893.9160	1893.9009	0.0152	7 -	23	0	---	QLEYLGGEQAWFGPGSR
1894.9233	1893.9160	1893.9009	0.0152	7 -	23	0	---	QLEYLGGEQAWFGPGSR

No match to: 1005.5212, 1141.5282, 1141.5282, 1151.7098, 1167.5533, 1184.5801, 1258.6058, 1287.5836, 1297.6268, 1297.6268, 1572.7245, 1572.7245, 1643.7699, 1738.8246, 1771.8645, 1817.9482, 2333.0603

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1

Protein View

Match to: **gi|16612200** Score: **373** Expect: **4.4e-035**
major allergen Arah1 [Arachis hypogaea]

Nominal mass (M_r): **71701**; Calculated pI value: **6.62**
NCBI BLAST search of gi|16612200 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```
   1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP
  51 DDLKQKACES RCTKLEYDPR CVYDPRGHTG TTNQRSPPGE RTRGRQPGDY
 101 DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE
 151 GREGEQEWGT PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD
 201 QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ GQATVTVANG
 251 NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED
 301 FFPASSRDQS SYLQGFSRNT LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ
 351 RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
 401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS
 451 KAMVIVVVNK GTGNLELVAV RKEQQQRGRR EEEEDEDEEE EGSNREVRRY
 501 TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV
 551 IDQIEKQAKD LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE
 601 SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
138 - 145	1005.5212	1004.5139	1004.5264	-0.0125	0	RPSHQQPR	(No match)
172 - 180	1141.5282	1140.5209	1140.5352	-0.0143	0	NNPFYFPSR	(Ions score 27)
172 - 180	1141.5282	1140.5209	1140.5352	-0.0143	0	NNPFYFPSR	(No match)
172 - 181	1297.6268	1296.6195	1296.6363	-0.0168	1	NNPFYFPSRR	(Ions score 32)
172 - 181	1297.6268	1296.6195	1296.6363	-0.0168	1	NNPFYFPSRR	(No match)
205 - 213	1184.5801	1183.5728	1183.5846	-0.0118	0	QFQNLQNHR	(No match)
255 - 265	1258.6058	1257.5985	1257.6101	-0.0116	0	SFNLDEGHALR	(No match)
266 - 277	1379.7531	1378.7458	1378.7608	-0.0150	0	IPSGFISYILNR	(Ions score 63)
266 - 277	1379.7531	1378.7458	1378.7608	-0.0150	0	IPSGFISYILNR	(No match)
308 - 318	1287.5836	1286.5763	1286.5891	-0.0128	0	DQSSYLQGFSR	(No match)
319 - 333	1738.8246	1737.8173	1737.8321	-0.0148	0	NTLEAAFNAEFNEIR	(No match)
319 - 334	1894.9233	1893.9160	1893.9332	-0.0172	1	NTLEAAFNAEFNEIRR	(No match)
319 - 334	1894.9233	1893.9160	1893.9332	-0.0172	1	NTLEAAFNAEFNEIRR	(Ions score 41)
335 - 348	1572.7245	1571.7172	1571.7426	-0.0254	0	VLLEENAGGEQEER	(No match)
335 - 348	1572.7245	1571.7172	1571.7426	-0.0254	0	VLLEENAGGEQEER	(Ions score 45)
386 - 401	1771.8645	1770.8572	1770.8747	-0.0175	1	KGSEEEGDITNPINLR	(No match)
387 - 401	1643.7699	1642.7626	1642.7798	-0.0171	0	GSEEEGDITNPINLR	(No match)
541 - 556	1817.9482	1816.9409	1816.9570	-0.0161	1	IFLAGDKDNVIDQIEK	(No match)

Spot 23

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:35:32 GMT**
Top Score : **65 for gi|16612200, major allergen Arah1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|16612200	71701	65	major allergen Arah1 [Arachis hypogaea]
2.	gi|1168391	71701	65	Allergen Ara h 1, clone P41B precursor (Ara h I)
3.	gi|602436	71701	65	Ara h I
4.	gi|46560476	48122	53	conarachin [Arachis hypogaea]
5.	gi|46560478	66934	35	conarachin [Arachis hypogaea]
6.	gi|620025	70639	33	Ara h I
7.	gi|1168390	70639	33	Allergen Ara h 1, clone P17 precursor (Ara h I)
8.	gi|46560474	33641	25	conarachin [Arachis hypogaea]
9.	gi|71040687	13451	22	auxin-repressed protein [Arachis hypogaea]
10.	gi|62177385	14731	21	resistance protein Cre [Arachis hypogaea]

Results List

1. gi|16612200 **Mass:** 71701 **Score:** 65 **Expect:** 0.00026 **Queries matched:** 13
major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5486	1004.5413	1004.5264	0.0149	138	145	0	RPSHQQPR
1175.5745	1174.5672	1174.5829	-0.0157	357	367	0	SSENNEGVIVK
1184.5933	1183.5860	1183.5846	0.0014	205	213	0	QFQNLQNHR
1287.6129	1286.6056	1286.5891	0.0165	308	318	0	DQSSYLQGFSR
1297.6498	1296.6425	1296.6363	0.0062	172	181	1	NNPFYFPSRR
1376.6731	1375.6658	1375.6619	0.0039	560	572	0	DLAFPGSGEQVEK
1427.7089	1426.7016	1426.7177	-0.0161	203	213	1	SRQFQNLQNHR
1568.7190	1567.7117	1567.7015	0.0103	153	166	0	EGEQEWGTPGSHVR
1572.7499	1571.7426	1571.7426	-0.0000	335	348	0	VLLEENAGGEQEER

1643.7924	1642.7851	1642.7798	0.0054	387 - 401	0	GSEEEGDITNPINLR
1728.8556	1727.8483	1727.8437	0.0046	334 - 348	1	RVLLEENAGGEQEER
1738.8312	1737.8239	1737.8321	-0.0082	319 - 333	0	NTLEAAFNAEFNEIR
1894.9730	1893.9657	1893.9332	0.0325	319 - 334	1	NTLEAAFNAEFNEIRR

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1277.1003, 1331.7030, 1400.6731, 1547.7455, 1618.7733, 1730.8704, 1731.8639, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2295.1536, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3137.4465, 3153.4587, 3211.5088, 3234.4561, 3300.7610, 3316.7498

2. gi|1168391 **Mass:** 71701 **Score:** 65 **Expect:** 0.00026 **Queries matched:** 13

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5486	1004.5413	1004.5264	0.0149	138 - 145		0	RPSHQQPR
1175.5745	1174.5672	1174.5829	-0.0157	357 - 367		0	SSENNEGVIVK
1184.5933	1183.5860	1183.5846	0.0014	205 - 213		0	QFQNLQNHR
1287.6129	1286.6056	1286.5891	0.0165	308 - 318		0	DQSSYLQGFSR
1297.6498	1296.6425	1296.6363	0.0062	172 - 181		1	NNPFYFPSRR
1376.6731	1375.6658	1375.6619	0.0039	560 - 572		0	DLAFPGSGEQVEK
1427.7089	1426.7016	1426.7177	-0.0161	203 - 213		1	SRQFQNLQNHR
1568.7190	1567.7117	1567.7015	0.0103	153 - 166		0	EGEQEWGTPGSHVR
1572.7499	1571.7426	1571.7426	-0.0000	335 - 348		0	VLLEENAGGEQEER
1643.7924	1642.7851	1642.7798	0.0054	387 - 401		0	GSEEEGDITNPINLR
1728.8556	1727.8483	1727.8437	0.0046	334 - 348		1	RVLLEENAGGEQEER
1738.8312	1737.8239	1737.8321	-0.0082	319 - 333		0	NTLEAAFNAEFNEIR
1894.9730	1893.9657	1893.9332	0.0325	319 - 334		1	NTLEAAFNAEFNEIRR

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1277.1003, 1331.7030, 1400.6731, 1547.7455, 1618.7733, 1730.8704, 1731.8639, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2295.1536, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3137.4465, 3153.4587, 3211.5088, 3234.4561, 3300.7610, 3316.7498

3. gi|602436 **Mass:** 71701 **Score:** 65 **Expect:** 0.00026 **Queries matched:** 13

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5486	1004.5413	1004.5264	0.0149	138 - 145		0	RPSHQQPR

1175.5745	1174.5672	1174.5829	-0.0157	357 - 367	0	SSENNEGVIVK
1184.5933	1183.5860	1183.5846	0.0014	205 - 213	0	QFQNLQNHR
1287.6129	1286.6056	1286.5891	0.0165	308 - 318	0	DQSSYLQGFSR
1297.6498	1296.6425	1296.6363	0.0062	172 - 181	1	NNPFYFPSRR
1376.6731	1375.6658	1375.6619	0.0039	560 - 572	0	DLAFPGSGEQVEK
1427.7089	1426.7016	1426.7177	-0.0161	203 - 213	1	SRQFQNLQNHR
1568.7190	1567.7117	1567.7015	0.0103	153 - 166	0	EGEQEWGTPGSHVR
1572.7499	1571.7426	1571.7426	-0.0000	335 - 348	0	VLLEENAGGEQEER
1643.7924	1642.7851	1642.7798	0.0054	387 - 401	0	GSEEEGDITNPINLR
1728.8556	1727.8483	1727.8437	0.0046	334 - 348	1	RVLLEENAGGEQEER
1738.8312	1737.8239	1737.8321	-0.0082	319 - 333	0	NTLEAAFNAEFNEIR
1894.9730	1893.9657	1893.9332	0.0325	319 - 334	1	NTLEAAFNAEFNEIRR

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1277.1003, 1331.7030, 1400.6731, 1547.7455, 1618.7733, 1730.8704, 1731.8639, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2295.1536, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3137.4465, 3153.4587, 3211.5088, 3234.4561, 3300.7610, 3316.7498

4. gi|46560476 **Mass:** 48122 **Score:** 53 **Expect:** 0.0047 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1175.5745	1174.5672	1174.5829	-0.0157	160	170	0	SSENNEGVIVK
1184.5933	1183.5860	1183.5846	0.0014	8	16	0	QFQNLQNHR
1287.6129	1286.6056	1286.5891	0.0165	111	121	0	DQSSYLQGFSR
1376.6731	1375.6658	1375.6619	0.0039	362	374	0	DLAFPGSGEQVEK
1427.7089	1426.7016	1426.7177	-0.0161	6	16	1	SRQFQNLQNHR
1572.7499	1571.7426	1571.7426	-0.0000	138	151	0	VLLEENAGGEQEER
1728.8556	1727.8483	1727.8437	0.0046	137	151	1	RVLLEENAGGEQEER
1738.8312	1737.8239	1737.8321	-0.0082	122	136	0	NTLEAAFNAEFNEIR
1894.9730	1893.9657	1893.9332	0.0325	122	137	1	NTLEAAFNAEFNEIRR

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1005.5486, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1277.1003, 1297.6498, 1331.7030, 1400.6731, 1547.7455, 1568.7190, 1618.7733, 1643.7924, 1730.8704, 1731.8639, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2295.1536, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3137.4465, 3153.4587, 3211.5088, 3234.4561, 3300.7610, 3316.7498

5. gi|46560478 **Mass:** 66934 **Score:** 35 **Expect:** 0.3 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5486	1004.5413	1004.5264	0.0149	132	139	0	RPSHQQPR
1184.5933	1183.5860	1183.5846	0.0014	199	207	0	QFQNLQNHR
1287.6129	1286.6056	1286.5891	0.0165	302	312	0	DQSSYLQGFSR
1297.6498	1296.6425	1296.6363	0.0062	166	175	1	NNPFYFPSRR
1376.6731	1375.6658	1375.6619	0.0039	555	567	0	DLAFPGSGEQVEK
1572.7499	1571.7426	1571.7426	-0.0000	329	342	0	VLLEENAGGEQEER
1728.8556	1727.8483	1727.8437	0.0046	328	342	1	RVLLEENAGGEQEER
1738.8312	1737.8239	1737.8321	-0.0082	313	327	0	NTLEAAFNAEFNEIR
1894.9730	1893.9657	1893.9332	0.0325	313	328	1	NTLEAAFNAEFNEIRR

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1175.5745, 1277.1003, 1331.7030, 1400.6731, 1427.7089, 1547.7455, 1568.7190, 1618.7733, 1643.7924, 1730.8704, 1731.8639, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2295.1536, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3137.4465, 3153.4587, 3211.5088, 3234.4561, 3300.7610, 3316.7498

6. gi|620025 **Mass:** 70639 **Score:** 33 **Expect:** 0.42 **Queries matched:** 9

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5486	1004.5413	1004.5264	0.0149	132	139	0	RPSHQQPR
1184.5933	1183.5860	1183.5846	0.0014	199	207	0	QFQNLQNHR
1287.6129	1286.6056	1286.5891	0.0165	302	312	0	DQSSYLQGFSR
1297.6498	1296.6425	1296.6363	0.0062	166	175	1	NNPFYFPSRR
1376.6731	1375.6658	1375.6619	0.0039	555	567	0	DLAFPGSGEQVEK
1572.7499	1571.7426	1571.7426	-0.0000	329	342	0	VLLEENAGGEQEER
1728.8556	1727.8483	1727.8437	0.0046	328	342	1	RVLLEENAGGEQEER
1738.8312	1737.8239	1737.8321	-0.0082	313	327	0	NTLEAAFNAEFNEIR
1894.9730	1893.9657	1893.9332	0.0325	313	328	1	NTLEAAFNAEFNEIRR

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1175.5745, 1277.1003, 1331.7030, 1400.6731, 1427.7089, 1547.7455, 1568.7190, 1618.7733, 1643.7924, 1730.8704, 1731.8639, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2295.1536, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3137.4465, 3153.4587, 3211.5088, 3234.4561, 3300.7610,

3316.7498

7. gi|1168390 **Mass:** 70639 **Score:** 33 **Expect:** 0.42 **Queries matched:** 9

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5486	1004.5413	1004.5264	0.0149	132	139	0	RPSHQQPR
1184.5933	1183.5860	1183.5846	0.0014	199	207	0	QFQNLQNHR
1287.6129	1286.6056	1286.5891	0.0165	302	312	0	DQSSYLQGFSR
1297.6498	1296.6425	1296.6363	0.0062	166	175	1	NNPFYFPSRR
1376.6731	1375.6658	1375.6619	0.0039	555	567	0	DLAFPGSGEQVEK
1572.7499	1571.7426	1571.7426	-0.0000	329	342	0	VLLEENAGGEQEER
1728.8556	1727.8483	1727.8437	0.0046	328	342	1	RVLLEENAGGEQEER
1738.8312	1737.8239	1737.8321	-0.0082	313	327	0	NTLEAAFNAEFNEIR
1894.9730	1893.9657	1893.9332	0.0325	313	328	1	NTLEAAFNAEFNEIRR

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1175.5745, 1277.1003, 1331.7030, 1400.6731, 1427.7089, 1547.7455, 1568.7190, 1618.7733, 1643.7924, 1730.8704, 1731.8639, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2295.1536, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3137.4465, 3153.4587, 3211.5088, 3234.4561, 3300.7610, 3316.7498

8. gi|46560474 **Mass:** 33641 **Score:** 25 **Expect:** 3 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1175.5745	1174.5672	1174.5829	-0.0157	37	47	0	SSENNEGVIVK
1376.6731	1375.6658	1375.6619	0.0039	240	252	0	DLAFPGSGEQVEK
1572.7499	1571.7426	1571.7426	-0.0000	15	28	0	VLLEENAGGEQEER
1643.7924	1642.7851	1642.7798	0.0054	67	81	0	GSEEEGDITNPINLR
1728.8556	1727.8483	1727.8437	0.0046	14	28	1	RVLLEENAGGEQEER

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1005.5486, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1184.5933, 1277.1003, 1287.6129, 1297.6498, 1331.7030, 1400.6731, 1427.7089, 1547.7455, 1568.7190, 1618.7733, 1730.8704, 1731.8639, 1738.8312, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1894.9730, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2295.1536, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3137.4465, 3153.4587, 3211.5088, 3234.4561, 3300.7610, 3316.7498

9. gi|71040687 **Mass:** 13451 **Score:** 22 **Expect:** 5.6 **Queries matched:** 2

auxin-repressed protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
3137.4465	3136.4392	3136.5029	-0.0636	91	-	117	0	TIGSDYFDKPLLNSPTVYDWLYSGETR
3211.5088	3210.5015	3210.5802	-0.0786	49	-	78	1	SMSMPATPTTPGTPTTPLSATPRKPDNVWR + Oxidation (M)

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1005.5486, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1175.5745, 1184.5933, 1277.1003, 1287.6129, 1297.6498, 1331.7030, 1376.6731, 1400.6731, 1427.7089, 1547.7455, 1568.7190, 1572.7499, 1618.7733, 1643.7924, 1728.8556, 1730.8704, 1731.8639, 1738.8312, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1894.9730, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2295.1536, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3153.4587, 3234.4561, 3300.7610, 3316.7498

10. gi|62177385 **Mass:** 14731 **Score:** 21 **Expect:** 6.8 **Queries matched:** 3

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1427.7089	1426.7016	1426.6986	0.0030	71	-	82	1	RNCPPELESIGR
1730.8704	1729.8631	1729.8787	-0.0156	1	-	14	1	NLILDDVWDSKAWR
2295.1536	2294.1463	2294.1147	0.0317	15	-	34	1	TIKNCFPENNNGGMILVTTR + Oxidation (M)

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1005.5486, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1175.5745, 1184.5933, 1277.1003, 1287.6129, 1297.6498, 1331.7030, 1376.6731, 1400.6731, 1547.7455, 1568.7190, 1572.7499, 1618.7733, 1643.7924, 1728.8556, 1731.8639, 1738.8312, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1894.9730, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3137.4465, 3153.4587, 3211.5088, 3234.4561, 3300.7610, 3316.7498

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 70

Protein View

Match to: **gi|16612200** Score: **65** Expect: **0.00026**
major allergen Arah1 [Arachis hypogaea]

Nominal mass (M_r): **71701**; Calculated pI value: **6.62**
NCBI BLAST search of gi|16612200 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **70**
Number of mass values matched: **13**
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP
    51 DDLKQKACES RCTKLEYDPR CVYDPRGHTG TTNQRSPPGE RTRGRQPGDY
   101 DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE
   151 GREGEQEWGT PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD
   201 QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ GQATVTVANG
   251 NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED
   301 FFPASSRDQS SYLQGFSRNT LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ
   351 RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
   401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS
   451 KAMVIVVVNK GTGNLELVAV RKEQQQRGRR EEEEDEDEEE EGSNREVRRY
   501 TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV
   551 IDQIEKQAKD LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE
   601 SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
138 - 145	1005.5486	1004.5413	1004.5264	0.0149	0	RPSHQQPR
153 - 166	1568.7190	1567.7117	1567.7015	0.0103	0	EGEQEWGTPGSHVR
172 - 181	1297.6498	1296.6425	1296.6363	0.0062	1	NNPFYFPSRR
203 - 213	1427.7089	1426.7016	1426.7177	-0.0161	1	SRQFQNLQNHR
205 - 213	1184.5933	1183.5860	1183.5846	0.0014	0	QFQNLQNHR
308 - 318	1287.6129	1286.6056	1286.5891	0.0165	0	DQSSYLQGFSR

319 - 333	**1738.8312**	**1737.8239**	**1737.8321**	**-0.0082**	**0**	**NTLEAAFNAEFNEIR**
319 - 334	**1894.9730**	**1893.9657**	**1893.9332**	**0.0325**	**1**	**NTLEAAFNAEFNEIRR**
334 - 348	**1728.8556**	**1727.8483**	**1727.8437**	**0.0046**	**1**	**RVLLEENAGGEQEER**
335 - 348	**1572.7499**	**1571.7426**	**1571.7426**	**-0.0000**	**0**	**VLLEENAGGEQEER**
357 - 367	**1175.5745**	**1174.5672**	**1174.5829**	**-0.0157**	**0**	**SSENNEGVIVK**
387 - 401	**1643.7924**	**1642.7851**	**1642.7798**	**0.0054**	**0**	**GSEEEGDITNPINLR**
560 - 572	**1376.6731**	**1375.6658**	**1375.6619**	**0.0039**	**0**	**DLAFPGSGEQVEK**

No match to: 805.4698, 839.0797, 845.0935, 855.0601, 861.0710, 877.0364, 881.2789, 1046.5946, 1066.0703, 1072.0830, 1080.5276, 1082.0248, 1111.5594, 1137.0791, 1137.5625, 1145.0785, 1145.5750, 1167.5708, 1277.1003, 1331.7030, 1400.6731, 1547.7455, 1618.7733, 1730.8704, 1731.8639, 1756.8510, 1770.8856, 1772.8700, 1774.8385, 1777.8568, 1778.9067, 1786.8491, 1830.9066, 1918.8964, 2145.0564, 2185.0396, 2225.0090, 2273.1641, 2295.1536, 2305.1423, 2311.1387, 2333.1282, 2335.0952, 2337.0981, 2351.1018, 2456.1990, 2514.3367, 2530.3350, 2612.1836, 2628.2019, 2783.3347, 3137.4465, 3153.4587, 3211.5088, 3234.4561, 3300.7610, 3316.7498

Spot 24

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:37:48 GMT**
Top Score : **95 for gi|16612200, major allergen Arah1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|16612200	71701	95	major allergen Arah1 [Arachis hypogaea]
2.	gi|1168391	71701	95	Allergen Ara h 1, clone P41B precursor (Ara h I)
3.	gi|602436	71701	95	Ara h I
4.	gi|46560474	33641	45	conarachin [Arachis hypogaea]
5.	gi|46560478	66934	41	conarachin [Arachis hypogaea]
6.	gi|620025	70639	40	Ara h I
7.	gi|1168390	70639	40	Allergen Ara h 1, clone P17 precursor (Ara h I)
8.	gi|46560476	48122	38	conarachin [Arachis hypogaea]
9.	gi|46560472	34169	17	conarachin [Arachis hypogaea]
10.	gi|2498261	2416	14	33.0 kDa cold shock protein (AHCSP33)

Results List

1. gi|16612200 **Mass:** 71701 **Score:** 95 **Expect:** 2.9e-007 **Queries matched:** 13
major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5333	1004.5260	1004.5264	-0.0004	138	145	0	RPSHQQPR
1175.5657	1174.5584	1174.5829	-0.0245	357	367	0	SSENNEGVIVK
1184.5958	1183.5885	1183.5846	0.0039	205	213	0	QFQNLQNHR
1287.6050	1286.5977	1286.5891	0.0086	308	318	0	DQSSYLQGFSR
1297.6477	1296.6404	1296.6363	0.0041	172	181	1	NNPFYFPSRR
1376.6771	1375.6698	1375.6619	0.0079	560	572	0	DLAFPGSGEQVEK
1568.7051	1567.6978	1567.7015	-0.0036	153	166	0	EGEQEWGTPGSHVR
1572.7500	1571.7427	1571.7426	0.0001	335	348	0	VLLEENAGGEQEER
1591.7729	1590.7656	1590.7763	-0.0107	134	145	1	EDWRRPSHQQPR

1643.8048	1642.7975	1642.7798	0.0178	387 - 401	0	GSEEEGDITNPINLR
1728.8701	1727.8628	1727.8437	0.0191	334 - 348	1	RVLLEENAGGEQEER
1771.8833	1770.8760	1770.8747	0.0013	386 - 401	1	KGSEEEGDITNPINLR
2170.9976	2169.9903	2169.9675	0.0229	153 - 171	1	EGEQEWGTPGSHVREETSR

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1277.0825, 1296.5740, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1547.7504, 1618.7946, 1638.7821, 1774.8478, 1830.8949, 2193.9246, 2273.1536, 3792.6909

2. gi|1168391 **Mass:** 71701 **Score:** 95 **Expect:** 2.9e-007 **Queries matched:** 13

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5333	1004.5260	1004.5264	-0.0004	138 - 145		0	RPSHQQPR
1175.5657	1174.5584	1174.5829	-0.0245	357 - 367		0	SSENNEGVIVK
1184.5958	1183.5885	1183.5846	0.0039	205 - 213		0	QFQNLQNHR
1287.6050	1286.5977	1286.5891	0.0086	308 - 318		0	DQSSYLQGFSR
1297.6477	1296.6404	1296.6363	0.0041	172 - 181		1	NNPFYFPSRR
1376.6771	1375.6698	1375.6619	0.0079	560 - 572		0	DLAFPGSGEQVEK
1568.7051	1567.6978	1567.7015	-0.0036	153 - 166		0	EGEQEWGTPGSHVR
1572.7500	1571.7427	1571.7426	0.0001	335 - 348		0	VLLEENAGGEQEER
1591.7729	1590.7656	1590.7763	-0.0107	134 - 145		1	EDWRRPSHQQPR
1643.8048	1642.7975	1642.7798	0.0178	387 - 401		0	GSEEEGDITNPINLR
1728.8701	1727.8628	1727.8437	0.0191	334 - 348		1	RVLLEENAGGEQEER
1771.8833	1770.8760	1770.8747	0.0013	386 - 401		1	KGSEEEGDITNPINLR
2170.9976	2169.9903	2169.9675	0.0229	153 - 171		1	EGEQEWGTPGSHVREETSR

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1277.0825, 1296.5740, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1547.7504, 1618.7946, 1638.7821, 1774.8478, 1830.8949, 2193.9246, 2273.1536, 3792.6909

3. gi|602436 **Mass:** 71701 **Score:** 95 **Expect:** 2.9e-007 **Queries matched:** 13

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5333	1004.5260	1004.5264	-0.0004	138 - 145		0	RPSHQQPR
1175.5657	1174.5584	1174.5829	-0.0245	357 - 367		0	SSENNEGVIVK
1184.5958	1183.5885	1183.5846	0.0039	205 - 213		0	QFQNLQNHR
1287.6050	1286.5977	1286.5891	0.0086	308 - 318		0	DQSSYLQGFSR

1297.6477	1296.6404	1296.6363	0.0041	172 - 181	1	NNPFYFPSRR
1376.6771	1375.6698	1375.6619	0.0079	560 - 572	0	DLAFPGSGEQVEK
1568.7051	1567.6978	1567.7015	-0.0036	153 - 166	0	EGEQEWGTPGSHVR
1572.7500	1571.7427	1571.7426	0.0001	335 - 348	0	VLLEENAGGEQEER
1591.7729	1590.7656	1590.7763	-0.0107	134 - 145	1	EDWRRPSHQQPR
1643.8048	1642.7975	1642.7798	0.0178	387 - 401	0	GSEEEGDITNPINLR
1728.8701	1727.8628	1727.8437	0.0191	334 - 348	1	RVLLEENAGGEQEER
1771.8833	1770.8760	1770.8747	0.0013	386 - 401	1	KGSEEEGDITNPINLR
2170.9976	2169.9903	2169.9675	0.0229	153 - 171	1	EGEQEWGTPGSHVREETSR

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1277.0825, 1296.5740, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1547.7504, 1618.7946, 1638.7821, 1774.8478, 1830.8949, 2193.9246, 2273.1536, 3792.6909

4. gi|46560474 **Mass:** 33641 **Score:** 45 **Expect:** 0.025 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1175.5657	1174.5584	1174.5829	-0.0245	37	47	0	SSENNEGVIVK
1376.6771	1375.6698	1375.6619	0.0079	240	252	0	DLAFPGSGEQVEK
1572.7500	1571.7427	1571.7426	0.0001	15	28	0	VLLEENAGGEQEER
1643.8048	1642.7975	1642.7798	0.0178	67	81	0	GSEEEGDITNPINLR
1728.8701	1727.8628	1727.8437	0.0191	14	28	1	RVLLEENAGGEQEER
1771.8833	1770.8760	1770.8747	0.0013	66	81	1	KGSEEEGDITNPINLR

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1005.5333, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1184.5958, 1277.0825, 1287.6050, 1296.5740, 1297.6477, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1547.7504, 1568.7051, 1591.7729, 1618.7946, 1638.7821, 1774.8478, 1830.8949, 2170.9976, 2193.9246, 2273.1536, 3792.6909

5. gi|46560478 **Mass:** 66934 **Score:** 41 **Expect:** 0.068 **Queries matched:** 8

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5333	1004.5260	1004.5264	-0.0004	132	139	0	RPSHQQPR
1184.5958	1183.5885	1183.5846	0.0039	199	207	0	QFQNLQNHR
1287.6050	1286.5977	1286.5891	0.0086	302	312	0	DQSSYLQGFSR
1297.6477	1296.6404	1296.6363	0.0041	166	175	1	NNPFYFPSRR
1376.6771	1375.6698	1375.6619	0.0079	555	567	0	DLAFPGSGEQVEK
1572.7500	1571.7427	1571.7426	0.0001	329	342	0	VLLEENAGGEQEER

1591.7729	1590.7656	1590.7763	-0.0107	128 - 139	1	EDWRRPSHQQPR
1728.8701	1727.8628	1727.8437	0.0191	328 - 342	1	RVLLEENAGGEQEER

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1175.5657, 1277.0825, 1296.5740, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1547.7504, 1568.7051, 1618.7946, 1638.7821, 1643.8048, 1771.8833, 1774.8478, 1830.8949, 2170.9976, 2193.9246, 2273.1536, 3792.6909

6. gi|620025 **Mass:** 70639 **Score:** 40 **Expect:** 0.092 **Queries matched:** 8

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5333	1004.5260	1004.5264	-0.0004	132 - 139		0	RPSHQQPR
1184.5958	1183.5885	1183.5846	0.0039	199 - 207		0	QFQNLQNHR
1287.6050	1286.5977	1286.5891	0.0086	302 - 312		0	DQSSYLQGFSR
1297.6477	1296.6404	1296.6363	0.0041	166 - 175		1	NNPFYFPSRR
1376.6771	1375.6698	1375.6619	0.0079	555 - 567		0	DLAFPGSGEQVEK
1572.7500	1571.7427	1571.7426	0.0001	329 - 342		0	VLLEENAGGEQEER
1591.7729	1590.7656	1590.7763	-0.0107	128 - 139		1	EDWRRPSHQQPR
1728.8701	1727.8628	1727.8437	0.0191	328 - 342		1	RVLLEENAGGEQEER

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1175.5657, 1277.0825, 1296.5740, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1547.7504, 1568.7051, 1618.7946, 1638.7821, 1643.8048, 1771.8833, 1774.8478, 1830.8949, 2170.9976, 2193.9246, 2273.1536, 3792.6909

7. gi|1168390 **Mass:** 70639 **Score:** 40 **Expect:** 0.092 **Queries matched:** 8

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5333	1004.5260	1004.5264	-0.0004	132 - 139		0	RPSHQQPR
1184.5958	1183.5885	1183.5846	0.0039	199 - 207		0	QFQNLQNHR
1287.6050	1286.5977	1286.5891	0.0086	302 - 312		0	DQSSYLQGFSR
1297.6477	1296.6404	1296.6363	0.0041	166 - 175		1	NNPFYFPSRR
1376.6771	1375.6698	1375.6619	0.0079	555 - 567		0	DLAFPGSGEQVEK
1572.7500	1571.7427	1571.7426	0.0001	329 - 342		0	VLLEENAGGEQEER
1591.7729	1590.7656	1590.7763	-0.0107	128 - 139		1	EDWRRPSHQQPR
1728.8701	1727.8628	1727.8437	0.0191	328 - 342		1	RVLLEENAGGEQEER

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1175.5657, 1277.0825, 1296.5740, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1547.7504, 1568.7051, 1618.7946, 1638.7821, 1643.8048, 1771.8833,

1774.8478, 1830.8949, 2170.9976, 2193.9246, 2273.1536, 3792.6909

8. gi|46560476 **Mass:** 48122 **Score:** 38 **Expect:** 0.15 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1175.5657	1174.5584	1174.5829	-0.0245	160	170	0	SSENNEGVIVK
1184.5958	1183.5885	1183.5846	0.0039	8	16	0	QFQNLQNHR
1287.6050	1286.5977	1286.5891	0.0086	111	121	0	DQSSYLQGFSR
1376.6771	1375.6698	1375.6619	0.0079	362	374	0	DLAFPGSGEQVEK
1572.7500	1571.7427	1571.7426	0.0001	138	151	0	VLLEENAGGEQEER
1728.8701	1727.8628	1727.8437	0.0191	137	151	1	RVLLEENAGGEQEER

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1005.5333, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1277.0825, 1296.5740, 1297.6477, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1547.7504, 1568.7051, 1591.7729, 1618.7946, 1638.7821, 1643.8048, 1771.8833, 1774.8478, 1830.8949, 2170.9976, 2193.9246, 2273.1536, 3792.6909

9. gi|46560472 **Mass:** 34169 **Score:** 17 **Expect:** 17 **Queries matched:** 3

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1376.6771	1375.6698	1375.6619	0.0079	244	256	0	DLAFPGSGEQVEK
1572.7500	1571.7427	1571.7426	0.0001	18	31	0	VLLEENAGGEQEER
1728.8701	1727.8628	1727.8437	0.0191	17	31	1	RVLLEENAGGEQEER

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1005.5333, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1175.5657, 1184.5958, 1277.0825, 1287.6050, 1296.5740, 1297.6477, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1547.7504, 1568.7051, 1591.7729, 1618.7946, 1638.7821, 1643.8048, 1771.8833, 1774.8478, 1830.8949, 2170.9976, 2193.9246, 2273.1536, 3792.6909

10. gi|2498261 **Mass:** 2416 **Score:** 14 **Expect:** 34 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1547.7504	1546.7431	1546.7263	0.0168	9	24	0	ASYTVTPPAQANAADA

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1005.5333, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1175.5657, 1184.5958, 1277.0825, 1287.6050, 1296.5740, 1297.6477, 1376.6771, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1568.7051, 1572.7500, 1591.7729, 1618.7946, 1638.7821, 1643.8048, 1728.8701, 1771.8833, 1774.8478, 1830.8949, 2170.9976,

2193.9246, 2273.1536, 3792.6909

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 44

Protein View

Match to: **gi|16612200** Score: **95** Expect: **2.9e-007**
major allergen Arah1 [Arachis hypogaea]

Nominal mass (M_r): **71701**; Calculated pI value: **6.62**
NCBI BLAST search of gi|16612200 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **44**
Number of mass values matched: **13**
Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP
    51 DDLKQKACES RCTKLEYDPR CVYDPRGHTG TTNQRSPPGE RTRGRQPGDY
   101 DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE
   151 GREGEQEWGT PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD
   201 QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ GQATVTVANG
   251 NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED
   301 FFPASSRDQS SYLQGFSRNT LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ
   351 RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
   401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS
   451 KAMVIVVVNK GTGNLELVAV RKEQQQRGRR EEEEDEDEEE EGSNREVRRY
   501 TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV
   551 IDQIEKQAKD LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE
   601 SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
134 - 145	1591.7729	1590.7656	1590.7763	-0.0107	1	EDWRRPSHQQPR
138 - 145	1005.5333	1004.5260	1004.5264	-0.0004	0	RPSHQQPR
153 - 166	1568.7051	1567.6978	1567.7015	-0.0036	0	EGEQEWGTPGSHVR
153 - 171	2170.9976	2169.9903	2169.9675	0.0229	1	EGEQEWGTPGSHVREETSR
172 - 181	1297.6477	1296.6404	1296.6363	0.0041	1	NNPFYFPSRR
205 - 213	1184.5958	1183.5885	1183.5846	0.0039	0	QFQNLQNHR
308 - 318	1287.6050	1286.5977	1286.5891	0.0086	0	DQSSYLQGFSR
334 - 348	1728.8701	1727.8628	1727.8437	0.0191	1	RVLLEENAGGEQEER
335 - 348	1572.7500	1571.7427	1571.7426	0.0001	0	VLLEENAGGEQEER
357 - 367	1175.5657	1174.5584	1174.5829	-0.0245	0	SSENNEGVIVK
386 - 401	1771.8833	1770.8760	1770.8747	0.0013	1	KGSEEEGDITNPINLR
387 - 401	1643.8048	1642.7975	1642.7798	0.0178	0	GSEEEGDITNPINLR
560 - 572	1376.6771	1375.6698	1375.6619	0.0079	0	DLAFPGSGEQVEK

No match to: 805.4381, 827.3657, 839.0717, 845.0814, 855.0585, 861.0620, 877.0328, 881.2643, 883.2606, 1046.6017, 1050.1027, 1066.0704, 1067.0804, 1072.0680, 1080.5221, 1167.5714, 1277.0825, 1296.5740, 1400.6774, 1464.5967, 1481.6234, 1529.7019, 1534.6705, 1547.7504, 1618.7946, 1638.7821, 1774.8478, 1830.8949, 2193.9246, 2273.1536, 3792.6909

Spot 25

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:38:52 GMT**
Top Score : **62 for gi|16612200, major allergen Arah1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|16612200	71701	62	major allergen Arah1 [Arachis hypogaea]
2.	gi|1168391	71701	62	Allergen Ara h 1, clone P41B precursor (Ara h I)
3.	gi|602436	71701	62	Ara h I
4.	gi|46560476	48122	51	conarachin [Arachis hypogaea]
5.	gi|46560478	66934	45	conarachin [Arachis hypogaea]
6.	gi|620025	70639	44	Ara h I
7.	gi|1168390	70639	44	Allergen Ara h 1, clone P17 precursor (Ara h I)
8.	gi|46560472	34169	26	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	26	conarachin [Arachis hypogaea]
10.	gi|47933675	58368	21	glycinin [Arachis hypogaea]

Results List

1. gi|16612200 **Mass:** 71701 **Score:** 62 **Expect:** 0.00052 **Queries matched:** 10
major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5382	1004.5309	1004.5264	0.0045	138	145	0	RPSHQQPR
1175.5707	1174.5634	1174.5829	-0.0195	357	367	0	SSENNEGVIVK
1184.5942	1183.5869	1183.5846	0.0023	205	213	0	QFQNLQNHR
1287.5958	1286.5885	1286.5891	-0.0006	308	318	0	DQSSYLQGFSR
1297.6378	1296.6305	1296.6363	-0.0058	172	181	1	NNPFYFPSRR
1376.6675	1375.6602	1375.6619	-0.0017	560	572	0	DLAFPGSGEQVEK

1427.6973	1426.6900	1426.7177	-0.0277	203 - 213	1	SRQFQNLQNHR
1568.7028	1567.6955	1567.7015	-0.0059	153 - 166	0	EGEQEWGTPGSHVR
1572.7581	1571.7508	1571.7426	0.0082	335 - 348	0	VLLEENAGGEQEER
1728.8640	1727.8567	1727.8437	0.0130	334 - 348	1	RVLLEENAGGEQEER

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1277.0908, 1299.6522, 1320.5942, 1464.6011, 1481.6090, 1529.6744, 1547.7467, 1618.7917, 1638.7450, 1730.8617, 1770.8802, 1774.8517, 2192.9968, 2273.1511

2. gi|1168391 **Mass:** 71701 **Score:** 62 **Expect:** 0.00052 **Queries matched:** 10

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5382	1004.5309	1004.5264	0.0045	138 - 145		0	RPSHQQPR
1175.5707	1174.5634	1174.5829	-0.0195	357 - 367		0	SSENNEGVIVK
1184.5942	1183.5869	1183.5846	0.0023	205 - 213		0	QFQNLQNHR
1287.5958	1286.5885	1286.5891	-0.0006	308 - 318		0	DQSSYLQGFSR
1297.6378	1296.6305	1296.6363	-0.0058	172 - 181		1	NNPFYFPSRR
1376.6675	1375.6602	1375.6619	-0.0017	560 - 572		0	DLAFPGSGEQVEK
1427.6973	1426.6900	1426.7177	-0.0277	203 - 213		1	SRQFQNLQNHR
1568.7028	1567.6955	1567.7015	-0.0059	153 - 166		0	EGEQEWGTPGSHVR
1572.7581	1571.7508	1571.7426	0.0082	335 - 348		0	VLLEENAGGEQEER
1728.8640	1727.8567	1727.8437	0.0130	334 - 348		1	RVLLEENAGGEQEER

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1277.0908, 1299.6522, 1320.5942, 1464.6011, 1481.6090, 1529.6744, 1547.7467, 1618.7917, 1638.7450, 1730.8617, 1770.8802, 1774.8517, 2192.9968, 2273.1511

3. gi|602436 **Mass:** 71701 **Score:** 62 **Expect:** 0.00052 **Queries matched:** 10

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5382	1004.5309	1004.5264	0.0045	138 - 145		0	RPSHQQPR
1175.5707	1174.5634	1174.5829	-0.0195	357 - 367		0	SSENNEGVIVK
1184.5942	1183.5869	1183.5846	0.0023	205 - 213		0	QFQNLQNHR
1287.5958	1286.5885	1286.5891	-0.0006	308 - 318		0	DQSSYLQGFSR
1297.6378	1296.6305	1296.6363	-0.0058	172 - 181		1	NNPFYFPSRR
1376.6675	1375.6602	1375.6619	-0.0017	560 - 572		0	DLAFPGSGEQVEK
1427.6973	1426.6900	1426.7177	-0.0277	203 - 213		1	SRQFQNLQNHR
1568.7028	1567.6955	1567.7015	-0.0059	153 - 166		0	EGEQEWGTPGSHVR
1572.7581	1571.7508	1571.7426	0.0082	335 - 348		0	VLLEENAGGEQEER

1728.8640	1727.8567	1727.8437	0.0130	334 - 348	1	RVLLEENAGGEQEER

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1277.0908, 1299.6522, 1320.5942, 1464.6011, 1481.6090, 1529.6744, 1547.7467, 1618.7917, 1638.7450, 1730.8617, 1770.8802, 1774.8517, 2192.9968, 2273.1511

4. gi|46560476 **Mass:** 48122 **Score:** 51 **Expect:** 0.0071 **Queries matched:** 7

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1175.5707	1174.5634	1174.5829	-0.0195	160 -	170	0	SSENNEGVIVK
1184.5942	1183.5869	1183.5846	0.0023	8 -	16	0	QFQNLQNHR
1287.5958	1286.5885	1286.5891	-0.0006	111 -	121	0	DQSSYLQGFSR
1376.6675	1375.6602	1375.6619	-0.0017	362 -	374	0	DLAFPGSGEQVEK
1427.6973	1426.6900	1426.7177	-0.0277	6 -	16	1	SRQFQNLQNHR
1572.7581	1571.7508	1571.7426	0.0082	138 -	151	0	VLLEENAGGEQEER
1728.8640	1727.8567	1727.8437	0.0130	137 -	151	1	RVLLEENAGGEQEER

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1005.5382, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1277.0908, 1297.6378, 1299.6522, 1320.5942, 1464.6011, 1481.6090, 1529.6744, 1547.7467, 1568.7028, 1618.7917, 1638.7450, 1730.8617, 1770.8802, 1774.8517, 2192.9968, 2273.1511

5. gi|46560478 **Mass:** 66934 **Score:** 45 **Expect:** 0.028 **Queries matched:** 8

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5382	1004.5309	1004.5264	0.0045	132 -	139	0	RPSHQQPR
1184.5942	1183.5869	1183.5846	0.0023	199 -	207	0	QFQNLQNHR
1287.5958	1286.5885	1286.5891	-0.0006	302 -	312	0	DQSSYLQGFSR
1297.6378	1296.6305	1296.6363	-0.0058	166 -	175	1	NNPFYFPSRR
1320.5942	1319.5869	1319.5741	0.0128	394 -	405	0	DGEPDLSNNFGR
1376.6675	1375.6602	1375.6619	-0.0017	555 -	567	0	DLAFPGSGEQVEK
1572.7581	1571.7508	1571.7426	0.0082	329 -	342	0	VLLEENAGGEQEER
1728.8640	1727.8567	1727.8437	0.0130	328 -	342	1	RVLLEENAGGEQEER

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1175.5707, 1277.0908, 1299.6522, 1427.6973, 1464.6011, 1481.6090, 1529.6744, 1547.7467, 1568.7028, 1618.7917, 1638.7450, 1730.8617, 1770.8802, 1774.8517, 2192.9968, 2273.1511

6. gi|620025 **Mass:** 70639 **Score:** 44 **Expect:** 0.038 **Queries matched:** 8

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1005.5382	1004.5309	1004.5264	0.0045	132	-	139	0	RPSHQQPR
1184.5942	1183.5869	1183.5846	0.0023	199	-	207	0	QFQNLQNHR
1287.5958	1286.5885	1286.5891	-0.0006	302	-	312	0	DQSSYLQGFSR
1297.6378	1296.6305	1296.6363	-0.0058	166	-	175	1	NNPFYFPSRR
1320.5942	1319.5869	1319.5741	0.0128	394	-	405	0	DGEPDLSNNFGR
1376.6675	1375.6602	1375.6619	-0.0017	555	-	567	0	DLAFPGSGEQVEK
1572.7581	1571.7508	1571.7426	0.0082	329	-	342	0	VLLEENAGGEQEER
1728.8640	1727.8567	1727.8437	0.0130	328	-	342	1	RVLLEENAGGEQEER

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1175.5707, 1277.0908, 1299.6522, 1427.6973, 1464.6011, 1481.6090, 1529.6744, 1547.7467, 1568.7028, 1618.7917, 1638.7450, 1730.8617, 1770.8802, 1774.8517, 2192.9968, 2273.1511

7. gi|1168390 **Mass:** 70639 **Score:** 44 **Expect:** 0.038 **Queries matched:** 8

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1005.5382	1004.5309	1004.5264	0.0045	132	-	139	0	RPSHQQPR
1184.5942	1183.5869	1183.5846	0.0023	199	-	207	0	QFQNLQNHR
1287.5958	1286.5885	1286.5891	-0.0006	302	-	312	0	DQSSYLQGFSR
1297.6378	1296.6305	1296.6363	-0.0058	166	-	175	1	NNPFYFPSRR
1320.5942	1319.5869	1319.5741	0.0128	394	-	405	0	DGEPDLSNNFGR
1376.6675	1375.6602	1375.6619	-0.0017	555	-	567	0	DLAFPGSGEQVEK
1572.7581	1571.7508	1571.7426	0.0082	329	-	342	0	VLLEENAGGEQEER
1728.8640	1727.8567	1727.8437	0.0130	328	-	342	1	RVLLEENAGGEQEER

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1175.5707, 1277.0908, 1299.6522, 1427.6973, 1464.6011, 1481.6090, 1529.6744, 1547.7467, 1568.7028, 1618.7917, 1638.7450, 1730.8617, 1770.8802, 1774.8517, 2192.9968, 2273.1511

8. gi|46560472 **Mass:** 34169 **Score:** 26 **Expect:** 2.1 **Queries matched:** 4

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1320.5942	1319.5869	1319.5741	0.0128	83	-	94	0	DGEPDLSNNFGR
1376.6675	1375.6602	1375.6619	-0.0017	244	-	256	0	DLAFPGSGEQVEK

1572.7581	1571.7508	1571.7426	0.0082	18 -	31	0	VLLEENAGGEQEER
1728.8640	1727.8567	1727.8437	0.0130	17 -	31	1	RVLLEENAGGEQEER

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1005.5382, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1175.5707, 1184.5942, 1277.0908, 1287.5958, 1297.6378, 1299.6522, 1427.6973, 1464.6011, 1481.6090, 1529.6744, 1547.7467, 1568.7028, 1618.7917, 1638.7450, 1730.8617, 1770.8802, 1774.8517, 2192.9968, 2273.1511

9. gi|46560474 **Mass:** 33641 **Score:** 26 **Expect:** 2.1 **Queries matched:** 4

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1175.5707	1174.5634	1174.5829	-0.0195	37 -	47	0	SSENNEGVIVK
1376.6675	1375.6602	1375.6619	-0.0017	240 -	252	0	DLAFPGSGEQVEK
1572.7581	1571.7508	1571.7426	0.0082	15 -	28	0	VLLEENAGGEQEER
1728.8640	1727.8567	1727.8437	0.0130	14 -	28	1	RVLLEENAGGEQEER

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1005.5382, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1184.5942, 1277.0908, 1287.5958, 1297.6378, 1299.6522, 1320.5942, 1427.6973, 1464.6011, 1481.6090, 1529.6744, 1547.7467, 1568.7028, 1618.7917, 1638.7450, 1730.8617, 1770.8802, 1774.8517, 2192.9968, 2273.1511

10. gi|47933675 **Mass:** 58368 **Score:** 21 **Expect:** 7 **Queries matched:** 4

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1481.6090	1480.6017	1480.6000	0.0017	23 -	34	0	QGGEENECQFQR
1547.7467	1546.7394	1546.7389	0.0005	209 -	220	0	YQQQQGSRPHYR
1618.7917	1617.7844	1617.7746	0.0098	342 -	356	0	SSNPDIYNPQAGSLR
1770.8802	1769.8729	1769.8848	-0.0119	195 -	208	1	RFYLAGNQEQEFLR

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1005.5382, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1175.5707, 1184.5942, 1277.0908, 1287.5958, 1297.6378, 1299.6522, 1320.5942, 1376.6675, 1427.6973, 1464.6011, 1529.6744, 1568.7028, 1572.7581, 1638.7450, 1728.8640, 1730.8617, 1774.8517, 2192.9968, 2273.1511

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)

Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 40

Protein View

Match to: **gi|16612200** Score: **62** Expect: **0.00052**
major allergen Arah1 [Arachis hypogaea]

Nominal mass (M_r): **71701**; Calculated pI value: **6.62**
NCBI BLAST search of gi|16612200 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **40**
Number of mass values matched: **10**
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

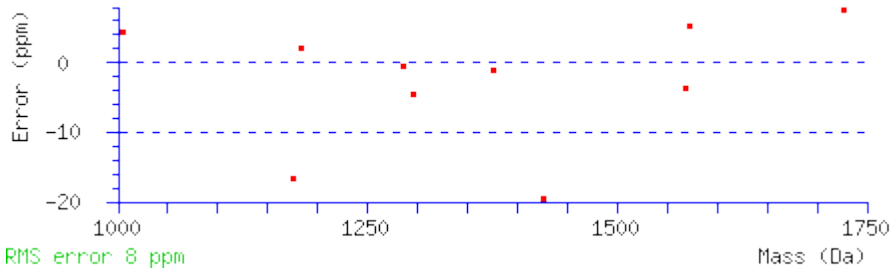
```
     1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP
    51 DDLKQKACES RCTKLEYDPR CVYDPRGHTG TTNQRSPPGE RTRGRQPGDY
   101 DDDRRQPRRE EGGRWGPAGP REREREEDWR QPREDWRRPS HQQPRKIRPE
   151 GREGEQEWGT PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD
   201 QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ GQATVTVANG
   251 NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED
   301 FFPASSRDQS SYLQGFSRNT LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ
   351 RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
   401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS
   451 KAMVIVVVNK GTGNLELVAV RKEQQQRGRR EEEEDEDEEE EGSNREVRRY
   501 TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV
   551 IDQIEKQAKD LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE
   601 SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence

138 - 145	1005.5382	1004.5309	1004.5264	0.0045	0	RPSHQQPR
153 - 166	1568.7028	1567.6955	1567.7015	-0.0059	0	EGEQEWGTPGSHVR
172 - 181	1297.6378	1296.6305	1296.6363	-0.0058	1	NNPFYFPSRR
203 - 213	1427.6973	1426.6900	1426.7177	-0.0277	1	SRQFQNLQNHR
205 - 213	1184.5942	1183.5869	1183.5846	0.0023	0	QFQNLQNHR
308 - 318	1287.5958	1286.5885	1286.5891	-0.0006	0	DQSSYLQGFSR
334 - 348	1728.8640	1727.8567	1727.8437	0.0130	1	RVLLEENAGGEQEER
335 - 348	1572.7581	1571.7508	1571.7426	0.0082	0	VLLEENAGGEQEER
357 - 367	1175.5707	1174.5634	1174.5829	-0.0195	0	SSENNEGVIVK
560 - 572	1376.6675	1375.6602	1375.6619	-0.0017	0	DLAFPGSGEQVEK

No match to: 805.4810, 839.1028, 845.1193, 855.0720, 861.0870, 871.0565, 877.0579, 881.2991, 893.0426, 1046.6058, 1050.0939, 1066.0735, 1072.1179, 1080.5459, 1082.0511, 1167.5688, 1277.0908, 1299.6522, 1320.5942, 1464.6011, 1481.6090, 1529.6744, 1547.7467, 1618.7917, 1638.7450, 1730.8617, 1770.8802, 1774.8517, 2192.9968, 2273.1511



Spot 26

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:31:13 GMT**
Top Score : **157 for gi|46560478, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	157	conarachin [Arachis hypogaea]
2.	gi|620025	70639	154	Ara h I
3.	gi|1168390	70639	154	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	145	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	145	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	145	Ara h I
7.	gi|46560476	48122	121	conarachin [Arachis hypogaea]
8.	gi|46560474	33641	35	conarachin [Arachis hypogaea]
9.	gi|46560472	34169	34	conarachin [Arachis hypogaea]
10.	gi|226258	10809	17	ferredoxin I

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 157 **Expect:** 1.7e-013 **Queries matched:** 19
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	272	278	0	HDNQNLR
1128.6416	1127.6343	1127.6298	0.0045	453	463	0	GTGNLELVAVR
1141.5464	1140.5391	1140.5352	0.0039	166	174	0	NNPFYFPSR
1184.5996	1183.5923	1183.5846	0.0077	199	207	0	QFQNLQNHR
1258.6265	1257.6192	1257.6101	0.0091	249	259	0	SFNLDEGHALR
1287.6080	1286.6007	1286.5891	0.0116	302	312	0	DQSSYLQGFSR
1297.6536	1296.6463	1296.6363	0.0100	166	175	1	NNPFYFPSRR
1320.5911	1319.5838	1319.5741	0.0097	394	405	0	DGEPDLSNNFGR
1379.7813	1378.7740	1378.7608	0.0132	260	271	0	IPSGFISYILNR
1560.7056	1559.6983	1559.6851	0.0132	147	160	0	EGEQEWGTPGSEVR

1572.7599	1571.7526	1571.7426	0.0100	329 - 342	0	VLLEENAGGEQEER
1691.0359	1690.0286	1690.0141	0.0146	208 - 222	0	IVQIEARPNTLVLPK
1738.8488	1737.8415	1737.8321	0.0094	313 - 327	0	NTLEAAFNAEFNEIR
1817.9735	1816.9662	1816.9570	0.0092	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9486	1893.9413	1893.9332	0.0081	313 - 328	1	NTLEAAFNAEFNEIRR
2082.2078	2081.2005	2081.2030	-0.0024	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	282 - 301	0	ISMPVNTPGQFEDFFPASSR
2243.0537	2242.0464	2242.0364	0.0100	282 - 301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2864	2618.2791	2618.3160	-0.0369	223 - 247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1167.5767, 1568.7229, 1771.8953, 2193.0051, 2256.6763, 2273.1592, 2295.1321, 2612.1487, 3153.3682, 3211.3804

2. gi|620025 **Mass:** 70639 **Score:** 154 **Expect:** 3.5e-013 **Queries matched:** 19

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	272 - 278		0	HDNQNLR
1128.6416	1127.6343	1127.6298	0.0045	453 - 463		0	GTGNLELVAVR
1141.5464	1140.5391	1140.5352	0.0039	166 - 174		0	NNPFYFPSR
1184.5996	1183.5923	1183.5846	0.0077	199 - 207		0	QFQNLQNHR
1258.6265	1257.6192	1257.6101	0.0091	249 - 259		0	SFNLDEGHALR
1287.6080	1286.6007	1286.5891	0.0116	302 - 312		0	DQSSYLQGFSR
1297.6536	1296.6463	1296.6363	0.0100	166 - 175		1	NNPFYFPSRR
1320.5911	1319.5838	1319.5741	0.0097	394 - 405		0	DGEPDLSNNFGR
1379.7813	1378.7740	1378.7608	0.0132	260 - 271		0	IPSGFISYILNR
1560.7056	1559.6983	1559.6851	0.0132	147 - 160		0	EGEQEWGTPGSEVR
1572.7599	1571.7526	1571.7426	0.0100	329 - 342		0	VLLEENAGGEQEER
1691.0359	1690.0286	1690.0141	0.0146	208 - 222		0	IVQIEARPNTLVLPK
1738.8488	1737.8415	1737.8321	0.0094	313 - 327		0	NTLEAAFNAEFNEIR
1817.9735	1816.9662	1816.9570	0.0092	536 - 551		1	IFLAGDKDNVIDQIEK
1894.9486	1893.9413	1893.9332	0.0081	313 - 328		1	NTLEAAFNAEFNEIRR
2082.2078	2081.2005	2081.2030	-0.0024	444 - 463		1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	282 - 301		0	ISMPVNTPGQFEDFFPASSR
2243.0537	2242.0464	2242.0364	0.0100	282 - 301		0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2864	2618.2791	2618.3160	-0.0369	223 - 247		0	HADADNILVIQQGQATVTVANGNNR

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1167.5767, 1568.7229, 1771.8953, 2193.0051, 2256.6763, 2273.1592, 2295.1321, 2612.1487, 3153.3682, 3211.3804

3. gi|1168390 **Mass:** 70639 **Score:** 154 **Expect:** 3.5e-013 **Queries matched:** 19

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	272	-	278	0	HDNQNLR
1128.6416	1127.6343	1127.6298	0.0045	453	-	463	0	GTGNLELVAVR
1141.5464	1140.5391	1140.5352	0.0039	166	-	174	0	NNPFYFPSR
1184.5996	1183.5923	1183.5846	0.0077	199	-	207	0	QFQNLQNHR
1258.6265	1257.6192	1257.6101	0.0091	249	-	259	0	SFNLDEGHALR
1287.6080	1286.6007	1286.5891	0.0116	302	-	312	0	DQSSYLQGFSR
1297.6536	1296.6463	1296.6363	0.0100	166	-	175	1	NNPFYFPSRR
1320.5911	1319.5838	1319.5741	0.0097	394	-	405	0	DGEPDLSNNFGR
1379.7813	1378.7740	1378.7608	0.0132	260	-	271	0	IPSGFISYILNR
1560.7056	1559.6983	1559.6851	0.0132	147	-	160	0	EGEQEWGTPGSEVR
1572.7599	1571.7526	1571.7426	0.0100	329	-	342	0	VLLEENAGGEQEER
1691.0359	1690.0286	1690.0141	0.0146	208	-	222	0	IVQIEARPNTLVLPK
1738.8488	1737.8415	1737.8321	0.0094	313	-	327	0	NTLEAAFNAEFNEIR
1817.9735	1816.9662	1816.9570	0.0092	536	-	551	1	IFLAGDKDNVIDQIEK
1894.9486	1893.9413	1893.9332	0.0081	313	-	328	1	NTLEAAFNAEFNEIRR
2082.2078	2081.2005	2081.2030	-0.0024	444	-	463	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	282	-	301	0	ISMPVNTPGQFEDFFPASSR
2243.0537	2242.0464	2242.0364	0.0100	282	-	301	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2864	2618.2791	2618.3160	-0.0369	223	-	247	0	HADADNILVIQQGQATVTVANGNNR

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1167.5767, 1568.7229, 1771.8953, 2193.0051, 2256.6763, 2273.1592, 2295.1321, 2612.1487, 3153.3682, 3211.3804

4. gi|16612200 **Mass:** 71701 **Score:** 145 **Expect:** 2.8e-012 **Queries matched:** 18

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	278	-	284	0	HDNQNLR
1128.6416	1127.6343	1127.6298	0.0045	461	-	471	0	GTGNLELVAVR
1141.5464	1140.5391	1140.5352	0.0039	172	-	180	0	NNPFYFPSR
1184.5996	1183.5923	1183.5846	0.0077	205	-	213	0	QFQNLQNHR
1258.6265	1257.6192	1257.6101	0.0091	255	-	265	0	SFNLDEGHALR
1287.6080	1286.6007	1286.5891	0.0116	308	-	318	0	DQSSYLQGFSR
1297.6536	1296.6463	1296.6363	0.0100	172	-	181	1	NNPFYFPSRR
1379.7813	1378.7740	1378.7608	0.0132	266	-	277	0	IPSGFISYILNR
1568.7229	1567.7156	1567.7015	0.0142	153	-	166	0	EGEQEWGTPGSHVR
1572.7599	1571.7526	1571.7426	0.0100	335	-	348	0	VLLEENAGGEQEER
1738.8488	1737.8415	1737.8321	0.0094	319	-	333	0	NTLEAAFNAEFNEIR
1771.8953	1770.8880	1770.8747	0.0133	386	-	401	1	KGSEEEGDITNPINLR
1817.9735	1816.9662	1816.9570	0.0092	541	-	556	1	IFLAGDKDNVIDQIEK

1894.9486	1893.9413	1893.9332	0.0081	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2078	2081.2005	2081.2030	-0.0024	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0537	2242.0464	2242.0364	0.0100	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2864	2618.2791	2618.3160	-0.0369	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1167.5767, 1320.5911, 1560.7056, 1691.0359, 2193.0051, 2256.6763, 2273.1592, 2295.1321, 2612.1487, 3153.3682, 3211.3804

5. gi|1168391 **Mass:** 71701 **Score:** 145 **Expect:** 2.8e-012 **Queries matched:** 18

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	278 - 284		0	HDNQNLR
1128.6416	1127.6343	1127.6298	0.0045	461 - 471		0	GTGNLELVAVR
1141.5464	1140.5391	1140.5352	0.0039	172 - 180		0	NNPFYFPSR
1184.5996	1183.5923	1183.5846	0.0077	205 - 213		0	QFQNLQNHR
1258.6265	1257.6192	1257.6101	0.0091	255 - 265		0	SFNLDEGHALR
1287.6080	1286.6007	1286.5891	0.0116	308 - 318		0	DQSSYLQGFSR
1297.6536	1296.6463	1296.6363	0.0100	172 - 181		1	NNPFYFPSRR
1379.7813	1378.7740	1378.7608	0.0132	266 - 277		0	IPSGFISYILNR
1568.7229	1567.7156	1567.7015	0.0142	153 - 166		0	EGEQEWGTPGSHVR
1572.7599	1571.7526	1571.7426	0.0100	335 - 348		0	VLLEENAGGEQEER
1738.8488	1737.8415	1737.8321	0.0094	319 - 333		0	NTLEAAFNAEFNEIR
1771.8953	1770.8880	1770.8747	0.0133	386 - 401		1	KGSEEEGDITNPINLR
1817.9735	1816.9662	1816.9570	0.0092	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9486	1893.9413	1893.9332	0.0081	319 - 334		1	NTLEAAFNAEFNEIRR
2082.2078	2081.2005	2081.2030	-0.0024	452 - 471		1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	288 - 307		0	ISMPVNTPGQFEDFFPASSR
2243.0537	2242.0464	2242.0364	0.0100	288 - 307		0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2864	2618.2791	2618.3160	-0.0369	229 - 253		0	HADADNILVIQQGQATVTVANGNNR

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1167.5767, 1320.5911, 1560.7056, 1691.0359, 2193.0051, 2256.6763, 2273.1592, 2295.1321, 2612.1487, 3153.3682, 3211.3804

6. gi|602436 **Mass:** 71701 **Score:** 145 **Expect:** 2.8e-012 **Queries matched:** 18

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	278 - 284		0	HDNQNLR
1128.6416	1127.6343	1127.6298	0.0045	461 - 471		0	GTGNLELVAVR

1141.5464	1140.5391	1140.5352	0.0039	172 - 180	0	NNPFYFPSR
1184.5996	1183.5923	1183.5846	0.0077	205 - 213	0	QFQNLQNHR
1258.6265	1257.6192	1257.6101	0.0091	255 - 265	0	SFNLDEGHALR
1287.6080	1286.6007	1286.5891	0.0116	308 - 318	0	DQSSYLQGFSR
1297.6536	1296.6463	1296.6363	0.0100	172 - 181	1	NNPFYFPSRR
1379.7813	1378.7740	1378.7608	0.0132	266 - 277	0	IPSGFISYILNR
1568.7229	1567.7156	1567.7015	0.0142	153 - 166	0	EGEQEWGTPGSHVR
1572.7599	1571.7526	1571.7426	0.0100	335 - 348	0	VLLEENAGGEQEER
1738.8488	1737.8415	1737.8321	0.0094	319 - 333	0	NTLEAAFNAEFNEIR
1771.8953	1770.8880	1770.8747	0.0133	386 - 401	1	KGSEEEGDITNPINLR
1817.9735	1816.9662	1816.9570	0.0092	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9486	1893.9413	1893.9332	0.0081	319 - 334	1	NTLEAAFNAEFNEIRR
2082.2078	2081.2005	2081.2030	-0.0024	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	288 - 307	0	ISMPVNTPGQFEDFFPASSR
2243.0537	2242.0464	2242.0364	0.0100	288 - 307	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2864	2618.2791	2618.3160	-0.0369	229 - 253	0	HADADNILVIQQGQATVTVANGNNR

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1167.5767, 1320.5911, 1560.7056, 1691.0359, 2193.0051, 2256.6763, 2273.1592, 2295.1321, 2612.1487, 3153.3682, 3211.3804

7. gi|46560476 **Mass:** 48122 **Score:** 121 **Expect:** 7e-010 **Queries matched:** 14

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
896.4271	895.4198	895.4260	-0.0062	81 -	87	0	HDNQNLR
1128.6416	1127.6343	1127.6298	0.0045	263 -	273	0	GTGNLELVAVR
1184.5996	1183.5923	1183.5846	0.0077	8 -	16	0	QFQNLQNHR
1258.6265	1257.6192	1257.6101	0.0091	58 -	68	0	SFNLDEGHALR
1287.6080	1286.6007	1286.5891	0.0116	111 -	121	0	DQSSYLQGFSR
1379.7813	1378.7740	1378.7608	0.0132	69 -	80	0	IPSGFISYILNR
1572.7599	1571.7526	1571.7426	0.0100	138 -	151	0	VLLEENAGGEQEER
1738.8488	1737.8415	1737.8321	0.0094	122 -	136	0	NTLEAAFNAEFNEIR
1817.9735	1816.9662	1816.9570	0.0092	343 -	358	1	IFLAGDKDNVIDQIEK
1894.9486	1893.9413	1893.9332	0.0081	122 -	137	1	NTLEAAFNAEFNEIRR
2082.2078	2081.2005	2081.2030	-0.0024	254 -	273	1	AMVIVVVNKGTGNLELVAVR
2227.0444	2226.0371	2226.0415	-0.0044	91 -	110	0	ISMPVNTPGQFEDFFPASSR
2243.0537	2242.0464	2242.0364	0.0100	91 -	110	0	ISMPVNTPGQFEDFFPASSR + Oxidation (M)
2619.2864	2618.2791	2618.3160	-0.0369	32 -	56	0	HADADNILVIQQGQATVTVANGNNR

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1141.5464, 1167.5767, 1297.6536, 1320.5911, 1560.7056, 1568.7229, 1691.0359, 1771.8953, 2193.0051, 2256.6763,

2273.1592, 2295.1321, 2612.1487, 3153.3682, 3211.3804

8. gi|46560474 **Mass:** 33641 **Score:** 35 **Expect:** 0.26 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6416	1127.6343	1127.6298	0.0045	141	151	0	GTGNLELVAVR
1572.7599	1571.7526	1571.7426	0.0100	15	28	0	VLLEENAGGEQEER
1771.8953	1770.8880	1770.8747	0.0133	66	81	1	KGSEEEGDITNPINLR
1817.9735	1816.9662	1816.9570	0.0092	221	236	1	IFLAGDKDNVIDQIEK
2082.2078	2081.2005	2081.2030	-0.0024	132	151	1	AMVIVVVNKGTGNLELVAVR

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 896.4271, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1141.5464, 1167.5767, 1184.5996, 1258.6265, 1287.6080, 1297.6536, 1320.5911, 1379.7813, 1560.7056, 1568.7229, 1691.0359, 1738.8488, 1894.9486, 2193.0051, 2227.0444, 2243.0537, 2256.6763, 2273.1592, 2295.1321, 2612.1487, 2619.2864, 3153.3682, 3211.3804

9. gi|46560472 **Mass:** 34169 **Score:** 34 **Expect:** 0.38 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6416	1127.6343	1127.6298	0.0045	142	152	0	GTGNLELVAVR
1320.5911	1319.5838	1319.5741	0.0097	83	94	0	DGEPDLSNNFGR
1572.7599	1571.7526	1571.7426	0.0100	18	31	0	VLLEENAGGEQEER
1817.9735	1816.9662	1816.9570	0.0092	225	240	1	IFLAGDKDNVIDQIEK
2082.2078	2081.2005	2081.2030	-0.0024	133	152	1	AMVIVVVNKGTGNLELVAVR

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 896.4271, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1141.5464, 1167.5767, 1184.5996, 1258.6265, 1287.6080, 1297.6536, 1379.7813, 1560.7056, 1568.7229, 1691.0359, 1738.8488, 1771.8953, 1894.9486, 2193.0051, 2227.0444, 2243.0537, 2256.6763, 2273.1592, 2295.1321, 2612.1487, 2619.2864, 3153.3682, 3211.3804

10. gi|226258 **Mass:** 10809 **Score:** 17 **Expect:** 19 **Queries matched:** 2

ferredoxin I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1141.5464	1140.5391	1140.5484	-0.0093	16	26	0	GDLAVAMASYK + Oxidation (M)
1297.6536	1296.6463	1296.6496	-0.0032	15	26	1	RGDLAVAMASYK + Oxidation (M)

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 896.4271, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1128.6416, 1167.5767, 1184.5996, 1258.6265, 1287.6080, 1320.5911, 1379.7813, 1560.7056, 1568.7229, 1572.7599, 1691.0359, 1738.8488, 1771.8953, 1817.9735, 1894.9486, 2082.2078, 2193.0051, 2227.0444, 2243.0537, 2256.6763, 2273.1592, 2295.1321, 2612.1487, 2619.2864, 3153.3682, 3211.3804

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|46560478** Score: **157** Expect: **1.7e-013**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **19**
Sequence Coverage: **36%**

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
147 - 160	1560.7056	1559.6983	1559.6851	0.0132	0	EGEQEWGTPGSEVR	
166 - 174	1141.5464	1140.5391	1140.5352	0.0039	0	NNPFYFPSR	
166 - 175	1297.6536	1296.6463	1296.6363	0.0100	1	NNPFYFPSRR	
199 - 207	1184.5996	1183.5923	1183.5846	0.0077	0	QFQNLQNHR	
208 - 222	1691.0359	1690.0286	1690.0141	0.0146	0	IVQIEARPNTLVLPK	
223 - 247	2619.2864	2618.2791	2618.3160	-0.0369	0	HADADNILVIQQGQATVTVANGNNR	
249 - 259	1258.6265	1257.6192	1257.6101	0.0091	0	SFNLDEGHALR	
260 - 271	1379.7813	1378.7740	1378.7608	0.0132	0	IPSGFISYILNR	
272 - 278	896.4271	895.4198	895.4260	-0.0062	0	HDNQNLR	
282 - 301	2227.0444	2226.0371	2226.0415	-0.0044	0	ISMPVNTPGQFEDFFPASSR	
282 - 301	2243.0537	2242.0464	2242.0364	0.0100	0	ISMPVNTPGQFEDFFPASSR	Oxidation (M)
302 - 312	1287.6080	1286.6007	1286.5891	0.0116	0	DQSSYLQGFSR	
313 - 327	1738.8488	1737.8415	1737.8321	0.0094	0	NTLEAAFNAEFNEIR	
313 - 328	1894.9486	1893.9413	1893.9332	0.0081	1	NTLEAAFNAEFNEIRR	
329 - 342	1572.7599	1571.7526	1571.7426	0.0100	0	VLLEENAGGEQEER	
394 - 405	1320.5911	1319.5838	1319.5741	0.0097	0	DGEPDLSNNFGR	
444 - 463	2082.2078	2081.2005	2081.2030	-0.0024	1	AMVIVVVNKGTGNLELVAVR	
453 - 463	1128.6416	1127.6343	1127.6298	0.0045	0	GTGNLELVAVR	
536 - 551	1817.9735	1816.9662	1816.9570	0.0092	1	IFLAGDKDNVIDQIEK	

No match to: 711.5172, 721.5340, 723.5375, 737.5273, 739.5438, 752.5684, 765.5609, 768.5731, 781.5546, 783.5774, 809.5963, 825.5858, 827.6053, 853.6208, 871.6320, 897.6557, 915.6580, 941.6829, 959.6893, 985.7008, 1111.5626, 1167.5767, 1568.7229, 1771.8953, 2193.0051, 2256.6763, 2273.1592, 2295.1321, 2612.1487, 3153.3682, 3211.3804

Spot 27

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 4 May 2007 at 11:31:17 GMT
Top Score : 91 for gi|46560478, conarachin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	gi|46560478	66934	91	conarachin [Arachis hypogaea]
2.	gi|620025	70639	88	Ara h I
3.	gi|1168390	70639	88	Allergen Ara h 1, clone P17 precursor (Ara h I)
4.	gi|16612200	71701	65	major allergen Arah1 [Arachis hypogaea]
5.	gi|1168391	71701	65	Allergen Ara h 1, clone P41B precursor (Ara h I)
6.	gi|602436	71701	65	Ara h I
7.	gi|46560476	48122	56	conarachin [Arachis hypogaea]
8.	gi|46560472	34169	49	conarachin [Arachis hypogaea]
9.	gi|46560474	33641	31	conarachin [Arachis hypogaea]
10.	gi|226258	10809	17	ferredoxin I

Results List

1. gi|46560478 **Mass:** 66934 **Score:** 91 **Expect:** 7.4e-007 **Queries matched:** 14
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1103.6443	1102.6370	1102.6386	-0.0016	406	414	1	LFEVKPDKK
1128.6412	1127.6339	1127.6298	0.0041	453	463	0	GTGNLELVAVR
1141.5514	1140.5441	1140.5352	0.0089	166	174	0	NNPFYFPSR
1184.6060	1183.5987	1183.5846	0.0141	199	207	0	QFQNLQNHR
1258.6398	1257.6325	1257.6101	0.0224	249	259	0	SFNLDEGHALR
1297.6683	1296.6610	1296.6363	0.0247	166	175	1	NNPFYFPSRR
1320.6041	1319.5968	1319.5741	0.0227	394	405	0	DGEPDLSNNFGR
1343.7043	1342.6970	1342.6703	0.0267	432	443	0	EGALMLPHFNSK

1359.6967	1358.6894	1358.6652	0.0242	432 - 443	0	EGALMLPHFNSK + Oxidation (M)
1586.7926	1585.7853	1585.7583	0.0270	380 - 393	0	GSEEEDITNPINLR
1714.8912	1713.8839	1713.8533	0.0307	379 - 393	1	KGSEEEDITNPINLR
1817.9984	1816.9911	1816.9570	0.0341	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9653	1893.9580	1893.9332	0.0248	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0474	2226.0401	2226.0415	-0.0014	282 - 301	0	ISMPVNTPGQFEDFFPASSR

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1167.5803, 1174.6575, 1287.6226, 1296.6287, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1643.8267, 1691.0629, 1738.8757, 1756.8650, 1771.9121, 1774.8794, 2185.0168, 2193.0049, 2200.9888, 2273.1589, 2295.1265, 2311.1106, 3211.2117

2. gi|620025 **Mass:** 70639 **Score:** 88 **Expect:** 1.3e-006 **Queries matched:** 14

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1103.6443	1102.6370	1102.6386	-0.0016	406 - 414		1	LFEVKPDKK
1128.6412	1127.6339	1127.6298	0.0041	453 - 463		0	GTGNLELVAVR
1141.5514	1140.5441	1140.5352	0.0089	166 - 174		0	NNPFYFPSR
1184.6060	1183.5987	1183.5846	0.0141	199 - 207		0	QFQNLQNHR
1258.6398	1257.6325	1257.6101	0.0224	249 - 259		0	SFNLDEGHALR
1297.6683	1296.6610	1296.6363	0.0247	166 - 175		1	NNPFYFPSRR
1320.6041	1319.5968	1319.5741	0.0227	394 - 405		0	DGEPDLSNNFGR
1343.7043	1342.6970	1342.6703	0.0267	432 - 443		0	EGALMLPHFNSK
1359.6967	1358.6894	1358.6652	0.0242	432 - 443		0	EGALMLPHFNSK + Oxidation (M)
1586.7926	1585.7853	1585.7583	0.0270	380 - 393		0	GSEEEDITNPINLR
1714.8912	1713.8839	1713.8533	0.0307	379 - 393		1	KGSEEEDITNPINLR
1817.9984	1816.9911	1816.9570	0.0341	536 - 551		1	IFLAGDKDNVIDQIEK
1894.9653	1893.9580	1893.9332	0.0248	313 - 328		1	NTLEAAFNAEFNEIRR
2227.0474	2226.0401	2226.0415	-0.0014	282 - 301		0	ISMPVNTPGQFEDFFPASSR

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1167.5803, 1174.6575, 1287.6226, 1296.6287, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1643.8267, 1691.0629, 1738.8757, 1756.8650, 1771.9121, 1774.8794, 2185.0168, 2193.0049, 2200.9888, 2273.1589, 2295.1265, 2311.1106, 3211.2117

3. gi|1168390 **Mass:** 70639 **Score:** 88 **Expect:** 1.3e-006 **Queries matched:** 14

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1103.6443	1102.6370	1102.6386	-0.0016	406 - 414		1	LFEVKPDKK
1128.6412	1127.6339	1127.6298	0.0041	453 - 463		0	GTGNLELVAVR
1141.5514	1140.5441	1140.5352	0.0089	166 - 174		0	NNPFYFPSR
1184.6060	1183.5987	1183.5846	0.0141	199 - 207		0	QFQNLQNHR
1258.6398	1257.6325	1257.6101	0.0224	249 - 259		0	SFNLDEGHALR

1297.6683	1296.6610	1296.6363	0.0247	166 - 175	1	NNPFYFPSRR
1320.6041	1319.5968	1319.5741	0.0227	394 - 405	0	DGEPDLSNNFGR
1343.7043	1342.6970	1342.6703	0.0267	432 - 443	0	EGALMLPHFNSK
1359.6967	1358.6894	1358.6652	0.0242	432 - 443	0	EGALMLPHFNSK + Oxidation (M)
1586.7926	1585.7853	1585.7583	0.0270	380 - 393	0	GSEEEDITNPINLR
1714.8912	1713.8839	1713.8533	0.0307	379 - 393	1	KGSEEEDITNPINLR
1817.9984	1816.9911	1816.9570	0.0341	536 - 551	1	IFLAGDKDNVIDQIEK
1894.9653	1893.9580	1893.9332	0.0248	313 - 328	1	NTLEAAFNAEFNEIRR
2227.0474	2226.0401	2226.0415	-0.0014	282 - 301	0	ISMPVNTPGQFEDFFPASSR

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1167.5803, 1174.6575, 1287.6226, 1296.6287, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1643.8267, 1691.0629, 1738.8757, 1756.8650, 1771.9121, 1774.8794, 2185.0168, 2193.0049, 2200.9888, 2273.1589, 2295.1265, 2311.1106, 3211.2117

4. gi|16612200 **Mass:** 71701 **Score:** 65 **Expect:** 0.00027 **Queries matched:** 12

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1103.6443	1102.6370	1102.6386	-0.0016	414 - 422		1	LFEVKPDKK
1128.6412	1127.6339	1127.6298	0.0041	461 - 471		0	GTGNLELVAVR
1141.5514	1140.5441	1140.5352	0.0089	172 - 180		0	NNPFYFPSR
1184.6060	1183.5987	1183.5846	0.0141	205 - 213		0	QFQNLQNHR
1258.6398	1257.6325	1257.6101	0.0224	255 - 265		0	SFNLDEGHALR
1297.6683	1296.6610	1296.6363	0.0247	172 - 181		1	NNPFYFPSRR
1343.7043	1342.6970	1342.6703	0.0267	440 - 451		0	EGALMLPHFNSK
1359.6967	1358.6894	1358.6652	0.0242	440 - 451		0	EGALMLPHFNSK + Oxidation (M)
1771.9121	1770.9048	1770.8747	0.0301	386 - 401		1	KGSEEEGDITNPINLR
1817.9984	1816.9911	1816.9570	0.0341	541 - 556		1	IFLAGDKDNVIDQIEK
1894.9653	1893.9580	1893.9332	0.0248	319 - 334		1	NTLEAAFNAEFNEIRR
2227.0474	2226.0401	2226.0415	-0.0014	288 - 307		0	ISMPVNTPGQFEDFFPASSR

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1167.5803, 1174.6575, 1287.6226, 1296.6287, 1320.6041, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1586.7926, 1643.8267, 1691.0629, 1714.8912, 1738.8757, 1756.8650, 1774.8794, 2185.0168, 2193.0049, 2200.9888, 2273.1589, 2295.1265, 2311.1106, 3211.2117

5. gi|1168391 **Mass:** 71701 **Score:** 65 **Expect:** 0.00027 **Queries matched:** 12

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1103.6443	1102.6370	1102.6386	-0.0016	414 - 422		1	LFEVKPDKK
1128.6412	1127.6339	1127.6298	0.0041	461 - 471		0	GTGNLELVAVR
1141.5514	1140.5441	1140.5352	0.0089	172 - 180		0	NNPFYFPSR
1184.6060	1183.5987	1183.5846	0.0141	205 - 213		0	QFQNLQNHR

1258.6398	1257.6325	1257.6101	0.0224	255 - 265	0	SFNLDEGHALR
1297.6683	1296.6610	1296.6363	0.0247	172 - 181	1	NNPFYFPSRR
1343.7043	1342.6970	1342.6703	0.0267	440 - 451	0	EGALMLPHFNSK
1359.6967	1358.6894	1358.6652	0.0242	440 - 451	0	EGALMLPHFNSK + Oxidation (M)
1771.9121	1770.9048	1770.8747	0.0301	386 - 401	1	KGSEEEGDITNPINLR
1817.9984	1816.9911	1816.9570	0.0341	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9653	1893.9580	1893.9332	0.0248	319 - 334	1	NTLEAAFNAEFNEIRR
2227.0474	2226.0401	2226.0415	-0.0014	288 - 307	0	ISMPVNTPGQFEDFFPASSR

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1167.5803, 1174.6575, 1287.6226, 1296.6287, 1320.6041, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1586.7926, 1643.8267, 1691.0629, 1714.8912, 1738.8757, 1756.8650, 1774.8794, 2185.0168, 2193.0049, 2200.9888, 2273.1589, 2295.1265, 2311.1106, 3211.2117

6. gi|602436 **Mass:** 71701 **Score:** 65 **Expect:** 0.00027 **Queries matched:** 12

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
1103.6443	1102.6370	1102.6386	-0.0016	414 - 422	1	LFEVKPDKK
1128.6412	1127.6339	1127.6298	0.0041	461 - 471	0	GTGNLELVAVR
1141.5514	1140.5441	1140.5352	0.0089	172 - 180	0	NNPFYFPSR
1184.6060	1183.5987	1183.5846	0.0141	205 - 213	0	QFQNLQNHR
1258.6398	1257.6325	1257.6101	0.0224	255 - 265	0	SFNLDEGHALR
1297.6683	1296.6610	1296.6363	0.0247	172 - 181	1	NNPFYFPSRR
1343.7043	1342.6970	1342.6703	0.0267	440 - 451	0	EGALMLPHFNSK
1359.6967	1358.6894	1358.6652	0.0242	440 - 451	0	EGALMLPHFNSK + Oxidation (M)
1771.9121	1770.9048	1770.8747	0.0301	386 - 401	1	KGSEEEGDITNPINLR
1817.9984	1816.9911	1816.9570	0.0341	541 - 556	1	IFLAGDKDNVIDQIEK
1894.9653	1893.9580	1893.9332	0.0248	319 - 334	1	NTLEAAFNAEFNEIRR
2227.0474	2226.0401	2226.0415	-0.0014	288 - 307	0	ISMPVNTPGQFEDFFPASSR

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1167.5803, 1174.6575, 1287.6226, 1296.6287, 1320.6041, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1586.7926, 1643.8267, 1691.0629, 1714.8912, 1738.8757, 1756.8650, 1774.8794, 2185.0168, 2193.0049, 2200.9888, 2273.1589, 2295.1265, 2311.1106, 3211.2117

7. gi|46560476 **Mass:** 48122 **Score:** 56 **Expect:** 0.002 **Queries matched:** 9

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
1103.6443	1102.6370	1102.6386	-0.0016	216 - 224	1	LFEVKPDKK
1128.6412	1127.6339	1127.6298	0.0041	263 - 273	0	GTGNLELVAVR
1184.6060	1183.5987	1183.5846	0.0141	8 - 16	0	QFQNLQNHR
1258.6398	1257.6325	1257.6101	0.0224	58 - 68	0	SFNLDEGHALR
1343.7043	1342.6970	1342.6703	0.0267	242 - 253	0	EGALMLPHFNSK

1359.6967	1358.6894	1358.6652	0.0242	242 - 253	0	EGALMLPHFNSK + Oxidation (M)
1817.9984	1816.9911	1816.9570	0.0341	343 - 358	1	IFLAGDKDNVIDQIEK
1894.9653	1893.9580	1893.9332	0.0248	122 - 137	1	NTLEAAFNAEFNEIRR
2227.0474	2226.0401	2226.0415	-0.0014	91 - 110	0	ISMPVNTPGQFEDFFPASSR

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1141.5514, 1167.5803, 1174.6575, 1287.6226, 1296.6287, 1297.6683, 1320.6041, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1586.7926, 1643.8267, 1691.0629, 1714.8912, 1738.8757, 1756.8650, 1771.9121, 1774.8794, 2185.0168, 2193.0049, 2200.9888, 2273.1589, 2295.1265, 2311.1106, 3211.2117

8. gi|46560472 **Mass:** 34169 **Score:** 49 **Expect:** 0.01 **Queries matched:** 8

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1103.6443	1102.6370	1102.6386	-0.0016	95 -	103	1	LFEVKPDKK
1128.6412	1127.6339	1127.6298	0.0041	142 -	152	0	GTGNLELVAVR
1320.6041	1319.5968	1319.5741	0.0227	83 -	94	0	DGEPDLSNNFGR
1343.7043	1342.6970	1342.6703	0.0267	121 -	132	0	EGALMLPHFNSK
1359.6967	1358.6894	1358.6652	0.0242	121 -	132	0	EGALMLPHFNSK + Oxidation (M)
1586.7926	1585.7853	1585.7583	0.0270	69 -	82	0	GSEEEDITNPINLR
1714.8912	1713.8839	1713.8533	0.0307	68 -	82	1	KGSEEEDITNPINLR
1817.9984	1816.9911	1816.9570	0.0341	225 -	240	1	IFLAGDKDNVIDQIEK

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1141.5514, 1167.5803, 1174.6575, 1184.6060, 1258.6398, 1287.6226, 1296.6287, 1297.6683, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1643.8267, 1691.0629, 1738.8757, 1756.8650, 1771.9121, 1774.8794, 1894.9653, 2185.0168, 2193.0049, 2200.9888, 2227.0474, 2273.1589, 2295.1265, 2311.1106, 3211.2117

9. gi|46560474 **Mass:** 33641 **Score:** 31 **Expect:** 0.74 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1103.6443	1102.6370	1102.6386	-0.0016	94 -	102	1	LFEVKPDKK
1128.6412	1127.6339	1127.6298	0.0041	141 -	151	0	GTGNLELVAVR
1343.7043	1342.6970	1342.6703	0.0267	120 -	131	0	EGALMLPHFNSK
1359.6967	1358.6894	1358.6652	0.0242	120 -	131	0	EGALMLPHFNSK + Oxidation (M)
1771.9121	1770.9048	1770.8747	0.0301	66 -	81	1	KGSEEEGDITNPINLR
1817.9984	1816.9911	1816.9570	0.0341	221 -	236	1	IFLAGDKDNVIDQIEK

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1141.5514, 1167.5803, 1174.6575, 1184.6060, 1258.6398, 1287.6226, 1296.6287, 1297.6683, 1320.6041, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1586.7926, 1643.8267, 1691.0629, 1714.8912, 1738.8757, 1756.8650, 1774.8794, 1894.9653, 2185.0168, 2193.0049, 2200.9888, 2227.0474, 2273.1589, 2295.1265, 2311.1106, 3211.2117

10. gi|226258 **Mass:** 10809 **Score:** 17 **Expect:** 20 **Queries matched:** 2

ferredoxin I

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1141.5514	1140.5441	1140.5484	-0.0043	16	-	26	0	GDLAVAMASYK + Oxidation (M)
1297.6683	1296.6610	1296.6496	0.0115	15	-	26	1	RGDLAVAMASYK + Oxidation (M)

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1103.6443, 1128.6412, 1167.5803, 1174.6575, 1184.6060, 1258.6398, 1287.6226, 1296.6287, 1320.6041, 1343.7043, 1359.6967, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1586.7926, 1643.8267, 1691.0629, 1714.8912, 1738.8757, 1756.8650, 1771.9121, 1774.8794, 1817.9984, 1894.9653, 2185.0168, 2193.0049, 2200.9888, 2227.0474, 2273.1589, 2295.1265, 2311.1106, 3211.2117

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|46560478** Score: **91** Expect: **7.4e-007**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **66934**; Calculated pI value: **6.72**
NCBI BLAST search of gi|46560478 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **14**
Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

```
  1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
 51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
166 - 174	1141.5514	1140.5441	1140.5352	0.0089	0	NNPFYFPSR
166 - 175	1297.6683	1296.6610	1296.6363	0.0247	1	NNPFYFPSRR
199 - 207	1184.6060	1183.5987	1183.5846	0.0141	0	QFQNLQNHR
249 - 259	1258.6398	1257.6325	1257.6101	0.0224	0	SFNLDEGHALR
282 - 301	2227.0474	2226.0401	2226.0415	-0.0014	0	ISMPVNTPGQFEDFFPASSR
313 - 328	1894.9653	1893.9580	1893.9332	0.0248	1	NTLEAAFNAEFNEIRR
379 - 393	1714.8912	1713.8839	1713.8533	0.0307	1	KGSEEEDITNPINLR
380 - 393	1586.7926	1585.7853	1585.7583	0.0270	0	GSEEEDITNPINLR
394 - 405	1320.6041	1319.5968	1319.5741	0.0227	0	DGEPDLSNNFGR
406 - 414	1103.6443	1102.6370	1102.6386	-0.0016	1	LFEVKPDKK
432 - 443	1343.7043	1342.6970	1342.6703	0.0267	0	EGALMLPHFNSK
432 - 443	1359.6967	1358.6894	1358.6652	0.0242	0	EGALMLPHFNSK Oxidation (M)
453 - 463	1128.6412	1127.6339	1127.6298	0.0041	0	GTGNLELVAVR
536 - 551	1817.9984	1816.9911	1816.9570	0.0341	1	IFLAGDKDNVIDQIEK

No match to: 805.3753, 808.3344, 811.3621, 816.3927, 828.4514, 855.4759, 883.4180, 896.4033, 906.4692, 932.4365, 1046.5906, 1080.5276, 1167.5803, 1174.6575, 1287.6226, 1296.6287, 1379.7987, 1386.7422, 1399.7501, 1431.6929, 1439.7024, 1568.7472, 1572.7866, 1643.8267, 1691.0629, 1738.8757, 1756.8650, 1771.9121, 1774.8794, 2185.0168, 2193.0049, 2200.9888, 2273.1589, 2295.1265, 2311.1106, 3211.2117

Spot 28

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:39:04 GMT
Top Score : 50 for gi|118776570, arachin 6 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	50	arachin 6 [Arachis hypogaea]
2.	gi|3703107	58543	39	glycinin [Arachis hypogaea]
3.	gi|9864777	60754	31	Gly1 [Arachis hypogaea]
4.	gi|52001219	61810	31	arachin Ahy-1 [Arachis hypogaea]
5.	gi|37789212	61803	31	storage protein [Arachis hypogaea]
6.	gi|57669861	61041	24	arachin Ahy-4 [Arachis hypogaea]
7.	gi|108595573	61041	24	arachin Ahy-4 [Arachis hypogaea]
8.	gi|21314465	62042	24	allergen Arah3/Arah4 [Arachis hypogaea]
9.	gi|52001221	61836	24	arachin Ahy-2 [Arachis hypogaea]
10.	gi|230338	23975	20	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 50 **Expect:** 0.009 **Queries matched:** 8
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5842	1101.5769	1101.5930	-0.0161	507	515	1	QLKNNNPFK
1269.7708	1268.7635	1268.7452	0.0183	377	387	0	TANELNLLILR
1295.6240	1294.6167	1294.6377	-0.0210	423	434	0	AHVQVVDSNGNR
1349.7216	1348.7143	1348.6927	0.0216	516	526	0	FFVPPFQQSPR
1389.7120	1388.7047	1388.6935	0.0112	364	376	0	SPDIYNPQAGSLK
1448.6774	1447.6701	1447.6619	0.0082	458	469	0	SQSENFEYVAFK
1636.7544	1635.7471	1635.7773	-0.0302	341	356	0	GSGNGIEETICTATVK
1659.8735	1658.8662	1658.8376	0.0287	362	376	1	NRSPDIYNPQAGSLK

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 906.4897, 1046.5922, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1255.7328, 1277.0940, 1289.6665, 1296.6388, 1305.6975, 1307.6860, 1365.6957, 1376.7419, 1377.7361, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1652.7588, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2273.1563, 2336.0764, 2383.9272

2. gi|3703107 **Mass:** 58543 **Score:** 39 **Expect:** 0.11 **Queries matched:** 7

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5842	1101.5769	1101.5930	-0.0161	485	493	1	QLKNNNPFK
1255.7328	1254.7255	1254.7295	-0.0040	355	365	0	TANDLNLLILR
1289.6665	1288.6592	1288.6564	0.0029	494	504	0	FFVPPSQQSPR
1295.6240	1294.6167	1294.6377	-0.0210	401	412	0	AHVQVVDSNGNR
1389.7120	1388.7047	1388.6935	0.0112	342	354	0	SPDIYNPQAGSLK
1448.6774	1447.6701	1447.6619	0.0082	436	447	0	SQSENFEYVAFK
1659.8735	1658.8662	1658.8376	0.0287	340	354	1	NRSPDIYNPQAGSLK

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 906.4897, 1046.5922, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1269.7708, 1277.0940, 1296.6388, 1305.6975, 1307.6860, 1349.7216, 1365.6957, 1376.7419, 1377.7361, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1636.7544, 1652.7588, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2273.1563, 2336.0764, 2383.9272

3. gi|9864777 **Mass:** 60754 **Score:** 31 **Expect:** 0.63 **Queries matched:** 6

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5842	1101.5769	1101.5930	-0.0161	507	515	1	QLKNNNPFK
1255.7328	1254.7255	1254.7295	-0.0040	377	387	0	TANDLNLLILR
1295.6240	1294.6167	1294.6377	-0.0210	423	434	0	AHVQVVDSNGNR
1305.6975	1304.6902	1304.6877	0.0026	516	526	0	FFVPPSQQSLR
1389.7120	1388.7047	1388.6935	0.0112	364	376	0	SPDIYNPQAGSLK
1659.8735	1658.8662	1658.8376	0.0287	362	376	1	NRSPDIYNPQAGSLK

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 906.4897, 1046.5922, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1269.7708, 1277.0940, 1289.6665, 1296.6388, 1307.6860, 1349.7216, 1365.6957, 1376.7419, 1377.7361, 1448.6774, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1636.7544, 1652.7588, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2273.1563, 2336.0764, 2383.9272

4. gi|52001219 **Mass:** 61810 **Score:** 31 **Expect:** 0.65 **Queries matched:** 6

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1102.5842	1101.5769	1101.5930	-0.0161	514	-	522	1	QLKNNNPFK
1269.7708	1268.7635	1268.7452	0.0183	384	-	394	0	TANELNLLILR
1296.6388	1295.6315	1295.6218	0.0098	430	-	441	0	AHVQVVDSNGDR
1389.7120	1388.7047	1388.6935	0.0112	371	-	383	0	SPDIYNPQAGSLK
1448.6774	1447.6701	1447.6619	0.0082	465	-	476	0	SQSENFEYVAFK
1659.8735	1658.8662	1658.8376	0.0287	369	-	383	1	NRSPDIYNPQAGSLK

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 906.4897, 1046.5922, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1255.7328, 1277.0940, 1289.6665, 1295.6240, 1305.6975, 1307.6860, 1349.7216, 1365.6957, 1376.7419, 1377.7361, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1636.7544, 1652.7588, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2273.1563, 2336.0764, 2383.9272

5. gi|37789212 **Mass:** 61803 **Score:** 31 **Expect:** 0.65 **Queries matched:** 6

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1102.5842	1101.5769	1101.5930	-0.0161	514	-	522	1	QLKNNNPFK
1269.7708	1268.7635	1268.7452	0.0183	384	-	394	0	TANELNLLILR
1296.6388	1295.6315	1295.6218	0.0098	430	-	441	0	AHVQVVDSNGDR
1389.7120	1388.7047	1388.6935	0.0112	371	-	383	0	SPDIYNPQAGSLK
1448.6774	1447.6701	1447.6619	0.0082	465	-	476	0	SQSENFEYVAFK
1659.8735	1658.8662	1658.8376	0.0287	369	-	383	1	NRSPDIYNPQAGSLK

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 906.4897, 1046.5922, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1255.7328, 1277.0940, 1289.6665, 1295.6240, 1305.6975, 1307.6860, 1349.7216, 1365.6957, 1376.7419, 1377.7361, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1636.7544, 1652.7588, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2273.1563, 2336.0764, 2383.9272

6. gi|57669861 **Mass:** 61041 **Score:** 24 **Expect:** 3.4 **Queries matched:** 5

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1255.7328	1254.7255	1254.7295	-0.0040	378	-	388	0	TANDLNLLILR
1289.6665	1288.6592	1288.6564	0.0029	518	-	528	0	FFVPPSQQSPR
1295.6240	1294.6167	1294.6377	-0.0210	424	-	435	0	AHVQVVDSNGNR
1389.7120	1388.7047	1388.6935	0.0112	365	-	377	0	SPDIYNPQAGSLK
1659.8735	1658.8662	1658.8376	0.0287	363	-	377	1	NRSPDIYNPQAGSLK

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 906.4897, 1046.5922, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1102.5842, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1269.7708, 1277.0940, 1296.6388, 1305.6975, 1307.6860, 1349.7216, 1365.6957, 1376.7419, 1377.7361, 1448.6774, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1636.7544, 1652.7588, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2273.1563, 2336.0764, 2383.9272

7. gi|108595573 **Mass:** 61041 **Score:** 24 **Expect:** 3.4 **Queries matched:** 5

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7328	1254.7255	1254.7295	-0.0040	378	388	0	TANDLNLLILR
1289.6665	1288.6592	1288.6564	0.0029	518	528	0	FFVPPSQQSPR
1295.6240	1294.6167	1294.6377	-0.0210	424	435	0	AHVQVVDSNGNR
1389.7120	1388.7047	1388.6935	0.0112	365	377	0	SPDIYNPQAGSLK
1659.8735	1658.8662	1658.8376	0.0287	363	377	1	NRSPDIYNPQAGSLK

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 906.4897, 1046.5922, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1102.5842, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1269.7708, 1277.0940, 1296.6388, 1305.6975, 1307.6860, 1349.7216, 1365.6957, 1376.7419, 1377.7361, 1448.6774, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1636.7544, 1652.7588, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2273.1563, 2336.0764, 2383.9272

8. gi|21314465 **Mass:** 62042 **Score:** 24 **Expect:** 3.6 **Queries matched:** 5

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5842	1101.5769	1101.5930	-0.0161	516	524	1	QLKNNNPFK
1296.6388	1295.6315	1295.6218	0.0098	432	443	0	AHVQVVDSNGDR
1389.7120	1388.7047	1388.6935	0.0112	371	383	0	SPDIYNPQAGSLK
1448.6774	1447.6701	1447.6619	0.0082	467	478	0	SQSENFEYVAFK
1659.8735	1658.8662	1658.8376	0.0287	369	383	1	NRSPDIYNPQAGSLK

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 906.4897, 1046.5922, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1255.7328, 1269.7708, 1277.0940, 1289.6665, 1295.6240, 1305.6975, 1307.6860, 1349.7216, 1365.6957, 1376.7419, 1377.7361, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1636.7544, 1652.7588, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2273.1563, 2336.0764, 2383.9272

9. gi|52001221 **Mass:** 61836 **Score:** 24 **Expect:** 3.8 **Queries matched:** 5

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1102.5842	1101.5769	1101.5930	-0.0161	515 - 523	1	QLKNNNPFK
1255.7328	1254.7255	1254.7295	-0.0040	385 - 395	0	TANDLNLLILR
1295.6240	1294.6167	1294.6377	-0.0210	431 - 442	0	AHVQVVDSNGNR
1389.7120	1388.7047	1388.6935	0.0112	372 - 384	0	SPDIYNPQAGSLK
1659.8735	1658.8662	1658.8376	0.0287	370 - 384	1	NRSPDIYNPQAGSLK

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 906.4897, 1046.5922, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1269.7708, 1277.0940, 1289.6665, 1296.6388, 1305.6975, 1307.6860, 1349.7216, 1365.6957, 1376.7419, 1377.7361, 1448.6774, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1636.7544, 1652.7588, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2273.1563, 2336.0764, 2383.9272

10. gi|230338 **Mass:** 23975 **Score:** 20 **Expect:** 8 **Queries matched:** 3

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
906.4897	905.4824	905.4970	-0.0146	201 -	208	0	NKPGVYTK
1046.5922	1045.5849	1045.5880	-0.0030	90 -	99	1	LKSAASLNSR
2273.1563	2272.1490	2272.1521	-0.0031	70 -	89	0	SIVHPSYNSNTLNNDIMLIK

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1102.5842, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1255.7328, 1269.7708, 1277.0940, 1289.6665, 1295.6240, 1296.6388, 1305.6975, 1307.6860, 1349.7216, 1365.6957, 1376.7419, 1377.7361, 1389.7120, 1448.6774, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1636.7544, 1652.7588, 1659.8735, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2336.0764, 2383.9272

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 48

Protein View

Match to: **gi|118776570** Score: **50** Expect: **0.009**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **48**
Number of mass values matched: **8**
Sequence Coverage: **16%**

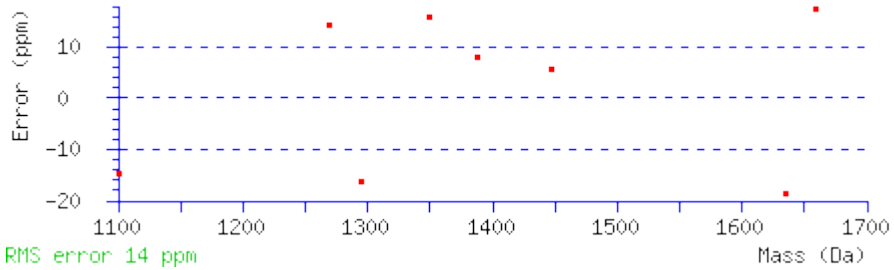
Matched peptides shown in **Bold Red**

```
     1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
    51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
   101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
   151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
   201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
   251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
   301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
   351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
   401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
   451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
   501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
341 - 356	1636.7544	1635.7471	1635.7773	-0.0302	0	GSGNGIEETICTATVK
362 - 376	1659.8735	1658.8662	1658.8376	0.0287	1	NRSPDIYNPQAGSLK
364 - 376	1389.7120	1388.7047	1388.6935	0.0112	0	SPDIYNPQAGSLK
377 - 387	1269.7708	1268.7635	1268.7452	0.0183	0	TANELNLLILR
423 - 434	1295.6240	1294.6167	1294.6377	-0.0210	0	AHVQVVDSNGNR
458 - 469	1448.6774	1447.6701	1447.6619	0.0082	0	SQSENFEYVAFK
507 - 515	1102.5842	1101.5769	1101.5930	-0.0161	1	QLKNNNPFK
516 - 526	1349.7216	1348.7143	1348.6927	0.0216	0	FFVPPFQQSPR

No match to: 805.4387, 839.0916, 845.0756, 855.0307, 861.0528, 877.0280, 906.4897, 1046.5922, 1050.0957, 1066.0604, 1072.0846, 1080.5132, 1082.0377, 1111.5480, 1174.6102, 1175.5587, 1215.5223, 1255.7328, 1277.0940, 1289.6665, 1296.6388, 1305.6975, 1307.6860, 1365.6957, 1376.7419, 1377.7361, 1462.6862, 1475.7637, 1493.7112, 1618.7968, 1652.7588, 1774.8490, 1796.8417, 2184.9966, 2194.0078, 2209.0105, 2227.0938, 2273.1563, 2336.0764, 2383.9272


Error (ppm)
10
0
-10
-20
1100
1200
1300
1400
1500
1600
1700
Mass (Da)
RMS error 14 ppm

Spot 29

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 4 May 2007 at 09:59:02 GMT
Top Score : 82 for gi|118776570, arachin 6 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	82	arachin 6 [Arachis hypogaea]
2.	gi|9864777	60754	52	Gly1 [Arachis hypogaea]
3.	gi|5712199	61430	43	glycinin [Arachis hypogaea]
4.	gi|52001219	61810	42	arachin Ahy-1 [Arachis hypogaea]
5.	gi|37789212	61803	42	storage protein [Arachis hypogaea]
6.	gi|57669861	61041	35	arachin Ahy-4 [Arachis hypogaea]
7.	gi|108595573	61041	35	arachin Ahy-4 [Arachis hypogaea]
8.	gi|21314465	62042	34	allergen Arah3/Arah4 [Arachis hypogaea]
9.	gi|52001221	61836	34	arachin Ahy-2 [Arachis hypogaea]
10.	gi|3703107	58543	31	glycinin [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 82 **Expect:** 5.9e-006 **Queries matched:** 12
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5988	1101.5915	1101.5930	-0.0015	507	515	1	QLKNNNPFK
1269.7687	1268.7614	1268.7452	0.0162	377	387	0	TANELNLLILR
1295.6569	1294.6496	1294.6377	0.0119	423	434	0	AHVQVVDSNGNR
1349.7191	1348.7118	1348.6927	0.0191	516	526	0	FFVPPFQQSPR
1389.7207	1388.7134	1388.6935	0.0199	364	376	0	SPDIYNPQAGSLK
1448.6886	1447.6813	1447.6619	0.0194	458	469	0	SQSENFEYVAFK
1541.7974	1540.7901	1540.7673	0.0228	388	400	0	WLGLSAEYGNLYR
1590.8185	1589.8112	1589.8354	-0.0241	516	529	1	FFVPPFQQSPRAVA

1636.7826	1635.7753	1635.7773	-0.0020	341 - 356	0	GSGNGIEETICTATVK
1659.8691	1658.8618	1658.8376	0.0243	362 - 376	1	NRSPDIYNPQAGSLK
2064.0422	2063.0349	2063.0376	-0.0027	510 - 526	1	NNNPFKFFVPPFQQSPR
2314.1636	2313.1563	2313.2018	-0.0454	401 - 420	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1111.5648, 1145.5807, 1175.5641, 1255.7523, 1289.6826, 1296.6492, 1305.7065, 1360.7144, 1365.7161, 1376.7495, 1377.7448, 1420.7631, 1434.6908, 1436.7437, 1462.7098, 1497.7458, 1523.7437, 1618.8027, 1640.7937, 1652.7723, 1757.8573, 1774.8885, 1861.9911, 2020.0276, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

2. gi|9864777 **Mass:** 60754 **Score:** 52 **Expect:** 0.0056 **Queries matched:** 9

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5988	1101.5915	1101.5930	-0.0015	507 - 515		1	QLKNNNPFK
1255.7523	1254.7450	1254.7295	0.0155	377 - 387		0	TANDLNLLILR
1295.6569	1294.6496	1294.6377	0.0119	423 - 434		0	AHVQVVDSNGNR
1305.7065	1304.6992	1304.6877	0.0116	516 - 526		0	FFVPPSQQSLR
1389.7207	1388.7134	1388.6935	0.0199	364 - 376		0	SPDIYNPQAGSLK
1541.7974	1540.7901	1540.7673	0.0228	388 - 400		0	WLGLSAEYGNLYR
1659.8691	1658.8618	1658.8376	0.0243	362 - 376		1	NRSPDIYNPQAGSLK
2020.0276	2019.0203	2019.0326	-0.0122	510 - 526		1	NNNPFKFFVPPSQQSLR
2314.1636	2313.1563	2313.2018	-0.0454	401 - 420		0	NALFVPHYNTNAHSIIYALR

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1111.5648, 1145.5807, 1175.5641, 1269.7687, 1289.6826, 1296.6492, 1349.7191, 1360.7144, 1365.7161, 1376.7495, 1377.7448, 1420.7631, 1434.6908, 1436.7437, 1448.6886, 1462.7098, 1497.7458, 1523.7437, 1590.8185, 1618.8027, 1636.7826, 1640.7937, 1652.7723, 1757.8573, 1774.8885, 1861.9911, 2064.0422, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

3. gi|5712199 **Mass:** 61430 **Score:** 43 **Expect:** 0.043 **Queries matched:** 8

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5988	1101.5915	1101.5930	-0.0015	508 - 516		1	QLKNNNPFK
1295.6569	1294.6496	1294.6377	0.0119	424 - 435		0	AHVQVVDSNGNR
1349.7191	1348.7118	1348.6927	0.0191	517 - 527		0	FFVPPFQQSPR
1448.6886	1447.6813	1447.6619	0.0194	459 - 470		0	SQSENFEYVAFK
1541.7974	1540.7901	1540.7673	0.0228	389 - 401		0	WLGLSAEYGNLYR
1590.8185	1589.8112	1589.8354	-0.0241	517 - 530		1	FFVPPFQQSPRAVA
2064.0422	2063.0349	2063.0376	-0.0027	511 - 527		1	NNNPFKFFVPPFQQSPR

2314.1636	2313.1563	2313.2018	-0.0454	402 - 421	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1111.5648, 1145.5807, 1175.5641, 1255.7523, 1269.7687, 1289.6826, 1296.6492, 1305.7065, 1360.7144, 1365.7161, 1376.7495, 1377.7448, 1389.7207, 1420.7631, 1434.6908, 1436.7437, 1462.7098, 1497.7458, 1523.7437, 1618.8027, 1636.7826, 1640.7937, 1652.7723, 1659.8691, 1757.8573, 1774.8885, 1861.9911, 2020.0276, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

4. gi|52001219 **Mass:** 61810 **Score:** 42 **Expect:** 0.054 **Queries matched:** 8

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5988	1101.5915	1101.5930	-0.0015	514 - 522		1	QLKNNNPFK
1269.7687	1268.7614	1268.7452	0.0162	384 - 394		0	TANELNLLILR
1296.6492	1295.6419	1295.6218	0.0202	430 - 441		0	AHVQVVDSNGDR
1389.7207	1388.7134	1388.6935	0.0199	371 - 383		0	SPDIYNPQAGSLK
1448.6886	1447.6813	1447.6619	0.0194	465 - 476		0	SQSENFEYVAFK
1541.7974	1540.7901	1540.7673	0.0228	395 - 407		0	WLGLSAEYGNLYR
1659.8691	1658.8618	1658.8376	0.0243	369 - 383		1	NRSPDIYNPQAGSLK
2314.1636	2313.1563	2313.2018	-0.0454	408 - 427		0	NALFVPHYNTNAHSIIYALR

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1111.5648, 1145.5807, 1175.5641, 1255.7523, 1289.6826, 1295.6569, 1305.7065, 1349.7191, 1360.7144, 1365.7161, 1376.7495, 1377.7448, 1420.7631, 1434.6908, 1436.7437, 1462.7098, 1497.7458, 1523.7437, 1590.8185, 1618.8027, 1636.7826, 1640.7937, 1652.7723, 1757.8573, 1774.8885, 1861.9911, 2020.0276, 2064.0422, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

5. gi|37789212 **Mass:** 61803 **Score:** 42 **Expect:** 0.054 **Queries matched:** 8

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5988	1101.5915	1101.5930	-0.0015	514 - 522		1	QLKNNNPFK
1269.7687	1268.7614	1268.7452	0.0162	384 - 394		0	TANELNLLILR
1296.6492	1295.6419	1295.6218	0.0202	430 - 441		0	AHVQVVDSNGDR
1389.7207	1388.7134	1388.6935	0.0199	371 - 383		0	SPDIYNPQAGSLK
1448.6886	1447.6813	1447.6619	0.0194	465 - 476		0	SQSENFEYVAFK
1541.7974	1540.7901	1540.7673	0.0228	395 - 407		0	WLGLSAEYGNLYR
1659.8691	1658.8618	1658.8376	0.0243	369 - 383		1	NRSPDIYNPQAGSLK
2314.1636	2313.1563	2313.2018	-0.0454	408 - 427		0	NALFVPHYNTNAHSIIYALR

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1111.5648, 1145.5807, 1175.5641, 1255.7523, 1289.6826, 1295.6569, 1305.7065, 1349.7191, 1360.7144, 1365.7161, 1376.7495,

1377.7448, 1420.7631, 1434.6908, 1436.7437, 1462.7098, 1497.7458, 1523.7437, 1590.8185, 1618.8027, 1636.7826, 1640.7937, 1652.7723, 1757.8573, 1774.8885, 1861.9911, 2020.0276, 2064.0422, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

6. gi|57669861 **Mass:** 61041 **Score:** 35 **Expect:** 0.29 **Queries matched:** 7

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1255.7523	1254.7450	1254.7295	0.0155	378	-	388	0	TANDLNLLILR
1289.6826	1288.6753	1288.6564	0.0190	518	-	528	0	FFVPPSQQSPR
1295.6569	1294.6496	1294.6377	0.0119	424	-	435	0	AHVQVVDSNGNR
1389.7207	1388.7134	1388.6935	0.0199	365	-	377	0	SPDIYNPQAGSLK
1541.7974	1540.7901	1540.7673	0.0228	389	-	401	0	WLGLSAEYGNLYR
1659.8691	1658.8618	1658.8376	0.0243	363	-	377	1	NRSPDIYNPQAGSLK
2314.1636	2313.1563	2313.2018	-0.0454	402	-	421	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1102.5988, 1111.5648, 1145.5807, 1175.5641, 1269.7687, 1296.6492, 1305.7065, 1349.7191, 1360.7144, 1365.7161, 1376.7495, 1377.7448, 1420.7631, 1434.6908, 1436.7437, 1448.6886, 1462.7098, 1497.7458, 1523.7437, 1590.8185, 1618.8027, 1636.7826, 1640.7937, 1652.7723, 1757.8573, 1774.8885, 1861.9911, 2020.0276, 2064.0422, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

7. gi|108595573 **Mass:** 61041 **Score:** 35 **Expect:** 0.29 **Queries matched:** 7

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1255.7523	1254.7450	1254.7295	0.0155	378	-	388	0	TANDLNLLILR
1289.6826	1288.6753	1288.6564	0.0190	518	-	528	0	FFVPPSQQSPR
1295.6569	1294.6496	1294.6377	0.0119	424	-	435	0	AHVQVVDSNGNR
1389.7207	1388.7134	1388.6935	0.0199	365	-	377	0	SPDIYNPQAGSLK
1541.7974	1540.7901	1540.7673	0.0228	389	-	401	0	WLGLSAEYGNLYR
1659.8691	1658.8618	1658.8376	0.0243	363	-	377	1	NRSPDIYNPQAGSLK
2314.1636	2313.1563	2313.2018	-0.0454	402	-	421	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1102.5988, 1111.5648, 1145.5807, 1175.5641, 1269.7687, 1296.6492, 1305.7065, 1349.7191, 1360.7144, 1365.7161, 1376.7495, 1377.7448, 1420.7631, 1434.6908, 1436.7437, 1448.6886, 1462.7098, 1497.7458, 1523.7437, 1590.8185, 1618.8027, 1636.7826, 1640.7937, 1652.7723, 1757.8573, 1774.8885, 1861.9911, 2020.0276, 2064.0422, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

8. gi|21314465 **Mass:** 62042 **Score:** 34 **Expect:** 0.32 **Queries matched:** 7

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5988	1101.5915	1101.5930	-0.0015	516	524	1	QLKNNNPFK
1296.6492	1295.6419	1295.6218	0.0202	432	443	0	AHVQVVDSNGDR
1389.7207	1388.7134	1388.6935	0.0199	371	383	0	SPDIYNPQAGSLK
1448.6886	1447.6813	1447.6619	0.0194	467	478	0	SQSENFEYVAFK
1541.7974	1540.7901	1540.7673	0.0228	397	409	0	WLGLSAEYGNLYR
1659.8691	1658.8618	1658.8376	0.0243	369	383	1	NRSPDIYNPQAGSLK
2314.1636	2313.1563	2313.2018	-0.0454	410	429	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1111.5648, 1145.5807, 1175.5641, 1255.7523, 1269.7687, 1289.6826, 1295.6569, 1305.7065, 1349.7191, 1360.7144, 1365.7161, 1376.7495, 1377.7448, 1420.7631, 1434.6908, 1436.7437, 1462.7098, 1497.7458, 1523.7437, 1590.8185, 1618.8027, 1636.7826, 1640.7937, 1652.7723, 1757.8573, 1774.8885, 1861.9911, 2020.0276, 2064.0422, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

9. gi|52001221 **Mass:** 61836 **Score:** 34 **Expect:** 0.33 **Queries matched:** 7

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5988	1101.5915	1101.5930	-0.0015	515	523	1	QLKNNNPFK
1255.7523	1254.7450	1254.7295	0.0155	385	395	0	TANDLNLLILR
1295.6569	1294.6496	1294.6377	0.0119	431	442	0	AHVQVVDSNGNR
1389.7207	1388.7134	1388.6935	0.0199	372	384	0	SPDIYNPQAGSLK
1541.7974	1540.7901	1540.7673	0.0228	396	408	0	WLGLSAEYGNLYR
1659.8691	1658.8618	1658.8376	0.0243	370	384	1	NRSPDIYNPQAGSLK
2314.1636	2313.1563	2313.2018	-0.0454	409	428	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1111.5648, 1145.5807, 1175.5641, 1269.7687, 1289.6826, 1296.6492, 1305.7065, 1349.7191, 1360.7144, 1365.7161, 1376.7495, 1377.7448, 1420.7631, 1434.6908, 1436.7437, 1448.6886, 1462.7098, 1497.7458, 1523.7437, 1590.8185, 1618.8027, 1636.7826, 1640.7937, 1652.7723, 1757.8573, 1774.8885, 1861.9911, 2020.0276, 2064.0422, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

10. gi|3703107 **Mass:** 58543 **Score:** 31 **Expect:** 0.65 **Queries matched:** 7

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1102.5988	1101.5915	1101.5930	-0.0015	485 - 493	1	QLKNNNPFK
1255.7523	1254.7450	1254.7295	0.0155	355 - 365	0	TANDLNLLILR
1289.6826	1288.6753	1288.6564	0.0190	494 - 504	0	FFVPPSQQSPR
1295.6569	1294.6496	1294.6377	0.0119	401 - 412	0	AHVQVVDSNGNR
1389.7207	1388.7134	1388.6935	0.0199	342 - 354	0	SPDIYNPQAGSLK
1448.6886	1447.6813	1447.6619	0.0194	436 - 447	0	SQSENFEYVAFK
1659.8691	1658.8618	1658.8376	0.0243	340 - 354	1	NRSPDIYNPQAGSLK

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1111.5648, 1145.5807, 1175.5641, 1269.7687, 1296.6492, 1305.7065, 1349.7191, 1360.7144, 1365.7161, 1376.7495, 1377.7448, 1420.7631, 1434.6908, 1436.7437, 1462.7098, 1497.7458, 1523.7437, 1541.7974, 1590.8185, 1618.8027, 1636.7826, 1640.7937, 1652.7723, 1757.8573, 1774.8885, 1861.9911, 2020.0276, 2064.0422, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2314.1636, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 62

Protein View

Match to: **gi|118776570** Score: **82** Expect: **5.9e-006**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr

Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **62**
Number of mass values matched: **12**
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
     1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
    51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
   101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
   151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
   201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
   251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
   301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
   351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
   401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
   451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
   501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
341 - 356	1636.7826	1635.7753	1635.7773	-0.0020	0	GSGNGIEETICTATVK
362 - 376	1659.8691	1658.8618	1658.8376	0.0243	1	NRSPDIYNPQAGSLK
364 - 376	1389.7207	1388.7134	1388.6935	0.0199	0	SPDIYNPQAGSLK
377 - 387	1269.7687	1268.7614	1268.7452	0.0162	0	TANELNLLILR
388 - 400	1541.7974	1540.7901	1540.7673	0.0228	0	WLGLSAEYGNLYR
401 - 420	2314.1636	2313.1563	2313.2018	-0.0454	0	NALFVPHYNTNAHSIIYALR
423 - 434	1295.6569	1294.6496	1294.6377	0.0119	0	AHVQVVDSNGNR
458 - 469	1448.6886	1447.6813	1447.6619	0.0194	0	SQSENFEYVAFK
507 - 515	1102.5988	1101.5915	1101.5930	-0.0015	1	QLKNNNPFK
510 - 526	2064.0422	2063.0349	2063.0376	-0.0027	1	NNNPFKFFVPPFQQSPR
516 - 526	1349.7191	1348.7118	1348.6927	0.0191	0	FFVPPFQQSPR
516 - 529	1590.8185	1589.8112	1589.8354	-0.0241	1	FFVPPFQQSPRAVA

No match to: 805.3811, 835.4734, 855.0240, 861.0449, 877.0218, 906.4791, 1046.5920, 1066.0759, 1080.5286, 1085.5692, 1111.5648, 1145.5807, 1175.5641, 1255.7523, 1289.6826, 1296.6492, 1305.7065, 1360.7144, 1365.7161, 1376.7495, 1377.7448, 1420.7631, 1434.6908, 1436.7437, 1462.7098, 1497.7458, 1523.7437, 1618.8027, 1640.7937, 1652.7723, 1757.8573, 1774.8885, 1861.9911, 2020.0276, 2092.0522, 2185.0137, 2200.9851, 2273.1431, 2311.1306, 2393.2581, 2454.2515, 2530.3196, 2542.2622, 2556.2742, 2652.3330, 2685.3132, 3153.2852, 3228.2988, 3245.4119, 3820.3582

Spot 30

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 4 May 2007 at 09:58:47 GMT
Top Score : 48 for gi|118776570, arachin 6 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	48	arachin 6 [Arachis hypogaea]
2.	gi|9864777	60754	47	Gly1 [Arachis hypogaea]
3.	gi|3703107	58543	47	glycinin [Arachis hypogaea]
4.	gi|57669861	61041	40	arachin Ahy-4 [Arachis hypogaea]
5.	gi|108595573	61041	40	arachin Ahy-4 [Arachis hypogaea]
6.	gi|5712199	61430	32	glycinin [Arachis hypogaea]
7.	gi|52001221	61836	30	arachin Ahy-2 [Arachis hypogaea]
8.	gi|52001219	61810	29	arachin Ahy-1 [Arachis hypogaea]
9.	gi|37789212	61803	29	storage protein [Arachis hypogaea]
10.	gi|47933675	58368	23	glycinin [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 48 **Expect:** 0.015 **Queries matched:** 8
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5974	1101.5901	1101.5930	-0.0029	507	515	1	QLKNNNPFK
1269.7736	1268.7663	1268.7452	0.0211	377	387	0	TANELNLLILR
1295.6582	1294.6509	1294.6377	0.0132	423	434	0	AHVQVVDSNGNR
1389.7239	1388.7166	1388.6935	0.0231	364	376	0	SPDIYNPQAGSLK
1448.6975	1447.6902	1447.6619	0.0283	458	469	0	SQSENFEYVAFK
2064.0437	2063.0364	2063.0376	-0.0012	510	526	1	NNNPFKFFVPPFQQSPR
2314.1755	2313.1682	2313.2018	-0.0335	401	420	0	NALFVPHYNTNAHSIIYALR
2541.2717	2540.2644	2540.2910	-0.0265	435	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1111.5662, 1145.0791, 1145.5741, 1255.7579, 1289.6870, 1296.6576, 1305.7136, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1421.7709, 1434.6984, 1436.7560, 1462.7122, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1618.8126, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2004.0181, 2020.0386, 2021.0405, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399, 2454.2397, 2530.2854, 2652.3311, 2685.3352, 3154.2932, 3820.4719

2. gi|9864777 **Mass:** 60754 **Score:** 47 **Expect:** 0.016 **Queries matched:** 8

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5974	1101.5901	1101.5930	-0.0029	507	515	1	QLKNNNPFK
1255.7579	1254.7506	1254.7295	0.0211	377	387	0	TANDLNLLILR
1295.6582	1294.6509	1294.6377	0.0132	423	434	0	AHVQVVDSNGNR
1305.7136	1304.7063	1304.6877	0.0187	516	526	0	FFVPPSQQSLR
1389.7239	1388.7166	1388.6935	0.0231	364	376	0	SPDIYNPQAGSLK
2020.0386	2019.0313	2019.0326	-0.0012	510	526	1	NNNPFKFFVPPSQQSLR
2314.1755	2313.1682	2313.2018	-0.0335	401	420	0	NALFVPHYNTNAHSIIYALR
2541.2717	2540.2644	2540.2910	-0.0265	435	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1111.5662, 1145.0791, 1145.5741, 1269.7736, 1289.6870, 1296.6576, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1421.7709, 1434.6984, 1436.7560, 1448.6975, 1462.7122, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1618.8126, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2004.0181, 2021.0405, 2064.0437, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399, 2454.2397, 2530.2854, 2652.3311, 2685.3352, 3154.2932, 3820.4719

3. gi|3703107 **Mass:** 58543 **Score:** 47 **Expect:** 0.018 **Queries matched:** 8

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5974	1101.5901	1101.5930	-0.0029	485	493	1	QLKNNNPFK
1255.7579	1254.7506	1254.7295	0.0211	355	365	0	TANDLNLLILR
1289.6870	1288.6797	1288.6564	0.0234	494	504	0	FFVPPSQQSPR
1295.6582	1294.6509	1294.6377	0.0132	401	412	0	AHVQVVDSNGNR
1389.7239	1388.7166	1388.6935	0.0231	342	354	0	SPDIYNPQAGSLK
1448.6975	1447.6902	1447.6619	0.0283	436	447	0	SQSENFEYVAFK
2004.0181	2003.0108	2003.0013	0.0096	488	504	1	NNNPFKFFVPPSQQSPR
2541.2717	2540.2644	2540.2910	-0.0265	413	435	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1111.5662, 1145.0791, 1145.5741, 1269.7736, 1296.6576, 1305.7136, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1421.7709, 1434.6984, 1436.7560, 1462.7122, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1618.8126, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2020.0386, 2021.0405, 2064.0437, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399,

2314.1755, 2454.2397, 2530.2854, 2652.3311, 2685.3352, 3154.2932, 3820.4719

4. gi|57669861 **Mass:** 61041 **Score:** 40 **Expect:** 0.096 **Queries matched:** 7

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7579	1254.7506	1254.7295	0.0211	378	388	0	TANDLNLLILR
1289.6870	1288.6797	1288.6564	0.0234	518	528	0	FFVPPSQQSPR
1295.6582	1294.6509	1294.6377	0.0132	424	435	0	AHVQVVDSNGNR
1389.7239	1388.7166	1388.6935	0.0231	365	377	0	SPDIYNPQAGSLK
2004.0181	2003.0108	2003.0013	0.0096	512	528	1	NNNPFKFFVPPSQQSPR
2314.1755	2313.1682	2313.2018	-0.0335	402	421	0	NALFVPHYNTNAHSIIYALR
2541.2717	2540.2644	2540.2910	-0.0265	436	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1102.5974, 1111.5662, 1145.0791, 1145.5741, 1269.7736, 1296.6576, 1305.7136, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1421.7709, 1434.6984, 1436.7560, 1448.6975, 1462.7122, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1618.8126, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2020.0386, 2021.0405, 2064.0437, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399, 2454.2397, 2530.2854, 2652.3311, 2685.3352, 3154.2932, 3820.4719

5. gi|108595573 **Mass:** 61041 **Score:** 40 **Expect:** 0.096 **Queries matched:** 7

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7579	1254.7506	1254.7295	0.0211	378	388	0	TANDLNLLILR
1289.6870	1288.6797	1288.6564	0.0234	518	528	0	FFVPPSQQSPR
1295.6582	1294.6509	1294.6377	0.0132	424	435	0	AHVQVVDSNGNR
1389.7239	1388.7166	1388.6935	0.0231	365	377	0	SPDIYNPQAGSLK
2004.0181	2003.0108	2003.0013	0.0096	512	528	1	NNNPFKFFVPPSQQSPR
2314.1755	2313.1682	2313.2018	-0.0335	402	421	0	NALFVPHYNTNAHSIIYALR
2541.2717	2540.2644	2540.2910	-0.0265	436	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1102.5974, 1111.5662, 1145.0791, 1145.5741, 1269.7736, 1296.6576, 1305.7136, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1421.7709, 1434.6984, 1436.7560, 1448.6975, 1462.7122, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1618.8126, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2020.0386, 2021.0405, 2064.0437, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399, 2454.2397, 2530.2854, 2652.3311, 2685.3352, 3154.2932, 3820.4719

6. gi|5712199 **Mass:** 61430 **Score:** 32 **Expect:** 0.59 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1102.5974	1101.5901	1101.5930	-0.0029	508 - 516	1	QLKNNNPFK
1295.6582	1294.6509	1294.6377	0.0132	424 - 435	0	AHVQVVDSNGNR
1448.6975	1447.6902	1447.6619	0.0283	459 - 470	0	SQSENFEYVAFK
2064.0437	2063.0364	2063.0376	-0.0012	511 - 527	1	NNNPFKFFVPPFQQSPR
2314.1755	2313.1682	2313.2018	-0.0335	402 - 421	0	NALFVPHYNTNAHSIIYALR
2541.2717	2540.2644	2540.2910	-0.0265	436 - 458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1111.5662, 1145.0791, 1145.5741, 1255.7579, 1269.7736, 1289.6870, 1296.6576, 1305.7136, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1389.7239, 1421.7709, 1434.6984, 1436.7560, 1462.7122, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1618.8126, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2004.0181, 2020.0386, 2021.0405, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399, 2454.2397, 2530.2854, 2652.3311, 2685.3352, 3154.2932, 3820.4719

7. gi|52001221 **Mass:** 61836 **Score:** 30 **Expect:** 0.8 **Queries matched:** 6

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5974	1101.5901	1101.5930	-0.0029	515 - 523		1	QLKNNNPFK
1255.7579	1254.7506	1254.7295	0.0211	385 - 395		0	TANDLNLLILR
1295.6582	1294.6509	1294.6377	0.0132	431 - 442		0	AHVQVVDSNGNR
1389.7239	1388.7166	1388.6935	0.0231	372 - 384		0	SPDIYNPQAGSLK
2314.1755	2313.1682	2313.2018	-0.0335	409 - 428		0	NALFVPHYNTNAHSIIYALR
2541.2717	2540.2644	2540.2910	-0.0265	443 - 465		0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1111.5662, 1145.0791, 1145.5741, 1269.7736, 1289.6870, 1296.6576, 1305.7136, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1421.7709, 1434.6984, 1436.7560, 1448.6975, 1462.7122, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1618.8126, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2004.0181, 2020.0386, 2021.0405, 2064.0437, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399, 2454.2397, 2530.2854, 2652.3311, 2685.3352, 3154.2932, 3820.4719

8. gi|52001219 **Mass:** 61810 **Score:** 29 **Expect:** 1.1 **Queries matched:** 6

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5974	1101.5901	1101.5930	-0.0029	514 - 522		1	QLKNNNPFK
1269.7736	1268.7663	1268.7452	0.0211	384 - 394		0	TANELNLLILR
1389.7239	1388.7166	1388.6935	0.0231	371 - 383		0	SPDIYNPQAGSLK
1448.6975	1447.6902	1447.6619	0.0283	465 - 476		0	SQSENFEYVAFK
2021.0405	2020.0332	2020.0166	0.0167	517 - 533		1	NNNPFKFFVPPSEQSLR
2314.1755	2313.1682	2313.2018	-0.0335	408 - 427		0	NALFVPHYNTNAHSIIYALR

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1111.5662,

1145.0791, 1145.5741, 1255.7579, 1289.6870, 1295.6582, 1296.6576, 1305.7136, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1421.7709, 1434.6984, 1436.7560, 1462.7122, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1618.8126, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2004.0181, 2020.0386, 2064.0437, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399, 2454.2397, 2530.2854, 2541.2717, 2652.3311, 2685.3352, 3154.2932, 3820.4719

9. gi|37789212 **Mass:** 61803 **Score:** 29 **Expect:** 1.1 **Queries matched:** 6

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5974	1101.5901	1101.5930	-0.0029	514	522	1	QLKNNNPFK
1269.7736	1268.7663	1268.7452	0.0211	384	394	0	TANELNLLILR
1389.7239	1388.7166	1388.6935	0.0231	371	383	0	SPDIYNPQAGSLK
1448.6975	1447.6902	1447.6619	0.0283	465	476	0	SQSENFEYVAFK
2021.0405	2020.0332	2020.0166	0.0167	517	533	1	NNNPFKFFVPPSEQSLR
2314.1755	2313.1682	2313.2018	-0.0335	408	427	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1111.5662, 1145.0791, 1145.5741, 1255.7579, 1289.6870, 1295.6582, 1296.6576, 1305.7136, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1421.7709, 1434.6984, 1436.7560, 1462.7122, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1618.8126, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2004.0181, 2020.0386, 2064.0437, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399, 2454.2397, 2530.2854, 2541.2717, 2652.3311, 2685.3352, 3154.2932, 3820.4719

10. gi|47933675 **Mass:** 58368 **Score:** 23 **Expect:** 4.4 **Queries matched:** 5

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5974	1101.5901	1101.5930	-0.0029	487	495	1	QLKNNNPFK
1295.6582	1294.6509	1294.6377	0.0132	403	414	0	AHVQVVDSNGNR
1462.7122	1461.7049	1461.6775	0.0274	438	449	0	AQSENYEYLAFK
1618.8126	1617.8053	1617.7746	0.0307	342	356	0	SSNPDIYNPQAGSLR
2454.2397	2453.2324	2453.2637	-0.0313	381	402	0	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1111.5662, 1145.0791, 1145.5741, 1255.7579, 1269.7736, 1289.6870, 1296.6576, 1305.7136, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1389.7239, 1421.7709, 1434.6984, 1436.7560, 1448.6975, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2004.0181, 2020.0386, 2021.0405, 2064.0437, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399, 2314.1755, 2530.2854, 2541.2717, 2652.3311, 2685.3352, 3154.2932, 3820.4719

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)

Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 58

Protein View

Match to: **gi|118776570** Score: **48** Expect: **0.015**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **58**
Number of mass values matched: **8**
Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

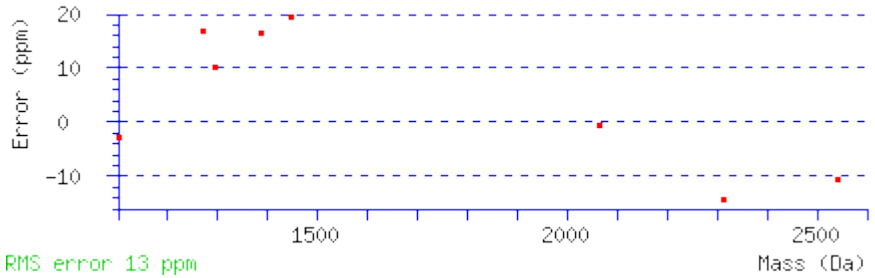
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     1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
    51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
   101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
   151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
   201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
   251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
   301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
   351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
   401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
   451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
   501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
364 - 376	1389.7239	1388.7166	1388.6935	0.0231	0	SPDIYNPQAGSLK
377 - 387	1269.7736	1268.7663	1268.7452	0.0211	0	TANELNLLILR
401 - 420	2314.1755	2313.1682	2313.2018	-0.0335	0	NALFVPHYNTNAHSIIYALR

423 - 434	1295.6582	1294.6509	1294.6377	0.0132	0	AHVQVVDSNGNR
435 - 457	2541.2717	2540.2644	2540.2910	-0.0265	0	VYDEELQEGHVLVVPQNFAVAGK
458 - 469	1448.6975	1447.6902	1447.6619	0.0283	0	SQSENFEYVAFK
507 - 515	1102.5974	1101.5901	1101.5930	-0.0029	1	QLKNNNPFK
510 - 526	2064.0437	2063.0364	2063.0376	-0.0012	1	NNNPFKFFVPPFQQSPR

No match to: 805.3774, 835.4649, 855.0188, 861.0392, 877.0193, 906.4772, 1046.5931, 1066.0718, 1080.5282, 1111.5662, 1145.0791, 1145.5741, 1255.7579, 1289.6870, 1296.6576, 1305.7136, 1306.7104, 1349.7284, 1360.7247, 1365.7220, 1376.7556, 1377.7515, 1421.7709, 1434.6984, 1436.7560, 1462.7122, 1523.7589, 1541.8062, 1557.8075, 1573.7985, 1618.8126, 1652.7816, 1659.8795, 1774.8867, 1862.0009, 2004.0181, 2020.0386, 2021.0405, 2080.0376, 2091.0632, 2092.0627, 2185.0251, 2273.1487, 2312.1399, 2454.2397, 2530.2854, 2652.3311, 2685.3352, 3154.2932, 3820.4719



Spot 31

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 09:58:57 GMT**
Top Score : **73 for gi|9864777, Gly1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|9864777	60754	73	Gly1 [Arachis hypogaea]
2.	gi|118776570	60681	68	arachin 6 [Arachis hypogaea]
3.	gi|3703107	58543	58	glycinin [Arachis hypogaea]
4.	gi|57669861	61041	50	arachin Ahy-4 [Arachis hypogaea]
5.	gi|108595573	61041	50	arachin Ahy-4 [Arachis hypogaea]
6.	gi|5712199	61430	40	glycinin [Arachis hypogaea]
7.	gi|52001221	61836	40	arachin Ahy-2 [Arachis hypogaea]
8.	gi|52001219	61810	37	arachin Ahy-1 [Arachis hypogaea]
9.	gi|37789212	61803	37	storage protein [Arachis hypogaea]
10.	gi|21314465	62042	29	allergen Arah3/Arah4 [Arachis hypogaea]

Results List

1. gi|9864777 **Mass:** 60754 **Score:** 73 **Expect:** 4.9e-005 **Queries matched:** 10
Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5983	1101.5910	1101.5930	-0.0020	507	515	1	QLKNNNPFK
1255.7587	1254.7514	1254.7295	0.0219	377	387	0	TANDLNLLILR
1295.6567	1294.6494	1294.6377	0.0117	423	434	0	AHVQVVDSNGNR
1305.7133	1304.7060	1304.6877	0.0184	516	526	0	FFVPPSQQSLR
1389.7252	1388.7179	1388.6935	0.0244	364	376	0	SPDIYNPQAGSLK
1659.8752	1658.8679	1658.8376	0.0304	362	376	1	NRSPDIYNPQAGSLK
2020.0286	2019.0213	2019.0326	-0.0112	510	526	1	NNNPFKFFVPPSQQSLR
2314.1658	2313.1585	2313.2018	-0.0432	401	420	0	NALFVPHYNTNAHSIIYALR
2541.2676	2540.2603	2540.2910	-0.0306	435	457	0	VYDEELQEGHVLVVPQNFAVAGK

3302.4380	3301.4307	3301.4798	-0.0491	250 - 279	0	AGQEEENEGGNIFSGFTPEFLAQAFQVDDR

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1111.5631, 1145.5807, 1175.5731, 1269.7749, 1289.6840, 1296.6511, 1306.7115, 1349.7262, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1420.7711, 1434.7007, 1436.7617, 1448.6957, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010, 1618.8129, 1637.7897, 1652.7880, 1876.0009, 2003.9983, 2064.0293, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2531.3118, 3155.2737, 3820.3909

2. gi|118776570 **Mass:** 60681 **Score:** 68 **Expect:** 0.00015 **Queries matched:** 10

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5983	1101.5910	1101.5930	-0.0020	507 -	515	1	QLKNNNPFK
1269.7749	1268.7676	1268.7452	0.0224	377 -	387	0	TANELNLLILR
1295.6567	1294.6494	1294.6377	0.0117	423 -	434	0	AHVQVVDSNGNR
1349.7262	1348.7189	1348.6927	0.0262	516 -	526	0	FFVPPFQQSPR
1389.7252	1388.7179	1388.6935	0.0244	364 -	376	0	SPDIYNPQAGSLK
1448.6957	1447.6884	1447.6619	0.0265	458 -	469	0	SQSENFEYVAFK
1659.8752	1658.8679	1658.8376	0.0304	362 -	376	1	NRSPDIYNPQAGSLK
2064.0293	2063.0220	2063.0376	-0.0156	510 -	526	1	NNNPFKFFVPPFQQSPR
2314.1658	2313.1585	2313.2018	-0.0432	401 -	420	0	NALFVPHYNTNAHSIIYALR
2541.2676	2540.2603	2540.2910	-0.0306	435 -	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1111.5631, 1145.5807, 1175.5731, 1255.7587, 1289.6840, 1296.6511, 1305.7133, 1306.7115, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1420.7711, 1434.7007, 1436.7617, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010, 1618.8129, 1637.7897, 1652.7880, 1876.0009, 2003.9983, 2020.0286, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2531.3118, 3155.2737, 3302.4380, 3820.3909

3. gi|3703107 **Mass:** 58543 **Score:** 58 **Expect:** 0.0014 **Queries matched:** 9

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5983	1101.5910	1101.5930	-0.0020	485 -	493	1	QLKNNNPFK
1255.7587	1254.7514	1254.7295	0.0219	355 -	365	0	TANDLNLLILR
1289.6840	1288.6767	1288.6564	0.0204	494 -	504	0	FFVPPSQQSPR
1295.6567	1294.6494	1294.6377	0.0117	401 -	412	0	AHVQVVDSNGNR
1389.7252	1388.7179	1388.6935	0.0244	342 -	354	0	SPDIYNPQAGSLK
1448.6957	1447.6884	1447.6619	0.0265	436 -	447	0	SQSENFEYVAFK
1659.8752	1658.8679	1658.8376	0.0304	340 -	354	1	NRSPDIYNPQAGSLK
2003.9983	2002.9910	2003.0013	-0.0102	488 -	504	1	NNNPFKFFVPPSQQSPR
2541.2676	2540.2603	2540.2910	-0.0306	413 -	435	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1111.5631, 1145.5807, 1175.5731, 1269.7749, 1296.6511, 1305.7133, 1306.7115, 1349.7262, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1420.7711, 1434.7007, 1436.7617, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010, 1618.8129, 1637.7897, 1652.7880, 1876.0009, 2020.0286, 2064.0293, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2314.1658, 2531.3118, 3155.2737, 3302.4380, 3820.3909

4. gi|57669861 **Mass:** 61041 **Score:** 50 **Expect:** 0.0096 **Queries matched:** 8

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1255.7587	1254.7514	1254.7295	0.0219	378	-	388	0	TANDLNLLILR
1289.6840	1288.6767	1288.6564	0.0204	518	-	528	0	FFVPPSQQSPR
1295.6567	1294.6494	1294.6377	0.0117	424	-	435	0	AHVQVVDSNGNR
1389.7252	1388.7179	1388.6935	0.0244	365	-	377	0	SPDIYNPQAGSLK
1659.8752	1658.8679	1658.8376	0.0304	363	-	377	1	NRSPDIYNPQAGSLK
2003.9983	2002.9910	2003.0013	-0.0102	512	-	528	1	NNNPFKFFVPPSQQSPR
2314.1658	2313.1585	2313.2018	-0.0432	402	-	421	0	NALFVPHYNTNAHSIIYALR
2541.2676	2540.2603	2540.2910	-0.0306	436	-	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1102.5983, 1111.5631, 1145.5807, 1175.5731, 1269.7749, 1296.6511, 1305.7133, 1306.7115, 1349.7262, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1420.7711, 1434.7007, 1436.7617, 1448.6957, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010, 1618.8129, 1637.7897, 1652.7880, 1876.0009, 2020.0286, 2064.0293, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2531.3118, 3155.2737, 3302.4380, 3820.3909

5. gi|108595573 **Mass:** 61041 **Score:** 50 **Expect:** 0.0096 **Queries matched:** 8

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1255.7587	1254.7514	1254.7295	0.0219	378	-	388	0	TANDLNLLILR
1289.6840	1288.6767	1288.6564	0.0204	518	-	528	0	FFVPPSQQSPR
1295.6567	1294.6494	1294.6377	0.0117	424	-	435	0	AHVQVVDSNGNR
1389.7252	1388.7179	1388.6935	0.0244	365	-	377	0	SPDIYNPQAGSLK
1659.8752	1658.8679	1658.8376	0.0304	363	-	377	1	NRSPDIYNPQAGSLK
2003.9983	2002.9910	2003.0013	-0.0102	512	-	528	1	NNNPFKFFVPPSQQSPR
2314.1658	2313.1585	2313.2018	-0.0432	402	-	421	0	NALFVPHYNTNAHSIIYALR
2541.2676	2540.2603	2540.2910	-0.0306	436	-	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1102.5983, 1111.5631, 1145.5807, 1175.5731, 1269.7749, 1296.6511, 1305.7133, 1306.7115, 1349.7262, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1420.7711, 1434.7007, 1436.7617, 1448.6957, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010,

1618.8129, 1637.7897, 1652.7880, 1876.0009, 2020.0286, 2064.0293, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2531.3118, 3155.2737, 3302.4380, 3820.3909

6. gi|5712199 **Mass:** 61430 **Score:** 40 **Expect:** 0.086 **Queries matched:** 7

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5983	1101.5910	1101.5930	-0.0020	508	516	1	QLKNNNPFK
1295.6567	1294.6494	1294.6377	0.0117	424	435	0	AHVQVVDSNGNR
1349.7262	1348.7189	1348.6927	0.0262	517	527	0	FFVPPFQQSPR
1448.6957	1447.6884	1447.6619	0.0265	459	470	0	SQSENFEYVAFK
2064.0293	2063.0220	2063.0376	-0.0156	511	527	1	NNNPFKFFVPPFQQSPR
2314.1658	2313.1585	2313.2018	-0.0432	402	421	0	NALFVPHYNTNAHSIIYALR
2541.2676	2540.2603	2540.2910	-0.0306	436	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1111.5631, 1145.5807, 1175.5731, 1255.7587, 1269.7749, 1289.6840, 1296.6511, 1305.7133, 1306.7115, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1389.7252, 1420.7711, 1434.7007, 1436.7617, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010, 1618.8129, 1637.7897, 1652.7880, 1659.8752, 1876.0009, 2003.9983, 2020.0286, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2531.3118, 3155.2737, 3302.4380, 3820.3909

7. gi|52001221 **Mass:** 61836 **Score:** 40 **Expect:** 0.096 **Queries matched:** 7

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5983	1101.5910	1101.5930	-0.0020	515	523	1	QLKNNNPFK
1255.7587	1254.7514	1254.7295	0.0219	385	395	0	TANDLNLLILR
1295.6567	1294.6494	1294.6377	0.0117	431	442	0	AHVQVVDSNGNR
1389.7252	1388.7179	1388.6935	0.0244	372	384	0	SPDIYNPQAGSLK
1659.8752	1658.8679	1658.8376	0.0304	370	384	1	NRSPDIYNPQAGSLK
2314.1658	2313.1585	2313.2018	-0.0432	409	428	0	NALFVPHYNTNAHSIIYALR
2541.2676	2540.2603	2540.2910	-0.0306	443	465	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1111.5631, 1145.5807, 1175.5731, 1269.7749, 1289.6840, 1296.6511, 1305.7133, 1306.7115, 1349.7262, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1420.7711, 1434.7007, 1436.7617, 1448.6957, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010, 1618.8129, 1637.7897, 1652.7880, 1876.0009, 2003.9983, 2020.0286, 2064.0293, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2531.3118, 3155.2737, 3302.4380, 3820.3909

8. gi|52001219 **Mass:** 61810 **Score:** 37 **Expect:** 0.17 **Queries matched:** 7

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1102.5983	1101.5910	1101.5930	-0.0020	514	-	522	1	QLKNNNPFK
1269.7749	1268.7676	1268.7452	0.0224	384	-	394	0	TANELNLLILR
1296.6511	1295.6438	1295.6218	0.0221	430	-	441	0	AHVQVVDSNGDR
1389.7252	1388.7179	1388.6935	0.0244	371	-	383	0	SPDIYNPQAGSLK
1448.6957	1447.6884	1447.6619	0.0265	465	-	476	0	SQSENFEYVAFK
1659.8752	1658.8679	1658.8376	0.0304	369	-	383	1	NRSPDIYNPQAGSLK
2314.1658	2313.1585	2313.2018	-0.0432	408	-	427	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1111.5631, 1145.5807, 1175.5731, 1255.7587, 1289.6840, 1295.6567, 1305.7133, 1306.7115, 1349.7262, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1420.7711, 1434.7007, 1436.7617, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010, 1618.8129, 1637.7897, 1652.7880, 1876.0009, 2003.9983, 2020.0286, 2064.0293, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2531.3118, 2541.2676, 3155.2737, 3302.4380, 3820.3909

9. gi|37789212 **Mass:** 61803 **Score:** 37 **Expect:** 0.17 **Queries matched:** 7

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1102.5983	1101.5910	1101.5930	-0.0020	514	-	522	1	QLKNNNPFK
1269.7749	1268.7676	1268.7452	0.0224	384	-	394	0	TANELNLLILR
1296.6511	1295.6438	1295.6218	0.0221	430	-	441	0	AHVQVVDSNGDR
1389.7252	1388.7179	1388.6935	0.0244	371	-	383	0	SPDIYNPQAGSLK
1448.6957	1447.6884	1447.6619	0.0265	465	-	476	0	SQSENFEYVAFK
1659.8752	1658.8679	1658.8376	0.0304	369	-	383	1	NRSPDIYNPQAGSLK
2314.1658	2313.1585	2313.2018	-0.0432	408	-	427	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1111.5631, 1145.5807, 1175.5731, 1255.7587, 1289.6840, 1295.6567, 1305.7133, 1306.7115, 1349.7262, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1420.7711, 1434.7007, 1436.7617, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010, 1618.8129, 1637.7897, 1652.7880, 1876.0009, 2003.9983, 2020.0286, 2064.0293, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2531.3118, 2541.2676, 3155.2737, 3302.4380, 3820.3909

10. gi|21314465 **Mass:** 62042 **Score:** 29 **Expect:** 1 **Queries matched:** 6

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1102.5983	1101.5910	1101.5930	-0.0020	516	-	524	1	QLKNNNPFK
1296.6511	1295.6438	1295.6218	0.0221	432	-	443	0	AHVQVVDSNGDR
1389.7252	1388.7179	1388.6935	0.0244	371	-	383	0	SPDIYNPQAGSLK
1448.6957	1447.6884	1447.6619	0.0265	467	-	478	0	SQSENFEYVAFK
1659.8752	1658.8679	1658.8376	0.0304	369	-	383	1	NRSPDIYNPQAGSLK

2314.1658 2313.1585 2313.2018 -0.0432 410 - 429 0 NALFVPHYNTNAHSIIYALR

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1111.5631, 1145.5807, 1175.5731, 1255.7587, 1269.7749, 1289.6840, 1295.6567, 1305.7133, 1306.7115, 1349.7262, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1420.7711, 1434.7007, 1436.7617, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010, 1618.8129, 1637.7897, 1652.7880, 1876.0009, 2003.9983, 2020.0286, 2064.0293, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2531.3118, 2541.2676, 3155.2737, 3302.4380, 3820.3909

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 56

Protein View

Match to: **gi|9864777** Score: **73** Expect: **4.9e-005**
Gly1 [Arachis hypogaea]

Nominal mass (M_r): **60754**; Calculated pI value: **5.48**
NCBI BLAST search of gi|9864777 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **56**
Number of mass values matched: **10**
Sequence Coverage: **24%**

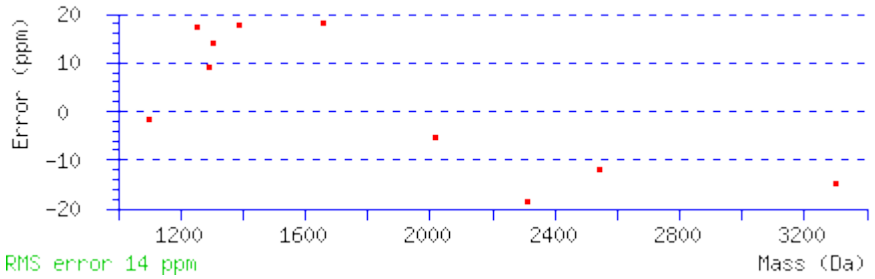
Matched peptides shown in **Bold Red**

```
   1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE
  51 GGYIETWNPN NQEFECAGVA LSRLVLRRNA LRRPFYSNAP QEIFIQQGRG
 101 YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR
 151 RFDEGDLIAV PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
 201 AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP RGQHSRRERA
 251 GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV
 301 KGGLRILSPD RKRGADEEEE YDEDEYEYDE EDRRRGRGSR GRGNGIEETI
 351 CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR
 401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
 451 NFAVAGKSQS DNFEYVAFKT DSRPNIANFA GENSIIDNLP EEVVANSYGL
 501 PREQARQLKN NNPFKFFVPP SQQSLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
250 - 279	3302.4380	3301.4307	3301.4798	-0.0491	0	AGQEEENEGGNIFSGFTPEFLAQAFQVDDR
362 - 376	1659.8752	1658.8679	1658.8376	0.0304	1	NRSPDIYNPQAGSLK
364 - 376	1389.7252	1388.7179	1388.6935	0.0244	0	SPDIYNPQAGSLK
377 - 387	1255.7587	1254.7514	1254.7295	0.0219	0	TANDLNLLILR
401 - 420	2314.1658	2313.1585	2313.2018	-0.0432	0	NALFVPHYNTNAHSIIYALR
423 - 434	1295.6567	1294.6494	1294.6377	0.0117	0	AHVQVVDSNGNR
435 - 457	2541.2676	2540.2603	2540.2910	-0.0306	0	VYDEELQEGHVLVVPQNFAVAGK
507 - 515	1102.5983	1101.5910	1101.5930	-0.0020	1	QLKNNNPFK
510 - 526	2020.0286	2019.0213	2019.0326	-0.0112	1	NNNPFKFFVPPSQQSLR
516 - 526	1305.7133	1304.7060	1304.6877	0.0184	0	FFVPPSQQSLR

No match to: 805.3788, 835.4684, 845.0682, 855.0266, 861.0447, 877.0233, 906.4748, 1046.5978, 1066.0748, 1080.5333, 1111.5631, 1145.5807, 1175.5731, 1269.7749, 1289.6840, 1296.6511, 1306.7115, 1349.7262, 1360.7295, 1365.7227, 1376.7556, 1377.7515, 1420.7711, 1434.7007, 1436.7617, 1448.6957, 1497.7532, 1524.7737, 1541.8064, 1557.8066, 1573.8010, 1618.8129, 1637.7897, 1652.7880, 1876.0009, 2003.9983, 2064.0293, 2091.0669, 2092.0642, 2185.0188, 2273.1492, 2295.1350, 2311.1208, 2531.3118, 3155.2737, 3820.3909



Spot 32

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:32:32 GMT**
Top Score : **51 for gi|118776570, arachin 6 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	51	arachin 6 [Arachis hypogaea]
2.	gi|52001219	61810	48	arachin Ahy-1 [Arachis hypogaea]
3.	gi|37789212	61803	48	storage protein [Arachis hypogaea]
4.	gi|57669861	61041	42	arachin Ahy-4 [Arachis hypogaea]
5.	gi|108595573	61041	42	arachin Ahy-4 [Arachis hypogaea]
6.	gi|21314465	62042	40	allergen Arah3/Arah4 [Arachis hypogaea]
7.	gi|9864777	60754	35	Gly1 [Arachis hypogaea]
8.	gi|5712199	61430	28	glycinin [Arachis hypogaea]
9.	gi|52001221	61836	28	arachin Ahy-2 [Arachis hypogaea]
10.	gi|3703107	58543	27	glycinin [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 51 **Expect:** 0.0071 **Queries matched:** 9
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1269.7527	1268.7454	1268.7452	0.0002	377	387	0	TANELNLLILR
1349.6990	1348.6917	1348.6927	-0.0010	516	526	0	FFVPPFQQSPR
1389.6942	1388.6869	1388.6935	-0.0066	364	376	0	SPDIYNPQAGSLK
1448.6555	1447.6482	1447.6619	-0.0137	458	469	0	SQSENFEYVAFK
1541.7686	1540.7613	1540.7673	-0.0060	388	400	0	WLGLSAEYGNLYR
1659.8676	1658.8603	1658.8376	0.0228	362	376	1	NRSPDIYNPQAGSLK
2064.0518	2063.0445	2063.0376	0.0069	510	526	1	NNNPFKFFVPPFQQSPR
2314.1758	2313.1685	2313.2018	-0.0332	401	420	0	NALFVPHYNTNAHSIIYALR
2541.3064	2540.2991	2540.2910	0.0082	435	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1255.7407, 1277.1042, 1289.6564, 1296.6444, 1305.6823, 1306.6963, 1365.6860, 1376.7327, 1435.6946, 1462.6788, 1529.7107, 1606.7324, 1618.7794, 1652.7349, 1756.8269, 1774.8324, 1934.8956, 2020.9919, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2315.1992, 2333.1455, 2351.1094, 2354.1138, 2514.3223, 2530.3555, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930

2. gi|52001219 **Mass:** 61810 **Score:** 48 **Expect:** 0.014 **Queries matched:** 9

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1269.7527	1268.7454	1268.7452	0.0002	384	394	0	TANELNLLILR
1296.6444	1295.6371	1295.6218	0.0154	430	441	0	AHVQVVDSNGDR
1306.6963	1305.6890	1305.6717	0.0173	523	533	0	FFVPPSEQSLR
1389.6942	1388.6869	1388.6935	-0.0066	371	383	0	SPDIYNPQAGSLK
1448.6555	1447.6482	1447.6619	-0.0137	465	476	0	SQSENFEYVAFK
1541.7686	1540.7613	1540.7673	-0.0060	395	407	0	WLGLSAEYGNLYR
1659.8676	1658.8603	1658.8376	0.0228	369	383	1	NRSPDIYNPQAGSLK
2020.9919	2019.9846	2020.0166	-0.0319	517	533	1	NNNPFKFFVPPSEQSLR
2314.1758	2313.1685	2313.2018	-0.0332	408	427	0	NALFVPHYNTNAHSIIYALR

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1255.7407, 1277.1042, 1289.6564, 1305.6823, 1349.6990, 1365.6860, 1376.7327, 1435.6946, 1462.6788, 1529.7107, 1606.7324, 1618.7794, 1652.7349, 1756.8269, 1774.8324, 1934.8956, 2064.0518, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2315.1992, 2333.1455, 2351.1094, 2354.1138, 2514.3223, 2530.3555, 2541.3064, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930

3. gi|37789212 **Mass:** 61803 **Score:** 48 **Expect:** 0.014 **Queries matched:** 9

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1269.7527	1268.7454	1268.7452	0.0002	384	394	0	TANELNLLILR
1296.6444	1295.6371	1295.6218	0.0154	430	441	0	AHVQVVDSNGDR
1306.6963	1305.6890	1305.6717	0.0173	523	533	0	FFVPPSEQSLR
1389.6942	1388.6869	1388.6935	-0.0066	371	383	0	SPDIYNPQAGSLK
1448.6555	1447.6482	1447.6619	-0.0137	465	476	0	SQSENFEYVAFK
1541.7686	1540.7613	1540.7673	-0.0060	395	407	0	WLGLSAEYGNLYR
1659.8676	1658.8603	1658.8376	0.0228	369	383	1	NRSPDIYNPQAGSLK
2020.9919	2019.9846	2020.0166	-0.0319	517	533	1	NNNPFKFFVPPSEQSLR
2314.1758	2313.1685	2313.2018	-0.0332	408	427	0	NALFVPHYNTNAHSIIYALR

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1255.7407, 1277.1042, 1289.6564, 1305.6823, 1349.6990, 1365.6860, 1376.7327, 1435.6946, 1462.6788, 1529.7107, 1606.7324, 1618.7794, 1652.7349, 1756.8269, 1774.8324, 1934.8956, 2064.0518, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2315.1992, 2333.1455, 2351.1094, 2354.1138,

2514.3223, 2530.3555, 2541.3064, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930

4. gi|57669861 **Mass:** 61041 **Score:** 42 **Expect:** 0.05 **Queries matched:** 8

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7407	1254.7334	1254.7295	0.0039	378	388	0	TANDLNLLILR
1289.6564	1288.6491	1288.6564	-0.0072	518	528	0	FFVPPSQQSPR
1389.6942	1388.6869	1388.6935	-0.0066	365	377	0	SPDIYNPQAGSLK
1541.7686	1540.7613	1540.7673	-0.0060	389	401	0	WLGLSAEYGNLYR
1618.7794	1617.7721	1617.7481	0.0240	288	302	0	GENESEEEGAIVTVR
1659.8676	1658.8603	1658.8376	0.0228	363	377	1	NRSPDIYNPQAGSLK
2314.1758	2313.1685	2313.2018	-0.0332	402	421	0	NALFVPHYNTNAHSIIYALR
2541.3064	2540.2991	2540.2910	0.0082	436	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1269.7527, 1277.1042, 1296.6444, 1305.6823, 1306.6963, 1349.6990, 1365.6860, 1376.7327, 1435.6946, 1448.6555, 1462.6788, 1529.7107, 1606.7324, 1652.7349, 1756.8269, 1774.8324, 1934.8956, 2020.9919, 2064.0518, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2315.1992, 2333.1455, 2351.1094, 2354.1138, 2514.3223, 2530.3555, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930

5. gi|108595573 **Mass:** 61041 **Score:** 42 **Expect:** 0.05 **Queries matched:** 8

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7407	1254.7334	1254.7295	0.0039	378	388	0	TANDLNLLILR
1289.6564	1288.6491	1288.6564	-0.0072	518	528	0	FFVPPSQQSPR
1389.6942	1388.6869	1388.6935	-0.0066	365	377	0	SPDIYNPQAGSLK
1541.7686	1540.7613	1540.7673	-0.0060	389	401	0	WLGLSAEYGNLYR
1618.7794	1617.7721	1617.7481	0.0240	288	302	0	GENESEEEGAIVTVR
1659.8676	1658.8603	1658.8376	0.0228	363	377	1	NRSPDIYNPQAGSLK
2314.1758	2313.1685	2313.2018	-0.0332	402	421	0	NALFVPHYNTNAHSIIYALR
2541.3064	2540.2991	2540.2910	0.0082	436	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1269.7527, 1277.1042, 1296.6444, 1305.6823, 1306.6963, 1349.6990, 1365.6860, 1376.7327, 1435.6946, 1448.6555, 1462.6788, 1529.7107, 1606.7324, 1652.7349, 1756.8269, 1774.8324, 1934.8956, 2020.9919, 2064.0518, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2315.1992, 2333.1455, 2351.1094, 2354.1138, 2514.3223, 2530.3555, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930

6. gi|21314465 **Mass:** 62042 **Score:** 40 **Expect:** 0.087 **Queries matched:** 8

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1296.6444	1295.6371	1295.6218	0.0154	432 -	443	0	AHVQVVDSNGDR
1306.6963	1305.6890	1305.6717	0.0173	525 -	535	0	FFVPPSEQSLR
1389.6942	1388.6869	1388.6935	-0.0066	371 -	383	0	SPDIYNPQAGSLK
1448.6555	1447.6482	1447.6619	-0.0137	467 -	478	0	SQSENFEYVAFK
1541.7686	1540.7613	1540.7673	-0.0060	397 -	409	0	WLGLSAEYGNLYR
1659.8676	1658.8603	1658.8376	0.0228	369 -	383	1	NRSPDIYNPQAGSLK
2020.9919	2019.9846	2020.0166	-0.0319	519 -	535	1	NNNPFKFFVPPSEQSLR
2314.1758	2313.1685	2313.2018	-0.0332	410 -	429	0	NALFVPHYNTNAHSIIYALR

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1255.7407, 1269.7527, 1277.1042, 1289.6564, 1305.6823, 1349.6990, 1365.6860, 1376.7327, 1435.6946, 1462.6788, 1529.7107, 1606.7324, 1618.7794, 1652.7349, 1756.8269, 1774.8324, 1934.8956, 2064.0518, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2315.1992, 2333.1455, 2351.1094, 2354.1138, 2514.3223, 2530.3555, 2541.3064, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930

7. gi|9864777 **Mass:** 60754 **Score:** 35 **Expect:** 0.31 **Queries matched:** 7

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7407	1254.7334	1254.7295	0.0039	377 -	387	0	TANDLNLLILR
1305.6823	1304.6750	1304.6877	-0.0126	516 -	526	0	FFVPPSQQSLR
1389.6942	1388.6869	1388.6935	-0.0066	364 -	376	0	SPDIYNPQAGSLK
1541.7686	1540.7613	1540.7673	-0.0060	388 -	400	0	WLGLSAEYGNLYR
1659.8676	1658.8603	1658.8376	0.0228	362 -	376	1	NRSPDIYNPQAGSLK
2314.1758	2313.1685	2313.2018	-0.0332	401 -	420	0	NALFVPHYNTNAHSIIYALR
2541.3064	2540.2991	2540.2910	0.0082	435 -	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1269.7527, 1277.1042, 1289.6564, 1296.6444, 1306.6963, 1349.6990, 1365.6860, 1376.7327, 1435.6946, 1448.6555, 1462.6788, 1529.7107, 1606.7324, 1618.7794, 1652.7349, 1756.8269, 1774.8324, 1934.8956, 2020.9919, 2064.0518, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2315.1992, 2333.1455, 2351.1094, 2354.1138, 2514.3223, 2530.3555, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930

8. gi|5712199 **Mass:** 61430 **Score:** 28 **Expect:** 1.3 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1349.6990	1348.6917	1348.6927	-0.0010	517 -	527	0	FFVPPFQQSPR
1448.6555	1447.6482	1447.6619	-0.0137	459 -	470	0	SQSENFEYVAFK
1541.7686	1540.7613	1540.7673	-0.0060	389 -	401	0	WLGLSAEYGNLYR
2064.0518	2063.0445	2063.0376	0.0069	511 -	527	1	NNNPFKFFVPPFQQSPR

2314.1758	2313.1685	2313.2018	-0.0332	402 - 421	0	NALFVPHYNTNAHSIIYALR
2541.3064	2540.2991	2540.2910	0.0082	436 - 458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1255.7407, 1269.7527, 1277.1042, 1289.6564, 1296.6444, 1305.6823, 1306.6963, 1365.6860, 1376.7327, 1389.6942, 1435.6946, 1462.6788, 1529.7107, 1606.7324, 1618.7794, 1652.7349, 1659.8676, 1756.8269, 1774.8324, 1934.8956, 2020.9919, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2315.1992, 2333.1455, 2351.1094, 2354.1138, 2514.3223, 2530.3555, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930

9. gi|52001221 **Mass:** 61836 **Score:** 28 **Expect:** 1.5 **Queries matched:** 6

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7407	1254.7334	1254.7295	0.0039	385 - 395		0	TANDLNLLILR
1389.6942	1388.6869	1388.6935	-0.0066	372 - 384		0	SPDIYNPQAGSLK
1541.7686	1540.7613	1540.7673	-0.0060	396 - 408		0	WLGLSAEYGNLYR
1659.8676	1658.8603	1658.8376	0.0228	370 - 384		1	NRSPDIYNPQAGSLK
2314.1758	2313.1685	2313.2018	-0.0332	409 - 428		0	NALFVPHYNTNAHSIIYALR
2541.3064	2540.2991	2540.2910	0.0082	443 - 465		0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1269.7527, 1277.1042, 1289.6564, 1296.6444, 1305.6823, 1306.6963, 1349.6990, 1365.6860, 1376.7327, 1435.6946, 1448.6555, 1462.6788, 1529.7107, 1606.7324, 1618.7794, 1652.7349, 1756.8269, 1774.8324, 1934.8956, 2020.9919, 2064.0518, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2315.1992, 2333.1455, 2351.1094, 2354.1138, 2514.3223, 2530.3555, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930

10. gi|3703107 **Mass:** 58543 **Score:** 27 **Expect:** 1.9 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7407	1254.7334	1254.7295	0.0039	355 - 365		0	TANDLNLLILR
1289.6564	1288.6491	1288.6564	-0.0072	494 - 504		0	FFVPPSQQSPR
1389.6942	1388.6869	1388.6935	-0.0066	342 - 354		0	SPDIYNPQAGSLK
1448.6555	1447.6482	1447.6619	-0.0137	436 - 447		0	SQSENFEYVAFK
1659.8676	1658.8603	1658.8376	0.0228	340 - 354		1	NRSPDIYNPQAGSLK
2541.3064	2540.2991	2540.2910	0.0082	413 - 435		0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1269.7527, 1277.1042, 1296.6444, 1305.6823, 1306.6963, 1349.6990, 1365.6860, 1376.7327, 1435.6946, 1462.6788, 1529.7107, 1541.7686, 1606.7324, 1618.7794, 1652.7349, 1756.8269, 1774.8324, 1934.8956, 2020.9919, 2064.0518, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2314.1758, 2315.1992, 2333.1455, 2351.1094, 2354.1138, 2514.3223, 2530.3555, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 69

Protein View

Match to: **gi|118776570** Score: **51** Expect: **0.0071**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **69**
Number of mass values matched: **9**
Sequence Coverage: **20%**

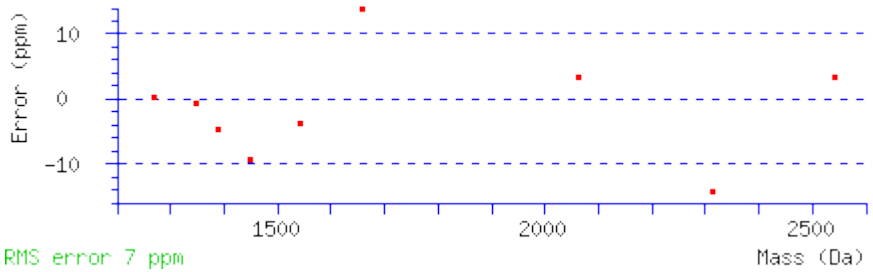
Matched peptides shown in **Bold Red**

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     1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
    51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
   101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
   151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
   201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
   251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
   301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
   351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
   401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
   451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
   501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
362 - 376	1659.8676	1658.8603	1658.8376	0.0228	1	NRSPDIYNPQAGSLK
364 - 376	1389.6942	1388.6869	1388.6935	-0.0066	0	SPDIYNPQAGSLK
377 - 387	1269.7527	1268.7454	1268.7452	0.0002	0	TANELNLLILR
388 - 400	1541.7686	1540.7613	1540.7673	-0.0060	0	WLGLSAEYGNLYR
401 - 420	2314.1758	2313.1685	2313.2018	-0.0332	0	NALFVPHYNTNAHSIIYALR
435 - 457	2541.3064	2540.2991	2540.2910	0.0082	0	VYDEELQEGHVLVVPQNFAVAGK
458 - 469	1448.6555	1447.6482	1447.6619	-0.0137	0	SQSENFEYVAFK
510 - 526	2064.0518	2063.0445	2063.0376	0.0069	1	NNNPFKFFVPPFQQSPR
516 - 526	1349.6990	1348.6917	1348.6927	-0.0010	0	FFVPPFQQSPR

No match to: 805.4623, 839.0889, 845.1064, 855.0725, 861.0878, 877.0505, 1046.6007, 1050.1095, 1066.0835, 1072.0830, 1080.5405, 1082.0316, 1082.5270, 1110.5571, 1111.5643, 1137.0651, 1137.5574, 1145.0698, 1145.5723, 1175.5519, 1255.7407, 1277.1042, 1289.6564, 1296.6444, 1305.6823, 1306.6963, 1365.6860, 1376.7327, 1435.6946, 1462.6788, 1529.7107, 1606.7324, 1618.7794, 1652.7349, 1756.8269, 1774.8324, 1934.8956, 2020.9919, 2091.0603, 2145.0728, 2146.5957, 2185.0337, 2225.0688, 2273.1675, 2295.1462, 2305.1714, 2311.1453, 2315.1992, 2333.1455, 2351.1094, 2354.1138, 2514.3223, 2530.3555, 2612.2063, 2653.4121, 3136.4814, 3137.4932, 3211.5269, 3300.7585, 3316.7930



Spot 33

User :
Email :
Search title : **SampleSetID: 262, AnalysisID: 1522, MaldiWellID: 5294, SpectrumID: 17272, Path=\261006\Ties Latendorf\Arachis Research 040507**
Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 09:58:27 GMT**
Top Score : **75 for gi|118776570, arachin 6 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	75	arachin 6 [Arachis hypogaea]
2.	gi|9864777	60754	66	Gly1 [Arachis hypogaea]
3.	gi|57669861	61041	57	arachin Ahy-4 [Arachis hypogaea]
4.	gi|108595573	61041	57	arachin Ahy-4 [Arachis hypogaea]
5.	gi|3703107	58543	56	glycinin [Arachis hypogaea]
6.	gi|5712199	61430	47	glycinin [Arachis hypogaea]
7.	gi|52001221	61836	46	arachin Ahy-2 [Arachis hypogaea]
8.	gi|52001219	61810	36	arachin Ahy-1 [Arachis hypogaea]
9.	gi|37789212	61803	36	storage protein [Arachis hypogaea]
10.	gi|21314465	62042	28	allergen Arah3/Arah4 [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 75 **Expect:** 2.6e-005 **Queries matched:** 11
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5908	1101.5835	1101.5930	-0.0095	507	515	1	QLKNNNPFK
1269.7710	1268.7637	1268.7452	0.0185	377	387	0	TANELNLLILR
1295.6559	1294.6486	1294.6377	0.0109	423	434	0	AHVQVVDSNGNR
1349.7261	1348.7188	1348.6927	0.0261	516	526	0	FFVPPFQQSPR

1389.7216	1388.7143	1388.6935	0.0208	364 - 376	0	SPDIYNPQAGSLK
1448.6935	1447.6862	1447.6619	0.0243	458 - 469	0	SQSENFEYVAFK
1541.8048	1540.7975	1540.7673	0.0302	388 - 400	0	WLGLSAEYGNLYR
1659.8755	1658.8682	1658.8376	0.0307	362 - 376	1	NRSPDIYNPQAGSLK
2064.0461	2063.0388	2063.0376	0.0012	510 - 526	1	NNNPFKFFVPPFQQSPR
2314.1763	2313.1690	2313.2018	-0.0327	401 - 420	0	NALFVPHYNTNAHSIIYALR
2541.2605	2540.2532	2540.2910	-0.0377	435 - 457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1255.7546, 1289.6857, 1296.6550, 1305.7095, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1420.7657, 1434.7029, 1436.7606, 1524.7937, 1557.7975, 1573.7949, 1774.8835, 1876.0176, 2004.0081, 2020.0453, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2461.2466, 2515.2876, 2530.2944, 2613.1318, 3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

2. gi|9864777 **Mass:** 60754 **Score:** 66 **Expect:** 0.00025 **Queries matched:** 10

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5908	1101.5835	1101.5930	-0.0095	507 - 515		1	QLKNNNPFK
1255.7546	1254.7473	1254.7295	0.0178	377 - 387		0	TANDLNLLILR
1295.6559	1294.6486	1294.6377	0.0109	423 - 434		0	AHVQVVDSNGNR
1305.7095	1304.7022	1304.6877	0.0146	516 - 526		0	FFVPPSQQSLR
1389.7216	1388.7143	1388.6935	0.0208	364 - 376		0	SPDIYNPQAGSLK
1541.8048	1540.7975	1540.7673	0.0302	388 - 400		0	WLGLSAEYGNLYR
1659.8755	1658.8682	1658.8376	0.0307	362 - 376		1	NRSPDIYNPQAGSLK
2020.0453	2019.0380	2019.0326	0.0055	510 - 526		1	NNNPFKFFVPPSQQSLR
2314.1763	2313.1690	2313.2018	-0.0327	401 - 420		0	NALFVPHYNTNAHSIIYALR
2541.2605	2540.2532	2540.2910	-0.0377	435 - 457		0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1269.7710, 1289.6857, 1296.6550, 1349.7261, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1420.7657, 1434.7029, 1436.7606, 1448.6935, 1524.7937, 1557.7975, 1573.7949, 1774.8835, 1876.0176, 2004.0081, 2064.0461, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2461.2466, 2515.2876, 2530.2944, 2613.1318, 3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

3. gi|57669861 **Mass:** 61041 **Score:** 57 **Expect:** 0.0019 **Queries matched:** 9

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7546	1254.7473	1254.7295	0.0178	378 - 388		0	TANDLNLLILR
1289.6857	1288.6784	1288.6564	0.0221	518 - 528		0	FFVPPSQQSPR
1295.6559	1294.6486	1294.6377	0.0109	424 - 435		0	AHVQVVDSNGNR
1389.7216	1388.7143	1388.6935	0.0208	365 - 377		0	SPDIYNPQAGSLK
1541.8048	1540.7975	1540.7673	0.0302	389 - 401		0	WLGLSAEYGNLYR
1659.8755	1658.8682	1658.8376	0.0307	363 - 377		1	NRSPDIYNPQAGSLK
2004.0081	2003.0008	2003.0013	-0.0004	512 - 528		1	NNNPFKFFVPPSQQSPR

2314.1763	2313.1690	2313.2018	-0.0327	402 - 421	0	NALFVPHYNTNAHSIIYALR
2541.2605	2540.2532	2540.2910	-0.0377	436 - 458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1102.5908, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1269.7710, 1296.6550, 1305.7095, 1349.7261, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1420.7657, 1434.7029, 1436.7606, 1448.6935, 1524.7937, 1557.7975, 1573.7949, 1774.8835, 1876.0176, 2020.0453, 2064.0461, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2461.2466, 2515.2876, 2530.2944, 2613.1318, 3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

4. gi|108595573 **Mass:** 61041 **Score:** 57 **Expect:** 0.0019 **Queries matched:** 9

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7546	1254.7473	1254.7295	0.0178	378 -	388	0	TANDLNLLILR
1289.6857	1288.6784	1288.6564	0.0221	518 -	528	0	FFVPPSQQSPR
1295.6559	1294.6486	1294.6377	0.0109	424 -	435	0	AHVQVVDSNGNR
1389.7216	1388.7143	1388.6935	0.0208	365 -	377	0	SPDIYNPQAGSLK
1541.8048	1540.7975	1540.7673	0.0302	389 -	401	0	WLGLSAEYGNLYR
1659.8755	1658.8682	1658.8376	0.0307	363 -	377	1	NRSPDIYNPQAGSLK
2004.0081	2003.0008	2003.0013	-0.0004	512 -	528	1	NNNPFKFFVPPSQQSPR
2314.1763	2313.1690	2313.2018	-0.0327	402 -	421	0	NALFVPHYNTNAHSIIYALR
2541.2605	2540.2532	2540.2910	-0.0377	436 -	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1102.5908, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1269.7710, 1296.6550, 1305.7095, 1349.7261, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1420.7657, 1434.7029, 1436.7606, 1448.6935, 1524.7937, 1557.7975, 1573.7949, 1774.8835, 1876.0176, 2020.0453, 2064.0461, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2461.2466, 2515.2876, 2530.2944, 2613.1318, 3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

5. gi|3703107 **Mass:** 58543 **Score:** 56 **Expect:** 0.0024 **Queries matched:** 9

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5908	1101.5835	1101.5930	-0.0095	485 -	493	1	QLKNNNPFK
1255.7546	1254.7473	1254.7295	0.0178	355 -	365	0	TANDLNLLILR
1289.6857	1288.6784	1288.6564	0.0221	494 -	504	0	FFVPPSQQSPR
1295.6559	1294.6486	1294.6377	0.0109	401 -	412	0	AHVQVVDSNGNR
1389.7216	1388.7143	1388.6935	0.0208	342 -	354	0	SPDIYNPQAGSLK
1448.6935	1447.6862	1447.6619	0.0243	436 -	447	0	SQSENFEYVAFK
1659.8755	1658.8682	1658.8376	0.0307	340 -	354	1	NRSPDIYNPQAGSLK
2004.0081	2003.0008	2003.0013	-0.0004	488 -	504	1	NNNPFKFFVPPSQQSPR
2541.2605	2540.2532	2540.2910	-0.0377	413 -	435	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1269.7710, 1296.6550, 1305.7095, 1349.7261, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1420.7657, 1434.7029, 1436.7606, 1524.7937, 1541.8048, 1557.7975, 1573.7949, 1774.8835, 1876.0176, 2020.0453, 2064.0461, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2314.1763, 2461.2466, 2515.2876, 2530.2944, 2613.1318,

3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

6. gi|5712199 **Mass:** 61430 **Score:** 47 **Expect:** 0.018 **Queries matched:** 8

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5908	1101.5835	1101.5930	-0.0095	508	516	1	QLKNNNPFK
1295.6559	1294.6486	1294.6377	0.0109	424	435	0	AHVQVVDSNGNR
1349.7261	1348.7188	1348.6927	0.0261	517	527	0	FFVPPFQQSPR
1448.6935	1447.6862	1447.6619	0.0243	459	470	0	SQSENFEYVAFK
1541.8048	1540.7975	1540.7673	0.0302	389	401	0	WLGLSAEYGNLYR
2064.0461	2063.0388	2063.0376	0.0012	511	527	1	NNNPFKFFVPPFQQSPR
2314.1763	2313.1690	2313.2018	-0.0327	402	421	0	NALFVPHYNTNAHSIIYALR
2541.2605	2540.2532	2540.2910	-0.0377	436	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1255.7546, 1269.7710, 1289.6857, 1296.6550, 1305.7095, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1389.7216, 1420.7657, 1434.7029, 1436.7606, 1524.7937, 1557.7975, 1573.7949, 1659.8755, 1774.8835, 1876.0176, 2004.0081, 2020.0453, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2461.2466, 2515.2876, 2530.2944, 2613.1318, 3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

7. gi|52001221 **Mass:** 61836 **Score:** 46 **Expect:** 0.021 **Queries matched:** 8

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5908	1101.5835	1101.5930	-0.0095	515	523	1	QLKNNNPFK
1255.7546	1254.7473	1254.7295	0.0178	385	395	0	TANDLNLLILR
1295.6559	1294.6486	1294.6377	0.0109	431	442	0	AHVQVVDSNGNR
1389.7216	1388.7143	1388.6935	0.0208	372	384	0	SPDIYNPQAGSLK
1541.8048	1540.7975	1540.7673	0.0302	396	408	0	WLGLSAEYGNLYR
1659.8755	1658.8682	1658.8376	0.0307	370	384	1	NRSPDIYNPQAGSLK
2314.1763	2313.1690	2313.2018	-0.0327	409	428	0	NALFVPHYNTNAHSIIYALR
2541.2605	2540.2532	2540.2910	-0.0377	443	465	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1269.7710, 1289.6857, 1296.6550, 1305.7095, 1349.7261, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1420.7657, 1434.7029, 1436.7606, 1448.6935, 1524.7937, 1557.7975, 1573.7949, 1774.8835, 1876.0176, 2004.0081, 2020.0453, 2064.0461, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2461.2466, 2515.2876, 2530.2944, 2613.1318, 3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

8. gi|52001219 **Mass:** 61810 **Score:** 36 **Expect:** 0.25 **Queries matched:** 7

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5908	1101.5835	1101.5930	-0.0095	514	522	1	QLKNNNPFK
1269.7710	1268.7637	1268.7452	0.0185	384	394	0	TANELNLLILR
1389.7216	1388.7143	1388.6935	0.0208	371	383	0	SPDIYNPQAGSLK

1448.6935	1447.6862	1447.6619	0.0243	465 - 476	0	SQSENFEYVAFK
1541.8048	1540.7975	1540.7673	0.0302	395 - 407	0	WLGLSAEYGNLYR
1659.8755	1658.8682	1658.8376	0.0307	369 - 383	1	NRSPDIYNPQAGSLK
2314.1763	2313.1690	2313.2018	-0.0327	408 - 427	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1255.7546, 1289.6857, 1295.6559, 1296.6550, 1305.7095, 1349.7261, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1420.7657, 1434.7029, 1436.7606, 1524.7937, 1557.7975, 1573.7949, 1774.8835, 1876.0176, 2004.0081, 2020.0453, 2064.0461, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2461.2466, 2515.2876, 2530.2944, 2541.2605, 2613.1318, 3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

9. gi|37789212 **Mass:** 61803 **Score:** 36 **Expect:** 0.25 **Queries matched:** 7

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5908	1101.5835	1101.5930	-0.0095	514 - 522		1	QLKNNNPFK
1269.7710	1268.7637	1268.7452	0.0185	384 - 394		0	TANELNLLILR
1389.7216	1388.7143	1388.6935	0.0208	371 - 383		0	SPDIYNPQAGSLK
1448.6935	1447.6862	1447.6619	0.0243	465 - 476		0	SQSENFEYVAFK
1541.8048	1540.7975	1540.7673	0.0302	395 - 407		0	WLGLSAEYGNLYR
1659.8755	1658.8682	1658.8376	0.0307	369 - 383		1	NRSPDIYNPQAGSLK
2314.1763	2313.1690	2313.2018	-0.0327	408 - 427		0	NALFVPHYNTNAHSIIYALR

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1255.7546, 1289.6857, 1295.6559, 1296.6550, 1305.7095, 1349.7261, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1420.7657, 1434.7029, 1436.7606, 1524.7937, 1557.7975, 1573.7949, 1774.8835, 1876.0176, 2004.0081, 2020.0453, 2064.0461, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2461.2466, 2515.2876, 2530.2944, 2541.2605, 2613.1318, 3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

10. gi|21314465 **Mass:** 62042 **Score:** 28 **Expect:** 1.3 **Queries matched:** 6

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5908	1101.5835	1101.5930	-0.0095	516 - 524		1	QLKNNNPFK
1389.7216	1388.7143	1388.6935	0.0208	371 - 383		0	SPDIYNPQAGSLK
1448.6935	1447.6862	1447.6619	0.0243	467 - 478		0	SQSENFEYVAFK
1541.8048	1540.7975	1540.7673	0.0302	397 - 409		0	WLGLSAEYGNLYR
1659.8755	1658.8682	1658.8376	0.0307	369 - 383		1	NRSPDIYNPQAGSLK
2314.1763	2313.1690	2313.2018	-0.0327	410 - 429		0	NALFVPHYNTNAHSIIYALR

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1255.7546, 1269.7710, 1289.6857, 1295.6559, 1296.6550, 1305.7095, 1349.7261, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1420.7657, 1434.7029, 1436.7606, 1524.7937, 1557.7975, 1573.7949, 1774.8835, 1876.0176, 2004.0081, 2020.0453, 2064.0461, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2461.2466, 2515.2876, 2530.2944, 2541.2605, 2613.1318, 3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 59

Protein View

Match to: **gi|118776570** Score: **75** Expect: **2.6e-005**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **59**
Number of mass values matched: **11**
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
     1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
    51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
   101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
   151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
   201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
   251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
   301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
   351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
   401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
   451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
   501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
362 - 376	1659.8755	1658.8682	1658.8376	0.0307	1	NRSPDIYNPQAGSLK
364 - 376	1389.7216	1388.7143	1388.6935	0.0208	0	SPDIYNPQAGSLK
377 - 387	1269.7710	1268.7637	1268.7452	0.0185	0	TANELNLLILR
388 - 400	1541.8048	1540.7975	1540.7673	0.0302	0	WLGLSAEYGNLYR
401 - 420	2314.1763	2313.1690	2313.2018	-0.0327	0	NALFVPHYNTNAHSIIYALR
423 - 434	1295.6559	1294.6486	1294.6377	0.0109	0	AHVQVVDSNGNR
435 - 457	2541.2605	2540.2532	2540.2910	-0.0377	0	VYDEELQEGHVLVVPQNFAVAGK
458 - 469	1448.6935	1447.6862	1447.6619	0.0243	0	SQSENFEYVAFK
507 - 515	1102.5908	1101.5835	1101.5930	-0.0095	1	QLKNNNPFK
510 - 526	2064.0461	2063.0388	2063.0376	0.0012	1	NNNPFKFFVPPFQQSPR
516 - 526	1349.7261	1348.7188	1348.6927	0.0261	0	FFVPPFQQSPR

No match to: 805.3787, 835.4728, 855.0343, 861.0455, 877.0241, 881.2499, 906.4744, 1046.5934, 1066.0745, 1080.5266, 1111.5601, 1145.0760, 1145.5691, 1175.5679, 1255.7546, 1289.6857, 1296.6550, 1305.7095, 1360.7295, 1365.7213, 1376.7538, 1377.7520, 1420.7657, 1434.7029, 1436.7606, 1524.7937, 1557.7975, 1573.7949, 1774.8835, 1876.0176, 2004.0081, 2020.0453, 2080.0322, 2091.0735, 2185.0354, 2273.1477, 2311.1230, 2461.2466, 2515.2876, 2530.2944, 2613.1318, 3154.2705, 3212.2720, 3227.2925, 3317.4917, 3513.4993, 3546.4314, 3818.3735

Spot 34

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 09:59:07 GMT**
Top Score : **67 for gi|118776570, arachin 6 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	67	arachin 6 [Arachis hypogaea]
2.	gi|9864777	60754	57	Gly1 [Arachis hypogaea]
3.	gi|3703107	58543	57	glycinin [Arachis hypogaea]
4.	gi|57669861	61041	49	arachin Ahy-4 [Arachis hypogaea]
5.	gi|108595573	61041	49	arachin Ahy-4 [Arachis hypogaea]
6.	gi|5712199	61430	39	glycinin [Arachis hypogaea]
7.	gi|52001221	61836	39	arachin Ahy-2 [Arachis hypogaea]
8.	gi|52001219	61810	36	arachin Ahy-1 [Arachis hypogaea]
9.	gi|37789212	61803	36	storage protein [Arachis hypogaea]
10.	gi|21314465	62042	29	allergen Arah3/Arah4 [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 67 **Expect:** 0.00018 **Queries matched:** 10
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6008	1101.5935	1101.5930	0.0005	507	515	1	QLKNNNPFK
1269.7712	1268.7639	1268.7452	0.0187	377	387	0	TANELNLLILR
1295.6625	1294.6552	1294.6377	0.0175	423	434	0	AHVQVVDSNGNR
1349.7252	1348.7179	1348.6927	0.0252	516	526	0	FFVPPFQQSPR
1389.7224	1388.7151	1388.6935	0.0216	364	376	0	SPDIYNPQAGSLK
1448.6938	1447.6865	1447.6619	0.0246	458	469	0	SQSENFEYVAFK
1659.8740	1658.8667	1658.8376	0.0292	362	376	1	NRSPDIYNPQAGSLK
2064.0425	2063.0352	2063.0376	-0.0024	510	526	1	NNNPFKFFVPPFQQSPR
2314.1763	2313.1690	2313.2018	-0.0327	401	420	0	NALFVPHYNTNAHSIIYALR
2541.2612	2540.2539	2540.2910	-0.0370	435	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1111.5520,

1145.0767, 1145.5686, 1255.7581, 1289.6864, 1296.6547, 1305.7128, 1360.7321, 1365.7252, 1376.7563, 1420.7695, 1434.6956, 1436.7593, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1774.8793, 1876.0122, 2004.0095, 2020.0443, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2508.2844, 2530.2986, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931

2. gi|9864777 **Mass:** 60754 **Score:** 57 **Expect:** 0.0016 **Queries matched:** 9

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6008	1101.5935	1101.5930	0.0005	507	515	1	QLKNNNPFK
1255.7581	1254.7508	1254.7295	0.0213	377	387	0	TANDLNLLILR
1295.6625	1294.6552	1294.6377	0.0175	423	434	0	AHVQVVDSNGNR
1305.7128	1304.7055	1304.6877	0.0179	516	526	0	FFVPPSQQSLR
1389.7224	1388.7151	1388.6935	0.0216	364	376	0	SPDIYNPQAGSLK
1659.8740	1658.8667	1658.8376	0.0292	362	376	1	NRSPDIYNPQAGSLK
2020.0443	2019.0370	2019.0326	0.0045	510	526	1	NNNPFKFFVPPSQQSLR
2314.1763	2313.1690	2313.2018	-0.0327	401	420	0	NALFVPHYNTNAHSIIYALR
2541.2612	2540.2539	2540.2910	-0.0370	435	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1111.5520, 1145.0767, 1145.5686, 1269.7712, 1289.6864, 1296.6547, 1349.7252, 1360.7321, 1365.7252, 1376.7563, 1420.7695, 1434.6956, 1436.7593, 1448.6938, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1774.8793, 1876.0122, 2004.0095, 2064.0425, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2508.2844, 2530.2986, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931

3. gi|3703107 **Mass:** 58543 **Score:** 57 **Expect:** 0.0018 **Queries matched:** 9

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6008	1101.5935	1101.5930	0.0005	485	493	1	QLKNNNPFK
1255.7581	1254.7508	1254.7295	0.0213	355	365	0	TANDLNLLILR
1289.6864	1288.6791	1288.6564	0.0228	494	504	0	FFVPPSQQSPR
1295.6625	1294.6552	1294.6377	0.0175	401	412	0	AHVQVVDSNGNR
1389.7224	1388.7151	1388.6935	0.0216	342	354	0	SPDIYNPQAGSLK
1448.6938	1447.6865	1447.6619	0.0246	436	447	0	SQSENFEYVAFK
1659.8740	1658.8667	1658.8376	0.0292	340	354	1	NRSPDIYNPQAGSLK
2004.0095	2003.0022	2003.0013	0.0010	488	504	1	NNNPFKFFVPPSQQSPR
2541.2612	2540.2539	2540.2910	-0.0370	413	435	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1111.5520, 1145.0767, 1145.5686, 1269.7712, 1296.6547, 1305.7128, 1349.7252, 1360.7321, 1365.7252, 1376.7563, 1420.7695, 1434.6956, 1436.7593, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1774.8793, 1876.0122, 2020.0443, 2064.0425, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2314.1763, 2508.2844, 2530.2986, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931

4. gi|57669861 **Mass:** 61041 **Score:** 49 **Expect:** 0.012 **Queries matched:** 8

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7581	1254.7508	1254.7295	0.0213	378	388	0	TANDLNLLILR
1289.6864	1288.6791	1288.6564	0.0228	518	528	0	FFVPPSQQSPR
1295.6625	1294.6552	1294.6377	0.0175	424	435	0	AHVQVVDSNGNR
1389.7224	1388.7151	1388.6935	0.0216	365	377	0	SPDIYNPQAGSLK
1659.8740	1658.8667	1658.8376	0.0292	363	377	1	NRSPDIYNPQAGSLK
2004.0095	2003.0022	2003.0013	0.0010	512	528	1	NNNPFKFFVPPSQQSPR
2314.1763	2313.1690	2313.2018	-0.0327	402	421	0	NALFVPHYNTNAHSIIYALR
2541.2612	2540.2539	2540.2910	-0.0370	436	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1102.6008, 1111.5520, 1145.0767, 1145.5686, 1269.7712, 1296.6547, 1305.7128, 1349.7252, 1360.7321, 1365.7252, 1376.7563, 1420.7695, 1434.6956, 1436.7593, 1448.6938, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1774.8793, 1876.0122, 2020.0443, 2064.0425, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2508.2844, 2530.2986, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931

5. gi|108595573 **Mass:** 61041 **Score:** 49 **Expect:** 0.012 **Queries matched:** 8

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7581	1254.7508	1254.7295	0.0213	378	388	0	TANDLNLLILR
1289.6864	1288.6791	1288.6564	0.0228	518	528	0	FFVPPSQQSPR
1295.6625	1294.6552	1294.6377	0.0175	424	435	0	AHVQVVDSNGNR
1389.7224	1388.7151	1388.6935	0.0216	365	377	0	SPDIYNPQAGSLK
1659.8740	1658.8667	1658.8376	0.0292	363	377	1	NRSPDIYNPQAGSLK
2004.0095	2003.0022	2003.0013	0.0010	512	528	1	NNNPFKFFVPPSQQSPR
2314.1763	2313.1690	2313.2018	-0.0327	402	421	0	NALFVPHYNTNAHSIIYALR
2541.2612	2540.2539	2540.2910	-0.0370	436	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1102.6008, 1111.5520, 1145.0767, 1145.5686, 1269.7712, 1296.6547, 1305.7128, 1349.7252, 1360.7321, 1365.7252, 1376.7563, 1420.7695, 1434.6956, 1436.7593, 1448.6938, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1774.8793, 1876.0122, 2020.0443, 2064.0425, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2508.2844, 2530.2986, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931

6. gi|5712199 **Mass:** 61430 **Score:** 39 **Expect:** 0.1 **Queries matched:** 7

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6008	1101.5935	1101.5930	0.0005	508	516	1	QLKNNNPFK
1295.6625	1294.6552	1294.6377	0.0175	424	435	0	AHVQVVDSNGNR
1349.7252	1348.7179	1348.6927	0.0252	517	527	0	FFVPPFQQSPR
1448.6938	1447.6865	1447.6619	0.0246	459	470	0	SQSENFEYVAFK
2064.0425	2063.0352	2063.0376	-0.0024	511	527	1	NNNPFKFFVPPFQQSPR
2314.1763	2313.1690	2313.2018	-0.0327	402	421	0	NALFVPHYNTNAHSIIYALR

2541.2612	2540.2539	2540.2910	-0.0370	436 - 458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1111.5520, 1145.0767, 1145.5686, 1255.7581, 1269.7712, 1289.6864, 1296.6547, 1305.7128, 1360.7321, 1365.7252, 1376.7563, 1389.7224, 1420.7695, 1434.6956, 1436.7593, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1659.8740, 1774.8793, 1876.0122, 2004.0095, 2020.0443, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2508.2844, 2530.2986, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931

7. gi|52001221 **Mass:** 61836 **Score:** 39 **Expect:** 0.12 **Queries matched:** 7

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6008	1101.5935	1101.5930	0.0005	515 - 523		1	QLKNNNPFK
1255.7581	1254.7508	1254.7295	0.0213	385 - 395		0	TANDLNLLILR
1295.6625	1294.6552	1294.6377	0.0175	431 - 442		0	AHVQVVDSNGNR
1389.7224	1388.7151	1388.6935	0.0216	372 - 384		0	SPDIYNPQAGSLK
1659.8740	1658.8667	1658.8376	0.0292	370 - 384		1	NRSPDIYNPQAGSLK
2314.1763	2313.1690	2313.2018	-0.0327	409 - 428		0	NALFVPHYNTNAHSIIYALR
2541.2612	2540.2539	2540.2910	-0.0370	443 - 465		0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1111.5520, 1145.0767, 1145.5686, 1269.7712, 1289.6864, 1296.6547, 1305.7128, 1349.7252, 1360.7321, 1365.7252, 1376.7563, 1420.7695, 1434.6956, 1436.7593, 1448.6938, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1774.8793, 1876.0122, 2004.0095, 2020.0443, 2064.0425, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2508.2844, 2530.2986, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931

8. gi|52001219 **Mass:** 61810 **Score:** 36 **Expect:** 0.21 **Queries matched:** 7

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6008	1101.5935	1101.5930	0.0005	514 - 522		1	QLKNNNPFK
1269.7712	1268.7639	1268.7452	0.0187	384 - 394		0	TANELNLLILR
1296.6547	1295.6474	1295.6218	0.0257	430 - 441		0	AHVQVVDSNGDR
1389.7224	1388.7151	1388.6935	0.0216	371 - 383		0	SPDIYNPQAGSLK
1448.6938	1447.6865	1447.6619	0.0246	465 - 476		0	SQSENFEYVAFK
1659.8740	1658.8667	1658.8376	0.0292	369 - 383		1	NRSPDIYNPQAGSLK
2314.1763	2313.1690	2313.2018	-0.0327	408 - 427		0	NALFVPHYNTNAHSIIYALR

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1111.5520, 1145.0767, 1145.5686, 1255.7581, 1289.6864, 1295.6625, 1305.7128, 1349.7252, 1360.7321, 1365.7252, 1376.7563, 1420.7695, 1434.6956, 1436.7593, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1774.8793, 1876.0122, 2004.0095, 2020.0443, 2064.0425, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2508.2844, 2530.2986, 2541.2612, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931

9. gi|37789212 **Mass:** 61803 **Score:** 36 **Expect:** 0.21 **Queries matched:** 7

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1102.6008	1101.5935	1101.5930	0.0005	514 - 522	1	QLKNNNPFK
1269.7712	1268.7639	1268.7452	0.0187	384 - 394	0	TANELNLLILR
1296.6547	1295.6474	1295.6218	0.0257	430 - 441	0	AHVQVVDSNGDR
1389.7224	1388.7151	1388.6935	0.0216	371 - 383	0	SPDIYNPQAGSLK
1448.6938	1447.6865	1447.6619	0.0246	465 - 476	0	SQSENFEYVAFK
1659.8740	1658.8667	1658.8376	0.0292	369 - 383	1	NRSPDIYNPQAGSLK
2314.1763	2313.1690	2313.2018	-0.0327	408 - 427	0	NALFVPHYNTNAHSIIYALR

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1111.5520, 1145.0767, 1145.5686, 1255.7581, 1289.6864, 1295.6625, 1305.7128, 1349.7252, 1360.7321, 1365.7252, 1376.7563, 1420.7695, 1434.6956, 1436.7593, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1774.8793, 1876.0122, 2004.0095, 2020.0443, 2064.0425, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2508.2844, 2530.2986, 2541.2612, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931

10. gi|21314465 **Mass:** 62042 **Score:** 29 **Expect:** 1.2 **Queries matched:** 6

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6008	1101.5935	1101.5930	0.0005	516 - 524		1	QLKNNNPFK
1296.6547	1295.6474	1295.6218	0.0257	432 - 443		0	AHVQVVDSNGDR
1389.7224	1388.7151	1388.6935	0.0216	371 - 383		0	SPDIYNPQAGSLK
1448.6938	1447.6865	1447.6619	0.0246	467 - 478		0	SQSENFEYVAFK
1659.8740	1658.8667	1658.8376	0.0292	369 - 383		1	NRSPDIYNPQAGSLK
2314.1763	2313.1690	2313.2018	-0.0327	410 - 429		0	NALFVPHYNTNAHSIIYALR

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1111.5520, 1145.0767, 1145.5686, 1255.7581, 1269.7712, 1289.6864, 1295.6625, 1305.7128, 1349.7252, 1360.7321, 1365.7252, 1376.7563, 1420.7695, 1434.6956, 1436.7593, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1774.8793, 1876.0122, 2004.0095, 2020.0443, 2064.0425, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2508.2844, 2530.2986, 2541.2612, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 57

Protein View

Match to: **gi|118776570** Score: **67** Expect: **0.00018**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **57**
Number of mass values matched: **10**
Sequence Coverage: **21%**

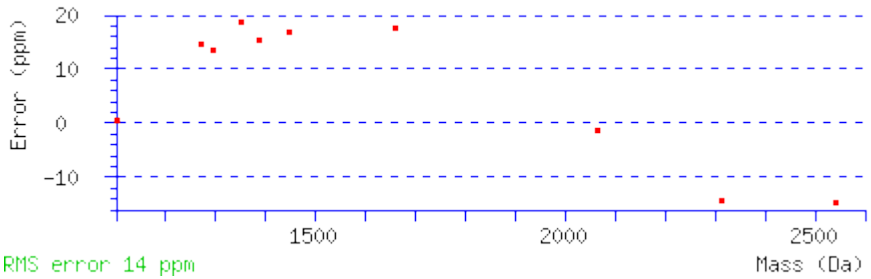
Matched peptides shown in **Bold Red**

```
     1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
    51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
   101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
   151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
   201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
   251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
   301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
   351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
   401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
   451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
   501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
362 - 376	1659.8740	1658.8667	1658.8376	0.0292	1	NRSPDIYNPQAGSLK
364 - 376	1389.7224	1388.7151	1388.6935	0.0216	0	SPDIYNPQAGSLK
377 - 387	1269.7712	1268.7639	1268.7452	0.0187	0	TANELNLLILR
401 - 420	2314.1763	2313.1690	2313.2018	-0.0327	0	NALFVPHYNTNAHSIIYALR
423 - 434	1295.6625	1294.6552	1294.6377	0.0175	0	AHVQVVDSNGNR
435 - 457	2541.2612	2540.2539	2540.2910	-0.0370	0	VYDEELQEGHVLVVPQNFAVAGK
458 - 469	1448.6938	1447.6865	1447.6619	0.0246	0	SQSENFEYVAFK
507 - 515	1102.6008	1101.5935	1101.5930	0.0005	1	QLKNNNPFK
510 - 526	2064.0425	2063.0352	2063.0376	-0.0024	1	NNNPFKFFVPPFQQSPR
516 - 526	1349.7252	1348.7179	1348.6927	0.0252	0	FFVPPFQQSPR

No match to: 805.3807, 835.4789, 855.0255, 861.0438, 877.0250, 906.4775, 1046.5964, 1066.0710, 1080.5311, 1111.5520, 1145.0767, 1145.5686, 1255.7581, 1289.6864, 1296.6547, 1305.7128, 1360.7321, 1365.7252, 1376.7563, 1420.7695, 1434.6956, 1436.7593, 1498.7629, 1523.8053, 1541.8060, 1557.8030, 1573.7982, 1638.8916, 1774.8793, 1876.0122, 2004.0095, 2020.0443, 2080.0332, 2091.0710, 2185.0286, 2202.0112, 2273.1484, 2311.1199, 2508.2844, 2530.2986, 2613.1123, 3153.2393, 3227.2446, 3318.4783, 3511.4304, 3546.4121, 3818.3931



Spot 35

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:31:52 GMT**
Top Score : **107 for gi|22135348, trypsin inhibitor [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	gi|22135348	25768	107	trypsin inhibitor [Arachis hypogaea]
2.	gi|52001219	61810	92	arachin Ahy-1 [Arachis hypogaea]
3.	gi|21314465	62042	92	allergen Arah3/Arah4 [Arachis hypogaea]
4.	gi|37789212	61803	79	storage protein [Arachis hypogaea]
5.	gi|118776572	24127	53	arachin 7 [Arachis hypogaea]
6.	gi|52001221	61836	50	arachin Ahy-2 [Arachis hypogaea]
7.	gi|9864777	60754	33	Gly1 [Arachis hypogaea]
8.	gi|118776570	60681	33	arachin 6 [Arachis hypogaea]
9.	gi|5712199	61430	33	glycinin [Arachis hypogaea]
10.	gi|57669861	61041	33	arachin Ahy-4 [Arachis hypogaea]

Results List

1. gi|22135348 **Mass:** 25768 **Score:** 107 **Expect:** 1.7e-008 **Queries matched:** 10
trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5240	1004.5167	1004.5264	-0.0097	124	131	0	HQSQRPPR
1083.5607	1082.5534	1082.5581	-0.0046	39	47	0	LNAQRPDNR
1161.6338	1160.6265	1160.6275	-0.0010	124	132	1	HQSQRPPRR
1534.6824	1533.6751	1533.6630	0.0121	27	38	0	QQPEENACQFQR
1574.7834	1573.7761	1573.7637	0.0125	198	210	0	FNLAGNHEQEFLR
1730.8826	1729.8753	1729.8648	0.0106	197	210	1	RFNLAGNHEQEFLR
1916.8501	1915.8428	1915.8409	0.0020	133	148	0	FQGQDQSQQQQDSHQK
2051.0413	2050.0340	2050.0384	-0.0044	84	100	0	RPFYSNAPQEIFIQQGR

2072.9436	2071.9363	2071.9420	-0.0056	132 - 148	1	RFQGQDQSQQQQDSHQK
2474.1160	2473.1087	2473.1371	-0.0284	101 - 122	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 884.5166, 906.4865, 958.4641, 990.5425, 1079.5360, 1111.5653, 1158.6116, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572, 1548.7029, 1603.7651, 1624.7952, 1650.8367, 1714.4330, 1756.8441, 1774.8589, 2034.5874, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960

2. gi|52001219 **Mass:** 61810 **Score:** 92 **Expect:** 5.3e-007 **Queries matched:** 12

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5166	883.5093	883.5239	-0.0146	278 -	284	0	QILQNLR
1005.5240	1004.5167	1004.5264	-0.0097	122 -	129	0	HQSQRPPR
1083.5607	1082.5534	1082.5581	-0.0046	37 -	45	0	LNAQRPDNR
1161.6338	1160.6265	1160.6275	-0.0010	122 -	130	1	HQSQRPPRR
1534.6824	1533.6751	1533.6630	0.0121	25 -	36	0	QQPEENACQFQR
1574.7834	1573.7761	1573.7637	0.0125	196 -	208	0	FNLAGNHEQEFLR
1603.7651	1602.7578	1602.7485	0.0094	285 -	299	0	GENESDEQGAIVTVR
1730.8826	1729.8753	1729.8648	0.0106	195 -	208	1	RFNLAGNHEQEFLR
1916.8501	1915.8428	1915.8409	0.0020	131 -	146	0	FQGQDQSQQQQDSHQK
2051.0413	2050.0340	2050.0384	-0.0044	82 -	98	0	RPFYSNAPQEIFIQQGR
2072.9436	2071.9363	2071.9420	-0.0056	130 -	146	1	RFQGQDQSQQQQDSHQK
2474.1160	2473.1087	2473.1371	-0.0284	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 906.4865, 958.4641, 990.5425, 1079.5360, 1111.5653, 1158.6116, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572, 1548.7029, 1624.7952, 1650.8367, 1714.4330, 1756.8441, 1774.8589, 2034.5874, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960

3. gi|21314465 **Mass:** 62042 **Score:** 92 **Expect:** 5.4e-007 **Queries matched:** 12

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5166	883.5093	883.5239	-0.0146	278 -	284	0	QILQNLR
1005.5240	1004.5167	1004.5264	-0.0097	122 -	129	0	HQSQRPPR
1083.5607	1082.5534	1082.5581	-0.0046	37 -	45	0	LNAQRPDNR
1161.6338	1160.6265	1160.6275	-0.0010	122 -	130	1	HQSQRPPRR
1534.6824	1533.6751	1533.6630	0.0121	25 -	36	0	QQPEENACQFQR
1574.7834	1573.7761	1573.7637	0.0125	196 -	208	0	FNLAGNHEQEFLR
1603.7651	1602.7578	1602.7485	0.0094	285 -	299	0	GENESDEQGAIVTVR
1730.8826	1729.8753	1729.8648	0.0106	195 -	208	1	RFNLAGNHEQEFLR
1916.8501	1915.8428	1915.8409	0.0020	131 -	146	0	FQGQDQSQQQQDSHQK
2051.0413	2050.0340	2050.0384	-0.0044	82 -	98	0	RPFYSNAPQEIFIQQGR

2072.9436	2071.9363	2071.9420	-0.0056	130 - 146	1	RFQGQDQSQQQQDSHQK
2474.1160	2473.1087	2473.1371	-0.0284	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 906.4865, 958.4641, 990.5425, 1079.5360, 1111.5653, 1158.6116, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572, 1548.7029, 1624.7952, 1650.8367, 1714.4330, 1756.8441, 1774.8589, 2034.5874, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960

4. gi|37789212 **Mass:** 61803 **Score:** 79 **Expect:** 1.2e-005 **Queries matched:** 11

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5166	883.5093	883.5239	-0.0146	278 - 284		0	QILQNLR
1005.5240	1004.5167	1004.5264	-0.0097	122 - 129		0	HQSQRPPR
1083.5607	1082.5534	1082.5581	-0.0046	37 - 45		0	LNAQRPDNR
1161.6338	1160.6265	1160.6275	-0.0010	122 - 130		1	HQSQRPPRR
1534.6824	1533.6751	1533.6630	0.0121	25 - 36		0	QQPEENACQFQR
1574.7834	1573.7761	1573.7637	0.0125	196 - 208		0	FNLAGNHEQEFLR
1603.7651	1602.7578	1602.7485	0.0094	285 - 299		0	GENESDEQGAIVTVR
1730.8826	1729.8753	1729.8648	0.0106	195 - 208		1	RFNLAGNHEQEFLR
1916.8501	1915.8428	1915.8409	0.0020	131 - 146		0	FQGQDQSQQQQDSHQK
2051.0413	2050.0340	2050.0384	-0.0044	82 - 98		0	RPFYSNAPQEIFIQQGR
2072.9436	2071.9363	2071.9420	-0.0056	130 - 146		1	RFQGQDQSQQQQDSHQK

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 906.4865, 958.4641, 990.5425, 1079.5360, 1111.5653, 1158.6116, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572, 1548.7029, 1624.7952, 1650.8367, 1714.4330, 1756.8441, 1774.8589, 2034.5874, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2474.1160, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960

5. gi|118776572 **Mass:** 24127 **Score:** 53 **Expect:** 0.004 **Queries matched:** 6

arachin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5240	1004.5167	1004.5264	-0.0097	122 - 129		0	HQSQRPPR
1161.6338	1160.6265	1160.6275	-0.0010	122 - 130		1	HQSQRPPRR
1534.6824	1533.6751	1533.6630	0.0121	25 - 36		0	QQPEENACQFQR
1916.8501	1915.8428	1915.8409	0.0020	131 - 146		0	FQGQDQSQQQQDSHQK
2051.0413	2050.0340	2050.0384	-0.0044	82 - 98		0	RPFYSNAPQEIFIQQGR
2072.9436	2071.9363	2071.9420	-0.0056	130 - 146		1	RFQGQDQSQQQQDSHQK

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 884.5166, 906.4865, 958.4641, 990.5425, 1079.5360, 1083.5607, 1111.5653, 1158.6116, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572, 1548.7029, 1574.7834, 1603.7651, 1624.7952, 1650.8367, 1714.4330, 1730.8826, 1756.8441, 1774.8589, 2034.5874, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2474.1160, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960

6. gi|52001221 **Mass:** 61836 **Score:** 50 **Expect:** 0.0086 **Queries matched:** 8

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5166	883.5093	883.5239	-0.0146	279 -	285	0	QILQNLR
1083.5607	1082.5534	1082.5581	-0.0046	37 -	45	0	LNAQRPDNR
1534.6824	1533.6751	1533.6630	0.0121	25 -	36	0	QQPEENACQFQR
1574.7834	1573.7761	1573.7637	0.0125	197 -	209	0	FNLAGNHEQEFLR
1603.7651	1602.7578	1602.7485	0.0094	286 -	300	0	GENESDEQGAIVTVR
1730.8826	1729.8753	1729.8648	0.0106	196 -	209	1	RFNLAGNHEQEFLR
2051.0413	2050.0340	2050.0384	-0.0044	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1160	2473.1087	2473.1371	-0.0284	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 906.4865, 958.4641, 990.5425, 1005.5240, 1079.5360, 1111.5653, 1158.6116, 1161.6338, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572, 1548.7029, 1624.7952, 1650.8367, 1714.4330, 1756.8441, 1774.8589, 1916.8501, 2034.5874, 2072.9436, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960

7. gi|9864777 **Mass:** 60754 **Score:** 33 **Expect:** 0.4 **Queries matched:** 6

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5607	1082.5534	1082.5581	-0.0046	38 -	46	0	LNAQRPDNR
1534.6824	1533.6751	1533.6630	0.0121	26 -	37	0	QQPEENACQFQR
1574.7834	1573.7761	1573.7637	0.0125	198 -	210	0	FNLAGNHEQEFLR
1730.8826	1729.8753	1729.8648	0.0106	197 -	210	1	RFNLAGNHEQEFLR
2051.0413	2050.0340	2050.0384	-0.0044	83 -	99	0	RPFYSNAPQEIFIQQGR
2474.1160	2473.1087	2473.1371	-0.0284	100 -	121	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 884.5166, 906.4865, 958.4641, 990.5425, 1005.5240, 1079.5360, 1111.5653, 1158.6116, 1161.6338, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572, 1548.7029, 1603.7651, 1624.7952, 1650.8367, 1714.4330, 1756.8441, 1774.8589, 1916.8501, 2034.5874, 2072.9436, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960

8. gi|118776570 **Mass:** 60681 **Score:** 33 **Expect:** 0.4 **Queries matched:** 6

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5607	1082.5534	1082.5581	-0.0046	37 -	45	0	LNAQRPDNR
1534.6824	1533.6751	1533.6630	0.0121	25 -	36	0	QQPEENACQFQR
1574.7834	1573.7761	1573.7637	0.0125	196 -	208	0	FNLAGNHEQEFLR
1730.8826	1729.8753	1729.8648	0.0106	195 -	208	1	RFNLAGNHEQEFLR
2051.0413	2050.0340	2050.0384	-0.0044	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1160	2473.1087	2473.1371	-0.0284	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 884.5166, 906.4865, 958.4641, 990.5425, 1005.5240, 1079.5360, 1111.5653, 1158.6116, 1161.6338, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572,

1548.7029, 1603.7651, 1624.7952, 1650.8367, 1714.4330, 1756.8441, 1774.8589, 1916.8501, 2034.5874, 2072.9436, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960

9. gi|5712199 **Mass:** 61430 **Score:** 33 **Expect:** 0.4 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5607	1082.5534	1082.5581	-0.0046	37	45	0	LNAQRPDNR
1534.6824	1533.6751	1533.6630	0.0121	25	36	0	QQPEENACQFQR
1574.7834	1573.7761	1573.7637	0.0125	196	208	0	FNLAGNHEQEFLR
1730.8826	1729.8753	1729.8648	0.0106	195	208	1	RFNLAGNHEQEFLR
2051.0413	2050.0340	2050.0384	-0.0044	82	98	0	RPFYSNAPQEIFIQQGR
2474.1160	2473.1087	2473.1371	-0.0284	99	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 884.5166, 906.4865, 958.4641, 990.5425, 1005.5240, 1079.5360, 1111.5653, 1158.6116, 1161.6338, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572, 1548.7029, 1603.7651, 1624.7952, 1650.8367, 1714.4330, 1756.8441, 1774.8589, 1916.8501, 2034.5874, 2072.9436, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960

10. gi|57669861 **Mass:** 61041 **Score:** 33 **Expect:** 0.41 **Queries matched:** 6

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5607	1082.5534	1082.5581	-0.0046	37	45	0	LNAQRPDNR
1534.6824	1533.6751	1533.6630	0.0121	25	36	0	QQPEENACQFQR
1574.7834	1573.7761	1573.7637	0.0125	196	208	0	FNLAGNHEQEFLR
1730.8826	1729.8753	1729.8648	0.0106	195	208	1	RFNLAGNHEQEFLR
2051.0413	2050.0340	2050.0384	-0.0044	82	98	0	RPFYSNAPQEIFIQQGR
2474.1160	2473.1087	2473.1371	-0.0284	99	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 884.5166, 906.4865, 958.4641, 990.5425, 1005.5240, 1079.5360, 1111.5653, 1158.6116, 1161.6338, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572, 1548.7029, 1603.7651, 1624.7952, 1650.8367, 1714.4330, 1756.8441, 1774.8589, 1916.8501, 2034.5874, 2072.9436, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted

Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|22135348** Score: **107** Expect: **1.7e-008**
trypsin inhibitor [Arachis hypogaea]

Nominal mass (M_r): **25768**; Calculated pI value: **6.66**
NCBI BLAST search of gi|22135348 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **10**
Sequence Coverage: **45%**

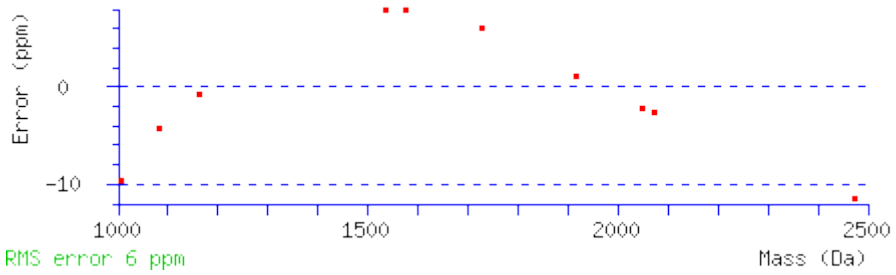
Matched peptides shown in **Bold Red**

```
    1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES
   51 EGGYIETWNP NNQEFECAGV ALSRLVLRRN ALRRPFYSNA PQEIFIQQGR
  101 GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH
  151 RFDEGDLIAV PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
  201 AGNHEQEFLR YQQQSRRRS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
27 - 38	1534.6824	1533.6751	1533.6630	0.0121	0	QQPEENACQFQR
39 - 47	1083.5607	1082.5534	1082.5581	-0.0046	0	LNAQRPDNR
84 - 100	2051.0413	2050.0340	2050.0384	-0.0044	0	RPFYSNAPQEIFIQQGR
101 - 122	2474.1160	2473.1087	2473.1371	-0.0284	0	GYFGLIFPGCPSTYEEPAQQGR
124 - 131	1005.5240	1004.5167	1004.5264	-0.0097	0	HQSQRPPR
124 - 132	1161.6338	1160.6265	1160.6275	-0.0010	1	HQSQRPPRR
132 - 148	2072.9436	2071.9363	2071.9420	-0.0056	1	RFQGQDQSQQQQDSHQK
133 - 148	1916.8501	1915.8428	1915.8409	0.0020	0	FQGQDQSQQQQDSHQK
197 - 210	1730.8826	1729.8753	1729.8648	0.0106	1	RFNLAGNHEQEFLR
198 - 210	1574.7834	1573.7761	1573.7637	0.0125	0	FNLAGNHEQEFLR

No match to: 805.3967, 809.3690, 861.4835, 867.4919, 884.5166, 906.4865, 958.4641, 990.5425, 1079.5360, 1111.5653, 1158.6116, 1174.6545, 1208.5692, 1286.6580, 1468.7272, 1487.7816, 1517.6572, 1548.7029, 1603.7651, 1624.7952, 1650.8367, 1714.4330, 1756.8441, 1774.8589, 2034.5874, 2185.0422, 2192.9983, 2256.7031, 2273.1602, 2295.1416, 2311.1089, 2488.1470, 2612.1519, 2796.9973, 2926.2881, 3070.2759, 3136.3115, 3153.3640, 3211.3855, 3301.3960



Spot 36

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:31:29 GMT
Top Score : 161 for gi|22135348, trypsin inhibitor [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|22135348	25768	161	trypsin inhibitor [Arachis hypogaea]
2.	gi|52001219	61810	154	arachin Ahy-1 [Arachis hypogaea]
3.	gi|21314465	62042	153	allergen Arah3/Arah4 [Arachis hypogaea]
4.	gi|37789212	61803	127	storage protein [Arachis hypogaea]
5.	gi|52001221	61836	98	arachin Ahy-2 [Arachis hypogaea]
6.	gi|118776572	24127	67	arachin 7 [Arachis hypogaea]
7.	gi|9864777	60754	60	Gly1 [Arachis hypogaea]
8.	gi|118776570	60681	52	arachin 6 [Arachis hypogaea]
9.	gi|5712199	61430	52	glycinin [Arachis hypogaea]
10.	gi|57669861	61041	52	arachin Ahy-4 [Arachis hypogaea]

Results List

1. gi|22135348 **Mass:** 25768 **Score:** 161 **Expect:** 7e-014 **Queries matched:** 15
trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
965.5071	964.4998	964.4838	0.0160	211	217	1	YQQQSRR
1005.5469	1004.5396	1004.5264	0.0132	124	131	0	HQSQRPPR
1083.5688	1082.5615	1082.5581	0.0035	39	47	0	LNAQRPDNR
1161.6273	1160.6200	1160.6275	-0.0075	124	132	1	HQSQRPPRR
1534.6646	1533.6573	1533.6630	-0.0057	27	38	0	QQPEENACQFQR
1574.7667	1573.7594	1573.7637	-0.0042	198	210	0	FNLAGNHEQEFLR
1730.8608	1729.8535	1729.8648	-0.0112	197	210	1	RFNLAGNHEQEFLR
1916.8315	1915.8242	1915.8409	-0.0166	133	148	0	FQGQDQSQQQQDSHQK
2051.0408	2050.0335	2050.0384	-0.0049	84	100	0	RPFYSNAPQEIFIQQGR
2072.9502	2071.9429	2071.9420	0.0010	132	148	1	RFQGQDQSQQQQDSHQK
2309.1033	2308.0960	2308.0693	0.0267	133	151	1	FQGQDQSQQQQDSHQKVHR

2474.1519	2473.1446	2473.1371	0.0075	101 - 122	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3293	2504.3220	2504.3036	0.0185	80 - 100	1	NALRRPFYSNAPQEIFIQQGR
2630.2595	2629.2522	2629.2383	0.0140	101 - 123	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4026	3069.3953	3069.3773	0.0180	48 - 74	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 884.5511, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1603.7527, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 1986.9550, 2035.5862, 2037.9482, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2469.2932, 2490.1853, 2521.2759, 2612.2136, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

2. gi|52001219 **Mass:** 61810 **Score:** 154 **Expect:** 3.5e-013 **Queries matched:** 19

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5511	883.5438	883.5239	0.0199	278 - 284		0	QILQNLR
965.5071	964.4998	964.4838	0.0160	209 - 215		1	YQQQSRR
1005.5469	1004.5396	1004.5264	0.0132	122 - 129		0	HQSQRPPR
1083.5688	1082.5615	1082.5581	0.0035	37 - 45		0	LNAQRPDNR
1161.6273	1160.6200	1160.6275	-0.0075	122 - 130		1	HQSQRPPRR
1534.6646	1533.6573	1533.6630	-0.0057	25 - 36		0	QQPEENACQFQR
1574.7667	1573.7594	1573.7637	-0.0042	196 - 208		0	FNLAGNHEQEFLR
1603.7527	1602.7454	1602.7485	-0.0030	285 - 299		0	GENESDEQGAIVTVR
1730.8608	1729.8535	1729.8648	-0.0112	195 - 208		1	RFNLAGNHEQEFLR
1916.8315	1915.8242	1915.8409	-0.0166	131 - 146		0	FQGQDQSQQQQDSHQK
1986.9550	1985.9477	1985.9765	-0.0288	285 - 303		1	GENESDEQGAIVTVRGGLR
2051.0408	2050.0335	2050.0384	-0.0049	82 - 98		0	RPFYSNAPQEIFIQQGR
2072.9502	2071.9429	2071.9420	0.0010	130 - 146		1	RFQGQDQSQQQQDSHQK
2309.1033	2308.0960	2308.0693	0.0267	131 - 149		1	FQGQDQSQQQQDSHQKVHR
2469.2932	2468.2859	2468.2618	0.0241	278 - 299		1	QILQNLRGENESDEQGAIVTVR
2474.1519	2473.1446	2473.1371	0.0075	99 - 120		0	GYFGLIFPGCPSTYEEPAQQGR
2505.3293	2504.3220	2504.3036	0.0185	78 - 98		1	NALRRPFYSNAPQEIFIQQGR
2630.2595	2629.2522	2629.2383	0.0140	99 - 121		1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4026	3069.3953	3069.3773	0.0180	46 - 72		0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 2035.5862, 2037.9482, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2490.1853, 2521.2759, 2612.2136, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

3. gi|21314465 **Mass:** 62042 **Score:** 153 **Expect:** 4.4e-013 **Queries matched:** 19

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5511	883.5438	883.5239	0.0199	278	284	0	QILQNLR
965.5071	964.4998	964.4838	0.0160	209	215	1	YQQQSRR
1005.5469	1004.5396	1004.5264	0.0132	122	129	0	HQSQRPPR
1083.5688	1082.5615	1082.5581	0.0035	37	45	0	LNAQRPDNR
1161.6273	1160.6200	1160.6275	-0.0075	122	130	1	HQSQRPPRR
1534.6646	1533.6573	1533.6630	-0.0057	25	36	0	QQPEENACQFQR
1574.7667	1573.7594	1573.7637	-0.0042	196	208	0	FNLAGNHEQEFLR
1603.7527	1602.7454	1602.7485	-0.0030	285	299	0	GENESDEQGAIVTVR
1730.8608	1729.8535	1729.8648	-0.0112	195	208	1	RFNLAGNHEQEFLR
1916.8315	1915.8242	1915.8409	-0.0166	131	146	0	FQGQDQSQQQQDSHQK
1986.9550	1985.9477	1985.9765	-0.0288	285	303	1	GENESDEQGAIVTVRGGLR
2051.0408	2050.0335	2050.0384	-0.0049	82	98	0	RPFYSNAPQEIFIQQGR
2072.9502	2071.9429	2071.9420	0.0010	130	146	1	RFQGQDQSQQQQDSHQK
2309.1033	2308.0960	2308.0693	0.0267	131	149	1	FQGQDQSQQQQDSHQKVHR
2469.2932	2468.2859	2468.2618	0.0241	278	299	1	QILQNLRGENESDEQGAIVTVR
2474.1519	2473.1446	2473.1371	0.0075	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3293	2504.3220	2504.3036	0.0185	78	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2595	2629.2522	2629.2383	0.0140	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4026	3069.3953	3069.3773	0.0180	46	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 2035.5862, 2037.9482, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2490.1853, 2521.2759, 2612.2136, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

4. gi|37789212 **Mass:** 61803 **Score:** 127 **Expect:** 1.7e-010 **Queries matched:** 17

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5511	883.5438	883.5239	0.0199	278	284	0	QILQNLR
965.5071	964.4998	964.4838	0.0160	209	215	1	YQQQSRR
1005.5469	1004.5396	1004.5264	0.0132	122	129	0	HQSQRPPR
1083.5688	1082.5615	1082.5581	0.0035	37	45	0	LNAQRPDNR
1161.6273	1160.6200	1160.6275	-0.0075	122	130	1	HQSQRPPRR
1534.6646	1533.6573	1533.6630	-0.0057	25	36	0	QQPEENACQFQR
1574.7667	1573.7594	1573.7637	-0.0042	196	208	0	FNLAGNHEQEFLR
1603.7527	1602.7454	1602.7485	-0.0030	285	299	0	GENESDEQGAIVTVR
1730.8608	1729.8535	1729.8648	-0.0112	195	208	1	RFNLAGNHEQEFLR
1916.8315	1915.8242	1915.8409	-0.0166	131	146	0	FQGQDQSQQQQDSHQK
1986.9550	1985.9477	1985.9765	-0.0288	285	303	1	GENESDEQGAIVTVRGGLR

2051.0408	2050.0335	2050.0384	-0.0049	82 - 98	0	RPFYSNAPQEIFIQQGR
2072.9502	2071.9429	2071.9420	0.0010	130 - 146	1	RFQGQDQSQQQQDSHQK
2309.1033	2308.0960	2308.0693	0.0267	131 - 149	1	FQGQDQSQQQQDSHQKVHR
2469.2932	2468.2859	2468.2618	0.0241	278 - 299	1	QILQNLRGENESDEQGAIVTVR
2505.3293	2504.3220	2504.3036	0.0185	78 - 98	1	NALRRPFYSNAPQEIFIQQGR
3070.4026	3069.3953	3069.3773	0.0180	46 - 72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 2035.5862, 2037.9482, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2474.1519, 2490.1853, 2521.2759, 2612.2136, 2630.2595, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

5. gi|52001221 **Mass:** 61836 **Score:** 98 **Expect:** 1.3e-007 **Queries matched:** 14

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
884.5511	883.5438	883.5239	0.0199	279 - 285	0	QILQNLR
965.5071	964.4998	964.4838	0.0160	210 - 216	1	YQQQSRR
1083.5688	1082.5615	1082.5581	0.0035	37 - 45	0	LNAQRPDNR
1534.6646	1533.6573	1533.6630	-0.0057	25 - 36	0	QQPEENACQFQR
1574.7667	1573.7594	1573.7637	-0.0042	197 - 209	0	FNLAGNHEQEFLR
1603.7527	1602.7454	1602.7485	-0.0030	286 - 300	0	GENESDEQGAIVTVR
1730.8608	1729.8535	1729.8648	-0.0112	196 - 209	1	RFNLAGNHEQEFLR
1986.9550	1985.9477	1985.9765	-0.0288	286 - 304	1	GENESDEQGAIVTVRGGLR
2051.0408	2050.0335	2050.0384	-0.0049	82 - 98	0	RPFYSNAPQEIFIQQGR
2469.2932	2468.2859	2468.2618	0.0241	279 - 300	1	QILQNLRGENESDEQGAIVTVR
2474.1519	2473.1446	2473.1371	0.0075	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3293	2504.3220	2504.3036	0.0185	78 - 98	1	NALRRPFYSNAPQEIFIQQGR
2630.2595	2629.2522	2629.2383	0.0140	99 - 121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4026	3069.3953	3069.3773	0.0180	46 - 72	0	LESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 1005.5469, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1161.6273, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 1916.8315, 2035.5862, 2037.9482, 2072.9502, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2309.1033, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2490.1853, 2521.2759, 2612.2136, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

6. gi|118776572 **Mass:** 24127 **Score:** 67 **Expect:** 0.00017 **Queries matched:** 8

arachin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
1005.5469	1004.5396	1004.5264	0.0132	122 - 129	0	HQSQRPPR
1161.6273	1160.6200	1160.6275	-0.0075	122 - 130	1	HQSQRPPRR

1534.6646	1533.6573	1533.6630	-0.0057	25 - 36	0	QQPEENACQFQR
1916.8315	1915.8242	1915.8409	-0.0166	131 - 146	0	FQGQDQSQQQQDSHQK
2051.0408	2050.0335	2050.0384	-0.0049	82 - 98	0	RPFYSNAPQEIFIQQGR
2072.9502	2071.9429	2071.9420	0.0010	130 - 146	1	RFQGQDQSQQQQDSHQK
2309.1033	2308.0960	2308.0693	0.0267	131 - 149	1	FQGQDQSQQQQDSHQKVHR
2505.3293	2504.3220	2504.3036	0.0185	78 - 98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 884.5511, 965.5071, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1083.5688, 1100.5778, 1145.0806, 1145.5693, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1574.7667, 1603.7527, 1608.7656, 1624.7751, 1730.8608, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 1986.9550, 2035.5862, 2037.9482, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2469.2932, 2474.1519, 2490.1853, 2521.2759, 2612.2136, 2630.2595, 2785.3833, 3070.4026, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

7. gi|9864777 **Mass:** 60754 **Score:** 60 **Expect:** 0.00098 **Queries matched:** 10

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
965.5071	964.4998	964.4838	0.0160	211 - 217		1	YQQQSRR
1083.5688	1082.5615	1082.5581	0.0035	38 - 46		0	LNAQRPDNR
1534.6646	1533.6573	1533.6630	-0.0057	26 - 37		0	QQPEENACQFQR
1574.7667	1573.7594	1573.7637	-0.0042	198 - 210		0	FNLAGNHEQEFLR
1730.8608	1729.8535	1729.8648	-0.0112	197 - 210		1	RFNLAGNHEQEFLR
2051.0408	2050.0335	2050.0384	-0.0049	83 - 99		0	RPFYSNAPQEIFIQQGR
2474.1519	2473.1446	2473.1371	0.0075	100 - 121		0	GYFGLIFPGCPSTYEEPAQQGR
2505.3293	2504.3220	2504.3036	0.0185	79 - 99		1	NALRRPFYSNAPQEIFIQQGR
2630.2595	2629.2522	2629.2383	0.0140	100 - 122		1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4026	3069.3953	3069.3773	0.0180	47 - 73		0	LESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 884.5511, 1005.5469, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1161.6273, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1603.7527, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 1916.8315, 1986.9550, 2035.5862, 2037.9482, 2072.9502, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2309.1033, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2469.2932, 2490.1853, 2521.2759, 2612.2136, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

8. gi|118776570 **Mass:** 60681 **Score:** 52 **Expect:** 0.005 **Queries matched:** 9

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5688	1082.5615	1082.5581	0.0035	37 - 45		0	LNAQRPDNR
1534.6646	1533.6573	1533.6630	-0.0057	25 - 36		0	QQPEENACQFQR
1574.7667	1573.7594	1573.7637	-0.0042	196 - 208		0	FNLAGNHEQEFLR
1730.8608	1729.8535	1729.8648	-0.0112	195 - 208		1	RFNLAGNHEQEFLR

2051.0408	2050.0335	2050.0384	-0.0049	82 - 98	0	RPFYSNAPQEIFIQQGR
2474.1519	2473.1446	2473.1371	0.0075	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3293	2504.3220	2504.3036	0.0185	78 - 98	1	NALRRPFYSNAPQEIFIQQGR
2630.2595	2629.2522	2629.2383	0.0140	99 - 121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4026	3069.3953	3069.3773	0.0180	46 - 72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 884.5511, 965.5071, 1005.5469, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1161.6273, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1603.7527, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 1916.8315, 1986.9550, 2035.5862, 2037.9482, 2072.9502, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2309.1033, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2469.2932, 2490.1853, 2521.2759, 2612.2136, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

9. gi|5712199 **Mass:** 61430 **Score:** 52 **Expect:** 0.0052 **Queries matched:** 9

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5688	1082.5615	1082.5581	0.0035	37 -	45	0	LNAQRPDNR
1534.6646	1533.6573	1533.6630	-0.0057	25 -	36	0	QQPEENACQFQR
1574.7667	1573.7594	1573.7637	-0.0042	196 -	208	0	FNLAGNHEQEFLR
1730.8608	1729.8535	1729.8648	-0.0112	195 -	208	1	RFNLAGNHEQEFLR
2051.0408	2050.0335	2050.0384	-0.0049	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1519	2473.1446	2473.1371	0.0075	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3293	2504.3220	2504.3036	0.0185	78 -	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2595	2629.2522	2629.2383	0.0140	99 -	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4026	3069.3953	3069.3773	0.0180	46 -	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 884.5511, 965.5071, 1005.5469, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1161.6273, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1603.7527, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 1916.8315, 1986.9550, 2035.5862, 2037.9482, 2072.9502, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2309.1033, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2469.2932, 2490.1853, 2521.2759, 2612.2136, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

10. gi|57669861 **Mass:** 61041 **Score:** 52 **Expect:** 0.0052 **Queries matched:** 9

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5688	1082.5615	1082.5581	0.0035	37 -	45	0	LNAQRPDNR
1534.6646	1533.6573	1533.6630	-0.0057	25 -	36	0	QQPEENACQFQR
1574.7667	1573.7594	1573.7637	-0.0042	196 -	208	0	FNLAGNHEQEFLR
1730.8608	1729.8535	1729.8648	-0.0112	195 -	208	1	RFNLAGNHEQEFLR
2051.0408	2050.0335	2050.0384	-0.0049	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1519	2473.1446	2473.1371	0.0075	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR

2505.3293	2504.3220	2504.3036	0.0185	78 - 98	1	NALRRPFYSNAPQEIFIQQGR
2630.2595	2629.2522	2629.2383	0.0140	99 - 121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4026	3069.3953	3069.3773	0.0180	46 - 72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 884.5511, 965.5071, 1005.5469, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1161.6273, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1603.7527, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 1916.8315, 1986.9550, 2035.5862, 2037.9482, 2072.9502, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2309.1033, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2469.2932, 2490.1853, 2521.2759, 2612.2136, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 78

1. Rank Protein View

Match to: **gi|22135348** Score: **161** Expect: **7e-014**
trypsin inhibitor [Arachis hypogaea]

Nominal mass (M_r): **25768**; Calculated pI value: **6.66**
NCBI BLAST search of gi|22135348 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **78**
Number of mass values matched: **15**
Sequence Coverage: **64%**

Matched peptides shown in **Bold Red**

```
  1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES
 51 EGGYIETWNP NNQEFECAGV ALSRLVLRRN ALRRPFYSNA PQEIFIQQGR
101 GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH
151 RFDEGDLIAV PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
201 AGNHEQEFLR YQQQSRRRS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
27 - 38	1534.6646	1533.6573	1533.6630	-0.0057	0	QQPEENACQFQR
39 - 47	1083.5688	1082.5615	1082.5581	0.0035	0	LNAQRPDNR
48 - 74	3070.4026	3069.3953	3069.3773	0.0180	0	IESEGGYIETWNPNNQEFECAGVALSR
80 - 100	2505.3293	2504.3220	2504.3036	0.0185	1	NALRRPFYSNAPQEIFIQQGR
84 - 100	2051.0408	2050.0335	2050.0384	-0.0049	0	RPFYSNAPQEIFIQQGR
101 - 122	2474.1519	2473.1446	2473.1371	0.0075	0	GYFGLIFPGCPSTYEEPAQQGR
101 - 123	2630.2595	2629.2522	2629.2383	0.0140	1	GYFGLIFPGCPSTYEEPAQQGRR
124 - 131	1005.5469	1004.5396	1004.5264	0.0132	0	HQSQRPPR
124 - 132	1161.6273	1160.6200	1160.6275	-0.0075	1	HQSQRPPRR
132 - 148	2072.9502	2071.9429	2071.9420	0.0010	1	RFQGQDQSQQQQDSHQK
133 - 148	1916.8315	1915.8242	1915.8409	-0.0166	0	FQGQDQSQQQQDSHQK
133 - 151	2309.1033	2308.0960	2308.0693	0.0267	1	FQGQDQSQQQQDSHQKVHR
197 - 210	1730.8608	1729.8535	1729.8648	-0.0112	1	RFNLAGNHEQEFLR
198 - 210	1574.7667	1573.7594	1573.7637	-0.0042	0	FNLAGNHEQEFLR
211 - 217	965.5071	964.4998	964.4838	0.0160	1	YQQQSRR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 884.5511, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1603.7527, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 1986.9550, 2035.5862, 2037.9482, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2469.2932, 2490.1853, 2521.2759, 2612.2136, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

2. Rank Protein View

Match to: **gi|52001219** Score: **154** Expect: **3.5e-013**
arachin Ahy-1 [Arachis hypogaea]

Nominal mass (M_r): **61810**; Calculated pI value: **5.57**
NCBI BLAST search of gi|52001219 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **78**
Number of mass values matched: **19**
Sequence Coverage: **31%**

Matched peptides shown in **Bold Red**

```
     1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
    51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
   101 FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
   201 NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG QHGRRERAGQ
   251 EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG
   301 GLRILSPDRK RRQQYERPDE EEEYDEDEYE YDEEERQHDR RRGRGSRGSG
   351 NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA
   401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG
   451 HVLVVPQNFA VAGKSQSENF EYVAFKTDSR PSIANLAGEN SFIDNLPEEV
   501 VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 36	1534.6646	1533.6573	1533.6630	-0.0057	0	QQPEENACQFQR
37 - 45	1083.5688	1082.5615	1082.5581	0.0035	0	LNAQRPDNR
46 - 72	3070.4026	3069.3953	3069.3773	0.0180	0	IESEGGYIETWNPNNQEFECAGVALSR
78 - 98	2505.3293	2504.3220	2504.3036	0.0185	1	NALRRPFYSNAPQEIFIQQGR
82 - 98	2051.0408	2050.0335	2050.0384	-0.0049	0	RPFYSNAPQEIFIQQGR
99 - 120	2474.1519	2473.1446	2473.1371	0.0075	0	GYFGLIFPGCPSTYEEPAQQGR
99 - 121	2630.2595	2629.2522	2629.2383	0.0140	1	GYFGLIFPGCPSTYEEPAQQGRR
122 - 129	1005.5469	1004.5396	1004.5264	0.0132	0	HQSQRPPR
122 - 130	1161.6273	1160.6200	1160.6275	-0.0075	1	HQSQRPPRR
130 - 146	2072.9502	2071.9429	2071.9420	0.0010	1	RFQGQDQSQQQQDSHQK
131 - 146	1916.8315	1915.8242	1915.8409	-0.0166	0	FQGQDQSQQQQDSHQK
131 - 149	2309.1033	2308.0960	2308.0693	0.0267	1	FQGQDQSQQQQDSHQKVHR
195 - 208	1730.8608	1729.8535	1729.8648	-0.0112	1	RFNLAGNHEQEFLR
196 - 208	1574.7667	1573.7594	1573.7637	-0.0042	0	FNLAGNHEQEFLR
209 - 215	965.5071	964.4998	964.4838	0.0160	1	YQQQSRR
278 - 284	884.5511	883.5438	883.5239	0.0199	0	QILQNLR
278 - 299	2469.2932	2468.2859	2468.2618	0.0241	1	QILQNLRGENESDEQGAIVTVR
285 - 299	1603.7527	1602.7454	1602.7485	-0.0030	0	GENESDEQGAIVTVR
285 - 303	1986.9550	1985.9477	1985.9765	-0.0288	1	GENESDEQGAIVTVRGGLR

No match to: 805.4823, 809.4392, 827.4273, 845.1008, 855.0770, 861.0867, 865.9586, 866.4548, 867.5010, 871.0408, 877.0644, 1019.5136, 1020.0039, 1026.0431, 1026.5428, 1037.4827, 1066.0824, 1080.5291, 1082.0525, 1100.5778, 1145.0806, 1145.5693, 1162.5248, 1175.5630, 1179.5425, 1253.6580, 1277.0992, 1318.6223, 1342.6791, 1517.6354, 1608.7656, 1624.7751, 1752.8438, 1756.8307, 1774.8339, 1778.8157, 1780.8662, 1792.7673, 1853.8578, 1870.8848, 2035.5862, 2037.9482, 2153.0095, 2185.0342, 2209.0166, 2273.1631, 2311.1111, 2333.1218, 2351.0764, 2452.2832, 2490.1853, 2521.2759, 2612.2136, 2785.3833, 3136.5469, 3211.5637, 3216.4624, 3301.6013, 3318.8306

Spot 37

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:38:10 GMT
Top Score : 110 for gi|22135348, trypsin inhibitor [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|22135348	25768	110	trypsin inhibitor [Arachis hypogaea]
2.	gi|52001219	61810	96	arachin Ahy-1 [Arachis hypogaea]
3.	gi|37789212	61803	96	storage protein [Arachis hypogaea]
4.	gi|21314465	62042	96	allergen Arah3/Arah4 [Arachis hypogaea]
5.	gi|118776572	24127	58	arachin 7 [Arachis hypogaea]
6.	gi|52001221	61836	50	arachin Ahy-2 [Arachis hypogaea]
7.	gi|118776570	60681	36	arachin 6 [Arachis hypogaea]
8.	gi|5712199	61430	36	glycinin [Arachis hypogaea]
9.	gi|57669861	61041	36	arachin Ahy-4 [Arachis hypogaea]
10.	gi|108595573	61041	36	arachin Ahy-4 [Arachis hypogaea]

Results List

1. gi|22135348 **Mass:** 25768 **Score:** 110 **Expect:** 8.7e-009 **Queries matched:** 10
trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
965.4828	964.4755	964.4838	-0.0083	211	217	1	YQQQSRR
1005.5358	1004.5285	1004.5264	0.0021	124	131	0	HQSQRPPR
1083.5725	1082.5652	1082.5581	0.0072	39	47	0	LNAQRPDNR
1534.6833	1533.6760	1533.6630	0.0130	27	38	0	QQPEENACQFQR
1574.7833	1573.7760	1573.7637	0.0124	198	210	0	FNLAGNHEQEFLR
1730.8890	1729.8817	1729.8648	0.0170	197	210	1	RFNLAGNHEQEFLR
1916.8605	1915.8532	1915.8409	0.0124	133	148	0	FQGQDQSQQQQDSHQK
2051.0603	2050.0530	2050.0384	0.0146	84	100	0	RPFYSNAPQEIFIQQGR
2072.9563	2071.9490	2071.9420	0.0071	132	148	1	RFQGQDQSQQQQDSHQK
2309.0925	2308.0852	2308.0693	0.0159	133	151	1	FQGQDQSQQQQDSHQKVHR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 884.5330, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1603.7629, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 2037.9637, 2094.9377, 2153.0156, 2273.1555, 2466.2058

2. gi|52001219 **Mass:** 61810 **Score:** 96 **Expect:** 2.1e-007 **Queries matched:** 12

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5330	883.5257	883.5239	0.0018	278	284	0	QILQNLR
965.4828	964.4755	964.4838	-0.0083	209	215	1	YQQQSRR
1005.5358	1004.5285	1004.5264	0.0021	122	129	0	HQSQRPPR
1083.5725	1082.5652	1082.5581	0.0072	37	45	0	LNAQRPDNR
1534.6833	1533.6760	1533.6630	0.0130	25	36	0	QQPEENACQFQR
1574.7833	1573.7760	1573.7637	0.0124	196	208	0	FNLAGNHEQEFLR
1603.7629	1602.7556	1602.7485	0.0072	285	299	0	GENESDEQGAIVTVR
1730.8890	1729.8817	1729.8648	0.0170	195	208	1	RFNLAGNHEQEFLR
1916.8605	1915.8532	1915.8409	0.0124	131	146	0	FQGQDQSQQQQDSHQK
2051.0603	2050.0530	2050.0384	0.0146	82	98	0	RPFYSNAPQEIFIQQGR
2072.9563	2071.9490	2071.9420	0.0071	130	146	1	RFQGQDQSQQQQDSHQK
2309.0925	2308.0852	2308.0693	0.0159	131	149	1	FQGQDQSQQQQDSHQKVHR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 2037.9637, 2094.9377, 2153.0156, 2273.1555, 2466.2058

3. gi|37789212 **Mass:** 61803 **Score:** 96 **Expect:** 2.1e-007 **Queries matched:** 12

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5330	883.5257	883.5239	0.0018	278	284	0	QILQNLR
965.4828	964.4755	964.4838	-0.0083	209	215	1	YQQQSRR
1005.5358	1004.5285	1004.5264	0.0021	122	129	0	HQSQRPPR
1083.5725	1082.5652	1082.5581	0.0072	37	45	0	LNAQRPDNR
1534.6833	1533.6760	1533.6630	0.0130	25	36	0	QQPEENACQFQR
1574.7833	1573.7760	1573.7637	0.0124	196	208	0	FNLAGNHEQEFLR
1603.7629	1602.7556	1602.7485	0.0072	285	299	0	GENESDEQGAIVTVR
1730.8890	1729.8817	1729.8648	0.0170	195	208	1	RFNLAGNHEQEFLR
1916.8605	1915.8532	1915.8409	0.0124	131	146	0	FQGQDQSQQQQDSHQK
2051.0603	2050.0530	2050.0384	0.0146	82	98	0	RPFYSNAPQEIFIQQGR
2072.9563	2071.9490	2071.9420	0.0071	130	146	1	RFQGQDQSQQQQDSHQK
2309.0925	2308.0852	2308.0693	0.0159	131	149	1	FQGQDQSQQQQDSHQKVHR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 1037.4762, 1046.5984, 1050.0861,

1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 2037.9637, 2094.9377, 2153.0156, 2273.1555, 2466.2058

4. gi|21314465 **Mass:** 62042 **Score:** 96 **Expect:** 2.1e-007 **Queries matched:** 12

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5330	883.5257	883.5239	0.0018	278	284	0	QILQNLR
965.4828	964.4755	964.4838	-0.0083	209	215	1	YQQQSRR
1005.5358	1004.5285	1004.5264	0.0021	122	129	0	HQSQRPPR
1083.5725	1082.5652	1082.5581	0.0072	37	45	0	LNAQRPDNR
1534.6833	1533.6760	1533.6630	0.0130	25	36	0	QQPEENACQFQR
1574.7833	1573.7760	1573.7637	0.0124	196	208	0	FNLAGNHEQEFLR
1603.7629	1602.7556	1602.7485	0.0072	285	299	0	GENESDEQGAIVTVR
1730.8890	1729.8817	1729.8648	0.0170	195	208	1	RFNLAGNHEQEFLR
1916.8605	1915.8532	1915.8409	0.0124	131	146	0	FQGQDQSQQQQDSHQK
2051.0603	2050.0530	2050.0384	0.0146	82	98	0	RPFYSNAPQEIFIQQGR
2072.9563	2071.9490	2071.9420	0.0071	130	146	1	RFQGQDQSQQQQDSHQK
2309.0925	2308.0852	2308.0693	0.0159	131	149	1	FQGQDQSQQQQDSHQKVHR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 2037.9637, 2094.9377, 2153.0156, 2273.1555, 2466.2058

5. gi|118776572 **Mass:** 24127 **Score:** 58 **Expect:** 0.0014 **Queries matched:** 6

arachin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5358	1004.5285	1004.5264	0.0021	122	129	0	HQSQRPPR
1534.6833	1533.6760	1533.6630	0.0130	25	36	0	QQPEENACQFQR
1916.8605	1915.8532	1915.8409	0.0124	131	146	0	FQGQDQSQQQQDSHQK
2051.0603	2050.0530	2050.0384	0.0146	82	98	0	RPFYSNAPQEIFIQQGR
2072.9563	2071.9490	2071.9420	0.0071	130	146	1	RFQGQDQSQQQQDSHQK
2309.0925	2308.0852	2308.0693	0.0159	131	149	1	FQGQDQSQQQQDSHQKVHR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 884.5330, 965.4828, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1083.5725, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1574.7833, 1603.7629, 1608.7889, 1624.7947, 1730.8890, 1774.8770, 1780.8928, 2037.9637, 2094.9377, 2153.0156, 2273.1555, 2466.2058

6. gi|52001221 **Mass:** 61836 **Score:** 50 **Expect:** 0.008 **Queries matched:** 8

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5330	883.5257	883.5239	0.0018	279	285	0	QILQNLR

965.4828	964.4755	964.4838	-0.0083	210 - 216	1	YQQQSRR
1083.5725	1082.5652	1082.5581	0.0072	37 - 45	0	LNAQRPDNR
1534.6833	1533.6760	1533.6630	0.0130	25 - 36	0	QQPEENACQFQR
1574.7833	1573.7760	1573.7637	0.0124	197 - 209	0	FNLAGNHEQEFLR
1603.7629	1602.7556	1602.7485	0.0072	286 - 300	0	GENESDEQGAIVTVR
1730.8890	1729.8817	1729.8648	0.0170	196 - 209	1	RFNLAGNHEQEFLR
2051.0603	2050.0530	2050.0384	0.0146	82 - 98	0	RPFYSNAPQEIFIQQGR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 1005.5358, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 1916.8605, 2037.9637, 2072.9563, 2094.9377, 2153.0156, 2273.1555, 2309.0925, 2466.2058

7. gi|118776570 **Mass:** 60681 **Score:** 36 **Expect:** 0.24 **Queries matched:** 6

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5725	1082.5652	1082.5581	0.0072	37 -	45	0	LNAQRPDNR
1534.6833	1533.6760	1533.6630	0.0130	25 -	36	0	QQPEENACQFQR
1574.7833	1573.7760	1573.7637	0.0124	196 -	208	0	FNLAGNHEQEFLR
1730.8890	1729.8817	1729.8648	0.0170	195 -	208	1	RFNLAGNHEQEFLR
2051.0603	2050.0530	2050.0384	0.0146	82 -	98	0	RPFYSNAPQEIFIQQGR
2466.2058	2465.1985	2465.2486	-0.0501	4 -	24	0	LLELSFCFCFLVLGASSISFR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 884.5330, 965.4828, 1005.5358, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1603.7629, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 1916.8605, 2037.9637, 2072.9563, 2094.9377, 2153.0156, 2273.1555, 2309.0925

8. gi|5712199 **Mass:** 61430 **Score:** 36 **Expect:** 0.24 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5725	1082.5652	1082.5581	0.0072	37 -	45	0	LNAQRPDNR
1534.6833	1533.6760	1533.6630	0.0130	25 -	36	0	QQPEENACQFQR
1574.7833	1573.7760	1573.7637	0.0124	196 -	208	0	FNLAGNHEQEFLR
1730.8890	1729.8817	1729.8648	0.0170	195 -	208	1	RFNLAGNHEQEFLR
2051.0603	2050.0530	2050.0384	0.0146	82 -	98	0	RPFYSNAPQEIFIQQGR
2466.2058	2465.1985	2465.2486	-0.0501	4 -	24	0	LLELSFCFCFLVLGASSISFR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 884.5330, 965.4828, 1005.5358, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1603.7629, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 1916.8605, 2037.9637, 2072.9563, 2094.9377, 2153.0156, 2273.1555, 2309.0925

9. gi|57669861 **Mass:** 61041 **Score:** 36 **Expect:** 0.25 **Queries matched:** 6

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5725	1082.5652	1082.5581	0.0072	37	45	0	LNAQRPDNR
1534.6833	1533.6760	1533.6630	0.0130	25	36	0	QQPEENACQFQR
1574.7833	1573.7760	1573.7637	0.0124	196	208	0	FNLAGNHEQEFLR
1730.8890	1729.8817	1729.8648	0.0170	195	208	1	RFNLAGNHEQEFLR
2051.0603	2050.0530	2050.0384	0.0146	82	98	0	RPFYSNAPQEIFIQQGR
2466.2058	2465.1985	2465.2486	-0.0501	4	24	0	LLELSFCFCFLVLGASSISFR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 884.5330, 965.4828, 1005.5358, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1603.7629, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 1916.8605, 2037.9637, 2072.9563, 2094.9377, 2153.0156, 2273.1555, 2309.0925

10. gi|108595573 **Mass:** 61041 **Score:** 36 **Expect:** 0.25 **Queries matched:** 6

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5725	1082.5652	1082.5581	0.0072	37	45	0	LNAQRPDNR
1534.6833	1533.6760	1533.6630	0.0130	25	36	0	QQPEENACQFQR
1574.7833	1573.7760	1573.7637	0.0124	196	208	0	FNLAGNHEQEFLR
1730.8890	1729.8817	1729.8648	0.0170	195	208	1	RFNLAGNHEQEFLR
2051.0603	2050.0530	2050.0384	0.0146	82	98	0	RPFYSNAPQEIFIQQGR
2466.2058	2465.1985	2465.2486	-0.0501	4	24	0	LLELSFCFCFLVLGASSISFR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 884.5330, 965.4828, 1005.5358, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1603.7629, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 1916.8605, 2037.9637, 2072.9563, 2094.9377, 2153.0156, 2273.1555, 2309.0925

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 46

Rank 1 Protein View

Match to: **gi|22135348** Score: **110** Expect: **8.7e-009**
trypsin inhibitor [Arachis hypogaea]

Nominal mass (M_r): **25768**; Calculated pI value: **6.66**
NCBI BLAST search of gi|22135348 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **46**
Number of mass values matched: **10**
Sequence Coverage: **39%**

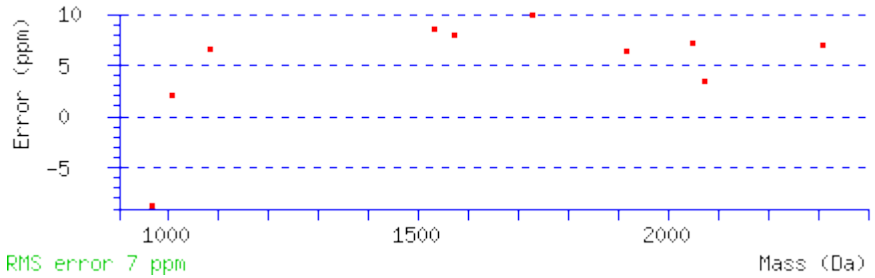
Matched peptides shown in **Bold Red**

```
     1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES
    51 EGGYIETWNP NNQEFECAGV ALSRLVLRRN ALRRPFYSNA PQEIFIQQGR
   101 GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH
   151 RFDEGDLIAV PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
   201 AGNHEQEFLR YQQQSRRRS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
27 - 38	1534.6833	1533.6760	1533.6630	0.0130	0	QQPEENACQFQR
39 - 47	1083.5725	1082.5652	1082.5581	0.0072	0	LNAQRPDNR
84 - 100	2051.0603	2050.0530	2050.0384	0.0146	0	RPFYSNAPQEIFIQQGR
124 - 131	1005.5358	1004.5285	1004.5264	0.0021	0	HQSQRPPR
132 - 148	2072.9563	2071.9490	2071.9420	0.0071	1	RFQGQDQSQQQQDSHQK
133 - 148	1916.8605	1915.8532	1915.8409	0.0124	0	FQGQDQSQQQQDSHQK
133 - 151	2309.0925	2308.0852	2308.0693	0.0159	1	FQGQDQSQQQQDSHQKVHR
197 - 210	1730.8890	1729.8817	1729.8648	0.0170	1	RFNLAGNHEQEFLR
198 - 210	1574.7833	1573.7760	1573.7637	0.0124	0	FNLAGNHEQEFLR
211 - 217	965.4828	964.4755	964.4838	-0.0083	1	YQQQSRR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 884.5330, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1603.7629, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 2037.9637, 2094.9377, 2153.0156, 2273.1555, 2466.2058



Rank 2 Protein View

Match to: **gi|52001219** Score: **96** Expect: **2.1e-007**
arachin Ahy-1 [Arachis hypogaea]

Nominal mass (M_r): **61810**; Calculated pI value: **5.57**
NCBI BLAST search of gi|52001219 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **46**
Number of mass values matched: **12**
Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

```
     1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
    51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
   101 FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
   201 NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG QHGRRERAGQ
   251 EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG
   301 GLRILSPDRK RRQQYERPDE EEEYDEDEYE YDEEERQHDR RRGRGSRGSG
   351 NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA
   401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG
   451 HVLVVPQNFA VAGKSQSENF EYVAFKTDSR PSIANLAGEN SFIDNLPEEV
   501 VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 36	1534.6833	1533.6760	1533.6630	0.0130	0	QQPEENACQFQR
37 - 45	1083.5725	1082.5652	1082.5581	0.0072	0	LNAQRPDNR
82 - 98	2051.0603	2050.0530	2050.0384	0.0146	0	RPFYSNAPQEIFIQQGR
122 - 129	1005.5358	1004.5285	1004.5264	0.0021	0	HQSQRPPR
130 - 146	2072.9563	2071.9490	2071.9420	0.0071	1	RFQGQDQSQQQQDSHQK
131 - 146	1916.8605	1915.8532	1915.8409	0.0124	0	FQGQDQSQQQQDSHQK
131 - 149	2309.0925	2308.0852	2308.0693	0.0159	1	FQGQDQSQQQQDSHQKVHR
195 - 208	1730.8890	1729.8817	1729.8648	0.0170	1	RFNLAGNHEQEFLR
196 - 208	1574.7833	1573.7760	1573.7637	0.0124	0	FNLAGNHEQEFLR
209 - 215	965.4828	964.4755	964.4838	-0.0083	1	YQQQSRR
278 - 284	884.5330	883.5257	883.5239	0.0018	0	QILQNLR
285 - 299	1603.7629	1602.7556	1602.7485	0.0072	0	GENESDEQGAIVTVR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 2037.9637, 2094.9377, 2153.0156, 2273.1555, 2466.2058

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 36	1534.6833	1533.6760	1533.6630	0.0130	0	QQPEENACQFQR
37 - 45	1083.5725	1082.5652	1082.5581	0.0072	0	LNAQRPDNR
82 - 98	2051.0603	2050.0530	2050.0384	0.0146	0	RPFYSNAPQEIFIQQGR
122 - 129	1005.5358	1004.5285	1004.5264	0.0021	0	HQSQRPPR
130 - 146	2072.9563	2071.9490	2071.9420	0.0071	1	RFQGQDQSQQQQDSHQK
131 - 146	1916.8605	1915.8532	1915.8409	0.0124	0	FQGQDQSQQQQDSHQK
131 - 149	2309.0925	2308.0852	2308.0693	0.0159	1	FQGQDQSQQQQDSHQKVHR
195 - 208	1730.8890	1729.8817	1729.8648	0.0170	1	RFNLAGNHEQEFLR
196 - 208	1574.7833	1573.7760	1573.7637	0.0124	0	FNLAGNHEQEFLR
209 - 215	965.4828	964.4755	964.4838	-0.0083	1	YQQQSRR
278 - 284	884.5330	883.5257	883.5239	0.0018	0	QILQNLR
285 - 299	1603.7629	1602.7556	1602.7485	0.0072	0	GENESDEQGAIVTVR

No match to: 805.4460, 809.4116, 845.0791, 855.0516, 861.0671, 867.4922, 877.0246, 1037.4762, 1046.5984, 1050.0861, 1066.0728, 1080.5206, 1100.5721, 1139.5829, 1146.5081, 1158.6107, 1162.5326, 1175.5774, 1179.5536, 1186.5433, 1277.0734, 1320.6095, 1342.6708, 1493.7369, 1517.6619, 1608.7889, 1624.7947, 1774.8770, 1780.8928, 2037.9637, 2094.9377, 2153.0156, 2273.1555, 2466.2058

Spot 38

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:37:05 GMT
Top Score : 83 for gi|22135348, trypsin inhibitor [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|22135348	25768	83	trypsin inhibitor [Arachis hypogaea]
2.	gi|52001219	61810	70	arachin Ahy-1 [Arachis hypogaea]
3.	gi|37789212	61803	70	storage protein [Arachis hypogaea]
4.	gi|21314465	62042	69	allergen Arah3/Arah4 [Arachis hypogaea]
5.	gi|118776572	24127	41	arachin 7 [Arachis hypogaea]
6.	gi|52001221	61836	34	arachin Ahy-2 [Arachis hypogaea]
7.	gi|9864777	60754	25	Gly1 [Arachis hypogaea]
8.	gi|118776570	60681	25	arachin 6 [Arachis hypogaea]
9.	gi|5712199	61430	25	glycinin [Arachis hypogaea]
10.	gi|57669861	61041	25	arachin Ahy-4 [Arachis hypogaea]

Results List

1. gi|22135348 **Mass:** 25768 **Score:** 83 **Expect:** 4e-006 **Queries matched:** 7
trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5311	1004.5238	1004.5264	-0.0026	124	131	0	HQSQRPPR
1083.5559	1082.5486	1082.5581	-0.0094	39	47	0	LNAQRPDNR
1534.6837	1533.6764	1533.6630	0.0134	27	38	0	QQPEENACQFQR
1574.8030	1573.7957	1573.7637	0.0321	198	210	0	FNLAGNHEQEFLR
1730.8853	1729.8780	1729.8648	0.0133	197	210	1	RFNLAGNHEQEFLR
1916.8632	1915.8559	1915.8409	0.0151	133	148	0	FQGQDQSQQQQDSHQK
2072.9546	2071.9473	2071.9420	0.0054	132	148	1	RFQGQDQSQQQQDSHQK

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 884.5185, 917.2738, 1046.5958, 1066.0782, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 2037.9781, 2052.0308, 2273.1653

2. gi|52001219 **Mass:** 61810 **Score:** 70 **Expect:** 9.6e-005 **Queries matched:** 8

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5185	883.5112	883.5239	-0.0127	278	284	0	QILQNLR
1005.5311	1004.5238	1004.5264	-0.0026	122	129	0	HQSQRPPR
1083.5559	1082.5486	1082.5581	-0.0094	37	45	0	LNAQRPDNR
1534.6837	1533.6764	1533.6630	0.0134	25	36	0	QQPEENACQFQR
1574.8030	1573.7957	1573.7637	0.0321	196	208	0	FNLAGNHEQEFLR
1730.8853	1729.8780	1729.8648	0.0133	195	208	1	RFNLAGNHEQEFLR
1916.8632	1915.8559	1915.8409	0.0151	131	146	0	FQGQDQSQQQQDSHQK
2072.9546	2071.9473	2071.9420	0.0054	130	146	1	RFQGQDQSQQQQDSHQK

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 917.2738, 1046.5958, 1066.0782, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 2037.9781, 2052.0308, 2273.1653

3. gi|37789212 **Mass:** 61803 **Score:** 70 **Expect:** 9.6e-005 **Queries matched:** 8

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5185	883.5112	883.5239	-0.0127	278	284	0	QILQNLR
1005.5311	1004.5238	1004.5264	-0.0026	122	129	0	HQSQRPPR
1083.5559	1082.5486	1082.5581	-0.0094	37	45	0	LNAQRPDNR
1534.6837	1533.6764	1533.6630	0.0134	25	36	0	QQPEENACQFQR
1574.8030	1573.7957	1573.7637	0.0321	196	208	0	FNLAGNHEQEFLR
1730.8853	1729.8780	1729.8648	0.0133	195	208	1	RFNLAGNHEQEFLR
1916.8632	1915.8559	1915.8409	0.0151	131	146	0	FQGQDQSQQQQDSHQK
2072.9546	2071.9473	2071.9420	0.0054	130	146	1	RFQGQDQSQQQQDSHQK

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 917.2738, 1046.5958, 1066.0782, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 2037.9781, 2052.0308, 2273.1653

4. gi|21314465 **Mass:** 62042 **Score:** 69 **Expect:** 0.0001 **Queries matched:** 8

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5185	883.5112	883.5239	-0.0127	278	284	0	QILQNLR
1005.5311	1004.5238	1004.5264	-0.0026	122	129	0	HQSQRPPR
1083.5559	1082.5486	1082.5581	-0.0094	37	45	0	LNAQRPDNR
1534.6837	1533.6764	1533.6630	0.0134	25	36	0	QQPEENACQFQR
1574.8030	1573.7957	1573.7637	0.0321	196	208	0	FNLAGNHEQEFLR
1730.8853	1729.8780	1729.8648	0.0133	195	208	1	RFNLAGNHEQEFLR
1916.8632	1915.8559	1915.8409	0.0151	131	146	0	FQGQDQSQQQQDSHQK
2072.9546	2071.9473	2071.9420	0.0054	130	146	1	RFQGQDQSQQQQDSHQK

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 917.2738, 1046.5958, 1066.0782, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 2037.9781, 2052.0308, 2273.1653

5. gi|118776572 **Mass:** 24127 **Score:** 41 **Expect:** 0.068 **Queries matched:** 4

arachin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1005.5311	1004.5238	1004.5264	-0.0026	122	129	0	HQSQRPPR
1534.6837	1533.6764	1533.6630	0.0134	25	36	0	QQPEENACQFQR
1916.8632	1915.8559	1915.8409	0.0151	131	146	0	FQGQDQSQQQQDSHQK
2072.9546	2071.9473	2071.9420	0.0054	130	146	1	RFQGQDQSQQQQDSHQK

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 884.5185, 917.2738, 1046.5958, 1066.0782, 1083.5559, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1574.8030, 1608.7963, 1624.7880, 1730.8853, 1774.8530, 2037.9781, 2052.0308, 2273.1653

6. gi|52001221 **Mass:** 61836 **Score:** 34 **Expect:** 0.34 **Queries matched:** 5

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
884.5185	883.5112	883.5239	-0.0127	279	285	0	QILQNLR
1083.5559	1082.5486	1082.5581	-0.0094	37	45	0	LNAQRPDNR
1534.6837	1533.6764	1533.6630	0.0134	25	36	0	QQPEENACQFQR
1574.8030	1573.7957	1573.7637	0.0321	197	209	0	FNLAGNHEQEFLR
1730.8853	1729.8780	1729.8648	0.0133	196	209	1	RFNLAGNHEQEFLR

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 917.2738, 1005.5311, 1046.5958, 1066.0782, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 1916.8632, 2037.9781, 2052.0308, 2072.9546, 2273.1653

7. gi|9864777 **Mass:** 60754 **Score:** 25 **Expect:** 2.5 **Queries matched:** 4

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	38	46	0	LNAQRPDNR
1534.6837	1533.6764	1533.6630	0.0134	26	37	0	QQPEENACQFQR
1574.8030	1573.7957	1573.7637	0.0321	198	210	0	FNLAGNHEQEFLR
1730.8853	1729.8780	1729.8648	0.0133	197	210	1	RFNLAGNHEQEFLR

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 884.5185, 917.2738, 1005.5311, 1046.5958, 1066.0782, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 1916.8632, 2037.9781, 2052.0308, 2072.9546, 2273.1653

8. gi|118776570 **Mass:** 60681 **Score:** 25 **Expect:** 2.5 **Queries matched:** 4

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37	45	0	LNAQRPDNR
1534.6837	1533.6764	1533.6630	0.0134	25	36	0	QQPEENACQFQR
1574.8030	1573.7957	1573.7637	0.0321	196	208	0	FNLAGNHEQEFLR
1730.8853	1729.8780	1729.8648	0.0133	195	208	1	RFNLAGNHEQEFLR

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 884.5185, 917.2738, 1005.5311, 1046.5958, 1066.0782,

1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 1916.8632, 2037.9781, 2052.0308, 2072.9546, 2273.1653

9. gi|5712199 **Mass:** 61430 **Score:** 25 **Expect:** 2.5 **Queries matched:** 4

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37	-	45	0	LNAQRPDNR
1534.6837	1533.6764	1533.6630	0.0134	25	-	36	0	QQPEENACQFQR
1574.8030	1573.7957	1573.7637	0.0321	196	-	208	0	FNLAGNHEQEFLR
1730.8853	1729.8780	1729.8648	0.0133	195	-	208	1	RFNLAGNHEQEFLR

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 884.5185, 917.2738, 1005.5311, 1046.5958, 1066.0782, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 1916.8632, 2037.9781, 2052.0308, 2072.9546, 2273.1653

10. gi|57669861 **Mass:** 61041 **Score:** 25 **Expect:** 2.5 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37	-	45	0	LNAQRPDNR
1534.6837	1533.6764	1533.6630	0.0134	25	-	36	0	QQPEENACQFQR
1574.8030	1573.7957	1573.7637	0.0321	196	-	208	0	FNLAGNHEQEFLR
1730.8853	1729.8780	1729.8648	0.0133	195	-	208	1	RFNLAGNHEQEFLR

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 884.5185, 917.2738, 1005.5311, 1046.5958, 1066.0782, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 1916.8632, 2037.9781, 2052.0308, 2072.9546, 2273.1653

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 27

1. Rank Protein View

Match to: **gi|22135348** Score: **83** Expect: **4e-006**
trypsin inhibitor [Arachis hypogaea]

Nominal mass (M_r): **25768**; Calculated pI value: **6.66**
NCBI BLAST search of gi|22135348 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **27**
Number of mass values matched: **7**
Sequence Coverage: **27%**

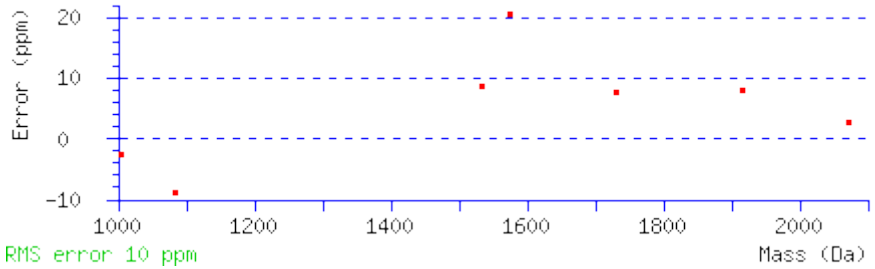
Matched peptides shown in **Bold Red**

```
     1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES
    51 EGGYIETWNP NNQEFECAGV ALSRLVLRRN ALRRPFYSNA PQEIFIQQGR
   101 GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH
   151 RFDEGDLIAV PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
   201 AGNHEQEFLR YQQQSRRRS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
27 - 38	1534.6837	1533.6764	1533.6630	0.0134	0	QQPEENACQFQR
39 - 47	1083.5559	1082.5486	1082.5581	-0.0094	0	LNAQRPDNR
124 - 131	1005.5311	1004.5238	1004.5264	-0.0026	0	HQSQRPPR
132 - 148	2072.9546	2071.9473	2071.9420	0.0054	1	RFQGQDQSQQQQDSHQK
133 - 148	1916.8632	1915.8559	1915.8409	0.0151	0	FQGQDQSQQQQDSHQK
197 - 210	1730.8853	1729.8780	1729.8648	0.0133	1	RFNLAGNHEQEFLR
198 - 210	1574.8030	1573.7957	1573.7637	0.0321	0	FNLAGNHEQEFLR

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 884.5185, 917.2738, 1046.5958, 1066.0782, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 2037.9781, 2052.0308, 2273.1653



2. Rank Protein View

Match to: **gi|52001219** Score: **70** Expect: **9.6e-005**
arachin Ahy-1 [Arachis hypogaea]

Nominal mass (M_r): **61810**; Calculated pI value: **5.57**
NCBI BLAST search of gi|52001219 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **27**
Number of mass values matched: **8**
Sequence Coverage: **12%**

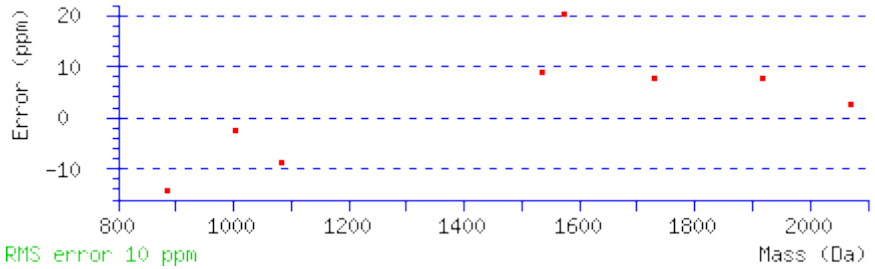
Matched peptides shown in **Bold Red**

```
    1 MGKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
   51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
  101 FGLIFPGCPS TYEEPAQQGR RHQSQRPPRR FQGQDQSQQQ QDSHQKVHRF
  151 DEGDLIAVPT GVAFWMYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
  201 NHEQEFLRYQ QQSRRRSLPY SPYSPQTQPK QEDREFSPRG QHGRRERAGQ
  251 EQENEGGNIF SGFTPEFLAQ AFQVDDRQIL QNLRGENESD EQGAIVTVRG
  301 GLRILSPDRK RRQQYERPDE EEEYDEDEYE YDEEERQHDR RRGRGSRGSG
  351 NGIEETICTA SFKKNIGRNR SPDIYNPQAG SLKTANELNL LILRWLGLSA
  401 EYGNLYRNAL FVPHYNTNAH SIIYALRGRA HVQVVDSNGD RVFDEELQEG
  451 HVLVVPQNFA VAGKSQSENF EYVAFKTDSR PSIANLAGEN SFIDNLPEEV
  501 VANSYGLPRE QARQLKNNNP FKFFVPPSEQ SLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 36	1534.6837	1533.6764	1533.6630	0.0134	0	QQPEENACQFQR
37 - 45	1083.5559	1082.5486	1082.5581	-0.0094	0	LNAQRPDNR
122 - 129	1005.5311	1004.5238	1004.5264	-0.0026	0	HQSQRPPR
130 - 146	2072.9546	2071.9473	2071.9420	0.0054	1	RFQGQDQSQQQQDSHQK
131 - 146	1916.8632	1915.8559	1915.8409	0.0151	0	FQGQDQSQQQQDSHQK
195 - 208	1730.8853	1729.8780	1729.8648	0.0133	1	RFNLAGNHEQEFLR
196 - 208	1574.8030	1573.7957	1573.7637	0.0321	0	FNLAGNHEQEFLR
278 - 284	884.5185	883.5112	883.5239	-0.0127	0	QILQNLR

No match to: 805.4496, 855.0427, 861.0593, 877.0269, 881.2643, 917.2738, 1046.5958, 1066.0782, 1175.5575, 1179.5482, 1215.5112, 1342.6681, 1517.6456, 1608.7963, 1624.7880, 1774.8530, 2037.9781, 2052.0308, 2273.1653



Spot 39

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:31:34 GMT
Top Score : 74 for gi|22135348, trypsin inhibitor [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|22135348	25768	74	trypsin inhibitor [Arachis hypogaea]
2.	gi|9864777	60754	64	Gly1 [Arachis hypogaea]
3.	gi|52001221	61836	63	arachin Ahy-2 [Arachis hypogaea]
4.	gi|118776570	60681	55	arachin 6 [Arachis hypogaea]
5.	gi|52001219	61810	54	arachin Ahy-1 [Arachis hypogaea]
6.	gi|21314465	62042	54	allergen Arah3/Arah4 [Arachis hypogaea]
7.	gi|57669861	61041	54	arachin Ahy-4 [Arachis hypogaea]
8.	gi|108595573	61041	54	arachin Ahy-4 [Arachis hypogaea]
9.	gi|5712199	61430	47	glycinin [Arachis hypogaea]
10.	gi|37789212	61803	35	storage protein [Arachis hypogaea]

Results List

1. gi|22135348 **Mass:** 25768 **Score:** 74 **Expect:** 3.5e-005 **Queries matched:** 8
trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1083.5647	1082.5574	1082.5581	-0.0006	39	-	47	0	LNAQRPDNR
1534.6725	1533.6652	1533.6630	0.0022	27	-	38	0	QQPEENACQFQR
1730.8733	1729.8660	1729.8648	0.0013	197	-	210	1	RFNLAGNHEQEFLR
2051.0461	2050.0388	2050.0384	0.0004	84	-	100	0	RPFYSNAPQEIFIQQGR
2474.1543	2473.1470	2473.1371	0.0099	101	-	122	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3113	2504.3040	2504.3036	0.0004	80	-	100	1	NALRRPFYSNAPQEIFIQQGR
2630.3052	2629.2979	2629.2383	0.0597	101	-	123	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3889	3069.3816	3069.3773	0.0043	48	-	74	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1177.5710, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1296.5981, 1372.6893, 1464.6021, 1481.6334,

1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2202.9834, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047

2. gi|9864777 **Mass:** 60754 **Score:** 64 **Expect:** 0.00038 **Queries matched:** 10

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5647	1082.5574	1082.5581	-0.0006	38	46	0	LNAQRPDNR
1177.5710	1176.5637	1176.5523	0.0114	233	241	1	QEEREFSPR
1534.6725	1533.6652	1533.6630	0.0022	26	37	0	QQPEENACQFQR
1730.8733	1729.8660	1729.8648	0.0013	197	210	1	RFNLAGNHEQEFLR
2051.0461	2050.0388	2050.0384	0.0004	83	99	0	RPFYSNAPQEIFIQQGR
2202.9834	2201.9761	2201.9686	0.0076	131	148	1	RFEGEDQSQQQQQDSHQK
2474.1543	2473.1470	2473.1371	0.0099	100	121	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3113	2504.3040	2504.3036	0.0004	79	99	1	NALRRPFYSNAPQEIFIQQGR
2630.3052	2629.2979	2629.2383	0.0597	100	122	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3889	3069.3816	3069.3773	0.0043	47	73	0	LESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1296.5981, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047

3. gi|52001221 **Mass:** 61836 **Score:** 63 **Expect:** 0.00044 **Queries matched:** 10

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5647	1082.5574	1082.5581	-0.0006	37	45	0	LNAQRPDNR
1177.5710	1176.5637	1176.5523	0.0114	232	240	1	QEEREFSPR
1534.6725	1533.6652	1533.6630	0.0022	25	36	0	QQPEENACQFQR
1730.8733	1729.8660	1729.8648	0.0013	196	209	1	RFNLAGNHEQEFLR
2051.0461	2050.0388	2050.0384	0.0004	82	98	0	RPFYSNAPQEIFIQQGR
2202.9834	2201.9761	2201.9686	0.0076	130	147	1	RFEGEDQSQQQQQDSHQK
2474.1543	2473.1470	2473.1371	0.0099	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3113	2504.3040	2504.3036	0.0004	78	98	1	NALRRPFYSNAPQEIFIQQGR
2630.3052	2629.2979	2629.2383	0.0597	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3889	3069.3816	3069.3773	0.0043	46	72	0	LESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1296.5981, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465,

2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047

4. gi|118776570 **Mass:** 60681 **Score:** 55 **Expect:** 0.0026 **Queries matched:** 9

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5647	1082.5574	1082.5581	-0.0006	37	45	0	LNAQRPDNR
1534.6725	1533.6652	1533.6630	0.0022	25	36	0	QQPEENACQFQR
1730.8733	1729.8660	1729.8648	0.0013	195	208	1	RFNLAGNHEQEFLR
1770.8901	1769.8828	1769.8584	0.0244	220	235	0	SLPLSPYSPQPGQEDR
2051.0461	2050.0388	2050.0384	0.0004	82	98	0	RPFYSNAPQEIFIQQGR
2474.1543	2473.1470	2473.1371	0.0099	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3113	2504.3040	2504.3036	0.0004	78	98	1	NALRRPFYSNAPQEIFIQQGR
2630.3052	2629.2979	2629.2383	0.0597	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3889	3069.3816	3069.3773	0.0043	46	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1177.5710, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1296.5981, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2202.9834, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047

5. gi|52001219 **Mass:** 61810 **Score:** 54 **Expect:** 0.0034 **Queries matched:** 9

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5647	1082.5574	1082.5581	-0.0006	37	45	0	LNAQRPDNR
1296.5981	1295.5908	1295.6218	-0.0309	430	441	0	AHVQVVDSNGDR
1534.6725	1533.6652	1533.6630	0.0022	25	36	0	QQPEENACQFQR
1730.8733	1729.8660	1729.8648	0.0013	195	208	1	RFNLAGNHEQEFLR
2051.0461	2050.0388	2050.0384	0.0004	82	98	0	RPFYSNAPQEIFIQQGR
2474.1543	2473.1470	2473.1371	0.0099	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3113	2504.3040	2504.3036	0.0004	78	98	1	NALRRPFYSNAPQEIFIQQGR
2630.3052	2629.2979	2629.2383	0.0597	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3889	3069.3816	3069.3773	0.0043	46	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1177.5710, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2202.9834, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047

6. gi|21314465 **Mass:** 62042 **Score:** 54 **Expect:** 0.0035 **Queries matched:** 9

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1083.5647	1082.5574	1082.5581	-0.0006	37	-	45	0	LNAQRPDNR
1296.5981	1295.5908	1295.6218	-0.0309	432	-	443	0	AHVQVVDSNGDR
1534.6725	1533.6652	1533.6630	0.0022	25	-	36	0	QQPEENACQFQR
1730.8733	1729.8660	1729.8648	0.0013	195	-	208	1	RFNLAGNHEQEFLR
2051.0461	2050.0388	2050.0384	0.0004	82	-	98	0	RPFYSNAPQEIFIQQGR
2474.1543	2473.1470	2473.1371	0.0099	99	-	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3113	2504.3040	2504.3036	0.0004	78	-	98	1	NALRRPFYSNAPQEIFIQQGR
2630.3052	2629.2979	2629.2383	0.0597	99	-	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3889	3069.3816	3069.3773	0.0043	46	-	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1177.5710, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2202.9834, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047

7. gi|57669861 **Mass:** 61041 **Score:** 54 **Expect:** 0.0035 **Queries matched:** 9

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1083.5647	1082.5574	1082.5581	-0.0006	37	-	45	0	LNAQRPDNR
1177.5710	1176.5637	1176.5523	0.0114	234	-	242	1	QEEREFSPR
1534.6725	1533.6652	1533.6630	0.0022	25	-	36	0	QQPEENACQFQR
1730.8733	1729.8660	1729.8648	0.0013	195	-	208	1	RFNLAGNHEQEFLR
2051.0461	2050.0388	2050.0384	0.0004	82	-	98	0	RPFYSNAPQEIFIQQGR
2474.1543	2473.1470	2473.1371	0.0099	99	-	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3113	2504.3040	2504.3036	0.0004	78	-	98	1	NALRRPFYSNAPQEIFIQQGR
2630.3052	2629.2979	2629.2383	0.0597	99	-	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3889	3069.3816	3069.3773	0.0043	46	-	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1296.5981, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2202.9834, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047

8. gi|108595573 **Mass:** 61041 **Score:** 54 **Expect:** 0.0035 **Queries matched:** 9

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1083.5647	1082.5574	1082.5581	-0.0006	37	-	45	0	LNAQRPDNR
1177.5710	1176.5637	1176.5523	0.0114	234	-	242	1	QEEREFSPR
1534.6725	1533.6652	1533.6630	0.0022	25	-	36	0	QQPEENACQFQR

1730.8733	1729.8660	1729.8648	0.0013	195 - 208	1	RFNLAGNHEQEFLR
2051.0461	2050.0388	2050.0384	0.0004	82 - 98	0	RPFYSNAPQEIFIQQGR
2474.1543	2473.1470	2473.1371	0.0099	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3113	2504.3040	2504.3036	0.0004	78 - 98	1	NALRRPFYSNAPQEIFIQQGR
2630.3052	2629.2979	2629.2383	0.0597	99 - 121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3889	3069.3816	3069.3773	0.0043	46 - 72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1296.5981, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2202.9834, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047

9. gi|5712199 **Mass:** 61430 **Score:** 47 **Expect:** 0.018 **Queries matched:** 8

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5647	1082.5574	1082.5581	-0.0006	37 -	45	0	LNAQRPDNR
1534.6725	1533.6652	1533.6630	0.0022	25 -	36	0	QQPEENACQFQR
1730.8733	1729.8660	1729.8648	0.0013	195 -	208	1	RFNLAGNHEQEFLR
2051.0461	2050.0388	2050.0384	0.0004	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1543	2473.1470	2473.1371	0.0099	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3113	2504.3040	2504.3036	0.0004	78 -	98	1	NALRRPFYSNAPQEIFIQQGR
2630.3052	2629.2979	2629.2383	0.0597	99 -	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3889	3069.3816	3069.3773	0.0043	46 -	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1177.5710, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1296.5981, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2202.9834, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047

10. gi|37789212 **Mass:** 61803 **Score:** 35 **Expect:** 0.3 **Queries matched:** 7

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5647	1082.5574	1082.5581	-0.0006	37 -	45	0	LNAQRPDNR
1296.5981	1295.5908	1295.6218	-0.0309	430 -	441	0	AHVQVVDSNGDR
1534.6725	1533.6652	1533.6630	0.0022	25 -	36	0	QQPEENACQFQR
1730.8733	1729.8660	1729.8648	0.0013	195 -	208	1	RFNLAGNHEQEFLR
2051.0461	2050.0388	2050.0384	0.0004	82 -	98	0	RPFYSNAPQEIFIQQGR
2505.3113	2504.3040	2504.3036	0.0004	78 -	98	1	NALRRPFYSNAPQEIFIQQGR
3070.3889	3069.3816	3069.3773	0.0043	46 -	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579,

928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1177.5710, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2202.9834, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2474.1543, 2612.1978, 2630.3052, 3136.4265, 3211.5405, 3303.6047

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 73

1. Rank

Match to: **gi|22135348** Score: **74** Expect: **3.5e-005**
trypsin inhibitor [Arachis hypogaea]

Nominal mass (M_r): **25768**; Calculated pI value: **6.66**
NCBI BLAST search of gi|22135348 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **73**
Number of mass values matched: **8**
Sequence Coverage: **48%**

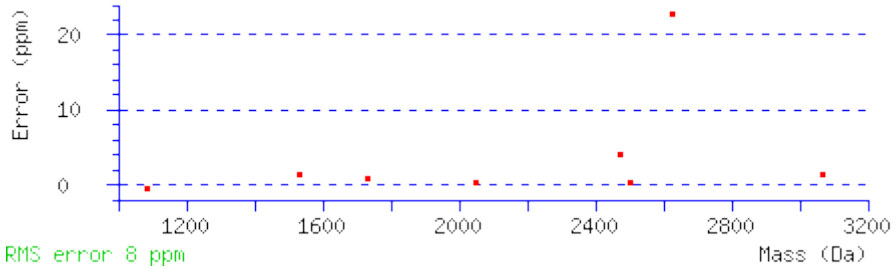
Matched peptides shown in **Bold Red**

```
  1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES
 51 EGGYIETWNP NNQEFECAGV ALSRLVLRRN ALRRPFYSNA PQEIFIQQGR
101 GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH
151 RFDEGDLIAV PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
201 AGNHEQEFLR YQQQSRRRS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
27 - 38	1534.6725	1533.6652	1533.6630	0.0022	0	QQPEENACQFQR
39 - 47	1083.5647	1082.5574	1082.5581	-0.0006	0	LNAQRPDNR
48 - 74	3070.3889	3069.3816	3069.3773	0.0043	0	IESEGGYIETWNPNNQEFECAGVALSR
80 - 100	2505.3113	2504.3040	2504.3036	0.0004	1	NALRRPFYSNAPQEIFIQQGR
84 - 100	2051.0461	2050.0388	2050.0384	0.0004	0	RPFYSNAPQEIFIQQGR
101 - 122	2474.1543	2473.1470	2473.1371	0.0099	0	GYFGLIFPGCPSTYEEPAQQGR
101 - 123	2630.3052	2629.2979	2629.2383	0.0597	1	GYFGLIFPGCPSTYEEPAQQGRR
197 - 210	1730.8733	1729.8660	1729.8648	0.0013	1	RFNLAGNHEQEFLR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1177.5710, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1296.5981, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2202.9834, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047



2. Rank Protein View

Match to: **gi|9864777** Score: **64** Expect: **0.00038**
Gly1 [Arachis hypogaea]

Nominal mass (M_r): **60754**; Calculated pI value: **5.48**
NCBI BLAST search of gi|9864777 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **73**
Number of mass values matched: **10**
Sequence Coverage: **25%**

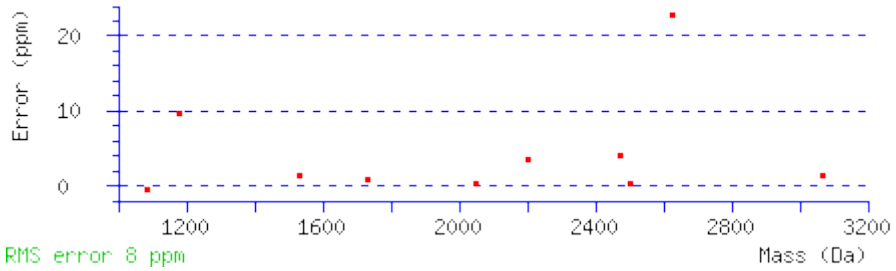
Matched peptides shown in **Bold Red**

```
   1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE
  51 GGYIETWNPN NQEFECAGVA LSRLVLRRNA LRRPFYSNAP QEIFIQQGRG
 101 YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR
 151 RFDEGDLIAV PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
 201 AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP RGQHSRRERA
 251 GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV
 301 KGGLRILSPD RKRGADEEEE YDEDEYEYDE EDRRRGRGSR GRGNGIEETI
 351 CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR
 401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
 451 NFAVAGKSQS DNFEYVAFKT DSRPNIANFA GENSIIDNLP EEVVANSYGL
 501 PREQARQLKN NNPFKFFVPP SQQSLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
26 - 37	1534.6725	1533.6652	1533.6630	0.0022	0	QQPEENACQFQR
38 - 46	1083.5647	1082.5574	1082.5581	-0.0006	0	LNAQRPDNR
47 - 73	3070.3889	3069.3816	3069.3773	0.0043	0	LESEGGYIETWNPNNQEFECAGVALSR
79 - 99	2505.3113	2504.3040	2504.3036	0.0004	1	NALRRPFYSNAPQEIFIQQGR
83 - 99	2051.0461	2050.0388	2050.0384	0.0004	0	RPFYSNAPQEIFIQQGR
100 - 121	2474.1543	2473.1470	2473.1371	0.0099	0	GYFGLIFPGCPSTYEEPAQQGR
100 - 122	2630.3052	2629.2979	2629.2383	0.0597	1	GYFGLIFPGCPSTYEEPAQQGRR
131 - 148	2202.9834	2201.9761	2201.9686	0.0076	1	RFEGEDQSQQQQQDSHQK
197 - 210	1730.8733	1729.8660	1729.8648	0.0013	1	RFNLAGNHEQEFLR
233 - 241	1177.5710	1176.5637	1176.5523	0.0114	1	QEEREFSPR

No match to: 805.4576, 809.4136, 827.4026, 839.0903, 845.1080, 854.1334, 855.0732, 861.0892, 871.0460, 877.0579, 928.5055, 970.4464, 1019.4733, 1026.5297, 1037.4834, 1050.1108, 1066.0823, 1072.0955, 1080.5431, 1082.0453, 1145.5715, 1149.6101, 1175.5698, 1193.5542, 1216.5612, 1277.0988, 1293.0728, 1296.5981, 1372.6893, 1464.6021, 1481.6334, 1517.6537, 1529.7211, 1547.7540, 1614.7852, 1622.7814, 1638.7782, 1756.8367, 1770.8901, 1774.8516, 1778.8392, 1794.8595, 1796.8254, 1984.8961, 2037.9513, 2099.9268, 2185.0410, 2194.0151, 2207.0063, 2209.0210, 2224.9968, 2227.0591, 2273.1619, 2295.1465, 2311.1460, 2335.0950, 2351.0854, 2355.0898, 2458.1758, 2612.1978, 3136.4265, 3211.5405, 3303.6047



Spot 40

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:32:37 GMT**
Top Score : **98 for gi|9864777, Gly1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|9864777	60754	98	Gly1 [Arachis hypogaea]
2.	gi|22135348	25768	93	trypsin inhibitor [Arachis hypogaea]
3.	gi|57669861	61041	67	arachin Ahy-4 [Arachis hypogaea]
4.	gi|108595573	61041	67	arachin Ahy-4 [Arachis hypogaea]
5.	gi|118776570	60681	66	arachin 6 [Arachis hypogaea]
6.	gi|5712199	61430	62	glycinin [Arachis hypogaea]
7.	gi|52001221	61836	58	arachin Ahy-2 [Arachis hypogaea]
8.	gi|52001219	61810	58	arachin Ahy-1 [Arachis hypogaea]
9.	gi|21314465	62042	58	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|37789212	61803	39	storage protein [Arachis hypogaea]

Results List

1. gi|9864777 **Mass:** 60754 **Score:** 98 **Expect:** 1.3e-007 **Queries matched:** 14
Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5206	869.5133	869.5083	0.0051	280	286	0	QIVQNLR
1083.5609	1082.5536	1082.5581	-0.0044	38	46	0	LNAQRPDNR
1534.6642	1533.6569	1533.6630	-0.0061	26	37	0	QQPEENACQFQR
1574.7723	1573.7650	1573.7637	0.0014	198	210	0	FNLAGNHEQEFLR
1730.8660	1729.8587	1729.8648	-0.0060	197	210	1	RFNLAGNHEQEFLR
1973.9684	1972.9611	1972.9700	-0.0089	287	305	1	GENESEEEGAIVTVKGGLR
2051.0386	2050.0313	2050.0384	-0.0071	83	99	0	RPFYSNAPQEIFIQQGR
2202.9910	2201.9837	2201.9686	0.0152	131	148	1	RFEGEDQSQQQQQDSHQK
2442.3008	2441.2935	2441.2397	0.0539	280	301	1	QIVQNLRGENESEEEGAIVTVK

2474.1514	2473.1441	2473.1371	0.0070	100 - 121	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3140	2504.3067	2504.3036	0.0032	79 - 99	1	NALRRPFYSNAPQEIFIQQGR
2528.8911	2527.8838	2527.8782	0.0056	314 - 333	0	GADEEEEYDEDEYEYDEEDR
2630.2368	2629.2295	2629.2383	-0.0087	100 - 122	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4138	3069.4065	3069.3773	0.0292	47 - 73	0	LESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1770.8713, 1774.8424, 1792.8030, 1794.8334, 2037.9451, 2056.0110, 2072.9775, 2145.0308, 2146.6199, 2185.0422, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2458.1621, 2522.2354, 2613.1790, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422, 3361.5156

2. gi|22135348 **Mass:** 25768 **Score:** 93 **Expect:** 4.4e-007 **Queries matched:** 10

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5609	1082.5536	1082.5581	-0.0044	39 -	47	0	LNAQRPDNR
1534.6642	1533.6569	1533.6630	-0.0061	27 -	38	0	QQPEENACQFQR
1574.7723	1573.7650	1573.7637	0.0014	198 -	210	0	FNLAGNHEQEFLR
1730.8660	1729.8587	1729.8648	-0.0060	197 -	210	1	RFNLAGNHEQEFLR
2051.0386	2050.0313	2050.0384	-0.0071	84 -	100	0	RPFYSNAPQEIFIQQGR
2072.9775	2071.9702	2071.9420	0.0283	132 -	148	1	RFQGQDQSQQQQDSHQK
2474.1514	2473.1441	2473.1371	0.0070	101 -	122	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3140	2504.3067	2504.3036	0.0032	80 -	100	1	NALRRPFYSNAPQEIFIQQGR
2630.2368	2629.2295	2629.2383	-0.0087	101 -	123	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4138	3069.4065	3069.3773	0.0292	48 -	74	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 870.5206, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1770.8713, 1774.8424, 1792.8030, 1794.8334, 1973.9684, 2037.9451, 2056.0110, 2145.0308, 2146.6199, 2185.0422, 2202.9910, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2442.3008, 2458.1621, 2522.2354, 2528.8911, 2613.1790, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422, 3361.5156

3. gi|57669861 **Mass:** 61041 **Score:** 67 **Expect:** 0.0002 **Queries matched:** 11

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

870.5206	869.5133	869.5083	0.0051	281 - 287	0	QIVQNLR
1083.5609	1082.5536	1082.5581	-0.0044	37 - 45	0	LNAQRPDNR
1534.6642	1533.6569	1533.6630	-0.0061	25 - 36	0	QQPEENACQFQR
1574.7723	1573.7650	1573.7637	0.0014	196 - 208	0	FNLAGNHEQEFLR
1730.8660	1729.8587	1729.8648	-0.0060	195 - 208	1	RFNLAGNHEQEFLR
2051.0386	2050.0313	2050.0384	-0.0071	82 - 98	0	RPFYSNAPQEIFIQQGR
2474.1514	2473.1441	2473.1371	0.0070	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3140	2504.3067	2504.3036	0.0032	78 - 98	1	NALRRPFYSNAPQEIFIQQGR
2528.8911	2527.8838	2527.8782	0.0056	315 - 334	0	GADEEEEYDEDEYEYDEEDR
2630.2368	2629.2295	2629.2383	-0.0087	99 - 121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4138	3069.4065	3069.3773	0.0292	46 - 72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1770.8713, 1774.8424, 1792.8030, 1794.8334, 1973.9684, 2037.9451, 2056.0110, 2072.9775, 2145.0308, 2146.6199, 2185.0422, 2202.9910, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2442.3008, 2458.1621, 2522.2354, 2613.1790, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422, 3361.5156

4. gi|108595573 **Mass:** 61041 **Score:** 67 **Expect:** 0.0002 **Queries matched:** 11

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5206	869.5133	869.5083	0.0051	281 - 287		0	QIVQNLR
1083.5609	1082.5536	1082.5581	-0.0044	37 - 45		0	LNAQRPDNR
1534.6642	1533.6569	1533.6630	-0.0061	25 - 36		0	QQPEENACQFQR
1574.7723	1573.7650	1573.7637	0.0014	196 - 208		0	FNLAGNHEQEFLR
1730.8660	1729.8587	1729.8648	-0.0060	195 - 208		1	RFNLAGNHEQEFLR
2051.0386	2050.0313	2050.0384	-0.0071	82 - 98		0	RPFYSNAPQEIFIQQGR
2474.1514	2473.1441	2473.1371	0.0070	99 - 120		0	GYFGLIFPGCPSTYEEPAQQGR
2505.3140	2504.3067	2504.3036	0.0032	78 - 98		1	NALRRPFYSNAPQEIFIQQGR
2528.8911	2527.8838	2527.8782	0.0056	315 - 334		0	GADEEEEYDEDEYEYDEEDR
2630.2368	2629.2295	2629.2383	-0.0087	99 - 121		1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4138	3069.4065	3069.3773	0.0292	46 - 72		0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1770.8713, 1774.8424, 1792.8030, 1794.8334, 1973.9684, 2037.9451, 2056.0110, 2072.9775, 2145.0308, 2146.6199, 2185.0422,

2202.9910, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2442.3008, 2458.1621, 2522.2354, 2613.1790, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422, 3361.5156

5. gi|118776570 **Mass:** 60681 **Score:** 66 **Expect:** 0.00024 **Queries matched:** 11

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5206	869.5133	869.5083	0.0051	279 -	285	0	QIVQNLR
1083.5609	1082.5536	1082.5581	-0.0044	37 -	45	0	LNAQRPDNR
1534.6642	1533.6569	1533.6630	-0.0061	25 -	36	0	QQPEENACQFQR
1574.7723	1573.7650	1573.7637	0.0014	196 -	208	0	FNLAGNHEQEFLR
1730.8660	1729.8587	1729.8648	-0.0060	195 -	208	1	RFNLAGNHEQEFLR
1770.8713	1769.8640	1769.8584	0.0056	220 -	235	0	SLPLSPYSPQPGQEDR
2051.0386	2050.0313	2050.0384	-0.0071	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1514	2473.1441	2473.1371	0.0070	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3140	2504.3067	2504.3036	0.0032	78 -	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2368	2629.2295	2629.2383	-0.0087	99 -	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4138	3069.4065	3069.3773	0.0292	46 -	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1774.8424, 1792.8030, 1794.8334, 1973.9684, 2037.9451, 2056.0110, 2072.9775, 2145.0308, 2146.6199, 2185.0422, 2202.9910, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2442.3008, 2458.1621, 2522.2354, 2528.8911, 2613.1790, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422, 3361.5156

6. gi|5712199 **Mass:** 61430 **Score:** 62 **Expect:** 0.00054 **Queries matched:** 10

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5609	1082.5536	1082.5581	-0.0044	37 -	45	0	LNAQRPDNR
1534.6642	1533.6569	1533.6630	-0.0061	25 -	36	0	QQPEENACQFQR
1574.7723	1573.7650	1573.7637	0.0014	196 -	208	0	FNLAGNHEQEFLR
1730.8660	1729.8587	1729.8648	-0.0060	195 -	208	1	RFNLAGNHEQEFLR
2051.0386	2050.0313	2050.0384	-0.0071	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1514	2473.1441	2473.1371	0.0070	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3140	2504.3067	2504.3036	0.0032	78 -	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2368	2629.2295	2629.2383	-0.0087	99 -	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4138	3069.4065	3069.3773	0.0292	46 -	72	0	IESEGGYIETWNPNNQEFECAGVALSR

3361.5156	3360.5083	3360.4693	0.0390	251 - 280	0	AGQEEEDEGGNIFSGFTPEFLEQAFQVDDR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 870.5206, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1770.8713, 1774.8424, 1792.8030, 1794.8334, 1973.9684, 2037.9451, 2056.0110, 2072.9775, 2145.0308, 2146.6199, 2185.0422, 2202.9910, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2442.3008, 2458.1621, 2522.2354, 2528.8911, 2613.1790, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422

7. gi|52001221 **Mass:** 61836 **Score:** 58 **Expect:** 0.0013 **Queries matched:** 10

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5609	1082.5536	1082.5581	-0.0044	37 -	45	0	LNAQRPDNR
1534.6642	1533.6569	1533.6630	-0.0061	25 -	36	0	QQPEENACQFQR
1574.7723	1573.7650	1573.7637	0.0014	197 -	209	0	FNLAGNHEQEFLR
1730.8660	1729.8587	1729.8648	-0.0060	196 -	209	1	RFNLAGNHEQEFLR
2051.0386	2050.0313	2050.0384	-0.0071	82 -	98	0	RPFYSNAPQEIFIQQGR
2202.9910	2201.9837	2201.9686	0.0152	130 -	147	1	RFEGEDQSQQQQQDSHQK
2474.1514	2473.1441	2473.1371	0.0070	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3140	2504.3067	2504.3036	0.0032	78 -	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2368	2629.2295	2629.2383	-0.0087	99 -	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4138	3069.4065	3069.3773	0.0292	46 -	72	0	LESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 870.5206, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1770.8713, 1774.8424, 1792.8030, 1794.8334, 1973.9684, 2037.9451, 2056.0110, 2072.9775, 2145.0308, 2146.6199, 2185.0422, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2442.3008, 2458.1621, 2522.2354, 2528.8911, 2613.1790, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422, 3361.5156

8. gi|52001219 **Mass:** 61810 **Score:** 58 **Expect:** 0.0014 **Queries matched:** 10

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5609	1082.5536	1082.5581	-0.0044	37 -	45	0	LNAQRPDNR
1534.6642	1533.6569	1533.6630	-0.0061	25 -	36	0	QQPEENACQFQR
1574.7723	1573.7650	1573.7637	0.0014	196 -	208	0	FNLAGNHEQEFLR
1730.8660	1729.8587	1729.8648	-0.0060	195 -	208	1	RFNLAGNHEQEFLR

2051.0386	2050.0313	2050.0384	-0.0071	82 - 98	0	RPFYSNAPQEIFIQQGR
2072.9775	2071.9702	2071.9420	0.0283	130 - 146	1	RFQGQDQSQQQQDSHQK
2474.1514	2473.1441	2473.1371	0.0070	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3140	2504.3067	2504.3036	0.0032	78 - 98	1	NALRRPFYSNAPQEIFIQQGR
2630.2368	2629.2295	2629.2383	-0.0087	99 - 121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4138	3069.4065	3069.3773	0.0292	46 - 72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 870.5206, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1770.8713, 1774.8424, 1792.8030, 1794.8334, 1973.9684, 2037.9451, 2056.0110, 2145.0308, 2146.6199, 2185.0422, 2202.9910, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2442.3008, 2458.1621, 2522.2354, 2528.8911, 2613.1790, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422, 3361.5156

9. gi|21314465 **Mass:** 62042 **Score:** 58 **Expect:** 0.0014 **Queries matched:** 10

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5609	1082.5536	1082.5581	-0.0044	37 -	45	0	LNAQRPDNR
1534.6642	1533.6569	1533.6630	-0.0061	25 -	36	0	QQPEENACQFQR
1574.7723	1573.7650	1573.7637	0.0014	196 -	208	0	FNLAGNHEQEFLR
1730.8660	1729.8587	1729.8648	-0.0060	195 -	208	1	RFNLAGNHEQEFLR
2051.0386	2050.0313	2050.0384	-0.0071	82 -	98	0	RPFYSNAPQEIFIQQGR
2072.9775	2071.9702	2071.9420	0.0283	130 -	146	1	RFQGQDQSQQQQDSHQK
2474.1514	2473.1441	2473.1371	0.0070	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3140	2504.3067	2504.3036	0.0032	78 -	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2368	2629.2295	2629.2383	-0.0087	99 -	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.4138	3069.4065	3069.3773	0.0292	46 -	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 870.5206, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1770.8713, 1774.8424, 1792.8030, 1794.8334, 1973.9684, 2037.9451, 2056.0110, 2145.0308, 2146.6199, 2185.0422, 2202.9910, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2442.3008, 2458.1621, 2522.2354, 2528.8911, 2613.1790, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422, 3361.5156

10. gi|37789212 **Mass:** 61803 **Score:** 39 **Expect:** 0.12 **Queries matched:** 8

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5609	1082.5536	1082.5581	-0.0044	37	45	0	LNAQRPDNR
1534.6642	1533.6569	1533.6630	-0.0061	25	36	0	QQPEENACQFQR
1574.7723	1573.7650	1573.7637	0.0014	196	208	0	FNLAGNHEQEFLR
1730.8660	1729.8587	1729.8648	-0.0060	195	208	1	RFNLAGNHEQEFLR
2051.0386	2050.0313	2050.0384	-0.0071	82	98	0	RPFYSNAPQEIFIQQGR
2072.9775	2071.9702	2071.9420	0.0283	130	146	1	RFQGQDQSQQQQDSHQK
2505.3140	2504.3067	2504.3036	0.0032	78	98	1	NALRRPFYSNAPQEIFIQQGR
3070.4138	3069.4065	3069.3773	0.0292	46	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 870.5206, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1770.8713, 1774.8424, 1792.8030, 1794.8334, 1973.9684, 2037.9451, 2056.0110, 2145.0308, 2146.6199, 2185.0422, 2202.9910, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2442.3008, 2458.1621, 2474.1514, 2522.2354, 2528.8911, 2613.1790, 2630.2368, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422, 3361.5156

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 83

Protein View

Match to: **gi|9864777** Score: **98** Expect: **1.3e-007**
Gly1 [Arachis hypogaea]

Nominal mass (M_r): **60754;** Calculated pI value: **5.48**
NCBI BLAST search of gi|9864777 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **83**
Number of mass values matched: **14**
Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

```
     1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE
    51 GGYIETWNPN NQEFECAGVA LSRLVLRRNA LRRPFYSNAP QEIFIQQGRG
   101 YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR
   151 RFDEGDLIAV PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
   201 AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP RGQHSRRERA
   251 GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV
   301 KGGLRILSPD RKRGADEEEE YDEDEYEYDE EDRRRGRGSR GRGNGIEETI
   351 CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR
   401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
   451 NFAVAGKSQS DNFEYVAFKT DSRPNIANFA GENSIIDNLP EEVVANSYGL
   501 PREQARQLKN NNPFKFFVPP SQQSLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
26 - 37	1534.6642	1533.6569	1533.6630	-0.0061	0	QQPEENACQFQR
38 - 46	1083.5609	1082.5536	1082.5581	-0.0044	0	LNAQRPDNR
47 - 73	3070.4138	3069.4065	3069.3773	0.0292	0	LESEGGYIETWNPNNQEFECAGVALSR
79 - 99	2505.3140	2504.3067	2504.3036	0.0032	1	NALRRPFYSNAPQEIFIQQGR
83 - 99	2051.0386	2050.0313	2050.0384	-0.0071	0	RPFYSNAPQEIFIQQGR
100 - 121	2474.1514	2473.1441	2473.1371	0.0070	0	GYFGLIFPGCPSTYEEPAQQGR
100 - 122	2630.2368	2629.2295	2629.2383	-0.0087	1	GYFGLIFPGCPSTYEEPAQQGRR
131 - 148	2202.9910	2201.9837	2201.9686	0.0152	1	RFEGEDQSQQQQQDSHQK
197 - 210	1730.8660	1729.8587	1729.8648	-0.0060	1	RFNLAGNHEQEFLR
198 - 210	1574.7723	1573.7650	1573.7637	0.0014	0	FNLAGNHEQEFLR
280 - 286	870.5206	869.5133	869.5083	0.0051	0	QIVQNLR
280 - 301	2442.3008	2441.2935	2441.2397	0.0539	1	QIVQNLRGENESEEEGAIVTVK
287 - 305	1973.9684	1972.9611	1972.9700	-0.0089	1	GENESEEEGAIVTVKGGLR
314 - 333	2528.8911	2527.8838	2527.8782	0.0056	0	GADEEEEYDEDEYEYDEEDR

No match to: 805.4643, 809.4140, 845.0879, 855.0638, 861.0670, 865.9457, 866.4460, 877.0416, 1019.4884, 1019.9838, 1021.4939, 1026.0206, 1026.5253, 1046.5898, 1050.0930, 1066.0669, 1072.0798, 1080.5284, 1111.5739, 1137.0812, 1137.5765, 1145.0592, 1145.5809, 1175.5845, 1176.5463, 1193.5466, 1216.5739, 1229.5825, 1253.6543, 1277.0780, 1372.6788, 1434.7100, 1458.7109, 1517.6381, 1547.7543, 1622.7739, 1638.7723, 1714.4275, 1756.8195, 1770.8713, 1774.8424, 1792.8030, 1794.8334, 2037.9451, 2056.0110, 2072.9775, 2145.0308, 2146.6199, 2185.0422, 2227.1409, 2273.1587, 2295.1399, 2311.1362, 2351.0833, 2425.2271, 2458.1621, 2522.2354, 2613.1790, 2808.4580, 2825.5261, 2841.1284, 3136.4326, 3211.5007, 3227.4839, 3300.8149, 3302.6477, 3303.5376, 3317.7422, 3361.5156

Spot 41

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:33:43 GMT**
Top Score : **131 for gi|9864777, Gly1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|9864777	60754	131	Gly1 [Arachis hypogaea]
2.	gi|57669861	61041	116	arachin Ahy-4 [Arachis hypogaea]
3.	gi|108595573	61041	116	arachin Ahy-4 [Arachis hypogaea]
4.	gi|22135348	25768	84	trypsin inhibitor [Arachis hypogaea]
5.	gi|52001221	61836	71	arachin Ahy-2 [Arachis hypogaea]
6.	gi|118776570	60681	69	arachin 6 [Arachis hypogaea]
7.	gi|5712199	61430	61	glycinin [Arachis hypogaea]
8.	gi|3703107	58543	53	glycinin [Arachis hypogaea]
9.	gi|52001219	61810	53	arachin Ahy-1 [Arachis hypogaea]
10.	gi|21314465	62042	53	allergen Arah3/Arah4 [Arachis hypogaea]

Results List

1. gi|9864777 **Mass:** 60754 **Score:** 131 **Expect:** 7e-011 **Queries matched:** 16
Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5316	869.5243	869.5083	0.0161	280	286	0	QIVQNLR
1083.5808	1082.5735	1082.5581	0.0155	38	46	0	LNAQRPDNR
1534.6830	1533.6757	1533.6630	0.0127	26	37	0	QQPEENACQFQR
1574.7706	1573.7633	1573.7637	-0.0003	198	210	0	FNLAGNHEQEFLR
1606.7828	1605.7755	1605.7787	-0.0032	219	232	0	SLPYSPYSPQSQPR
1730.8671	1729.8598	1729.8648	-0.0049	197	210	1	RFNLAGNHEQEFLR
2051.0420	2050.0347	2050.0384	-0.0037	83	99	0	RPFYSNAPQEIFIQQGR
2202.9885	2201.9812	2201.9686	0.0127	131	148	1	RFEGEDQSQQQQQDSHQK
2442.2183	2441.2110	2441.2397	-0.0286	280	301	1	QIVQNLRGENESEEEGAIVTVK
2474.1443	2473.1370	2473.1371	-0.0001	100	121	0	GYFGLIFPGCPSTYEEPAQQGR

2505.3066	2504.2993	2504.3036	-0.0043	79 - 99	1	NALRRPFYSNAPQEIFIQQGR
2528.8921	2527.8848	2527.8782	0.0066	314 - 333	0	GADEEEEYDEDEYEYDEEDR
2630.2502	2629.2429	2629.2383	0.0047	100 - 122	1	GYFGLIFPGCPSTYEEPAQQGRR
2685.0342	2684.0269	2683.9793	0.0476	314 - 334	1	GADEEEEYDEDEYEYDEEDRR
3070.3884	3069.3811	3069.3773	0.0038	47 - 73	0	LESEGGYIETWNPNNQEFECAGVALSR
3302.5583	3301.5510	3301.4798	0.0712	250 - 279	0	AGQEEENEGGNIFSGFTPEFLAQAFQVDDR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 877.0414, 881.2761, 1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1111.6124, 1137.5815, 1176.5317, 1187.6499, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1622.7891, 1638.7802, 1714.3816, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2458.1538, 2521.2507, 2613.1743, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3360.5269, 3588.5938

2. gi|57669861 **Mass:** 61041 **Score:** 116 **Expect:** 2.2e-009 **Queries matched:** 15

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5316	869.5243	869.5083	0.0161	281	287	0	QIVQNLR
1083.5808	1082.5735	1082.5581	0.0155	37	45	0	LNAQRPDNR
1111.6124	1110.6051	1110.6006	0.0045	122	130	1	SQSQRPPRR
1534.6830	1533.6757	1533.6630	0.0127	25	36	0	QQPEENACQFQR
1574.7706	1573.7633	1573.7637	-0.0003	196	208	0	FNLAGNHEQEFLR
1606.7828	1605.7755	1605.7787	-0.0032	220	233	0	SLPYSPYSPQSQPR
1730.8671	1729.8598	1729.8648	-0.0049	195	208	1	RFNLAGNHEQEFLR
2051.0420	2050.0347	2050.0384	-0.0037	82	98	0	RPFYSNAPQEIFIQQGR
2474.1443	2473.1370	2473.1371	-0.0001	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3066	2504.2993	2504.3036	-0.0043	78	98	1	NALRRPFYSNAPQEIFIQQGR
2528.8921	2527.8848	2527.8782	0.0066	315	334	0	GADEEEEYDEDEYEYDEEDR
2630.2502	2629.2429	2629.2383	0.0047	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
2685.0342	2684.0269	2683.9793	0.0476	315	335	1	GADEEEEYDEDEYEYDEEDRR
3070.3884	3069.3811	3069.3773	0.0038	46	72	0	IESEGGYIETWNPNNQEFECAGVALSR
3360.5269	3359.5196	3359.4853	0.0343	251	280	0	AGQEEENEGGNIFSGFTPEFLEQAFQVDDR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 877.0414, 881.2761, 1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1137.5815, 1176.5317, 1187.6499, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1622.7891, 1638.7802, 1714.3816, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2202.9885, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2442.2183, 2458.1538, 2521.2507, 2613.1743, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3302.5583, 3588.5938

3. gi|108595573 **Mass:** 61041 **Score:** 116 **Expect:** 2.2e-009 **Queries matched:** 15

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5316	869.5243	869.5083	0.0161	281	287	0	QIVQNLR
1083.5808	1082.5735	1082.5581	0.0155	37	45	0	LNAQRPDNR
1111.6124	1110.6051	1110.6006	0.0045	122	130	1	SQSQRPPRR
1534.6830	1533.6757	1533.6630	0.0127	25	36	0	QQPEENACQFQR
1574.7706	1573.7633	1573.7637	-0.0003	196	208	0	FNLAGNHEQEFLR
1606.7828	1605.7755	1605.7787	-0.0032	220	233	0	SLPYSPYSPQSQPR
1730.8671	1729.8598	1729.8648	-0.0049	195	208	1	RFNLAGNHEQEFLR
2051.0420	2050.0347	2050.0384	-0.0037	82	98	0	RPFYSNAPQEIFIQQGR
2474.1443	2473.1370	2473.1371	-0.0001	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3066	2504.2993	2504.3036	-0.0043	78	98	1	NALRRPFYSNAPQEIFIQQGR
2528.8921	2527.8848	2527.8782	0.0066	315	334	0	GADEEEEYDEDEYEYDEEDR
2630.2502	2629.2429	2629.2383	0.0047	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
2685.0342	2684.0269	2683.9793	0.0476	315	335	1	GADEEEEYDEDEYEYDEEDRR
3070.3884	3069.3811	3069.3773	0.0038	46	72	0	IESEGGYIETWNPNNQEFECAGVALSR
3360.5269	3359.5196	3359.4853	0.0343	251	280	0	AGQEEENEGGNIFSGFTPEFLEQAFQVDDR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 877.0414, 881.2761, 1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1137.5815, 1176.5317, 1187.6499, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1622.7891, 1638.7802, 1714.3816, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2202.9885, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2442.2183, 2458.1538, 2521.2507, 2613.1743, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3302.5583, 3588.5938

4. gi|22135348 **Mass:** 25768 **Score:** 84 **Expect:** 3.2e-006 **Queries matched:** 9

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5808	1082.5735	1082.5581	0.0155	39	47	0	LNAQRPDNR
1534.6830	1533.6757	1533.6630	0.0127	27	38	0	QQPEENACQFQR
1574.7706	1573.7633	1573.7637	-0.0003	198	210	0	FNLAGNHEQEFLR
1730.8671	1729.8598	1729.8648	-0.0049	197	210	1	RFNLAGNHEQEFLR
2051.0420	2050.0347	2050.0384	-0.0037	84	100	0	RPFYSNAPQEIFIQQGR
2474.1443	2473.1370	2473.1371	-0.0001	101	122	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3066	2504.2993	2504.3036	-0.0043	80	100	1	NALRRPFYSNAPQEIFIQQGR
2630.2502	2629.2429	2629.2383	0.0047	101	123	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3884	3069.3811	3069.3773	0.0038	48	74	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 870.5316, 877.0414, 881.2761,

1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1111.6124, 1137.5815, 1176.5317, 1187.6499, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1606.7828, 1622.7891, 1638.7802, 1714.3816, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2202.9885, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2442.2183, 2458.1538, 2521.2507, 2528.8921, 2613.1743, 2685.0342, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3302.5583, 3360.5269, 3588.5938

5. gi|52001221 **Mass:** 61836 **Score:** 71 **Expect:** 7e-005 **Queries matched:** 11

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5808	1082.5735	1082.5581	0.0155	37	45	0	LNAQRPDNR
1534.6830	1533.6757	1533.6630	0.0127	25	36	0	QQPEENACQFQR
1574.7706	1573.7633	1573.7637	-0.0003	197	209	0	FNLAGNHEQEFLR
1606.7828	1605.7755	1605.7787	-0.0032	218	231	0	SLPYSPYSPQSQPR
1730.8671	1729.8598	1729.8648	-0.0049	196	209	1	RFNLAGNHEQEFLR
2051.0420	2050.0347	2050.0384	-0.0037	82	98	0	RPFYSNAPQEIFIQQGR
2202.9885	2201.9812	2201.9686	0.0127	130	147	1	RFEGEDQSQQQQQDSHQK
2474.1443	2473.1370	2473.1371	-0.0001	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3066	2504.2993	2504.3036	-0.0043	78	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2502	2629.2429	2629.2383	0.0047	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3884	3069.3811	3069.3773	0.0038	46	72	0	LESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 870.5316, 877.0414, 881.2761, 1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1111.6124, 1137.5815, 1176.5317, 1187.6499, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1622.7891, 1638.7802, 1714.3816, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2442.2183, 2458.1538, 2521.2507, 2528.8921, 2613.1743, 2685.0342, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3302.5583, 3360.5269, 3588.5938

6. gi|118776570 **Mass:** 60681 **Score:** 69 **Expect:** 0.00012 **Queries matched:** 11

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5316	869.5243	869.5083	0.0161	279	285	0	QIVQNLR
1083.5808	1082.5735	1082.5581	0.0155	37	45	0	LNAQRPDNR
1187.6499	1186.6426	1186.6319	0.0107	122	130	1	YQSQRPPRR
1534.6830	1533.6757	1533.6630	0.0127	25	36	0	QQPEENACQFQR
1574.7706	1573.7633	1573.7637	-0.0003	196	208	0	FNLAGNHEQEFLR
1730.8671	1729.8598	1729.8648	-0.0049	195	208	1	RFNLAGNHEQEFLR
2051.0420	2050.0347	2050.0384	-0.0037	82	98	0	RPFYSNAPQEIFIQQGR

2474.1443	2473.1370	2473.1371	-0.0001	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3066	2504.2993	2504.3036	-0.0043	78 - 98	1	NALRRPFYSNAPQEIFIQQGR
2630.2502	2629.2429	2629.2383	0.0047	99 - 121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3884	3069.3811	3069.3773	0.0038	46 - 72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 877.0414, 881.2761, 1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1111.6124, 1137.5815, 1176.5317, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1606.7828, 1622.7891, 1638.7802, 1714.3816, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2202.9885, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2442.2183, 2458.1538, 2521.2507, 2528.8921, 2613.1743, 2685.0342, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3302.5583, 3360.5269, 3588.5938

7. gi|5712199 **Mass:** 61430 **Score:** 61 **Expect:** 0.00073 **Queries matched:** 10

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5808	1082.5735	1082.5581	0.0155	37 -	45	0	LNAQRPDNR
1187.6499	1186.6426	1186.6319	0.0107	122 -	130	1	YQSQRPPRR
1534.6830	1533.6757	1533.6630	0.0127	25 -	36	0	QQPEENACQFQR
1574.7706	1573.7633	1573.7637	-0.0003	196 -	208	0	FNLAGNHEQEFLR
1730.8671	1729.8598	1729.8648	-0.0049	195 -	208	1	RFNLAGNHEQEFLR
2051.0420	2050.0347	2050.0384	-0.0037	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1443	2473.1370	2473.1371	-0.0001	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3066	2504.2993	2504.3036	-0.0043	78 -	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2502	2629.2429	2629.2383	0.0047	99 -	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3884	3069.3811	3069.3773	0.0038	46 -	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 870.5316, 877.0414, 881.2761, 1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1111.6124, 1137.5815, 1176.5317, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1606.7828, 1622.7891, 1638.7802, 1714.3816, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2202.9885, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2442.2183, 2458.1538, 2521.2507, 2528.8921, 2613.1743, 2685.0342, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3302.5583, 3360.5269, 3588.5938

8. gi|3703107 **Mass:** 58543 **Score:** 53 **Expect:** 0.0043 **Queries matched:** 9

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5316	869.5243	869.5083	0.0161	258 -	264	0	QIVQNLR
1083.5808	1082.5735	1082.5581	0.0155	14 -	22	0	LNAQRPDNR

1111.6124	1110.6051	1110.6006	0.0045	99 - 107	1	SQSQRPPRR
1534.6830	1533.6757	1533.6630	0.0127	2 - 13	0	QQPEENACQFQR
1606.7828	1605.7755	1605.7787	-0.0032	197 - 210	0	SLPYSPYSPQSQPR
2051.0420	2050.0347	2050.0384	-0.0037	59 - 75	0	RPFYSNAPQEIFIQQGR
2505.3066	2504.2993	2504.3036	-0.0043	55 - 75	1	NALRRPFYSNAPQEIFIQQGR
3070.3884	3069.3811	3069.3773	0.0038	23 - 49	0	IESEGGYIETWNPNNQEFECAGVALSR
3360.5269	3359.5196	3359.4853	0.0343	228 - 257	0	AGQEEENEGGNIFSGFTPEFLEQAFQVDDR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 877.0414, 881.2761, 1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1137.5815, 1176.5317, 1187.6499, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1574.7706, 1622.7891, 1638.7802, 1714.3816, 1730.8671, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2202.9885, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2442.2183, 2458.1538, 2474.1443, 2521.2507, 2528.8921, 2613.1743, 2630.2502, 2685.0342, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3302.5583, 3588.5938

9. gi|52001219 **Mass:** 61810 **Score:** 53 **Expect:** 0.0045 **Queries matched:** 9

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5808	1082.5735	1082.5581	0.0155	37 -	45	0	LNAQRPDNR
1534.6830	1533.6757	1533.6630	0.0127	25 -	36	0	QQPEENACQFQR
1574.7706	1573.7633	1573.7637	-0.0003	196 -	208	0	FNLAGNHEQEFLR
1730.8671	1729.8598	1729.8648	-0.0049	195 -	208	1	RFNLAGNHEQEFLR
2051.0420	2050.0347	2050.0384	-0.0037	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1443	2473.1370	2473.1371	-0.0001	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3066	2504.2993	2504.3036	-0.0043	78 -	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2502	2629.2429	2629.2383	0.0047	99 -	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3884	3069.3811	3069.3773	0.0038	46 -	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 870.5316, 877.0414, 881.2761, 1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1111.6124, 1137.5815, 1176.5317, 1187.6499, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1606.7828, 1622.7891, 1638.7802, 1714.3816, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2202.9885, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2442.2183, 2458.1538, 2521.2507, 2528.8921, 2613.1743, 2685.0342, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3302.5583, 3360.5269, 3588.5938

10. gi|21314465 **Mass:** 62042 **Score:** 53 **Expect:** 0.0046 **Queries matched:** 9

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1083.5808	1082.5735	1082.5581	0.0155	37 - 45	0	LNAQRPDNR
1534.6830	1533.6757	1533.6630	0.0127	25 - 36	0	QQPEENACQFQR
1574.7706	1573.7633	1573.7637	-0.0003	196 - 208	0	FNLAGNHEQEFLR
1730.8671	1729.8598	1729.8648	-0.0049	195 - 208	1	RFNLAGNHEQEFLR
2051.0420	2050.0347	2050.0384	-0.0037	82 - 98	0	RPFYSNAPQEIFIQQGR
2474.1443	2473.1370	2473.1371	-0.0001	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3066	2504.2993	2504.3036	-0.0043	78 - 98	1	NALRRPFYSNAPQEIFIQQGR
2630.2502	2629.2429	2629.2383	0.0047	99 - 121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3884	3069.3811	3069.3773	0.0038	46 - 72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 870.5316, 877.0414, 881.2761, 1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1111.6124, 1137.5815, 1176.5317, 1187.6499, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1606.7828, 1622.7891, 1638.7802, 1714.3816, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2202.9885, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2442.2183, 2458.1538, 2521.2507, 2528.8921, 2613.1743, 2685.0342, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3302.5583, 3360.5269, 3588.5938

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 75

Protein View

Match to: **gi|9864777** Score: **131** Expect: **7e-011**
Gly1 [Arachis hypogaea]

Nominal mass (M_r): **60754**; Calculated pI value: **5.48**
NCBI BLAST search of gi|9864777 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: **75**
Number of mass values matched: **16**
Sequence Coverage: **39%**

Matched peptides shown in **Bold Red**

```
   1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE
  51 GGYIETWNPN NQEFECAGVA LSRLVLRRNA LRRPFYSNAP QEIFIQQGRG
 101 YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR
 151 RFDEGDLIAV PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
 201 AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP RGQHSRRERA
 251 GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV
 301 KGGLRILSPD RKRGADEEEE YDEDEYEYDE EDRRRGRGSR GRGNGIEETI
 351 CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR
 401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
 451 NFAVAGKSQS DNFEYVAFKT DSRPNIANFA GENSIIDNLP EEVVANSYGL
 501 PREQARQLKN NNPFKFFVPP SQQSLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
26 - 37	1534.6830	1533.6757	1533.6630	0.0127	0	QQPEENACQFQR
38 - 46	1083.5808	1082.5735	1082.5581	0.0155	0	LNAQRPDNR
47 - 73	3070.3884	3069.3811	3069.3773	0.0038	0	LESEGGYIETWNPNNQEFECAGVALSR
79 - 99	2505.3066	2504.2993	2504.3036	-0.0043	1	NALRRPFYSNAPQEIFIQQGR
83 - 99	2051.0420	2050.0347	2050.0384	-0.0037	0	RPFYSNAPQEIFIQQGR
100 - 121	2474.1443	2473.1370	2473.1371	-0.0001	0	GYFGLIFPGCPSTYEEPAQQGR
100 - 122	2630.2502	2629.2429	2629.2383	0.0047	1	GYFGLIFPGCPSTYEEPAQQGRR
131 - 148	2202.9885	2201.9812	2201.9686	0.0127	1	RFEGEDQSQQQQQDSHQK
197 - 210	1730.8671	1729.8598	1729.8648	-0.0049	1	RFNLAGNHEQEFLR
198 - 210	1574.7706	1573.7633	1573.7637	-0.0003	0	FNLAGNHEQEFLR
219 - 232	1606.7828	1605.7755	1605.7787	-0.0032	0	SLPYSPYSPQSQPR
250 - 279	3302.5583	3301.5510	3301.4798	0.0712	0	AGQEEENEGGNIFSGFTPEFLAQAFQVDDR
280 - 286	870.5316	869.5243	869.5083	0.0161	0	QIVQNLR
280 - 301	2442.2183	2441.2110	2441.2397	-0.0286	1	QIVQNLRGENESEEEGAIVTVK
314 - 333	2528.8921	2527.8848	2527.8782	0.0066	0	GADEEEEYDEDEYEYDEEDR
314 - 334	2685.0342	2684.0269	2683.9793	0.0476	1	GADEEEEYDEDEYEYDEEDRR

No match to: 805.4750, 809.4346, 853.5126, 855.0565, 861.0674, 865.9595, 866.4498, 877.0414, 881.2761, 1019.4967, 1019.9947, 1026.0327, 1026.5487, 1046.6075, 1111.6124, 1137.5815, 1176.5317, 1187.6499, 1193.5599, 1216.5692, 1229.5898, 1230.0876, 1253.1597, 1253.6714, 1372.6968, 1413.7648, 1517.6521, 1533.6990, 1622.7891, 1638.7802, 1714.3816, 1758.8390, 1792.7953, 1794.8525, 1914.9344, 2037.9534, 2067.0249, 2112.9749, 2181.0125, 2185.0186, 2225.0322, 2227.1338, 2273.1599, 2296.1365, 2336.1169, 2351.0894, 2425.2310, 2458.1538, 2521.2507, 2613.1743, 2809.4763, 2825.4739, 2841.1216, 3137.4338, 3211.5117, 3228.5056, 3300.7358, 3360.5269, 3588.5938

Spot 42

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:34:53 GMT
Top Score : 134 for gi|9864777, Gly1 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|9864777	60754	134	Gly1 [Arachis hypogaea]
2.	gi|57669861	61041	111	arachin Ahy-4 [Arachis hypogaea]
3.	gi|108595573	61041	111	arachin Ahy-4 [Arachis hypogaea]
4.	gi|22135348	25768	92	trypsin inhibitor [Arachis hypogaea]
5.	gi|52001221	61836	84	arachin Ahy-2 [Arachis hypogaea]
6.	gi|118776570	60681	65	arachin 6 [Arachis hypogaea]
7.	gi|5712199	61430	65	glycinin [Arachis hypogaea]
8.	gi|52001219	61810	57	arachin Ahy-1 [Arachis hypogaea]
9.	gi|21314465	62042	57	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|3703107	58543	50	glycinin [Arachis hypogaea]

Results List

1. gi|9864777 **Mass:** 60754 **Score:** 134 **Expect:** 3.5e-011 **Queries matched:** 17
Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3909	808.3836	808.3827	0.0009	211 -	216	0	YQQQSR
979.5104	978.5031	978.5107	-0.0076	123 -	130	1	HQSQRAPR
1083.5477	1082.5404	1082.5581	-0.0176	38 -	46	0	LNAQRPDNR
1534.6632	1533.6559	1533.6630	-0.0071	26 -	37	0	QQPEENACQFQR
1574.7633	1573.7560	1573.7637	-0.0076	198 -	210	0	FNLAGNHEQEFLR
1606.7750	1605.7677	1605.7787	-0.0110	219 -	232	0	SLPYSPYSPQSQPR
1730.8651	1729.8578	1729.8648	-0.0069	197 -	210	1	RFNLAGNHEQEFLR
1973.9591	1972.9518	1972.9700	-0.0182	287 -	305	1	GENESEEEGAIVTVKGGLR
2051.0371	2050.0298	2050.0384	-0.0086	83 -	99	0	RPFYSNAPQEIFIQQGR
2202.9751	2201.9678	2201.9686	-0.0007	131 -	148	1	RFEGEDQSQQQQQDSHQK
2442.2388	2441.2315	2441.2397	-0.0081	280 -	301	1	QIVQNLRGENESEEEGAIVTVK

2474.1382	2473.1309	2473.1371	-0.0062	100 - 121	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3042	2504.2969	2504.3036	-0.0066	79 - 99	1	NALRRPFYSNAPQEIFIQQGR
2528.8914	2527.8841	2527.8782	0.0059	314 - 333	0	GADEEEEYDEDEYEYDEEDR
2630.2800	2629.2727	2629.2383	0.0345	100 - 122	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3977	3069.3904	3069.3773	0.0131	47 - 73	0	LESEGGYIETWNPNNQEFECAGVALSR
3302.5366	3301.5293	3301.4798	0.0495	250 - 279	0	AGQEEENEGGNIFSGFTPEFLAQAFQVDDR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 955.5024, 958.4595, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1187.6337, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1622.7775, 1638.7738, 1714.4171, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2273.1641, 2366.1201, 2425.2405, 2458.1357, 2470.2500, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3305.4414, 3360.5444, 3588.6704, 3957.7244

2. gi|57669861 **Mass:** 61041 **Score:** 111 **Expect:** 7e-009 **Queries matched:** 15

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3909	808.3836	808.3827	0.0009	209 - 214		0	YQQQSR
955.5024	954.4951	954.4995	-0.0044	122 - 129		0	SQSQRPPR
1083.5477	1082.5404	1082.5581	-0.0176	37 - 45		0	LNAQRPDNR
1534.6632	1533.6559	1533.6630	-0.0071	25 - 36		0	QQPEENACQFQR
1574.7633	1573.7560	1573.7637	-0.0076	196 - 208		0	FNLAGNHEQEFLR
1606.7750	1605.7677	1605.7787	-0.0110	220 - 233		0	SLPYSPYSPQSQPR
1730.8651	1729.8578	1729.8648	-0.0069	195 - 208		1	RFNLAGNHEQEFLR
2051.0371	2050.0298	2050.0384	-0.0086	82 - 98		0	RPFYSNAPQEIFIQQGR
2470.2500	2469.2427	2469.2458	-0.0031	281 - 302		1	QIVQNLRGENESEEEGAIVTVR
2474.1382	2473.1309	2473.1371	-0.0062	99 - 120		0	GYFGLIFPGCPSTYEEPAQQGR
2505.3042	2504.2969	2504.3036	-0.0066	78 - 98		1	NALRRPFYSNAPQEIFIQQGR
2528.8914	2527.8841	2527.8782	0.0059	315 - 334		0	GADEEEEYDEDEYEYDEEDR
2630.2800	2629.2727	2629.2383	0.0345	99 - 121		1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3977	3069.3904	3069.3773	0.0131	46 - 72		0	IESEGGYIETWNPNNQEFECAGVALSR
3360.5444	3359.5371	3359.4853	0.0518	251 - 280		0	AGQEEENEGGNIFSGFTPEFLEQAFQVDDR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 958.4595, 979.5104, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1187.6337, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1622.7775, 1638.7738, 1714.4171, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 1973.9591, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2202.9751, 2273.1641, 2366.1201, 2425.2405, 2442.2388, 2458.1357, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3302.5366, 3305.4414, 3588.6704, 3957.7244

3. gi|108595573 **Mass:** 61041 **Score:** 111 **Expect:** 7e-009 **Queries matched:** 15

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3909	808.3836	808.3827	0.0009	209	214	0	YQQQSR
955.5024	954.4951	954.4995	-0.0044	122	129	0	SQSQRPPR
1083.5477	1082.5404	1082.5581	-0.0176	37	45	0	LNAQRPDNR
1534.6632	1533.6559	1533.6630	-0.0071	25	36	0	QQPEENACQFQR
1574.7633	1573.7560	1573.7637	-0.0076	196	208	0	FNLAGNHEQEFLR
1606.7750	1605.7677	1605.7787	-0.0110	220	233	0	SLPYSPYSPQSQPR
1730.8651	1729.8578	1729.8648	-0.0069	195	208	1	RFNLAGNHEQEFLR
2051.0371	2050.0298	2050.0384	-0.0086	82	98	0	RPFYSNAPQEIFIQQGR
2470.2500	2469.2427	2469.2458	-0.0031	281	302	1	QIVQNLRGENESEEEGAIVTVR
2474.1382	2473.1309	2473.1371	-0.0062	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3042	2504.2969	2504.3036	-0.0066	78	98	1	NALRRPFYSNAPQEIFIQQGR
2528.8914	2527.8841	2527.8782	0.0059	315	334	0	GADEEEEYDEDEYEYDEEDR
2630.2800	2629.2727	2629.2383	0.0345	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3977	3069.3904	3069.3773	0.0131	46	72	0	IESEGGYIETWNPNNQEFECAGVALSR
3360.5444	3359.5371	3359.4853	0.0518	251	280	0	AGQEEENEGGNIFSGFTPEFLEQAFQVDDR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 958.4595, 979.5104, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1187.6337, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1622.7775, 1638.7738, 1714.4171, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 1973.9591, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2202.9751, 2273.1641, 2366.1201, 2425.2405, 2442.2388, 2458.1357, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3302.5366, 3305.4414, 3588.6704, 3957.7244

4. gi|22135348 **Mass:** 25768 **Score:** 92 **Expect:** 5.6e-007 **Queries matched:** 10

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3909	808.3836	808.3827	0.0009	211	216	0	YQQQSR
1083.5477	1082.5404	1082.5581	-0.0176	39	47	0	LNAQRPDNR
1534.6632	1533.6559	1533.6630	-0.0071	27	38	0	QQPEENACQFQR
1574.7633	1573.7560	1573.7637	-0.0076	198	210	0	FNLAGNHEQEFLR
1730.8651	1729.8578	1729.8648	-0.0069	197	210	1	RFNLAGNHEQEFLR
2051.0371	2050.0298	2050.0384	-0.0086	84	100	0	RPFYSNAPQEIFIQQGR
2474.1382	2473.1309	2473.1371	-0.0062	101	122	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3042	2504.2969	2504.3036	-0.0066	80	100	1	NALRRPFYSNAPQEIFIQQGR
2630.2800	2629.2727	2629.2383	0.0345	101	123	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3977	3069.3904	3069.3773	0.0131	48	74	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 955.5024, 958.4595, 979.5104, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1187.6337, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1606.7750, 1622.7775, 1638.7738, 1714.4171, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 1973.9591, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2202.9751,

2273.1641, 2366.1201, 2425.2405, 2442.2388, 2458.1357, 2470.2500, 2528.8914, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3302.5366, 3305.4414, 3360.5444, 3588.6704, 3957.7244

5. gi|52001221 **Mass:** 61836 **Score:** 84 **Expect:** 3.9e-006 **Queries matched:** 13

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3909	808.3836	808.3827	0.0009	210	215	0	YQQQSR
979.5104	978.5031	978.5107	-0.0076	122	129	1	HQSQRAPR
1083.5477	1082.5404	1082.5581	-0.0176	37	45	0	LNAQRPDNR
1534.6632	1533.6559	1533.6630	-0.0071	25	36	0	QQPEENACQFQR
1574.7633	1573.7560	1573.7637	-0.0076	197	209	0	FNLAGNHEQEFLR
1606.7750	1605.7677	1605.7787	-0.0110	218	231	0	SLPYSPYSPQSQPR
1730.8651	1729.8578	1729.8648	-0.0069	196	209	1	RFNLAGNHEQEFLR
2051.0371	2050.0298	2050.0384	-0.0086	82	98	0	RPFYSNAPQEIFIQQGR
2202.9751	2201.9678	2201.9686	-0.0007	130	147	1	RFEGEDQSQQQQQDSHQK
2474.1382	2473.1309	2473.1371	-0.0062	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3042	2504.2969	2504.3036	-0.0066	78	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2800	2629.2727	2629.2383	0.0345	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3977	3069.3904	3069.3773	0.0131	46	72	0	LESEGGYIETWNPNNQEFECAGVALSR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 955.5024, 958.4595, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1187.6337, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1622.7775, 1638.7738, 1714.4171, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 1973.9591, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2273.1641, 2366.1201, 2425.2405, 2442.2388, 2458.1357, 2470.2500, 2528.8914, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3302.5366, 3305.4414, 3360.5444, 3588.6704, 3957.7244

6. gi|118776570 **Mass:** 60681 **Score:** 65 **Expect:** 0.00027 **Queries matched:** 11

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3909	808.3836	808.3827	0.0009	209	214	0	YQQQSR
1083.5477	1082.5404	1082.5581	-0.0176	37	45	0	LNAQRPDNR
1187.6337	1186.6264	1186.6319	-0.0055	122	130	1	YQSQRPPRR
1534.6632	1533.6559	1533.6630	-0.0071	25	36	0	QQPEENACQFQR
1574.7633	1573.7560	1573.7637	-0.0076	196	208	0	FNLAGNHEQEFLR
1730.8651	1729.8578	1729.8648	-0.0069	195	208	1	RFNLAGNHEQEFLR
2051.0371	2050.0298	2050.0384	-0.0086	82	98	0	RPFYSNAPQEIFIQQGR
2474.1382	2473.1309	2473.1371	-0.0062	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3042	2504.2969	2504.3036	-0.0066	78	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2800	2629.2727	2629.2383	0.0345	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3977	3069.3904	3069.3773	0.0131	46	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 955.5024, 958.4595, 979.5104, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1606.7750, 1622.7775, 1638.7738, 1714.4171, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 1973.9591, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2202.9751, 2273.1641, 2366.1201, 2425.2405, 2442.2388, 2458.1357, 2470.2500, 2528.8914, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3302.5366, 3305.4414, 3360.5444, 3588.6704, 3957.7244

7. gi|5712199 **Mass:** 61430 **Score:** 65 **Expect:** 0.00028 **Queries matched:** 11

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3909	808.3836	808.3827	0.0009	209	214	0	YQQQSR
1083.5477	1082.5404	1082.5581	-0.0176	37	45	0	LNAQRPDNR
1187.6337	1186.6264	1186.6319	-0.0055	122	130	1	YQSQRPPRR
1534.6632	1533.6559	1533.6630	-0.0071	25	36	0	QQPEENACQFQR
1574.7633	1573.7560	1573.7637	-0.0076	196	208	0	FNLAGNHEQEFLR
1730.8651	1729.8578	1729.8648	-0.0069	195	208	1	RFNLAGNHEQEFLR
2051.0371	2050.0298	2050.0384	-0.0086	82	98	0	RPFYSNAPQEIFIQQGR
2474.1382	2473.1309	2473.1371	-0.0062	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3042	2504.2969	2504.3036	-0.0066	78	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2800	2629.2727	2629.2383	0.0345	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3977	3069.3904	3069.3773	0.0131	46	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 955.5024, 958.4595, 979.5104, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1606.7750, 1622.7775, 1638.7738, 1714.4171, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 1973.9591, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2202.9751, 2273.1641, 2366.1201, 2425.2405, 2442.2388, 2458.1357, 2470.2500, 2528.8914, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3302.5366, 3305.4414, 3360.5444, 3588.6704, 3957.7244

8. gi|52001219 **Mass:** 61810 **Score:** 57 **Expect:** 0.0018 **Queries matched:** 10

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3909	808.3836	808.3827	0.0009	209	214	0	YQQQSR
1083.5477	1082.5404	1082.5581	-0.0176	37	45	0	LNAQRPDNR
1534.6632	1533.6559	1533.6630	-0.0071	25	36	0	QQPEENACQFQR
1574.7633	1573.7560	1573.7637	-0.0076	196	208	0	FNLAGNHEQEFLR
1730.8651	1729.8578	1729.8648	-0.0069	195	208	1	RFNLAGNHEQEFLR
2051.0371	2050.0298	2050.0384	-0.0086	82	98	0	RPFYSNAPQEIFIQQGR
2474.1382	2473.1309	2473.1371	-0.0062	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3042	2504.2969	2504.3036	-0.0066	78	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2800	2629.2727	2629.2383	0.0345	99	121	1	GYFGLIFPGCPSTYEEPAQQGRR

3070.3977	3069.3904	3069.3773	0.0131	46 - 72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 955.5024, 958.4595, 979.5104, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1187.6337, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1606.7750, 1622.7775, 1638.7738, 1714.4171, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 1973.9591, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2202.9751, 2273.1641, 2366.1201, 2425.2405, 2442.2388, 2458.1357, 2470.2500, 2528.8914, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3302.5366, 3305.4414, 3360.5444, 3588.6704, 3957.7244

9. gi|21314465 **Mass:** 62042 **Score:** 57 **Expect:** 0.0018 **Queries matched:** 10

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3909	808.3836	808.3827	0.0009	209 -	214	0	YQQQSR
1083.5477	1082.5404	1082.5581	-0.0176	37 -	45	0	LNAQRPDNR
1534.6632	1533.6559	1533.6630	-0.0071	25 -	36	0	QQPEENACQFQR
1574.7633	1573.7560	1573.7637	-0.0076	196 -	208	0	FNLAGNHEQEFLR
1730.8651	1729.8578	1729.8648	-0.0069	195 -	208	1	RFNLAGNHEQEFLR
2051.0371	2050.0298	2050.0384	-0.0086	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1382	2473.1309	2473.1371	-0.0062	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3042	2504.2969	2504.3036	-0.0066	78 -	98	1	NALRRPFYSNAPQEIFIQQGR
2630.2800	2629.2727	2629.2383	0.0345	99 -	121	1	GYFGLIFPGCPSTYEEPAQQGRR
3070.3977	3069.3904	3069.3773	0.0131	46 -	72	0	IESEGGYIETWNPNNQEFECAGVALSR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 955.5024, 958.4595, 979.5104, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1187.6337, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1606.7750, 1622.7775, 1638.7738, 1714.4171, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 1973.9591, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2202.9751, 2273.1641, 2366.1201, 2425.2405, 2442.2388, 2458.1357, 2470.2500, 2528.8914, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3302.5366, 3305.4414, 3360.5444, 3588.6704, 3957.7244

10. gi|3703107 **Mass:** 58543 **Score:** 50 **Expect:** 0.0087 **Queries matched:** 9

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3909	808.3836	808.3827	0.0009	186 -	191	0	YQQQSR
955.5024	954.4951	954.4995	-0.0044	99 -	106	0	SQSQRPPR
1083.5477	1082.5404	1082.5581	-0.0176	14 -	22	0	LNAQRPDNR
1534.6632	1533.6559	1533.6630	-0.0071	2 -	13	0	QQPEENACQFQR
1606.7750	1605.7677	1605.7787	-0.0110	197 -	210	0	SLPYSPYSPQSQPR
2051.0371	2050.0298	2050.0384	-0.0086	59 -	75	0	RPFYSNAPQEIFIQQGR
2505.3042	2504.2969	2504.3036	-0.0066	55 -	75	1	NALRRPFYSNAPQEIFIQQGR
3070.3977	3069.3904	3069.3773	0.0131	23 -	49	0	IESEGGYIETWNPNNQEFECAGVALSR

3360.5444 3359.5371 3359.4853 0.0518 228 - 257 0 AGQEEENEGGNIFSGFTPEFLEQAFQVDDR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 958.4595, 979.5104, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1187.6337, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1574.7633, 1622.7775, 1638.7738, 1714.4171, 1730.8651, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 1973.9591, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2202.9751, 2273.1641, 2366.1201, 2425.2405, 2442.2388, 2458.1357, 2470.2500, 2474.1382, 2528.8914, 2630.2800, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3302.5366, 3305.4414, 3588.6704, 3957.7244

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 81

Protein View

Match to: **gi|9864777** Score: **134** Expect: **3.5e-011**
Gly1 [Arachis hypogaea]

Nominal mass (M_r): **60754**; Calculated pI value: **5.48**
NCBI BLAST search of gi|9864777 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **81**
Number of mass values matched: **17**
Sequence Coverage: **43%**

Matched peptides shown in **Bold Red**

```
  1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE
 51 GGYIETWNPN NQEFECAGVA LSRLVLRRNA LRRPFYSNAP QEIFIQQGRG
101 YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR
151 RFDEGDLIAV PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
201 AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP RGQHSRRERA
```

```
251 GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV
301 KGGLRILSPD RKRGADEEEE YDEDEYEYDE EDRRRGRGSR GRGNGIEETI
351 CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
451 NFAVAGKSQS DNFEYVAFKT DSRPNIANFA GENSIIDNLP EEVVANSYGL
501 PREQARQLKN NNPFKFFVPP SQQSLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
26 - 37	1534.6632	1533.6559	1533.6630	-0.0071	0	QQPEENACQFQR
38 - 46	1083.5477	1082.5404	1082.5581	-0.0176	0	LNAQRPDNR
47 - 73	3070.3977	3069.3904	3069.3773	0.0131	0	LESEGGYIETWNPNNQEFECAGVALSR
79 - 99	2505.3042	2504.2969	2504.3036	-0.0066	1	NALRRPFYSNAPQEIFIQQGR
83 - 99	2051.0371	2050.0298	2050.0384	-0.0086	0	RPFYSNAPQEIFIQQGR
100 - 121	2474.1382	2473.1309	2473.1371	-0.0062	0	GYFGLIFPGCPSTYEEPAQQGR
100 - 122	2630.2800	2629.2727	2629.2383	0.0345	1	GYFGLIFPGCPSTYEEPAQQGRR
123 - 130	979.5104	978.5031	978.5107	-0.0076	1	HQSQRAPR
131 - 148	2202.9751	2201.9678	2201.9686	-0.0007	1	RFEGEDQSQQQQQDSHQK
197 - 210	1730.8651	1729.8578	1729.8648	-0.0069	1	RFNLAGNHEQEFLR
198 - 210	1574.7633	1573.7560	1573.7637	-0.0076	0	FNLAGNHEQEFLR
211 - 216	809.3909	808.3836	808.3827	0.0009	0	YQQQSR
219 - 232	1606.7750	1605.7677	1605.7787	-0.0110	0	SLPYSPYSPQSQPR
250 - 279	3302.5366	3301.5293	3301.4798	0.0495	0	AGQEEENEGGNIFSGFTPEFLAQAFQVDDR
280 - 301	2442.2388	2441.2315	2441.2397	-0.0081	1	QIVQNLRGENESEEEGAIVTVK
287 - 305	1973.9591	1972.9518	1972.9700	-0.0182	1	GENESEEEGAIVTVKGGLR
314 - 333	2528.8914	2527.8841	2527.8782	0.0059	0	GADEEEEYDEDEYEYDEEDR

No match to: 861.0342, 865.9244, 866.4233, 870.4919, 877.0131, 955.5024, 958.4595, 1019.4702, 1019.9630, 1026.0040, 1026.5114, 1111.5667, 1129.5361, 1137.5607, 1176.5038, 1187.6337, 1193.5358, 1216.5763, 1229.5471, 1230.0543, 1253.1527, 1253.6627, 1372.6497, 1477.6219, 1517.6324, 1553.6410, 1622.7775, 1638.7738, 1714.4171, 1757.8521, 1792.7863, 1794.8450, 1884.8612, 1894.9648, 1897.9104, 1899.3738, 1914.9631, 2021.4386, 2034.6188, 2037.9460, 2056.9624, 2057.9270, 2067.9998, 2073.0400, 2181.0288, 2185.0178, 2273.1641, 2366.1201, 2425.2405, 2458.1357, 2470.2500, 2685.9951, 2808.4539, 2814.2751, 2824.4888, 2825.4651, 2841.0952, 3154.5183, 3211.5132, 3300.6892, 3305.4414, 3360.5444, 3588.6704, 3957.7244

Spot 43

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:37:11 GMT
Top Score : 107 for gi|57669861, arachin Ahy-4 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|57669861	61041	107	arachin Ahy-4 [Arachis hypogaea]
2.	gi|108595573	61041	107	arachin Ahy-4 [Arachis hypogaea]
3.	gi|3703107	58543	67	glycinin [Arachis hypogaea]
4.	gi|9864777	60754	55	Gly1 [Arachis hypogaea]
5.	gi|52001221	61836	47	arachin Ahy-2 [Arachis hypogaea]
6.	gi|22135348	25768	43	trypsin inhibitor [Arachis hypogaea]
7.	gi|118776570	60681	30	arachin 6 [Arachis hypogaea]
8.	gi|5712199	61430	24	glycinin [Arachis hypogaea]
9.	gi|52001219	61810	24	arachin Ahy-1 [Arachis hypogaea]
10.	gi|37789212	61803	24	storage protein [Arachis hypogaea]

Results List

1. gi|57669861 **Mass:** 61041 **Score:** 107 **Expect:** 1.7e-008 **Queries matched:** 15
arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.4070	808.3997	808.3827	0.0170	209	214	0	YQQQSR
870.5183	869.5110	869.5083	0.0028	281	287	0	QIVQNLR
955.5049	954.4976	954.4995	-0.0019	122	129	0	SQSQRPPR
1083.5571	1082.5498	1082.5581	-0.0082	37	45	0	LNAQRPDNR
1111.6038	1110.5965	1110.6006	-0.0041	122	130	1	SQSQRPPRR
1177.5394	1176.5321	1176.5523	-0.0202	234	242	1	QEEREFSPR
1534.6613	1533.6540	1533.6630	-0.0090	25	36	0	QQPEENACQFQR
1574.7548	1573.7475	1573.7637	-0.0161	196	208	0	FNLAGNHEQEFLR
1606.7793	1605.7720	1605.7787	-0.0067	220	233	0	SLPYSPYSPQSQPR
1618.7587	1617.7514	1617.7481	0.0033	288	302	0	GENESEEEGAIVTVR

1730.8621	1729.8548	1729.8648	-0.0099	195 - 208	1	RFNLAGNHEQEFLR
1883.8375	1882.8302	1882.8405	-0.0103	131 - 146	0	LQGEDQSQQQQDSHQK
2039.9423	2038.9350	2038.9416	-0.0066	130 - 146	1	RLQGEDQSQQQQDSHQK
2051.0286	2050.0213	2050.0384	-0.0171	82 - 98	0	RPFYSNAPQEIFIQQGR
2276.0933	2275.0860	2275.0689	0.0171	131 - 149	1	LQGEDQSQQQQDSHQKVHR

No match to: 805.4454, 827.4073, 853.4749, 877.0261, 881.2617, 883.2652, 897.2622, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1160.5341, 1175.5282, 1176.5338, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2203.0024, 2273.1440, 2432.1707, 2454.2466, 2458.1355, 2471.8638, 2627.9663, 2784.0745, 2941.1960

2. gi|108595573 **Mass:** 61041 **Score:** 107 **Expect:** 1.7e-008 **Queries matched:** 15

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.4070	808.3997	808.3827	0.0170	209 - 214		0	YQQQSR
870.5183	869.5110	869.5083	0.0028	281 - 287		0	QIVQNLR
955.5049	954.4976	954.4995	-0.0019	122 - 129		0	SQSQRPPR
1083.5571	1082.5498	1082.5581	-0.0082	37 - 45		0	LNAQRPDNR
1111.6038	1110.5965	1110.6006	-0.0041	122 - 130		1	SQSQRPPRR
1177.5394	1176.5321	1176.5523	-0.0202	234 - 242		1	QEEREFSPR
1534.6613	1533.6540	1533.6630	-0.0090	25 - 36		0	QQPEENACQFQR
1574.7548	1573.7475	1573.7637	-0.0161	196 - 208		0	FNLAGNHEQEFLR
1606.7793	1605.7720	1605.7787	-0.0067	220 - 233		0	SLPYSPYSPQSQPR
1618.7587	1617.7514	1617.7481	0.0033	288 - 302		0	GENESEEEGAIVTVR
1730.8621	1729.8548	1729.8648	-0.0099	195 - 208		1	RFNLAGNHEQEFLR
1883.8375	1882.8302	1882.8405	-0.0103	131 - 146		0	LQGEDQSQQQQDSHQK
2039.9423	2038.9350	2038.9416	-0.0066	130 - 146		1	RLQGEDQSQQQQDSHQK
2051.0286	2050.0213	2050.0384	-0.0171	82 - 98		0	RPFYSNAPQEIFIQQGR
2276.0933	2275.0860	2275.0689	0.0171	131 - 149		1	LQGEDQSQQQQDSHQKVHR

No match to: 805.4454, 827.4073, 853.4749, 877.0261, 881.2617, 883.2652, 897.2622, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1160.5341, 1175.5282, 1176.5338, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2203.0024, 2273.1440, 2432.1707, 2454.2466, 2458.1355, 2471.8638, 2627.9663, 2784.0745, 2941.1960

3. gi|3703107 **Mass:** 58543 **Score:** 67 **Expect:** 0.00018 **Queries matched:** 11

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.4070	808.3997	808.3827	0.0170	186 -	191	0	YQQQSR
870.5183	869.5110	869.5083	0.0028	258 -	264	0	QIVQNLR
955.5049	954.4976	954.4995	-0.0019	99 -	106	0	SQSQRPPR
1083.5571	1082.5498	1082.5581	-0.0082	14 -	22	0	LNAQRPDNR
1111.6038	1110.5965	1110.6006	-0.0041	99 -	107	1	SQSQRPPRR
1177.5394	1176.5321	1176.5523	-0.0202	211 -	219	1	QEEREFSPR
1534.6613	1533.6540	1533.6630	-0.0090	2 -	13	0	QQPEENACQFQR
1606.7793	1605.7720	1605.7787	-0.0067	197 -	210	0	SLPYSPYSPQSQPR
2051.0286	2050.0213	2050.0384	-0.0171	59 -	75	0	RPFYSNAPQEIFIQQGR
2471.8638	2470.8565	2470.8567	-0.0002	293 -	311	0	ADEEEEYDEDEYEYDEEDR
2627.9663	2626.9590	2626.9579	0.0012	293 -	312	1	ADEEEEYDEDEYEYDEEDRR

No match to: 805.4454, 827.4073, 853.4749, 877.0261, 881.2617, 883.2652, 897.2622, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1160.5341, 1175.5282, 1176.5338, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1574.7548, 1618.7587, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1730.8621, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1883.8375, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2039.9423, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2203.0024, 2273.1440, 2276.0933, 2432.1707, 2454.2466, 2458.1355, 2784.0745, 2941.1960

4. gi|9864777 **Mass:** 60754 **Score:** 55 **Expect:** 0.0026 **Queries matched:** 10

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.4070	808.3997	808.3827	0.0170	211 -	216	0	YQQQSR
870.5183	869.5110	869.5083	0.0028	280 -	286	0	QIVQNLR
1083.5571	1082.5498	1082.5581	-0.0082	38 -	46	0	LNAQRPDNR
1177.5394	1176.5321	1176.5523	-0.0202	233 -	241	1	QEEREFSPR
1534.6613	1533.6540	1533.6630	-0.0090	26 -	37	0	QQPEENACQFQR
1574.7548	1573.7475	1573.7637	-0.0161	198 -	210	0	FNLAGNHEQEFLR
1606.7793	1605.7720	1605.7787	-0.0067	219 -	232	0	SLPYSPYSPQSQPR
1730.8621	1729.8548	1729.8648	-0.0099	197 -	210	1	RFNLAGNHEQEFLR
2051.0286	2050.0213	2050.0384	-0.0171	83 -	99	0	RPFYSNAPQEIFIQQGR
2203.0024	2201.9951	2201.9686	0.0266	131 -	148	1	RFEGEDQSQQQQQDSHQK

No match to: 805.4454, 827.4073, 853.4749, 877.0261, 881.2617, 883.2652, 897.2622, 955.5049, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1111.6038, 1160.5341, 1175.5282, 1176.5338, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1618.7587, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1883.8375, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2039.9423, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2273.1440, 2276.0933, 2432.1707, 2454.2466, 2458.1355, 2471.8638, 2627.9663, 2784.0745, 2941.1960

5. gi|52001221 **Mass:** 61836 **Score:** 47 **Expect:** 0.017 **Queries matched:** 9

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.4070	808.3997	808.3827	0.0170	210 -	215	0	YQQQSR
1083.5571	1082.5498	1082.5581	-0.0082	37 -	45	0	LNAQRPDNR
1177.5394	1176.5321	1176.5523	-0.0202	232 -	240	1	QEEREFSPR
1534.6613	1533.6540	1533.6630	-0.0090	25 -	36	0	QQPEENACQFQR
1574.7548	1573.7475	1573.7637	-0.0161	197 -	209	0	FNLAGNHEQEFLR
1606.7793	1605.7720	1605.7787	-0.0067	218 -	231	0	SLPYSPYSPQSQPR
1730.8621	1729.8548	1729.8648	-0.0099	196 -	209	1	RFNLAGNHEQEFLR
2051.0286	2050.0213	2050.0384	-0.0171	82 -	98	0	RPFYSNAPQEIFIQQGR
2203.0024	2201.9951	2201.9686	0.0266	130 -	147	1	RFEGEDQSQQQQQDSHQK

No match to: 805.4454, 827.4073, 853.4749, 870.5183, 877.0261, 881.2617, 883.2652, 897.2622, 955.5049, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1111.6038, 1160.5341, 1175.5282, 1176.5338, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1618.7587, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1883.8375, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2039.9423, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2273.1440, 2276.0933, 2432.1707, 2454.2466, 2458.1355, 2471.8638, 2627.9663, 2784.0745, 2941.1960

6. gi|22135348 **Mass:** 25768 **Score:** 43 **Expect:** 0.043 **Queries matched:** 6

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.4070	808.3997	808.3827	0.0170	211 -	216	0	YQQQSR
1083.5571	1082.5498	1082.5581	-0.0082	39 -	47	0	LNAQRPDNR
1534.6613	1533.6540	1533.6630	-0.0090	27 -	38	0	QQPEENACQFQR
1574.7548	1573.7475	1573.7637	-0.0161	198 -	210	0	FNLAGNHEQEFLR
1730.8621	1729.8548	1729.8648	-0.0099	197 -	210	1	RFNLAGNHEQEFLR
2051.0286	2050.0213	2050.0384	-0.0171	84 -	100	0	RPFYSNAPQEIFIQQGR

No match to: 805.4454, 827.4073, 853.4749, 870.5183, 877.0261, 881.2617, 883.2652, 897.2622, 955.5049, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1111.6038, 1160.5341, 1175.5282, 1176.5338, 1177.5394, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1606.7793, 1618.7587, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1883.8375, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2039.9423, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2203.0024, 2273.1440, 2276.0933, 2432.1707, 2454.2466, 2458.1355, 2471.8638, 2627.9663, 2784.0745, 2941.1960

7. gi|118776570 **Mass:** 60681 **Score:** 30 **Expect:** 0.84 **Queries matched:** 7

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.4070	808.3997	808.3827	0.0170	209 -	214	0	YQQQSR
870.5183	869.5110	869.5083	0.0028	279 -	285	0	QIVQNLR
1083.5571	1082.5498	1082.5581	-0.0082	37 -	45	0	LNAQRPDNR
1534.6613	1533.6540	1533.6630	-0.0090	25 -	36	0	QQPEENACQFQR
1574.7548	1573.7475	1573.7637	-0.0161	196 -	208	0	FNLAGNHEQEFLR
1730.8621	1729.8548	1729.8648	-0.0099	195 -	208	1	RFNLAGNHEQEFLR
2051.0286	2050.0213	2050.0384	-0.0171	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 805.4454, 827.4073, 853.4749, 877.0261, 881.2617, 883.2652, 897.2622, 955.5049, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1111.6038, 1160.5341, 1175.5282, 1176.5338, 1177.5394, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1606.7793, 1618.7587, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1883.8375, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2039.9423, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2203.0024, 2273.1440, 2276.0933, 2432.1707, 2454.2466, 2458.1355, 2471.8638, 2627.9663, 2784.0745, 2941.1960

8. gi|5712199 **Mass:** 61430 **Score:** 24 **Expect:** 3.5 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.4070	808.3997	808.3827	0.0170	209 -	214	0	YQQQSR
1083.5571	1082.5498	1082.5581	-0.0082	37 -	45	0	LNAQRPDNR
1534.6613	1533.6540	1533.6630	-0.0090	25 -	36	0	QQPEENACQFQR
1574.7548	1573.7475	1573.7637	-0.0161	196 -	208	0	FNLAGNHEQEFLR
1730.8621	1729.8548	1729.8648	-0.0099	195 -	208	1	RFNLAGNHEQEFLR
2051.0286	2050.0213	2050.0384	-0.0171	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 805.4454, 827.4073, 853.4749, 870.5183, 877.0261, 881.2617, 883.2652, 897.2622, 955.5049, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1111.6038, 1160.5341, 1175.5282, 1176.5338, 1177.5394, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1606.7793, 1618.7587, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1883.8375, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2039.9423, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2203.0024, 2273.1440, 2276.0933, 2432.1707, 2454.2466, 2458.1355, 2471.8638, 2627.9663, 2784.0745, 2941.1960

9. gi|52001219 **Mass:** 61810 **Score:** 24 **Expect:** 3.7 **Queries matched:** 6

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.4070	808.3997	808.3827	0.0170	209 -	214	0	YQQQSR
1083.5571	1082.5498	1082.5581	-0.0082	37 -	45	0	LNAQRPDNR
1534.6613	1533.6540	1533.6630	-0.0090	25 -	36	0	QQPEENACQFQR

1574.7548	1573.7475	1573.7637	-0.0161	196 - 208	0	FNLAGNHEQEFLR
1730.8621	1729.8548	1729.8648	-0.0099	195 - 208	1	RFNLAGNHEQEFLR
2051.0286	2050.0213	2050.0384	-0.0171	82 - 98	0	RPFYSNAPQEIFIQQGR

No match to: 805.4454, 827.4073, 853.4749, 870.5183, 877.0261, 881.2617, 883.2652, 897.2622, 955.5049, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1111.6038, 1160.5341, 1175.5282, 1176.5338, 1177.5394, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1606.7793, 1618.7587, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1883.8375, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2039.9423, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2203.0024, 2273.1440, 2276.0933, 2432.1707, 2454.2466, 2458.1355, 2471.8638, 2627.9663, 2784.0745, 2941.1960

10. gi|37789212 **Mass:** 61803 **Score:** 24 **Expect:** 3.7 **Queries matched:** 6

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.4070	808.3997	808.3827	0.0170	209 -	214	0	YQQQSR
1083.5571	1082.5498	1082.5581	-0.0082	37 -	45	0	LNAQRPDNR
1534.6613	1533.6540	1533.6630	-0.0090	25 -	36	0	QQPEENACQFQR
1574.7548	1573.7475	1573.7637	-0.0161	196 -	208	0	FNLAGNHEQEFLR
1730.8621	1729.8548	1729.8648	-0.0099	195 -	208	1	RFNLAGNHEQEFLR
2051.0286	2050.0213	2050.0384	-0.0171	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 805.4454, 827.4073, 853.4749, 870.5183, 877.0261, 881.2617, 883.2652, 897.2622, 955.5049, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1111.6038, 1160.5341, 1175.5282, 1176.5338, 1177.5394, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1606.7793, 1618.7587, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1883.8375, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2039.9423, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2203.0024, 2273.1440, 2276.0933, 2432.1707, 2454.2466, 2458.1355, 2471.8638, 2627.9663, 2784.0745, 2941.1960

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 67

Protein View

Match to: **gi|57669861** Score: **107** Expect: **1.7e-008**
arachin Ahy-4 [Arachis hypogaea]

Nominal mass (M_r): **61041**; Calculated pI value: **5.36**
NCBI BLAST search of gi|57669861 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **67**
Number of mass values matched: **15**
Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

```
    1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
   51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
  101 FGLIFPGCPS TYEEPAQQGR RSQSQRPPRR LQGEDQSQQQ QDSHQKVHRF
  151 DEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
  201 NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS PRGQHSRRER
  251 AGQEEENEGG NIFSGFTPEF LEQAFQVDDR QIVQNLRGEN ESEEEGAIVT
  301 VRGGLRILSP DRKRGADEEE EYDEDEYEYD EEDRRRGRGS RGRGNGIEET
  351 ICTASVKKNI GRNRSPDIYN PQAGSLKTAN DLNLLILRWL GLSAEYGNLY
  401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP
  451 QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL AGENSVIDNL PEEVVANSYG
  501 LQREQARQQL KNNNPFKFFV PPSQQSPRAV A
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 36	1534.6613	1533.6540	1533.6630	-0.0090	0	QQPEENACQFQR
37 - 45	1083.5571	1082.5498	1082.5581	-0.0082	0	LNAQRPDNR
82 - 98	2051.0286	2050.0213	2050.0384	-0.0171	0	RPFYSNAPQEIFIQQGR
122 - 129	955.5049	954.4976	954.4995	-0.0019	0	SQSQRPPR
122 - 130	1111.6038	1110.5965	1110.6006	-0.0041	1	SQSQRPPRR
130 - 146	2039.9423	2038.9350	2038.9416	-0.0066	1	RLQGEDQSQQQQDSHQK
131 - 146	1883.8375	1882.8302	1882.8405	-0.0103	0	LQGEDQSQQQQDSHQK
131 - 149	2276.0933	2275.0860	2275.0689	0.0171	1	LQGEDQSQQQQDSHQKVHR
195 - 208	1730.8621	1729.8548	1729.8648	-0.0099	1	RFNLAGNHEQEFLR
196 - 208	1574.7548	1573.7475	1573.7637	-0.0161	0	FNLAGNHEQEFLR

209 - 214	809.4070	808.3997	808.3827	0.0170	0	YQQQSR
220 - 233	1606.7793	1605.7720	1605.7787	-0.0067	0	SLPYSPYSPQSQPR
234 - 242	1177.5394	1176.5321	1176.5523	-0.0202	1	QEEREFSPR
281 - 287	870.5183	869.5110	869.5083	0.0028	0	QIVQNLR
288 - 302	1618.7587	1617.7514	1617.7481	0.0033	0	GENESEEEGAIVTVR

No match to: 805.4454, 827.4073, 853.4749, 877.0261, 881.2617, 883.2652, 897.2622, 984.5844, 1020.4728, 1046.5872, 1080.5287, 1160.5341, 1175.5282, 1176.5338, 1193.5458, 1216.5693, 1239.6340, 1314.6071, 1372.6732, 1477.6404, 1517.6348, 1533.6385, 1551.6726, 1553.6453, 1622.7706, 1638.7670, 1651.8263, 1654.7682, 1660.7371, 1741.7983, 1758.8064, 1774.8326, 1778.8605, 1793.8044, 1794.8481, 1897.8975, 1914.9091, 2021.9342, 2037.9460, 2061.9336, 2101.9045, 2181.0054, 2185.0181, 2203.0024, 2273.1440, 2432.1707, 2454.2466, 2458.1355, 2471.8638, 2627.9663, 2784.0745, 2941.1960

Spot 44

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:39:22 GMT
Top Score : 102 for gi|57669861, arachin Ahy-4 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|57669861	61041	102	arachin Ahy-4 [Arachis hypogaea]
2.	gi|108595573	61041	102	arachin Ahy-4 [Arachis hypogaea]
3.	gi|3703107	58543	69	glycinin [Arachis hypogaea]
4.	gi|9864777	60754	56	Gly1 [Arachis hypogaea]
5.	gi|52001221	61836	56	arachin Ahy-2 [Arachis hypogaea]
6.	gi|22135348	25768	56	trypsin inhibitor [Arachis hypogaea]
7.	gi|118776570	60681	35	arachin 6 [Arachis hypogaea]
8.	gi|5712199	61430	35	glycinin [Arachis hypogaea]
9.	gi|52001219	61810	35	arachin Ahy-1 [Arachis hypogaea]
10.	gi|37789212	61803	35	storage protein [Arachis hypogaea]

Results List

1. gi|57669861 **Mass:** 61041 **Score:** 102 **Expect:** 5.5e-008 **Queries matched:** 12
arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3698	808.3625	808.3827	-0.0202	209	214	0	YQQQSR
955.5025	954.4952	954.4995	-0.0043	122	129	0	SQSQRPPR
1083.5602	1082.5529	1082.5581	-0.0051	37	45	0	LNAQRPDNR
1111.6030	1110.5957	1110.6006	-0.0049	122	130	1	SQSQRPPRR
1534.6929	1533.6856	1533.6630	0.0226	25	36	0	QQPEENACQFQR
1574.7852	1573.7779	1573.7637	0.0143	196	208	0	FNLAGNHEQEFLR
1606.8230	1605.8157	1605.8031	0.0126	344	358	1	GNGIEETICTASVKK
1618.7788	1617.7715	1617.7481	0.0234	288	302	0	GENESEEEGAIVTVR
1730.8938	1729.8865	1729.8648	0.0218	195	208	1	RFNLAGNHEQEFLR
1883.8575	1882.8502	1882.8405	0.0097	131	146	0	LQGEDQSQQQQDSHQK

2039.9790	2038.9717	2038.9416	0.0301	130 - 146	1	RLQGEDQSQQQQDSHQK
2051.0596	2050.0523	2050.0384	0.0139	82 - 98	0	RPFYSNAPQEIFIQQGR

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 1046.5958, 1066.0715, 1080.5363, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1622.8041, 1637.7511, 1638.7970, 1774.8638, 1794.8792, 2037.9725, 2182.0530, 2202.9868, 2273.1580, 2275.1536, 2458.1426, 2471.8423, 2627.9443, 2785.0386

2. gi|108595573 **Mass:** 61041 **Score:** 102 **Expect:** 5.5e-008 **Queries matched:** 12

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3698	808.3625	808.3827	-0.0202	209 -	214	0	YQQQSR
955.5025	954.4952	954.4995	-0.0043	122 -	129	0	SQSQRPPR
1083.5602	1082.5529	1082.5581	-0.0051	37 -	45	0	LNAQRPDNR
1111.6030	1110.5957	1110.6006	-0.0049	122 -	130	1	SQSQRPPRR
1534.6929	1533.6856	1533.6630	0.0226	25 -	36	0	QQPEENACQFQR
1574.7852	1573.7779	1573.7637	0.0143	196 -	208	0	FNLAGNHEQEFLR
1606.8230	1605.8157	1605.8031	0.0126	344 -	358	1	GNGIEETICTASVKK
1618.7788	1617.7715	1617.7481	0.0234	288 -	302	0	GENESEEEGAIVTVR
1730.8938	1729.8865	1729.8648	0.0218	195 -	208	1	RFNLAGNHEQEFLR
1883.8575	1882.8502	1882.8405	0.0097	131 -	146	0	LQGEDQSQQQQDSHQK
2039.9790	2038.9717	2038.9416	0.0301	130 -	146	1	RLQGEDQSQQQQDSHQK
2051.0596	2050.0523	2050.0384	0.0139	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 1046.5958, 1066.0715, 1080.5363, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1622.8041, 1637.7511, 1638.7970, 1774.8638, 1794.8792, 2037.9725, 2182.0530, 2202.9868, 2273.1580, 2275.1536, 2458.1426, 2471.8423, 2627.9443, 2785.0386

3. gi|3703107 **Mass:** 58543 **Score:** 69 **Expect:** 0.00012 **Queries matched:** 9

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3698	808.3625	808.3827	-0.0202	186 -	191	0	YQQQSR
955.5025	954.4952	954.4995	-0.0043	99 -	106	0	SQSQRPPR
1083.5602	1082.5529	1082.5581	-0.0051	14 -	22	0	LNAQRPDNR
1111.6030	1110.5957	1110.6006	-0.0049	99 -	107	1	SQSQRPPRR
1534.6929	1533.6856	1533.6630	0.0226	2 -	13	0	QQPEENACQFQR
1606.8230	1605.8157	1605.7787	0.0370	197 -	210	0	SLPYSPYSPQSQPR
2051.0596	2050.0523	2050.0384	0.0139	59 -	75	0	RPFYSNAPQEIFIQQGR
2471.8423	2470.8350	2470.8567	-0.0217	293 -	311	0	ADEEEEYDEDEYEYDEEDR
2627.9443	2626.9370	2626.9579	-0.0208	293 -	312	1	ADEEEEYDEDEYEYDEEDRR

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 1046.5958, 1066.0715, 1080.5363, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1574.7852, 1618.7788, 1622.8041, 1637.7511, 1638.7970, 1730.8938, 1774.8638, 1794.8792, 1883.8575, 2037.9725, 2039.9790, 2182.0530, 2202.9868, 2273.1580, 2275.1536, 2458.1426, 2785.0386

4. gi|9864777 **Mass:** 60754 **Score:** 56 **Expect:** 0.0021 **Queries matched:** 8

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3698	808.3625	808.3827	-0.0202	211	216	0	YQQQSR
1083.5602	1082.5529	1082.5581	-0.0051	38	46	0	LNAQRPDNR
1534.6929	1533.6856	1533.6630	0.0226	26	37	0	QQPEENACQFQR
1574.7852	1573.7779	1573.7637	0.0143	198	210	0	FNLAGNHEQEFLR
1606.8230	1605.8157	1605.8031	0.0126	343	357	1	GNGIEETICTASVKK
1730.8938	1729.8865	1729.8648	0.0218	197	210	1	RFNLAGNHEQEFLR
2051.0596	2050.0523	2050.0384	0.0139	83	99	0	RPFYSNAPQEIFIQQGR
2202.9868	2201.9795	2201.9686	0.0110	131	148	1	RFEGEDQSQQQQQDSHQK

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 955.5025, 1046.5958, 1066.0715, 1080.5363, 1111.6030, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1618.7788, 1622.8041, 1637.7511, 1638.7970, 1774.8638, 1794.8792, 1883.8575, 2037.9725, 2039.9790, 2182.0530, 2273.1580, 2275.1536, 2458.1426, 2471.8423, 2627.9443, 2785.0386

5. gi|52001221 **Mass:** 61836 **Score:** 56 **Expect:** 0.0022 **Queries matched:** 8

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3698	808.3625	808.3827	-0.0202	210	215	0	YQQQSR
1083.5602	1082.5529	1082.5581	-0.0051	37	45	0	LNAQRPDNR
1534.6929	1533.6856	1533.6630	0.0226	25	36	0	QQPEENACQFQR
1574.7852	1573.7779	1573.7637	0.0143	197	209	0	FNLAGNHEQEFLR
1606.8230	1605.8157	1605.8031	0.0126	351	365	1	GNGIEETICTASVKK
1730.8938	1729.8865	1729.8648	0.0218	196	209	1	RFNLAGNHEQEFLR
2051.0596	2050.0523	2050.0384	0.0139	82	98	0	RPFYSNAPQEIFIQQGR
2202.9868	2201.9795	2201.9686	0.0110	130	147	1	RFEGEDQSQQQQQDSHQK

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 955.5025, 1046.5958, 1066.0715, 1080.5363, 1111.6030, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1618.7788, 1622.8041, 1637.7511, 1638.7970, 1774.8638, 1794.8792, 1883.8575, 2037.9725, 2039.9790, 2182.0530, 2273.1580, 2275.1536, 2458.1426, 2471.8423, 2627.9443, 2785.0386

6. gi|22135348 **Mass:** 25768 **Score:** 56 **Expect:** 0.0024 **Queries matched:** 6

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3698	808.3625	808.3827	-0.0202	211	216	0	YQQQSR
1083.5602	1082.5529	1082.5581	-0.0051	39	47	0	LNAQRPDNR
1534.6929	1533.6856	1533.6630	0.0226	27	38	0	QQPEENACQFQR
1574.7852	1573.7779	1573.7637	0.0143	198	210	0	FNLAGNHEQEFLR
1730.8938	1729.8865	1729.8648	0.0218	197	210	1	RFNLAGNHEQEFLR
2051.0596	2050.0523	2050.0384	0.0139	84	100	0	RPFYSNAPQEIFIQQGR

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 955.5025, 1046.5958, 1066.0715, 1080.5363, 1111.6030, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1606.8230, 1618.7788, 1622.8041, 1637.7511, 1638.7970, 1774.8638, 1794.8792, 1883.8575, 2037.9725, 2039.9790, 2182.0530, 2202.9868, 2273.1580, 2275.1536, 2458.1426, 2471.8423, 2627.9443, 2785.0386

7. gi|118776570 **Mass:** 60681 **Score:** 35 **Expect:** 0.26 **Queries matched:** 6

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3698	808.3625	808.3827	-0.0202	209	214	0	YQQQSR
1083.5602	1082.5529	1082.5581	-0.0051	37	45	0	LNAQRPDNR
1534.6929	1533.6856	1533.6630	0.0226	25	36	0	QQPEENACQFQR
1574.7852	1573.7779	1573.7637	0.0143	196	208	0	FNLAGNHEQEFLR
1730.8938	1729.8865	1729.8648	0.0218	195	208	1	RFNLAGNHEQEFLR
2051.0596	2050.0523	2050.0384	0.0139	82	98	0	RPFYSNAPQEIFIQQGR

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 955.5025, 1046.5958, 1066.0715, 1080.5363, 1111.6030, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1606.8230, 1618.7788, 1622.8041, 1637.7511, 1638.7970, 1774.8638, 1794.8792, 1883.8575, 2037.9725, 2039.9790, 2182.0530, 2202.9868, 2273.1580, 2275.1536, 2458.1426, 2471.8423, 2627.9443, 2785.0386

8. gi|5712199 **Mass:** 61430 **Score:** 35 **Expect:** 0.27 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3698	808.3625	808.3827	-0.0202	209	214	0	YQQQSR
1083.5602	1082.5529	1082.5581	-0.0051	37	45	0	LNAQRPDNR
1534.6929	1533.6856	1533.6630	0.0226	25	36	0	QQPEENACQFQR
1574.7852	1573.7779	1573.7637	0.0143	196	208	0	FNLAGNHEQEFLR
1730.8938	1729.8865	1729.8648	0.0218	195	208	1	RFNLAGNHEQEFLR

2051.0596	2050.0523	2050.0384	0.0139	82 - 98	0	RPFYSNAPQEIFIQQGR

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 955.5025, 1046.5958, 1066.0715, 1080.5363, 1111.6030, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1606.8230, 1618.7788, 1622.8041, 1637.7511, 1638.7970, 1774.8638, 1794.8792, 1883.8575, 2037.9725, 2039.9790, 2182.0530, 2202.9868, 2273.1580, 2275.1536, 2458.1426, 2471.8423, 2627.9443, 2785.0386

9. gi|52001219 **Mass:** 61810 **Score:** 35 **Expect:** 0.28 **Queries matched:** 6

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3698	808.3625	808.3827	-0.0202	209 -	214	0	YQQQSR
1083.5602	1082.5529	1082.5581	-0.0051	37 -	45	0	LNAQRPDNR
1534.6929	1533.6856	1533.6630	0.0226	25 -	36	0	QQPEENACQFQR
1574.7852	1573.7779	1573.7637	0.0143	196 -	208	0	FNLAGNHEQEFLR
1730.8938	1729.8865	1729.8648	0.0218	195 -	208	1	RFNLAGNHEQEFLR
2051.0596	2050.0523	2050.0384	0.0139	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 955.5025, 1046.5958, 1066.0715, 1080.5363, 1111.6030, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1606.8230, 1618.7788, 1622.8041, 1637.7511, 1638.7970, 1774.8638, 1794.8792, 1883.8575, 2037.9725, 2039.9790, 2182.0530, 2202.9868, 2273.1580, 2275.1536, 2458.1426, 2471.8423, 2627.9443, 2785.0386

10. gi|37789212 **Mass:** 61803 **Score:** 35 **Expect:** 0.28 **Queries matched:** 6

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3698	808.3625	808.3827	-0.0202	209 -	214	0	YQQQSR
1083.5602	1082.5529	1082.5581	-0.0051	37 -	45	0	LNAQRPDNR
1534.6929	1533.6856	1533.6630	0.0226	25 -	36	0	QQPEENACQFQR
1574.7852	1573.7779	1573.7637	0.0143	196 -	208	0	FNLAGNHEQEFLR
1730.8938	1729.8865	1729.8648	0.0218	195 -	208	1	RFNLAGNHEQEFLR
2051.0596	2050.0523	2050.0384	0.0139	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 955.5025, 1046.5958, 1066.0715, 1080.5363, 1111.6030, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1606.8230, 1618.7788, 1622.8041, 1637.7511, 1638.7970, 1774.8638, 1794.8792, 1883.8575, 2037.9725, 2039.9790, 2182.0530, 2202.9868, 2273.1580, 2275.1536, 2458.1426, 2471.8423, 2627.9443, 2785.0386

Search Parameters

Type of search : **Peptide Mass Fingerprint**
Enzyme : **Trypsin**
Fixed modifications : **Carbamidomethyl (C)**
Variable modifications : **Oxidation (M)**
Mass values : **MONOISOTOPIC**
Protein Mass : **Unrestricted**
Peptide Mass Tolerance : **± 25 ppm**
Peptide Charge State : **1+**
Max Missed Cleavages : **1**
Number of queries : **41**

Protein View

Match to: **gi|57669861** Score: **102** Expect: **5.5e-008**
arachin Ahy-4 [Arachis hypogaea]

Nominal mass (M_r): **61041**; Calculated pI value: **5.36**
NCBI BLAST search of gi|57669861 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **41**
Number of mass values matched: **12**
Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

```
    1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
   51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
  101 FGLIFPGCPS TYEEPAQQGR RSQSQRPPRR LQGEDQSQQQ QDSHQKVHRF
  151 DEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
  201 NHEQEFLRYQ QQSRQSRRRS LPYSPYSPQS QPRQEEREFS PRGQHSRRER
  251 AGQEEENEGG NIFSGFTPEF LEQAFQVDDR QIVQNLRGEN ESEEEGAIVT
  301 VRGGLRILSP DRKRGADEEE EYDEDEYEYD EEDRRRGRGS RGRGNGIEET
  351 ICTASVKKNI GRNRSPDIYN PQAGSLKTAN DLNLLILRWL GLSAEYGNLY
  401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP
  451 QNFAVAGKSQ SDNFEYVAFK TDSRPSIANL AGENSVIDNL PEEVVANSYG
  501 LQREQARQQL KNNNPFKFFV PPSQQSPRAV A
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 36	1534.6929	1533.6856	1533.6630	0.0226	0	QQPEENACQFQR
37 - 45	1083.5602	1082.5529	1082.5581	-0.0051	0	LNAQRPDNR
82 - 98	2051.0596	2050.0523	2050.0384	0.0139	0	RPFYSNAPQEIFIQQGR
122 - 129	955.5025	954.4952	954.4995	-0.0043	0	SQSQRPPR
122 - 130	1111.6030	1110.5957	1110.6006	-0.0049	1	SQSQRPPRR
130 - 146	2039.9790	2038.9717	2038.9416	0.0301	1	RLQGEDQSQQQQDSHQK
131 - 146	1883.8575	1882.8502	1882.8405	0.0097	0	LQGEDQSQQQQDSHQK
195 - 208	1730.8938	1729.8865	1729.8648	0.0218	1	RFNLAGNHEQEFLR
196 - 208	1574.7852	1573.7779	1573.7637	0.0143	0	FNLAGNHEQEFLR
209 - 214	809.3698	808.3625	808.3827	-0.0202	0	YQQQSR
288 - 302	1618.7788	1617.7715	1617.7481	0.0234	0	GENESEEEGAIVTVR
344 - 358	1606.8230	1605.8157	1605.8031	0.0126	1	GNGIEETICTASVKK

No match to: 855.0315, 861.0535, 870.4847, 877.0236, 906.4882, 1046.5958, 1066.0715, 1080.5363, 1175.5483, 1176.5482, 1193.5632, 1215.4912, 1216.5698, 1372.7052, 1517.6642, 1622.8041, 1637.7511, 1638.7970, 1774.8638, 1794.8792, 2037.9725, 2182.0530, 2202.9868, 2273.1580, 2275.1536, 2458.1426, 2471.8423, 2627.9443, 2785.0386

Spot 45

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:36:08 GMT
Top Score : 138 for gi|47933675, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	138	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	138	iso-Ara h3 [Arachis hypogaea]
3.	gi|230338	23975	21	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
4.	gi|28194657	13874	17	putative caffeic acid methyl transferase [Arachis hypogaea]
5.	gi|62177385	14731	16	resistance protein Cre [Arachis hypogaea]
6.	gi|2498261	2416	13	33.0 kDa cold shock protein (AHCSP33)
7.	gi|62177393	21055	12	resistance protein Cre [Arachis hypogaea]
8.	gi|62177626	19671	12	resistance protein PRG [Arachis hypogaea]
9.	gi|60594911	28600	12	N-acetylglucosaminyl-transferase [Rhizobium sp. NET30]
10.	gi|60594909	28570	12	N-acetylglucosaminyl-transferase [Rhizobium sp. NCHA22]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 138 **Expect:** 1.4e-011 **Queries matched:** 16
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
859.4807	858.4734	858.4559	0.0175	256	262	0	QTVENLR
993.5130	992.5057	992.5039	0.0018	120	127	0	YQSQKPSR
1083.5750	1082.5677	1082.5581	0.0097	35	43	0	LNAQRPDNR
1095.4679	1094.4606	1094.4628	-0.0022	299	306	1	REEFDEDR
1149.6213	1148.6140	1148.6050	0.0090	120	128	1	YQSQKPSRR
1481.6130	1480.6057	1480.6000	0.0057	23	34	0	QGGEENECQFQR
1547.7567	1546.7494	1546.7389	0.0105	209	220	0	YQQQQGSRPHYR
1614.7960	1613.7887	1613.7837	0.0050	196	208	0	FYLAGNQEQEFLR
1658.8499	1657.8426	1657.8270	0.0156	263	277	1	GENEREEQGAIVTVK
1691.7894	1690.7821	1690.7659	0.0163	300	312	1	EEFDEDRSRPQQR

1770.8993	1769.8920	1769.8848	0.0072	195 - 208	1	RFYLAGNQEQEFLR
2099.9412	2098.9339	2098.9304	0.0035	129 - 146	0	FQVGQDDPSQQQQDSHQK
2256.0696	2255.0623	2255.0315	0.0308	128 - 146	1	RFQVGQDDPSQQQQDSHQK
2492.1494	2491.1421	2491.1588	-0.0167	129 - 149	1	FQVGQDDPSQQQQDSHQKVHR
3069.3899	3068.3826	3068.3933	-0.0107	44 - 70	0	IESEGGYIETWNPNNQEFQCAGVALSR
3199.4573	3198.4500	3198.4277	0.0223	228 - 255	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 805.4572, 845.1028, 855.0690, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1307.6849, 1464.5979, 1475.7537, 1638.8511, 1754.4689, 1832.8914, 1984.8966, 2088.9976, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2499.2644, 2514.3379, 2613.1792, 3211.5134, 3228.4553, 3300.7080, 3455.6265

2. gi|112380623 **Mass:** 58570 **Score:** 138 **Expect:** 1.4e-011 **Queries matched:** 16

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
859.4807	858.4734	858.4559	0.0175	258 - 264		0	QTVENLR
993.5130	992.5057	992.5039	0.0018	122 - 129		0	YQSQKPSR
1083.5750	1082.5677	1082.5581	0.0097	37 - 45		0	LNAQRPDNR
1095.4679	1094.4606	1094.4628	-0.0022	301 - 308		1	REEFDEDR
1149.6213	1148.6140	1148.6050	0.0090	122 - 130		1	YQSQKPSRR
1481.6130	1480.6057	1480.6000	0.0057	25 - 36		0	QGGEENECQFQR
1547.7567	1546.7494	1546.7389	0.0105	211 - 222		0	YQQQQGSRPHYR
1614.7960	1613.7887	1613.7837	0.0050	198 - 210		0	FYLAGNQEQEFLR
1658.8499	1657.8426	1657.8270	0.0156	265 - 279		1	GENEREEQGAIVTVK
1691.7894	1690.7821	1690.7659	0.0163	302 - 314		1	EEFDEDRSRPQQR
1770.8993	1769.8920	1769.8848	0.0072	197 - 210		1	RFYLAGNQEQEFLR
2099.9412	2098.9339	2098.9304	0.0035	131 - 148		0	FQVGQDDPSQQQQDSHQK
2256.0696	2255.0623	2255.0315	0.0308	130 - 148		1	RFQVGQDDPSQQQQDSHQK
2492.1494	2491.1421	2491.1588	-0.0167	131 - 151		1	FQVGQDDPSQQQQDSHQKVHR
3069.3899	3068.3826	3068.3933	-0.0107	46 - 72		0	IESEGGYIETWNPNNQEFQCAGVALSR
3199.4573	3198.4500	3198.4277	0.0223	230 - 257		0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 805.4572, 845.1028, 855.0690, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1307.6849, 1464.5979, 1475.7537, 1638.8511, 1754.4689, 1832.8914, 1984.8966, 2088.9976, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2499.2644, 2514.3379, 2613.1792, 3211.5134, 3228.4553, 3300.7080, 3455.6265

3. gi|230338 **Mass:** 23975 **Score:** 21 **Expect:** 7.1 **Queries matched:** 3

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1046.6045	1045.5972	1045.5880	0.0093	90	-	99	1	LKSAASLNSR
2273.1533	2272.1460	2272.1521	-0.0061	70	-	89	0	SIVHPSYNSNTLNNDIMLIK
2514.3379	2513.3306	2513.3311	-0.0005	70	-	91	1	SIVHPSYNSNTLNNDIMLIKLK

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

4. gi|28194657 **Mass:** 13874 **Score:** 17 **Expect:** 18 **Queries matched:** 2

putative caffeic acid methyl transferase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1658.8499	1657.8426	1657.8133	0.0293	1	-	16	0	DGITHVGGDMFVSVPK
2483.2200	2482.2127	2482.1871	0.0256	1	-	23	1	DGITHVGGDMFVSVPKADAIYMK + 2 Oxidation (M)

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

5. gi|62177385 **Mass:** 14731 **Score:** 16 **Expect:** 21 **Queries matched:** 2

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
2088.9976	2087.9903	2087.9979	-0.0076	72	-	89	1	NCPPELESIGRSIVETCK
2295.1426	2294.1353	2294.1147	0.0207	15	-	34	1	TIKNCFPENNNGGMILVTTR + Oxidation (M)

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2273.1533, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

6. gi|2498261 **Mass:** 2416 **Score:** 13 **Expect:** 46 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1547.7567	1546.7494	1546.7263	0.0231	9	-	24	0	ASYTVTPPAQANAADA

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

7. gi|62177393 **Mass:** 21055 **Score:** 12 **Expect:** 54 **Queries matched:** 3

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1691.7894	1690.7821	1690.7991	-0.0169	112	-	124	1	SDWIYFRDVEFSK
2295.1426	2294.1353	2294.1326	0.0027	42	-	61	1	IMGTEPPLFLKGMDVETSWK + Oxidation (M)
2311.1426	2310.1353	2310.1275	0.0078	42	-	61	1	IMGTEPPLFLKGMDVETSWK + 2 Oxidation (M)

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2273.1533, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

8. gi|62177626 **Mass:** 19671 **Score:** 12 **Expect:** 56 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1145.5767	1144.5694	1144.5724	-0.0029	32	-	41	0	ISDQEEGLVR
2335.1172	2334.1099	2334.1280	-0.0181	151	-	171	0	ANYEDLSNQAIHYAQGLPFAL

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2273.1533, 2295.1426, 2311.1426, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

9. gi|60594911 **Mass:** 28600 **Score:** 12 **Expect:** 59 **Queries matched:** 2

N-acetylglucosaminyl-transferase [Rhizobium sp. NET30]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2162.0383	2161.0310	2161.0547	-0.0237	135	152	1	TALTMLLDQYETQMFRGK + Oxidation (M)
2227.1443	2226.1370	2226.1612	-0.0242	71	92	1	LALKMQDPAIGAAMGQLAASNR

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2185.0366, 2226.0540, 2256.0696, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

10. gi|60594909 **Mass:** 28570 **Score:** 12 **Expect:** 61 **Queries matched:** 2

N-acetylglucosaminyl-transferase [Rhizobium sp. NCHA22]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2162.0383	2161.0310	2161.0547	-0.0237	135	152	1	TALTMLLDQYETQMFRGK + Oxidation (M)
2227.1443	2226.1370	2226.1612	-0.0242	71	92	1	LALKMQDPAIGAAMGQLAASNR

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2185.0366, 2226.0540, 2256.0696, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 59

Protein View

Match to: **gi|47933675** Score: **138** Expect: **1.4e-011**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **59**
Number of mass values matched: **16**
Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

```
     1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
    51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
   101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
   201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
   251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
   301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
   351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
   401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
   451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
   501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6130	1480.6057	1480.6000	0.0057	0	QGGEENECQFQR
35 - 43	1083.5750	1082.5677	1082.5581	0.0097	0	LNAQRPDNR
44 - 70	3069.3899	3068.3826	3068.3933	-0.0107	0	IESEGGYIETWNPNNQEFQCAGVALSR
120 - 127	993.5130	992.5057	992.5039	0.0018	0	YQSQKPSR
120 - 128	1149.6213	1148.6140	1148.6050	0.0090	1	YQSQKPSRR
128 - 146	2256.0696	2255.0623	2255.0315	0.0308	1	RFQVGQDDPSQQQQDSHQK
129 - 146	2099.9412	2098.9339	2098.9304	0.0035	0	FQVGQDDPSQQQQDSHQK
129 - 149	2492.1494	2491.1421	2491.1588	-0.0167	1	FQVGQDDPSQQQQDSHQKVHR
195 - 208	1770.8993	1769.8920	1769.8848	0.0072	1	RFYLAGNQEQEFLR
196 - 208	1614.7960	1613.7887	1613.7837	0.0050	0	FYLAGNQEQEFLR

209 - 220	1547.7567	1546.7494	1546.7389	0.0105	0	YQQQQGSRPHYR
228 - 255	3199.4573	3198.4500	3198.4277	0.0223	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR
256 - 262	859.4807	858.4734	858.4559	0.0175	0	QTVENLR
263 - 277	1658.8499	1657.8426	1657.8270	0.0156	1	GENEREEQGAIVTVK
299 - 306	1095.4679	1094.4606	1094.4628	-0.0022	1	REEFDEDR
300 - 312	1691.7894	1690.7821	1690.7659	0.0163	1	EEFDEDRSRPQQR

No match to: 805.4572, 845.1028, 855.0690, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1307.6849, 1464.5979, 1475.7537, 1638.8511, 1754.4689, 1832.8914, 1984.8966, 2088.9976, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2499.2644, 2514.3379, 2613.1792, 3211.5134, 3228.4553, 3300.7080, 3455.6265

Spot 46

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:37:16 GMT
Top Score : 128 for gi|47933675, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	128	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	128	iso-Ara h3 [Arachis hypogaea]
3.	gi|230338	23975	23	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
4.	gi|2498261	2416	14	33.0 kDa cold shock protein (AHCSP33)
5.	gi|62177393	21055	13	resistance protein Cre [Arachis hypogaea]
6.	gi|1834333	4154	12	unknown [Arachis hypogaea]
7.	gi|2736182	32367	12	coat protein [cowpea mild mottle virus]
8.	gi|1709314	4568	10	Chitooligosaccharide deacetylase (Nodulation protein B)
9.	gi|988275	4568	10	NodB
10.	gi|40738310	112681	10	1a protein [Cucumber mosaic virus]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 128 **Expect:** 1.4e-010 **Queries matched:** 14
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
939.3691	938.3618	938.3617	0.0001	300	306	0	EEFDEDR
993.5040	992.4967	992.5039	-0.0072	120	127	0	YQSQKPSR
1083.5684	1082.5611	1082.5581	0.0031	35	43	0	LNAQRPDNR
1095.4774	1094.4701	1094.4628	0.0073	299	306	1	REEFDEDR
1149.6135	1148.6062	1148.6050	0.0012	120	128	1	YQSQKPSRR
1481.6066	1480.5993	1480.6000	-0.0007	23	34	0	QGGEENECQFQR
1547.7479	1546.7406	1546.7389	0.0017	209	220	0	YQQQQGSRPHYR
1614.7954	1613.7881	1613.7837	0.0044	196	208	0	FYLAGNQEQEFLR
1658.8303	1657.8230	1657.8270	-0.0040	263	277	1	GENEREEQGAIVTVK
1691.7769	1690.7696	1690.7659	0.0038	300	312	1	EEFDEDRSRPQQR

1770.8834	1769.8761	1769.8848	-0.0087	195 - 208	1	RFYLAGNQEQEFLR
2099.9395	2098.9322	2098.9304	0.0018	129 - 146	0	FQVGQDDPSQQQQDSHQK
2256.0303	2255.0230	2255.0315	-0.0085	128 - 146	1	RFQVGQDDPSQQQQDSHQK
2492.1650	2491.1577	2491.1588	-0.0011	129 - 149	1	FQVGQDDPSQQQQDSHQKVHR

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 992.9540, 1046.6029, 1050.1044, 1066.0920, 1072.1031, 1175.5537, 1277.0929, 1424.6067, 1464.5776, 1500.5861, 1531.3519, 1563.7388, 1569.7230, 1609.6785, 1847.8778, 1984.8951, 2088.9807, 2121.9194, 2161.9651, 2273.1624

2. gi|112380623 **Mass:** 58570 **Score:** 128 **Expect:** 1.4e-010 **Queries matched:** 14

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
939.3691	938.3618	938.3617	0.0001	302 -	308	0	EEFDEDR
993.5040	992.4967	992.5039	-0.0072	122 -	129	0	YQSQKPSR
1083.5684	1082.5611	1082.5581	0.0031	37 -	45	0	LNAQRPDNR
1095.4774	1094.4701	1094.4628	0.0073	301 -	308	1	REEFDEDR
1149.6135	1148.6062	1148.6050	0.0012	122 -	130	1	YQSQKPSRR
1481.6066	1480.5993	1480.6000	-0.0007	25 -	36	0	QGGEENECQFQR
1547.7479	1546.7406	1546.7389	0.0017	211 -	222	0	YQQQQGSRPHYR
1614.7954	1613.7881	1613.7837	0.0044	198 -	210	0	FYLAGNQEQEFLR
1658.8303	1657.8230	1657.8270	-0.0040	265 -	279	1	GENEREEQGAIVTVK
1691.7769	1690.7696	1690.7659	0.0038	302 -	314	1	EEFDEDRSRPQQR
1770.8834	1769.8761	1769.8848	-0.0087	197 -	210	1	RFYLAGNQEQEFLR
2099.9395	2098.9322	2098.9304	0.0018	131 -	148	0	FQVGQDDPSQQQQDSHQK
2256.0303	2255.0230	2255.0315	-0.0085	130 -	148	1	RFQVGQDDPSQQQQDSHQK
2492.1650	2491.1577	2491.1588	-0.0011	131 -	151	1	FQVGQDDPSQQQQDSHQKVHR

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 992.9540, 1046.6029, 1050.1044, 1066.0920, 1072.1031, 1175.5537, 1277.0929, 1424.6067, 1464.5776, 1500.5861, 1531.3519, 1563.7388, 1569.7230, 1609.6785, 1847.8778, 1984.8951, 2088.9807, 2121.9194, 2161.9651, 2273.1624

3. gi|230338 **Mass:** 23975 **Score:** 23 **Expect:** 4.2 **Queries matched:** 3

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.6029	1045.5956	1045.5880	0.0077	90 -	99	1	LKSAASLNSR
1609.6785	1608.6712	1608.6508	0.0205	171 -	186	0	DSCQGDSGGPVVCSGK
2273.1624	2272.1551	2272.1521	0.0030	70 -	89	0	SIVHPSYNSNTLNNDIMLIK

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 939.3691,

992.9540, 993.5040, 1050.1044, 1066.0920, 1072.1031, 1083.5684, 1095.4774, 1149.6135, 1175.5537, 1277.0929, 1424.6067, 1464.5776, 1481.6066, 1500.5861, 1531.3519, 1547.7479, 1563.7388, 1569.7230, 1614.7954, 1658.8303, 1691.7769, 1770.8834, 1847.8778, 1984.8951, 2088.9807, 2099.9395, 2121.9194, 2161.9651, 2256.0303, 2492.1650

4. gi|2498261 **Mass:** 2416 **Score:** 14 **Expect:** 34 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1547.7479	1546.7406	1546.7263	0.0143	9 -	24	0	ASYTVTPPAQANAADA

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 939.3691, 992.9540, 993.5040, 1046.6029, 1050.1044, 1066.0920, 1072.1031, 1083.5684, 1095.4774, 1149.6135, 1175.5537, 1277.0929, 1424.6067, 1464.5776, 1481.6066, 1500.5861, 1531.3519, 1563.7388, 1569.7230, 1609.6785, 1614.7954, 1658.8303, 1691.7769, 1770.8834, 1847.8778, 1984.8951, 2088.9807, 2099.9395, 2121.9194, 2161.9651, 2256.0303, 2273.1624, 2492.1650

5. gi|62177393 **Mass:** 21055 **Score:** 13 **Expect:** 41 **Queries matched:** 2

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1691.7769	1690.7696	1690.7991	-0.0294	112 -	124	1	SDWIYFRDVEFSK
2161.9651	2160.9578	2160.9471	0.0108	149 -	165	1	NCFSYCSLFPKGFMFEK

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 939.3691, 992.9540, 993.5040, 1046.6029, 1050.1044, 1066.0920, 1072.1031, 1083.5684, 1095.4774, 1149.6135, 1175.5537, 1277.0929, 1424.6067, 1464.5776, 1481.6066, 1500.5861, 1531.3519, 1547.7479, 1563.7388, 1569.7230, 1609.6785, 1614.7954, 1658.8303, 1770.8834, 1847.8778, 1984.8951, 2088.9807, 2099.9395, 2121.9194, 2256.0303, 2273.1624, 2492.1650

6. gi|1834333 **Mass:** 4154 **Score:** 12 **Expect:** 61 **Queries matched:** 1

unknown [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1658.8303	1657.8230	1657.8034	0.0196	4 -	17	1	KFDDSFMRPVFGGR

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 939.3691, 992.9540, 993.5040, 1046.6029, 1050.1044, 1066.0920, 1072.1031, 1083.5684, 1095.4774, 1149.6135, 1175.5537, 1277.0929, 1424.6067, 1464.5776, 1481.6066, 1500.5861, 1531.3519, 1547.7479, 1563.7388, 1569.7230, 1609.6785, 1614.7954, 1691.7769, 1770.8834, 1847.8778, 1984.8951, 2088.9807, 2099.9395, 2121.9194, 2161.9651, 2256.0303, 2273.1624, 2492.1650

7. gi|2736182 **Mass:** 32367 **Score:** 12 **Expect:** 62 **Queries matched:** 2

coat protein [cowpea mild mottle virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1569.7230	1568.7157	1568.7174	-0.0017	100 -	113	1	KISNNMATAEEMAK + 2 Oxidation (M)

2088.9807	2087.9734	2087.9754	-0.0020	1 -	18	1	MESIFDLNKLLDDSMGTK + 2 Oxidation (M)

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 939.3691, 992.9540, 993.5040, 1046.6029, 1050.1044, 1066.0920, 1072.1031, 1083.5684, 1095.4774, 1149.6135, 1175.5537, 1277.0929, 1424.6067, 1464.5776, 1481.6066, 1500.5861, 1531.3519, 1547.7479, 1563.7388, 1609.6785, 1614.7954, 1658.8303, 1691.7769, 1770.8834, 1847.8778, 1984.8951, 2099.9395, 2121.9194, 2161.9651, 2256.0303, 2273.1624, 2492.1650

8. gi|1709314 **Mass:** 4568 **Score:** 10 **Expect:** 82 **Queries matched:** 1

Chitooligosaccharide deacetylase (Nodulation protein B)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5684	1082.5611	1082.5581	0.0031	3 -	11	1	HSDNLRSVR

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 939.3691, 992.9540, 993.5040, 1046.6029, 1050.1044, 1066.0920, 1072.1031, 1095.4774, 1149.6135, 1175.5537, 1277.0929, 1424.6067, 1464.5776, 1481.6066, 1500.5861, 1531.3519, 1547.7479, 1563.7388, 1569.7230, 1609.6785, 1614.7954, 1658.8303, 1691.7769, 1770.8834, 1847.8778, 1984.8951, 2088.9807, 2099.9395, 2121.9194, 2161.9651, 2256.0303, 2273.1624, 2492.1650

9. gi|988275 **Mass:** 4568 **Score:** 10 **Expect:** 82 **Queries matched:** 1

NodB

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5684	1082.5611	1082.5581	0.0031	3 -	11	1	HSDNLRSVR

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 939.3691, 992.9540, 993.5040, 1046.6029, 1050.1044, 1066.0920, 1072.1031, 1095.4774, 1149.6135, 1175.5537, 1277.0929, 1424.6067, 1464.5776, 1481.6066, 1500.5861, 1531.3519, 1547.7479, 1563.7388, 1569.7230, 1609.6785, 1614.7954, 1658.8303, 1691.7769, 1770.8834, 1847.8778, 1984.8951, 2088.9807, 2099.9395, 2121.9194, 2161.9651, 2256.0303, 2273.1624, 2492.1650

10. gi|40738310 **Mass:** 112681 **Score:** 10 **Expect:** 90 **Queries matched:** 3

1a protein [Cucumber mosaic virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1464.5776	1463.5703	1463.6061	-0.0357	440 -	451	0	MYDMWNASSISK + 2 Oxidation (M)
1691.7769	1690.7696	1690.8009	-0.0313	565 -	579	0	EQEVSELDSLSAQTR
2273.1624	2272.1551	2272.1958	-0.0407	780 -	799	0	VLVDEVVLLHFGQLCAVMSK + Oxidation (M)

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 939.3691, 992.9540, 993.5040, 1046.6029, 1050.1044, 1066.0920, 1072.1031, 1083.5684, 1095.4774, 1149.6135, 1175.5537, 1277.0929, 1424.6067, 1481.6066, 1500.5861, 1531.3519, 1547.7479, 1563.7388, 1569.7230, 1609.6785, 1614.7954, 1658.8303, 1770.8834, 1847.8778, 1984.8951, 2088.9807, 2099.9395, 2121.9194, 2161.9651, 2256.0303, 2492.1650

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 43

Protein View

Match to: **gi|47933675** Score: **128** Expect: **1.4e-010**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **43**
Number of mass values matched: **14**
Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

```
     1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
    51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
   101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
   201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
   251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
   301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
   351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
   401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
   451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
   501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6066	1480.5993	1480.6000	-0.0007	0	QGGEENECQFQR
35 - 43	1083.5684	1082.5611	1082.5581	0.0031	0	LNAQRPDNR
120 - 127	993.5040	992.4967	992.5039	-0.0072	0	YQSQKPSR
120 - 128	1149.6135	1148.6062	1148.6050	0.0012	1	YQSQKPSRR
128 - 146	2256.0303	2255.0230	2255.0315	-0.0085	1	RFQVGQDDPSQQQQDSHQK
129 - 146	2099.9395	2098.9322	2098.9304	0.0018	0	FQVGQDDPSQQQQDSHQK
129 - 149	2492.1650	2491.1577	2491.1588	-0.0011	1	FQVGQDDPSQQQQDSHQKVHR
195 - 208	1770.8834	1769.8761	1769.8848	-0.0087	1	RFYLAGNQEQEFLR
196 - 208	1614.7954	1613.7881	1613.7837	0.0044	0	FYLAGNQEQEFLR
209 - 220	1547.7479	1546.7406	1546.7389	0.0017	0	YQQQQGSRPHYR
263 - 277	1658.8303	1657.8230	1657.8270	-0.0040	1	GENEREEQGAIVTVK
299 - 306	1095.4774	1094.4701	1094.4628	0.0073	1	REEFDEDR
300 - 306	939.3691	938.3618	938.3617	0.0001	0	EEFDEDR
300 - 312	1691.7769	1690.7696	1690.7659	0.0038	1	EEFDEDRSRPQQR

No match to: 805.4550, 845.1116, 855.0529, 861.0714, 870.0411, 877.0459, 885.9858, 893.0499, 917.2999, 992.9540, 1046.6029, 1050.1044, 1066.0920, 1072.1031, 1175.5537, 1277.0929, 1424.6067, 1464.5776, 1500.5861, 1531.3519, 1563.7388, 1569.7230, 1609.6785, 1847.8778, 1984.8951, 2088.9807, 2121.9194, 2161.9651, 2273.1624

Spot 47

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:32:42 GMT**
Top Score : **110 for gi|47933675, glycinin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	110	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	110	iso-Ara h3 [Arachis hypogaea]
3.	gi|22135348	25768	26	trypsin inhibitor [Arachis hypogaea]
4.	gi|62177385	14731	23	resistance protein Cre [Arachis hypogaea]
5.	gi|71040687	13451	22	auxin-repressed protein [Arachis hypogaea]
6.	gi|118776570	60681	20	arachin 6 [Arachis hypogaea]
7.	gi|230338	23975	17	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
8.	gi|9864777	60754	15	Gly1 [Arachis hypogaea]
9.	gi|5712199	61430	15	glycinin [Arachis hypogaea]
10.	gi|108595573	61041	15	arachin Ahy-4 [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 110 **Expect:** 8.7e-009 **Queries matched:** 15
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
939.3778	938.3705	938.3617	0.0088	300	306	0	EEFDEDR
993.4865	992.4792	992.5039	-0.0247	120	127	0	YQSQKPSR
1083.5681	1082.5608	1082.5581	0.0028	35	43	0	LNAQRPDNR
1095.4639	1094.4566	1094.4628	-0.0062	299	306	1	REEFDEDR
1149.6158	1148.6085	1148.6050	0.0035	120	128	1	YQSQKPSRR
1481.6080	1480.6007	1480.6000	0.0007	23	34	0	QGGEENECQFQR
1547.7444	1546.7371	1546.7389	-0.0018	209	220	0	YQQQQGSRPHYR
1614.7821	1613.7748	1613.7837	-0.0089	196	208	0	FYLAGNQEQEFLR

1658.8350	1657.8277	1657.8270	0.0007	263 - 277	1	GENEREEQGAIVTVK
1691.7625	1690.7552	1690.7659	-0.0106	300 - 312	1	EEFDEDRSRPQQR
1770.8872	1769.8799	1769.8848	-0.0049	195 - 208	1	RFYLAGNQEQEFLR
2099.9412	2098.9339	2098.9304	0.0035	129 - 146	0	FQVGQDDPSQQQQDSHQK
2256.0591	2255.0518	2255.0315	0.0203	128 - 146	1	RFQVGQDDPSQQQQDSHQK
2492.1794	2491.1721	2491.1588	0.0133	129 - 149	1	FQVGQDDPSQQQQDSHQKVHR
3069.4404	3068.4331	3068.3933	0.0398	44 - 70	0	IESEGGYIETWNPNNQEFQCAGVALSR

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 949.4711, 992.9482, 1046.6041, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1145.5537, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1569.7112, 1609.6650, 1638.7699, 1728.8016, 1730.8545, 1769.8712, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885, 2051.0366, 2088.9785, 2185.0520, 2224.9932, 2227.1077, 2273.1599, 2295.1458, 2311.1348, 2334.1301, 2351.0981, 2474.1187, 2482.2668, 2499.2917, 2612.1426, 3137.4878, 3155.5068, 3200.4990, 3211.5098, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

2. gi|112380623 **Mass:** 58570 **Score:** 110 **Expect:** 8.7e-009 **Queries matched:** 15

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
939.3778	938.3705	938.3617	0.0088	302 - 308		0	EEFDEDR
993.4865	992.4792	992.5039	-0.0247	122 - 129		0	YQSQKPSR
1083.5681	1082.5608	1082.5581	0.0028	37 - 45		0	LNAQRPDNR
1095.4639	1094.4566	1094.4628	-0.0062	301 - 308		1	REEFDEDR
1149.6158	1148.6085	1148.6050	0.0035	122 - 130		1	YQSQKPSRR
1481.6080	1480.6007	1480.6000	0.0007	25 - 36		0	QGGEENECQFQR
1547.7444	1546.7371	1546.7389	-0.0018	211 - 222		0	YQQQQGSRPHYR
1614.7821	1613.7748	1613.7837	-0.0089	198 - 210		0	FYLAGNQEQEFLR
1658.8350	1657.8277	1657.8270	0.0007	265 - 279		1	GENEREEQGAIVTVK
1691.7625	1690.7552	1690.7659	-0.0106	302 - 314		1	EEFDEDRSRPQQR
1770.8872	1769.8799	1769.8848	-0.0049	197 - 210		1	RFYLAGNQEQEFLR
2099.9412	2098.9339	2098.9304	0.0035	131 - 148		0	FQVGQDDPSQQQQDSHQK
2256.0591	2255.0518	2255.0315	0.0203	130 - 148		1	RFQVGQDDPSQQQQDSHQK
2492.1794	2491.1721	2491.1588	0.0133	131 - 151		1	FQVGQDDPSQQQQDSHQKVHR
3069.4404	3068.4331	3068.3933	0.0398	46 - 72		0	IESEGGYIETWNPNNQEFQCAGVALSR

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 949.4711, 992.9482, 1046.6041, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1145.5537, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1569.7112, 1609.6650, 1638.7699, 1728.8016, 1730.8545, 1769.8712, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885, 2051.0366, 2088.9785, 2185.0520, 2224.9932, 2227.1077, 2273.1599, 2295.1458, 2311.1348, 2334.1301, 2351.0981, 2474.1187, 2482.2668, 2499.2917, 2612.1426, 3137.4878, 3155.5068, 3200.4990, 3211.5098, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

3. gi|22135348 **Mass:** 25768 **Score:** 26 **Expect:** 2 **Queries matched:** 4

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5681	1082.5608	1082.5581	0.0028	39	47	0	LNAQRPDNR
1730.8545	1729.8472	1729.8648	-0.0175	197	210	1	RFNLAGNHEQEFLR
2051.0366	2050.0293	2050.0384	-0.0091	84	100	0	RPFYSNAPQEIFIQQGR
2474.1187	2473.1114	2473.1371	-0.0257	101	122	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 939.3778, 949.4711, 992.9482, 993.4865, 1046.6041, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1095.4639, 1145.5537, 1149.6158, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1481.6080, 1547.7444, 1569.7112, 1609.6650, 1614.7821, 1638.7699, 1658.8350, 1691.7625, 1728.8016, 1769.8712, 1770.8872, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885, 2088.9785, 2099.9412, 2185.0520, 2224.9932, 2227.1077, 2256.0591, 2273.1599, 2295.1458, 2311.1348, 2334.1301, 2351.0981, 2482.2668, 2492.1794, 2499.2917, 2612.1426, 3069.4404, 3137.4878, 3155.5068, 3200.4990, 3211.5098, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

4. gi|62177385 **Mass:** 14731 **Score:** 23 **Expect:** 4.4 **Queries matched:** 3

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1730.8545	1729.8472	1729.8787	-0.0315	1	14	1	NLILDDVWDSKAWR
2088.9785	2087.9712	2087.9979	-0.0267	72	89	1	NCPPELESIGRSIVETCK
2295.1458	2294.1385	2294.1147	0.0239	15	34	1	TIKNCFPENNNGGMILVTTR + Oxidation (M)

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 939.3778, 949.4711, 992.9482, 993.4865, 1046.6041, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1083.5681, 1095.4639, 1145.5537, 1149.6158, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1481.6080, 1547.7444, 1569.7112, 1609.6650, 1614.7821, 1638.7699, 1658.8350, 1691.7625, 1728.8016, 1769.8712, 1770.8872, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885, 2051.0366, 2099.9412, 2185.0520, 2224.9932, 2227.1077, 2256.0591, 2273.1599, 2311.1348, 2334.1301, 2351.0981, 2474.1187, 2482.2668, 2492.1794, 2499.2917, 2612.1426, 3069.4404, 3137.4878, 3155.5068, 3200.4990, 3211.5098, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

5. gi|71040687 **Mass:** 13451 **Score:** 22 **Expect:** 5.8 **Queries matched:** 2

auxin-repressed protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
3137.4878	3136.4805	3136.5029	-0.0223	91	117	0	TIGSDYFDKPLLNSPTVYDWLYSGETR
3211.5098	3210.5025	3210.5802	-0.0776	49	78	1	SMSMPATPTTPGTPTTPLSATPRKPDNVWR + Oxidation (M)

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 939.3778, 949.4711, 992.9482, 993.4865, 1046.6041, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1083.5681, 1095.4639, 1145.5537, 1149.6158, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1481.6080, 1547.7444, 1569.7112, 1609.6650, 1614.7821,

1638.7699, 1658.8350, 1691.7625, 1728.8016, 1730.8545, 1769.8712, 1770.8872, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885, 2051.0366, 2088.9785, 2099.9412, 2185.0520, 2224.9932, 2227.1077, 2256.0591, 2273.1599, 2295.1458, 2311.1348, 2334.1301, 2351.0981, 2474.1187, 2482.2668, 2492.1794, 2499.2917, 2612.1426, 3069.4404, 3155.5068, 3200.4990, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

6. gi|118776570 **Mass:** 60681 **Score:** 20 **Expect:** 8 **Queries matched:** 5

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5681	1082.5608	1082.5581	0.0028	37	45	0	LNAQRPDNR
1730.8545	1729.8472	1729.8648	-0.0175	195	208	1	RFNLAGNHEQEFLR
1770.8872	1769.8799	1769.8584	0.0215	220	235	0	SLPLSPYSPQPGQEDR
2051.0366	2050.0293	2050.0384	-0.0091	82	98	0	RPFYSNAPQEIFIQQGR
2474.1187	2473.1114	2473.1371	-0.0257	99	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 939.3778, 949.4711, 992.9482, 993.4865, 1046.6041, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1095.4639, 1145.5537, 1149.6158, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1481.6080, 1547.7444, 1569.7112, 1609.6650, 1614.7821, 1638.7699, 1658.8350, 1691.7625, 1728.8016, 1769.8712, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885, 2088.9785, 2099.9412, 2185.0520, 2224.9932, 2227.1077, 2256.0591, 2273.1599, 2295.1458, 2311.1348, 2334.1301, 2351.0981, 2482.2668, 2492.1794, 2499.2917, 2612.1426, 3069.4404, 3137.4878, 3155.5068, 3200.4990, 3211.5098, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

7. gi|230338 **Mass:** 23975 **Score:** 17 **Expect:** 16 **Queries matched:** 3

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.6041	1045.5968	1045.5880	0.0089	90	99	1	LKSAASLNSR
1609.6650	1608.6577	1608.6508	0.0070	171	186	0	DSCQGDSGGPVVCSGK
2273.1599	2272.1526	2272.1521	0.0005	70	89	0	SIVHPSYNSNTLNNDIMLIK

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 939.3778, 949.4711, 992.9482, 993.4865, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1083.5681, 1095.4639, 1145.5537, 1149.6158, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1481.6080, 1547.7444, 1569.7112, 1614.7821, 1638.7699, 1658.8350, 1691.7625, 1728.8016, 1730.8545, 1769.8712, 1770.8872, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885, 2051.0366, 2088.9785, 2099.9412, 2185.0520, 2224.9932, 2227.1077, 2256.0591, 2295.1458, 2311.1348, 2334.1301, 2351.0981, 2474.1187, 2482.2668, 2492.1794, 2499.2917, 2612.1426, 3069.4404, 3137.4878, 3155.5068, 3200.4990, 3211.5098, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

8. gi|9864777 **Mass:** 60754 **Score:** 15 **Expect:** 31 **Queries matched:** 4

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1083.5681	1082.5608	1082.5581	0.0028	38 - 46	0	LNAQRPDNR
1730.8545	1729.8472	1729.8648	-0.0175	197 - 210	1	RFNLAGNHEQEFLR
2051.0366	2050.0293	2050.0384	-0.0091	83 - 99	0	RPFYSNAPQEIFIQQGR
2474.1187	2473.1114	2473.1371	-0.0257	100 - 121	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 939.3778, 949.4711, 992.9482, 993.4865, 1046.6041, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1095.4639, 1145.5537, 1149.6158, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1481.6080, 1547.7444, 1569.7112, 1609.6650, 1614.7821, 1638.7699, 1658.8350, 1691.7625, 1728.8016, 1769.8712, 1770.8872, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885, 2088.9785, 2099.9412, 2185.0520, 2224.9932, 2227.1077, 2256.0591, 2273.1599, 2295.1458, 2311.1348, 2334.1301, 2351.0981, 2482.2668, 2492.1794, 2499.2917, 2612.1426, 3069.4404, 3137.4878, 3155.5068, 3200.4990, 3211.5098, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

9. gi|5712199 **Mass:** 61430 **Score:** 15 **Expect:** 31 **Queries matched:** 4

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
1083.5681	1082.5608	1082.5581	0.0028	37 - 45	0	LNAQRPDNR
1730.8545	1729.8472	1729.8648	-0.0175	195 - 208	1	RFNLAGNHEQEFLR
2051.0366	2050.0293	2050.0384	-0.0091	82 - 98	0	RPFYSNAPQEIFIQQGR
2474.1187	2473.1114	2473.1371	-0.0257	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 939.3778, 949.4711, 992.9482, 993.4865, 1046.6041, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1095.4639, 1145.5537, 1149.6158, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1481.6080, 1547.7444, 1569.7112, 1609.6650, 1614.7821, 1638.7699, 1658.8350, 1691.7625, 1728.8016, 1769.8712, 1770.8872, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885, 2088.9785, 2099.9412, 2185.0520, 2224.9932, 2227.1077, 2256.0591, 2273.1599, 2295.1458, 2311.1348, 2334.1301, 2351.0981, 2482.2668, 2492.1794, 2499.2917, 2612.1426, 3069.4404, 3137.4878, 3155.5068, 3200.4990, 3211.5098, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

10. gi|108595573 **Mass:** 61041 **Score:** 15 **Expect:** 31 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
1083.5681	1082.5608	1082.5581	0.0028	37 - 45	0	LNAQRPDNR
1730.8545	1729.8472	1729.8648	-0.0175	195 - 208	1	RFNLAGNHEQEFLR
2051.0366	2050.0293	2050.0384	-0.0091	82 - 98	0	RPFYSNAPQEIFIQQGR
2474.1187	2473.1114	2473.1371	-0.0257	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 939.3778, 949.4711, 992.9482, 993.4865, 1046.6041, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1095.4639, 1145.5537, 1149.6158, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1481.6080, 1547.7444, 1569.7112, 1609.6650, 1614.7821, 1638.7699, 1658.8350, 1691.7625, 1728.8016, 1769.8712, 1770.8872, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885,

2088.9785, 2099.9412, 2185.0520, 2224.9932, 2227.1077, 2256.0591, 2273.1599, 2295.1458, 2311.1348, 2334.1301, 2351.0981, 2482.2668, 2492.1794, 2499.2917, 2612.1426, 3069.4404, 3137.4878, 3155.5068, 3200.4990, 3211.5098, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 70

Protein View

Match to: **gi|47933675** Score: **110** Expect: **8.7e-009**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **70**
Number of mass values matched: **15**
Sequence Coverage: **26%**

Matched peptides shown in **Bold Red**

```
     1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
    51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
   101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
   201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
   251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
   301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
   351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
   401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
   451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6080	1480.6007	1480.6000	0.0007	0	QGGEENECQFQR
35 - 43	1083.5681	1082.5608	1082.5581	0.0028	0	LNAQRPDNR
44 - 70	3069.4404	3068.4331	3068.3933	0.0398	0	IESEGGYIETWNPNNQEFQCAGVALSR
120 - 127	993.4865	992.4792	992.5039	-0.0247	0	YQSQKPSR
120 - 128	1149.6158	1148.6085	1148.6050	0.0035	1	YQSQKPSRR
128 - 146	2256.0591	2255.0518	2255.0315	0.0203	1	RFQVGQDDPSQQQQDSHQK
129 - 146	2099.9412	2098.9339	2098.9304	0.0035	0	FQVGQDDPSQQQQDSHQK
129 - 149	2492.1794	2491.1721	2491.1588	0.0133	1	FQVGQDDPSQQQQDSHQKVHR
195 - 208	1770.8872	1769.8799	1769.8848	-0.0049	1	RFYLAGNQEQEFLR
196 - 208	1614.7821	1613.7748	1613.7837	-0.0089	0	FYLAGNQEQEFLR
209 - 220	1547.7444	1546.7371	1546.7389	-0.0018	0	YQQQQGSRPHYR
263 - 277	1658.8350	1657.8277	1657.8270	0.0007	1	GENEREEQGAIVTVK
299 - 306	1095.4639	1094.4566	1094.4628	-0.0062	1	REEFDEDR
300 - 306	939.3778	938.3705	938.3617	0.0088	0	EEFDEDR
300 - 312	1691.7625	1690.7552	1690.7659	-0.0106	1	EEFDEDRSRPQQR

No match to: 805.4669, 839.0811, 845.0983, 855.0562, 861.0745, 877.0483, 885.9694, 886.4550, 949.4711, 992.9482, 1046.6041, 1050.0892, 1066.0703, 1080.5348, 1082.0385, 1082.5297, 1145.5537, 1175.5522, 1277.0856, 1464.5793, 1480.5800, 1569.7112, 1609.6650, 1638.7699, 1728.8016, 1730.8545, 1769.8712, 1775.8522, 1792.8787, 1832.8510, 1847.8613, 1984.8885, 2051.0366, 2088.9785, 2185.0520, 2224.9932, 2227.1077, 2273.1599, 2295.1458, 2311.1348, 2334.1301, 2351.0981, 2474.1187, 2482.2668, 2499.2917, 2612.1426, 3137.4878, 3155.5068, 3200.4990, 3211.5098, 3214.6257, 3228.5815, 3301.7705, 3455.6279, 3456.7529

Spot 48

User :
Email :
Search title : **SampleSetID: 741, AnalysisID: 1089, MaldiWellID: 13822, SpectrumID: 9627, Path=\Janssen\TLatendorf_190207_1\Arachis_190107_1**
Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:33:49 GMT**
Top Score : **47 for gi|47933675, glycinin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	47	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	47	iso-Ara h3 [Arachis hypogaea]
3.	gi|22135348	25768	32	trypsin inhibitor [Arachis hypogaea]
4.	gi|52001221	61836	27	arachin Ahy-2 [Arachis hypogaea]
5.	gi|118776570	60681	26	arachin 6 [Arachis hypogaea]
6.	gi|62177385	14731	23	resistance protein Cre [Arachis hypogaea]
7.	gi|9864777	60754	19	Gly1 [Arachis hypogaea]
8.	gi|5712199	61430	19	glycinin [Arachis hypogaea]
9.	gi|57669861	61041	19	arachin Ahy-4 [Arachis hypogaea]
10.	gi|108595573	61041	19	arachin Ahy-4 [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 47 **Expect:** 0.016 **Queries matched:** 8
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
993.4908	992.4835	992.5039	-0.0204	120	127	0	YQSQKPSR
1149.6226	1148.6153	1148.6050	0.0103	120	128	1	YQSQKPSRR
1481.6139	1480.6066	1480.6000	0.0066	23	34	0	QGGEENECQFQR
1547.7374	1546.7301	1546.7389	-0.0088	209	220	0	YQQQQGSRPHYR
1614.7792	1613.7719	1613.7837	-0.0118	196	208	0	FYLAGNQEQEFLR

1770.8821	1769.8748	1769.8848	-0.0100	195 - 208	1	RFYLAGNQEQEFLR
2099.9297	2098.9224	2098.9304	-0.0080	129 - 146	0	FQVGQDDPSQQQQDSHQK
3069.4749	3068.4676	3068.3933	0.0743	44 - 70	0	IESEGGYIETWNPNNQEFQCAGVALSR

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1159.4990, 1427.6747, 1464.5830, 1609.6544, 1638.7902, 1730.8549, 1984.8816, 2003.8466, 2037.9452, 2051.0186, 2145.0508, 2146.6165, 2162.0508, 2185.0471, 2224.9927, 2273.1665, 2295.1592, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2474.1714, 2492.2480, 2499.2798, 2505.3228, 2612.2568, 3136.5059, 3211.6523, 3302.8564, 3317.7808

2. gi|112380623 **Mass:** 58570 **Score:** 47 **Expect:** 0.016 **Queries matched:** 8

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
993.4908	992.4835	992.5039	-0.0204	122 - 129		0	YQSQKPSR
1149.6226	1148.6153	1148.6050	0.0103	122 - 130		1	YQSQKPSRR
1481.6139	1480.6066	1480.6000	0.0066	25 - 36		0	QGGEENECQFQR
1547.7374	1546.7301	1546.7389	-0.0088	211 - 222		0	YQQQQGSRPHYR
1614.7792	1613.7719	1613.7837	-0.0118	198 - 210		0	FYLAGNQEQEFLR
1770.8821	1769.8748	1769.8848	-0.0100	197 - 210		1	RFYLAGNQEQEFLR
2099.9297	2098.9224	2098.9304	-0.0080	131 - 148		0	FQVGQDDPSQQQQDSHQK
3069.4749	3068.4676	3068.3933	0.0743	46 - 72		0	IESEGGYIETWNPNNQEFQCAGVALSR

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1159.4990, 1427.6747, 1464.5830, 1609.6544, 1638.7902, 1730.8549, 1984.8816, 2003.8466, 2037.9452, 2051.0186, 2145.0508, 2146.6165, 2162.0508, 2185.0471, 2224.9927, 2273.1665, 2295.1592, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2474.1714, 2492.2480, 2499.2798, 2505.3228, 2612.2568, 3136.5059, 3211.6523, 3302.8564, 3317.7808

3. gi|22135348 **Mass:** 25768 **Score:** 32 **Expect:** 0.58 **Queries matched:** 4

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1730.8549	1729.8476	1729.8648	-0.0171	197 - 210		1	RFNLAGNHEQEFLR
2051.0186	2050.0113	2050.0384	-0.0271	84 - 100		0	RPFYSNAPQEIFIQQGR
2474.1714	2473.1641	2473.1371	0.0270	101 - 122		0	GYFGLIFPGCPSTYEEPAQQGR
2505.3228	2504.3155	2504.3036	0.0120	80 - 100		1	NALRRPFYSNAPQEIFIQQGR

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 993.4908, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1149.6226, 1159.4990, 1427.6747, 1464.5830, 1481.6139, 1547.7374, 1609.6544, 1614.7792, 1638.7902, 1770.8821, 1984.8816, 2003.8466, 2037.9452, 2099.9297, 2145.0508, 2146.6165, 2162.0508, 2185.0471, 2224.9927, 2273.1665,

2295.1592, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2492.2480, 2499.2798, 2612.2568, 3069.4749, 3136.5059, 3211.6523, 3302.8564, 3317.7808

4. gi|52001221 **Mass:** 61836 **Score:** 27 **Expect:** 1.9 **Queries matched:** 5

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1730.8549	1729.8476	1729.8648	-0.0171	196	209	1	RFNLAGNHEQEFLR
2051.0186	2050.0113	2050.0384	-0.0271	82	98	0	RPFYSNAPQEIFIQQGR
2162.0508	2161.0435	2161.0955	-0.0520	518	537	1	NNNPFKFFVPPSQQSLGAVA
2474.1714	2473.1641	2473.1371	0.0270	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3228	2504.3155	2504.3036	0.0120	78	98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 993.4908, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1149.6226, 1159.4990, 1427.6747, 1464.5830, 1481.6139, 1547.7374, 1609.6544, 1614.7792, 1638.7902, 1770.8821, 1984.8816, 2003.8466, 2037.9452, 2099.9297, 2145.0508, 2146.6165, 2185.0471, 2224.9927, 2273.1665, 2295.1592, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2492.2480, 2499.2798, 2612.2568, 3069.4749, 3136.5059, 3211.6523, 3302.8564, 3317.7808

5. gi|118776570 **Mass:** 60681 **Score:** 26 **Expect:** 2.2 **Queries matched:** 5

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1730.8549	1729.8476	1729.8648	-0.0171	195	208	1	RFNLAGNHEQEFLR
1770.8821	1769.8748	1769.8584	0.0164	220	235	0	SLPLSPYSPQPGQEDR
2051.0186	2050.0113	2050.0384	-0.0271	82	98	0	RPFYSNAPQEIFIQQGR
2474.1714	2473.1641	2473.1371	0.0270	99	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3228	2504.3155	2504.3036	0.0120	78	98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 993.4908, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1149.6226, 1159.4990, 1427.6747, 1464.5830, 1481.6139, 1547.7374, 1609.6544, 1614.7792, 1638.7902, 1984.8816, 2003.8466, 2037.9452, 2099.9297, 2145.0508, 2146.6165, 2162.0508, 2185.0471, 2224.9927, 2273.1665, 2295.1592, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2492.2480, 2499.2798, 2612.2568, 3069.4749, 3136.5059, 3211.6523, 3302.8564, 3317.7808

6. gi|62177385 **Mass:** 14731 **Score:** 23 **Expect:** 4.3 **Queries matched:** 3

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1427.6747	1426.6674	1426.6986	-0.0312	71	82	1	RNCPPELESIGR

1730.8549	1729.8476	1729.8787	-0.0311	1 - 14	1	NLILDDVWDSKAWR
2295.1592	2294.1519	2294.1147	0.0373	15 - 34	1	TIKNCFPENNNGGMILVTTR + Oxidation (M)

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 993.4908, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1149.6226, 1159.4990, 1464.5830, 1481.6139, 1547.7374, 1609.6544, 1614.7792, 1638.7902, 1770.8821, 1984.8816, 2003.8466, 2037.9452, 2051.0186, 2099.9297, 2145.0508, 2146.6165, 2162.0508, 2185.0471, 2224.9927, 2273.1665, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2474.1714, 2492.2480, 2499.2798, 2505.3228, 2612.2568, 3069.4749, 3136.5059, 3211.6523, 3302.8564, 3317.7808

7. gi|9864777 **Mass:** 60754 **Score:** 19 **Expect:** 10 **Queries matched:** 4

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1730.8549	1729.8476	1729.8648	-0.0171	197 -	210	1	RFNLAGNHEQEFLR
2051.0186	2050.0113	2050.0384	-0.0271	83 -	99	0	RPFYSNAPQEIFIQQGR
2474.1714	2473.1641	2473.1371	0.0270	100 -	121	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3228	2504.3155	2504.3036	0.0120	79 -	99	1	NALRRPFYSNAPQEIFIQQGR

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 993.4908, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1149.6226, 1159.4990, 1427.6747, 1464.5830, 1481.6139, 1547.7374, 1609.6544, 1614.7792, 1638.7902, 1770.8821, 1984.8816, 2003.8466, 2037.9452, 2099.9297, 2145.0508, 2146.6165, 2162.0508, 2185.0471, 2224.9927, 2273.1665, 2295.1592, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2492.2480, 2499.2798, 2612.2568, 3069.4749, 3136.5059, 3211.6523, 3302.8564, 3317.7808

8. gi|5712199 **Mass:** 61430 **Score:** 19 **Expect:** 10 **Queries matched:** 4

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1730.8549	1729.8476	1729.8648	-0.0171	195 -	208	1	RFNLAGNHEQEFLR
2051.0186	2050.0113	2050.0384	-0.0271	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1714	2473.1641	2473.1371	0.0270	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3228	2504.3155	2504.3036	0.0120	78 -	98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 993.4908, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1149.6226, 1159.4990, 1427.6747, 1464.5830, 1481.6139, 1547.7374, 1609.6544, 1614.7792, 1638.7902, 1770.8821, 1984.8816, 2003.8466, 2037.9452, 2099.9297, 2145.0508, 2146.6165, 2162.0508, 2185.0471, 2224.9927, 2273.1665, 2295.1592, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2492.2480, 2499.2798, 2612.2568, 3069.4749, 3136.5059, 3211.6523, 3302.8564, 3317.7808

9. gi|57669861 **Mass:** 61041 **Score:** 19 **Expect:** 10 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1730.8549	1729.8476	1729.8648	-0.0171	195	-	208	1	RFNLAGNHEQEFLR
2051.0186	2050.0113	2050.0384	-0.0271	82	-	98	0	RPFYSNAPQEIFIQQGR
2474.1714	2473.1641	2473.1371	0.0270	99	-	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3228	2504.3155	2504.3036	0.0120	78	-	98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 993.4908, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1149.6226, 1159.4990, 1427.6747, 1464.5830, 1481.6139, 1547.7374, 1609.6544, 1614.7792, 1638.7902, 1770.8821, 1984.8816, 2003.8466, 2037.9452, 2099.9297, 2145.0508, 2146.6165, 2162.0508, 2185.0471, 2224.9927, 2273.1665, 2295.1592, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2492.2480, 2499.2798, 2612.2568, 3069.4749, 3136.5059, 3211.6523, 3302.8564, 3317.7808

10. gi|108595573 **Mass:** 61041 **Score:** 19 **Expect:** 10 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1730.8549	1729.8476	1729.8648	-0.0171	195	-	208	1	RFNLAGNHEQEFLR
2051.0186	2050.0113	2050.0384	-0.0271	82	-	98	0	RPFYSNAPQEIFIQQGR
2474.1714	2473.1641	2473.1371	0.0270	99	-	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3228	2504.3155	2504.3036	0.0120	78	-	98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 993.4908, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1149.6226, 1159.4990, 1427.6747, 1464.5830, 1481.6139, 1547.7374, 1609.6544, 1614.7792, 1638.7902, 1770.8821, 1984.8816, 2003.8466, 2037.9452, 2099.9297, 2145.0508, 2146.6165, 2162.0508, 2185.0471, 2224.9927, 2273.1665, 2295.1592, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2492.2480, 2499.2798, 2612.2568, 3069.4749, 3136.5059, 3211.6523, 3302.8564, 3317.7808

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 59

Protein View

Match to: **gi|47933675** Score: **47** Expect: **0.016**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **59**
Number of mass values matched: **8**
Sequence Coverage: **18%**

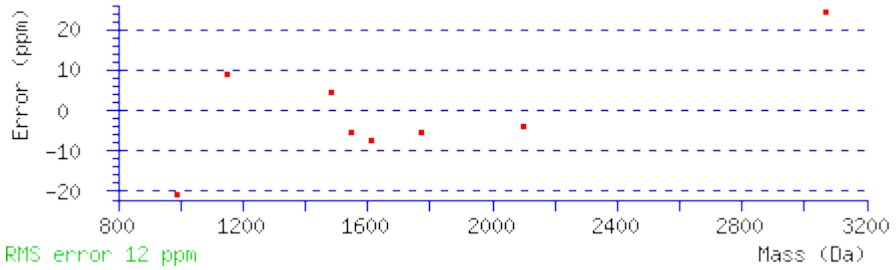
Matched peptides shown in **Bold Red**

```
     1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
    51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
   101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
   201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
   251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
   301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
   351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
   401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
   451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
   501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6139	1480.6066	1480.6000	0.0066	0	QGGEENECQFQR
44 - 70	3069.4749	3068.4676	3068.3933	0.0743	0	IESEGGYIETWNPNNQEFQCAGVALSR
120 - 127	993.4908	992.4835	992.5039	-0.0204	0	YQSQKPSR
120 - 128	1149.6226	1148.6153	1148.6050	0.0103	1	YQSQKPSRR
129 - 146	2099.9297	2098.9224	2098.9304	-0.0080	0	FQVGQDDPSQQQQDSHQK
195 - 208	1770.8821	1769.8748	1769.8848	-0.0100	1	RFYLAGNQEQEFLR
196 - 208	1614.7792	1613.7719	1613.7837	-0.0118	0	FYLAGNQEQEFLR
209 - 220	1547.7374	1546.7301	1546.7389	-0.0088	0	YQQQQGSRPHYR

No match to: 805.4622, 816.5531, 854.0650, 855.0682, 860.6512, 861.0908, 870.0447, 871.0472, 877.0542, 881.2918, 885.9778, 886.4695, 893.0164, 1082.0294, 1082.5330, 1111.5524, 1137.0891, 1137.5675, 1145.0718, 1145.5720, 1159.4990, 1427.6747, 1464.5830, 1609.6544, 1638.7902, 1730.8549, 1984.8816, 2003.8466, 2037.9452, 2051.0186, 2145.0508, 2146.6165, 2162.0508, 2185.0471, 2224.9927, 2273.1665, 2295.1592, 2305.1560, 2311.1509, 2333.1621, 2336.0872, 2351.1055, 2474.1714, 2492.2480, 2499.2798, 2505.3228, 2612.2568, 3136.5059, 3211.6523, 3302.8564, 3317.7808



Spot 49

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:39:44 GMT**
Top Score : **123 for Mixture 1, gi|47933675 + gi|22135348**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	Mixture 1		123	gi|47933675 + gi|22135348
2.	gi|47933675	58368	76	glycinin [Arachis hypogaea]
3.	gi|112380623	58570	76	iso-Ara h3 [Arachis hypogaea]
4.	gi|22135348	25768	59	trypsin inhibitor [Arachis hypogaea]
5.	gi|118776570	60681	52	arachin 6 [Arachis hypogaea]
6.	gi|9864777	60754	41	Gly1 [Arachis hypogaea]
7.	gi|5712199	61430	41	glycinin [Arachis hypogaea]
8.	gi|57669861	61041	41	arachin Ahy-4 [Arachis hypogaea]
9.	gi|108595573	61041	41	arachin Ahy-4 [Arachis hypogaea]
10.	gi|52001219	61810	41	arachin Ahy-1 [Arachis hypogaea]

Results List

1. Mixture 1 **Total score: 123** **Expect:** 4.4e-010 **Queries matched:** 12

Components: 1. gi|47933675 glycinin [Arachis hypogaea]
2. gi|22135348 trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Comp	Peptide
1083.5483	1082.5410	1082.5581	-0.0170	35	43	0	1	LNAQRPDNR
1149.6107	1148.6034	1148.6050	-0.0016	120	128	1	1	YQSQKPSRR
1481.5973	1480.5900	1480.6000	-0.0100	23	34	0	1	QGGEENECQFQR
1547.7334	1546.7261	1546.7389	-0.0128	209	220	0	1	YQQQQGSRPHYR
1614.7852	1613.7779	1613.7837	-0.0058	196	208	0	1	FYLAGNQEQEFLR
1691.7585	1690.7512	1690.7659	-0.0146	300	312	1	1	EEFDEDRSRPQQR
1730.8666	1729.8593	1729.8648	-0.0054	197	210	1	2	RFNLAGNHEQEFLR
1770.8693	1769.8620	1769.8848	-0.0228	195	208	1	1	RFYLAGNQEQEFLR
2051.0349	2050.0276	2050.0384	-0.0108	84	100	0	2	RPFYSNAPQEIFIQQGR

2474.1531	2473.1458	2473.1371	0.0087	101 - 122	0	2	GYFGLIFPGCPSTYEEPAQQGR
2505.3188	2504.3115	2504.3036	0.0080	80 - 100	1	2	NALRRPFYSNAPQEIFIQQGR
3199.3984	3198.3911	3198.4277	-0.0366	228 - 255	0	1	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1638.7784, 2311.1038, 2530.3315, 3303.4795, 3316.7529, 3455.6177

2. gi|47933675 **Mass:** 58368 **Score:** 76 **Expect:** 2.4e-005 **Queries matched:** 8

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5483	1082.5410	1082.5581	-0.0170	35 -	43	0	LNAQRPDNR
1149.6107	1148.6034	1148.6050	-0.0016	120 -	128	1	YQSQKPSRR
1481.5973	1480.5900	1480.6000	-0.0100	23 -	34	0	QGGEENECQFQR
1547.7334	1546.7261	1546.7389	-0.0128	209 -	220	0	YQQQQGSRPHYR
1614.7852	1613.7779	1613.7837	-0.0058	196 -	208	0	FYLAGNQEQEFLR
1691.7585	1690.7512	1690.7659	-0.0146	300 -	312	1	EEFDEDRSRPQQR
1770.8693	1769.8620	1769.8848	-0.0228	195 -	208	1	RFYLAGNQEQEFLR
3199.3984	3198.3911	3198.4277	-0.0366	228 -	255	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1638.7784, 1730.8666, 2051.0349, 2311.1038, 2474.1531, 2505.3188, 2530.3315, 3303.4795, 3316.7529, 3455.6177

3. gi|112380623 **Mass:** 58570 **Score:** 76 **Expect:** 2.5e-005 **Queries matched:** 8

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5483	1082.5410	1082.5581	-0.0170	37 -	45	0	LNAQRPDNR
1149.6107	1148.6034	1148.6050	-0.0016	122 -	130	1	YQSQKPSRR
1481.5973	1480.5900	1480.6000	-0.0100	25 -	36	0	QGGEENECQFQR
1547.7334	1546.7261	1546.7389	-0.0128	211 -	222	0	YQQQQGSRPHYR
1614.7852	1613.7779	1613.7837	-0.0058	198 -	210	0	FYLAGNQEQEFLR
1691.7585	1690.7512	1690.7659	-0.0146	302 -	314	1	EEFDEDRSRPQQR
1770.8693	1769.8620	1769.8848	-0.0228	197 -	210	1	RFYLAGNQEQEFLR
3199.3984	3198.3911	3198.4277	-0.0366	230 -	257	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1638.7784, 1730.8666, 2051.0349, 2311.1038, 2474.1531, 2505.3188, 2530.3315, 3303.4795, 3316.7529, 3455.6177

4. gi|22135348 **Mass:** 25768 **Score:** 59 **Expect:** 0.0012 **Queries matched:** 5

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5483	1082.5410	1082.5581	-0.0170	39 -	47	0	LNAQRPDNR
1730.8666	1729.8593	1729.8648	-0.0054	197 -	210	1	RFNLAGNHEQEFLR
2051.0349	2050.0276	2050.0384	-0.0108	84 -	100	0	RPFYSNAPQEIFIQQGR
2474.1531	2473.1458	2473.1371	0.0087	101 -	122	0	GYFGLIFPGCPSTYEEPAQQGR

2505.3188	2504.3115	2504.3036	0.0080	80 - 100	1	NALRRPFYSNAPQEIFIQQGR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1149.6107, 1481.5973, 1547.7334, 1614.7852, 1638.7784, 1691.7585, 1770.8693, 2311.1038, 2530.3315, 3199.3984, 3303.4795, 3316.7529, 3455.6177

5. gi|118776570 **Mass:** 60681 **Score:** 52 **Expect:** 0.005 **Queries matched:** 6

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5483	1082.5410	1082.5581	-0.0170	37 -	45	0	LNAQRPDNR
1730.8666	1729.8593	1729.8648	-0.0054	195 -	208	1	RFNLAGNHEQEFLR
1770.8693	1769.8620	1769.8584	0.0036	220 -	235	0	SLPLSPYSPQPGQEDR
2051.0349	2050.0276	2050.0384	-0.0108	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1531	2473.1458	2473.1371	0.0087	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3188	2504.3115	2504.3036	0.0080	78 -	98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1149.6107, 1481.5973, 1547.7334, 1614.7852, 1638.7784, 1691.7585, 2311.1038, 2530.3315, 3199.3984, 3303.4795, 3316.7529, 3455.6177

6. gi|9864777 **Mass:** 60754 **Score:** 41 **Expect:** 0.073 **Queries matched:** 5

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5483	1082.5410	1082.5581	-0.0170	38 -	46	0	LNAQRPDNR
1730.8666	1729.8593	1729.8648	-0.0054	197 -	210	1	RFNLAGNHEQEFLR
2051.0349	2050.0276	2050.0384	-0.0108	83 -	99	0	RPFYSNAPQEIFIQQGR
2474.1531	2473.1458	2473.1371	0.0087	100 -	121	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3188	2504.3115	2504.3036	0.0080	79 -	99	1	NALRRPFYSNAPQEIFIQQGR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1149.6107, 1481.5973, 1547.7334, 1614.7852, 1638.7784, 1691.7585, 1770.8693, 2311.1038, 2530.3315, 3199.3984, 3303.4795, 3316.7529, 3455.6177

7. gi|5712199 **Mass:** 61430 **Score:** 41 **Expect:** 0.074 **Queries matched:** 5

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5483	1082.5410	1082.5581	-0.0170	37 -	45	0	LNAQRPDNR
1730.8666	1729.8593	1729.8648	-0.0054	195 -	208	1	RFNLAGNHEQEFLR
2051.0349	2050.0276	2050.0384	-0.0108	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1531	2473.1458	2473.1371	0.0087	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3188	2504.3115	2504.3036	0.0080	78 -	98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1149.6107, 1481.5973, 1547.7334, 1614.7852, 1638.7784, 1691.7585, 1770.8693, 2311.1038, 2530.3315, 3199.3984, 3303.4795, 3316.7529, 3455.6177

8. gi|57669861 **Mass:** 61041 **Score:** 41 **Expect:** 0.074 **Queries matched:** 5

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1083.5483	1082.5410	1082.5581	-0.0170	37 - 45	0	LNAQRPDNR
1730.8666	1729.8593	1729.8648	-0.0054	195 - 208	1	RFNLAGNHEQEFLR
2051.0349	2050.0276	2050.0384	-0.0108	82 - 98	0	RPFYSNAPQEIFIQQGR
2474.1531	2473.1458	2473.1371	0.0087	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3188	2504.3115	2504.3036	0.0080	78 - 98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1149.6107, 1481.5973, 1547.7334, 1614.7852, 1638.7784, 1691.7585, 1770.8693, 2311.1038, 2530.3315, 3199.3984, 3303.4795, 3316.7529, 3455.6177

9. gi|108595573 **Mass:** 61041 **Score:** 41 **Expect:** 0.074 **Queries matched:** 5

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5483	1082.5410	1082.5581	-0.0170	37 -	45	0	LNAQRPDNR
1730.8666	1729.8593	1729.8648	-0.0054	195 -	208	1	RFNLAGNHEQEFLR
2051.0349	2050.0276	2050.0384	-0.0108	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1531	2473.1458	2473.1371	0.0087	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3188	2504.3115	2504.3036	0.0080	78 -	98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1149.6107, 1481.5973, 1547.7334, 1614.7852, 1638.7784, 1691.7585, 1770.8693, 2311.1038, 2530.3315, 3199.3984, 3303.4795, 3316.7529, 3455.6177

10. gi|52001219 **Mass:** 61810 **Score:** 41 **Expect:** 0.078 **Queries matched:** 5

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5483	1082.5410	1082.5581	-0.0170	37 -	45	0	LNAQRPDNR
1730.8666	1729.8593	1729.8648	-0.0054	195 -	208	1	RFNLAGNHEQEFLR
2051.0349	2050.0276	2050.0384	-0.0108	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1531	2473.1458	2473.1371	0.0087	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR
2505.3188	2504.3115	2504.3036	0.0080	78 -	98	1	NALRRPFYSNAPQEIFIQQGR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1149.6107, 1481.5973, 1547.7334, 1614.7852, 1638.7784, 1691.7585, 1770.8693, 2311.1038, 2530.3315, 3199.3984, 3303.4795, 3316.7529, 3455.6177

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1

Number of queries : 26

Mixture: 1. Protein Protein View

Match to: **gi|47933675** Score: **76** Expect: **2.4e-005**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **26**
Number of mass values matched: **8**
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

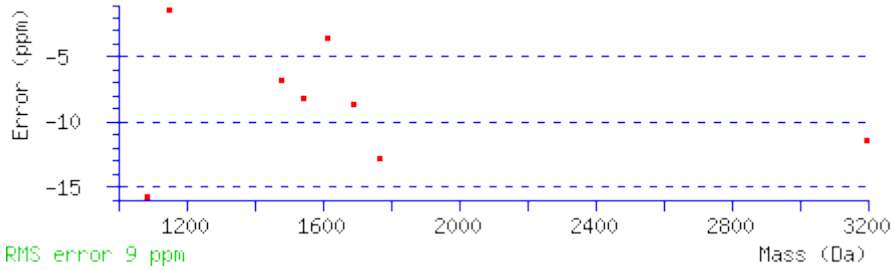
```
    1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
   51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
  101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
  151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
  201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
  251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
  301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
  351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
  401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
  451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
  501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.5973	1480.5900	1480.6000	-0.0100	0	QGGEENECQFQR
35 - 43	1083.5483	1082.5410	1082.5581	-0.0170	0	LNAQRPDNR
120 - 128	1149.6107	1148.6034	1148.6050	-0.0016	1	YQSQKPSRR
195 - 208	1770.8693	1769.8620	1769.8848	-0.0228	1	RFYLAGNQEQEFLR
196 - 208	1614.7852	1613.7779	1613.7837	-0.0058	0	FYLAGNQEQEFLR
209 - 220	1547.7334	1546.7261	1546.7389	-0.0128	0	YQQQQGSRPHYR
228 - 255	3199.3984	3198.3911	3198.4277	-0.0366	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

300 - 312	**1691.7585**	**1690.7512**	**1690.7659**	**-0.0146**	**1**	**EEFDEDRSRPQQR**

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1638.7784, 1730.8666, 2051.0349, 2311.1038, 2474.1531, 2505.3188, 2530.3315, 3303.4795, 3316.7529, 3455.6177



Mixture: 2. Protein Protein View

Match to: **gi|22135348** Score: **59** Expect: **0.0012**
trypsin inhibitor [Arachis hypogaea]

Nominal mass (M_r): **25768**; Calculated pI value: **6.66**
NCBI BLAST search of gi|22135348 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **26**
Number of mass values matched: **5**
Sequence Coverage: **30%**

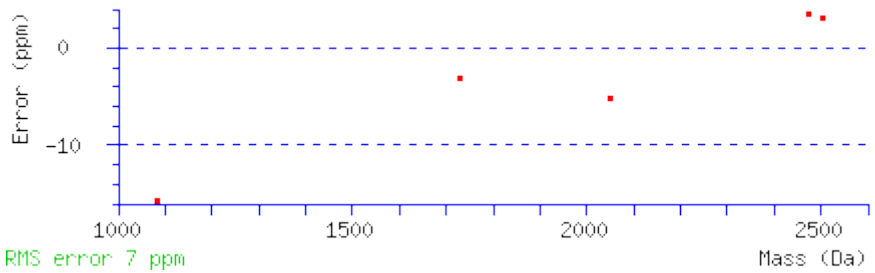
Matched peptides shown in **Bold Red**

```
   1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES
  51 EGGYIETWNP NNQEFECAGV ALSRLVLRRN ALRRPFYSNA PQEIFIQQGR
 101 GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH
 151 RFDEGDLIAV PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
 201 AGNHEQEFLR YQQQSRRRS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
39 - 47	1083.5483	1082.5410	1082.5581	-0.0170	0	LNAQRPDNR
80 - 100	2505.3188	2504.3115	2504.3036	0.0080	1	NALRRPFYSNAPQEIFIQQGR
84 - 100	2051.0349	2050.0276	2050.0384	-0.0108	0	RPFYSNAPQEIFIQQGR
101 - 122	2474.1531	2473.1458	2473.1371	0.0087	0	GYFGLIFPGCPSTYEEPAQQGR
197 - 210	1730.8666	1729.8593	1729.8648	-0.0054	1	RFNLAGNHEQEFLR

No match to: 881.2808, 932.4442, 949.4701, 958.4711, 990.5214, 1080.5199, 1120.5297, 1129.5408, 1149.6107, 1481.5973, 1547.7334, 1614.7852, 1638.7784, 1691.7585, 1770.8693, 2311.1038, 2530.3315, 3199.3984, 3303.4795, 3316.7529, 3455.6177



Spot 50

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:39:48 GMT**
Top Score : **100 for gi|47933675, glycinin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	100	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	100	iso-Ara h3 [Arachis hypogaea]
3.	gi|22135348	25768	25	trypsin inhibitor [Arachis hypogaea]
4.	gi|118776570	60681	23	arachin 6 [Arachis hypogaea]
5.	gi|230338	23975	17	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
6.	gi|9864777	60754	15	Gly1 [Arachis hypogaea]
7.	gi|5712199	61430	15	glycinin [Arachis hypogaea]
8.	gi|57669861	61041	15	arachin Ahy-4 [Arachis hypogaea]
9.	gi|108595573	61041	15	arachin Ahy-4 [Arachis hypogaea]
10.	gi|52001219	61810	15	arachin Ahy-1 [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 100 **Expect:** 8.7e-008 **Queries matched:** 11
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5582	1082.5509	1082.5581	-0.0071	35	43	0	LNAQRPDNR
1149.6095	1148.6022	1148.6050	-0.0028	120	128	1	YQSQKPSRR
1481.6079	1480.6006	1480.6000	0.0006	23	34	0	QGGEENECQFQR
1547.7476	1546.7403	1546.7389	0.0014	209	220	0	YQQQQGSRPHYR
1614.7950	1613.7877	1613.7837	0.0040	196	208	0	FYLAGNQEQEFLR
1658.8304	1657.8231	1657.8270	-0.0039	263	277	1	GENEREEQGAIVTVK
1691.7700	1690.7627	1690.7659	-0.0031	300	312	1	EEFDEDRSRPQQR
1770.8900	1769.8827	1769.8848	-0.0021	195	208	1	RFYLAGNQEQEFLR
2099.9451	2098.9378	2098.9304	0.0074	129	146	0	FQVGQDDPSQQQQDSHQK
3069.3582	3068.3509	3068.3933	-0.0424	44	70	0	IESEGGYIETWNPNNQEFQCAGVALSR

3199.4026	3198.3953	3198.4277	-0.0324	228 - 255	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1111.5560, 1120.5461, 1425.6030, 1464.5890, 1638.7993, 1984.8745, 2051.0212, 2273.1528, 2474.1089, 2530.3464, 2613.1572, 3154.4604, 3227.4558, 3303.4529, 3316.6902, 3455.5583

2. gi|112380623 **Mass:** 58570 **Score:** 100 **Expect:** 9e-008 **Queries matched:** 11

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5582	1082.5509	1082.5581	-0.0071	37 -	45	0	LNAQRPDNR
1149.6095	1148.6022	1148.6050	-0.0028	122 -	130	1	YQSQKPSRR
1481.6079	1480.6006	1480.6000	0.0006	25 -	36	0	QGGEENECQFQR
1547.7476	1546.7403	1546.7389	0.0014	211 -	222	0	YQQQQGSRPHYR
1614.7950	1613.7877	1613.7837	0.0040	198 -	210	0	FYLAGNQEQEFLR
1658.8304	1657.8231	1657.8270	-0.0039	265 -	279	1	GENEREEQGAIVTVK
1691.7700	1690.7627	1690.7659	-0.0031	302 -	314	1	EEFDEDRSRPQQR
1770.8900	1769.8827	1769.8848	-0.0021	197 -	210	1	RFYLAGNQEQEFLR
2099.9451	2098.9378	2098.9304	0.0074	131 -	148	0	FQVGQDDPSQQQQDSHQK
3069.3582	3068.3509	3068.3933	-0.0424	46 -	72	0	IESEGGYIETWNPNNQEFQCAGVALSR
3199.4026	3198.3953	3198.4277	-0.0324	230 -	257	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1111.5560, 1120.5461, 1425.6030, 1464.5890, 1638.7993, 1984.8745, 2051.0212, 2273.1528, 2474.1089, 2530.3464, 2613.1572, 3154.4604, 3227.4558, 3303.4529, 3316.6902, 3455.5583

3. gi|22135348 **Mass:** 25768 **Score:** 25 **Expect:** 3 **Queries matched:** 3

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5582	1082.5509	1082.5581	-0.0071	39 -	47	0	LNAQRPDNR
2051.0212	2050.0139	2050.0384	-0.0245	84 -	100	0	RPFYSNAPQEIFIQQGR
2474.1089	2473.1016	2473.1371	-0.0355	101 -	122	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1111.5560, 1120.5461, 1149.6095, 1425.6030, 1464.5890, 1481.6079, 1547.7476, 1614.7950, 1638.7993, 1658.8304, 1691.7700, 1770.8900, 1984.8745, 2099.9451, 2273.1528, 2530.3464, 2613.1572, 3069.3582, 3154.4604, 3199.4026, 3227.4558, 3303.4529, 3316.6902, 3455.5583

4. gi|118776570 **Mass:** 60681 **Score:** 23 **Expect:** 4.7 **Queries matched:** 4

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5582	1082.5509	1082.5581	-0.0071	37 -	45	0	LNAQRPDNR
1770.8900	1769.8827	1769.8584	0.0243	220 -	235	0	SLPLSPYSPQPGQEDR
2051.0212	2050.0139	2050.0384	-0.0245	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1089	2473.1016	2473.1371	-0.0355	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1111.5560, 1120.5461, 1149.6095, 1425.6030, 1464.5890, 1481.6079, 1547.7476, 1614.7950, 1638.7993, 1658.8304, 1691.7700, 1984.8745, 2099.9451, 2273.1528, 2530.3464, 2613.1572, 3069.3582, 3154.4604, 3199.4026, 3227.4558, 3303.4529, 3316.6902, 3455.5583

5. gi|230338 **Mass:** 23975 **Score:** 17 **Expect:** 18 **Queries matched:** 2

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2273.1528	2272.1455	2272.1521	-0.0066	70 -	89	0	SIVHPSYNSNTLNNDIMLIK
2530.3464	2529.3391	2529.3260	0.0131	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1083.5582, 1111.5560, 1120.5461, 1149.6095, 1425.6030, 1464.5890, 1481.6079, 1547.7476, 1614.7950, 1638.7993, 1658.8304, 1691.7700, 1770.8900, 1984.8745, 2051.0212, 2099.9451, 2474.1089, 2613.1572, 3069.3582, 3154.4604, 3199.4026, 3227.4558, 3303.4529, 3316.6902, 3455.5583

6. gi|9864777 **Mass:** 60754 **Score:** 15 **Expect:** 26 **Queries matched:** 3

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5582	1082.5509	1082.5581	-0.0071	38 -	46	0	LNAQRPDNR
2051.0212	2050.0139	2050.0384	-0.0245	83 -	99	0	RPFYSNAPQEIFIQQGR
2474.1089	2473.1016	2473.1371	-0.0355	100 -	121	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1111.5560, 1120.5461, 1149.6095, 1425.6030, 1464.5890, 1481.6079, 1547.7476, 1614.7950, 1638.7993, 1658.8304, 1691.7700, 1770.8900, 1984.8745, 2099.9451, 2273.1528, 2530.3464, 2613.1572, 3069.3582, 3154.4604, 3199.4026, 3227.4558, 3303.4529, 3316.6902, 3455.5583

7. gi|5712199 **Mass:** 61430 **Score:** 15 **Expect:** 26 **Queries matched:** 3

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5582	1082.5509	1082.5581	-0.0071	37 -	45	0	LNAQRPDNR

2051.0212	2050.0139	2050.0384	-0.0245	82 - 98	0	RPFYSNAPQEIFIQQGR
2474.1089	2473.1016	2473.1371	-0.0355	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1111.5560, 1120.5461, 1149.6095, 1425.6030, 1464.5890, 1481.6079, 1547.7476, 1614.7950, 1638.7993, 1658.8304, 1691.7700, 1770.8900, 1984.8745, 2099.9451, 2273.1528, 2530.3464, 2613.1572, 3069.3582, 3154.4604, 3199.4026, 3227.4558, 3303.4529, 3316.6902, 3455.5583

8. gi|57669861 **Mass:** 61041 **Score:** 15 **Expect:** 26 **Queries matched:** 3

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5582	1082.5509	1082.5581	-0.0071	37 -	45	0	LNAQRPDNR
2051.0212	2050.0139	2050.0384	-0.0245	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1089	2473.1016	2473.1371	-0.0355	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1111.5560, 1120.5461, 1149.6095, 1425.6030, 1464.5890, 1481.6079, 1547.7476, 1614.7950, 1638.7993, 1658.8304, 1691.7700, 1770.8900, 1984.8745, 2099.9451, 2273.1528, 2530.3464, 2613.1572, 3069.3582, 3154.4604, 3199.4026, 3227.4558, 3303.4529, 3316.6902, 3455.5583

9. gi|108595573 **Mass:** 61041 **Score:** 15 **Expect:** 26 **Queries matched:** 3

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5582	1082.5509	1082.5581	-0.0071	37 -	45	0	LNAQRPDNR
2051.0212	2050.0139	2050.0384	-0.0245	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1089	2473.1016	2473.1371	-0.0355	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1111.5560, 1120.5461, 1149.6095, 1425.6030, 1464.5890, 1481.6079, 1547.7476, 1614.7950, 1638.7993, 1658.8304, 1691.7700, 1770.8900, 1984.8745, 2099.9451, 2273.1528, 2530.3464, 2613.1572, 3069.3582, 3154.4604, 3199.4026, 3227.4558, 3303.4529, 3316.6902, 3455.5583

10. gi|52001219 **Mass:** 61810 **Score:** 15 **Expect:** 27 **Queries matched:** 3

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5582	1082.5509	1082.5581	-0.0071	37 -	45	0	LNAQRPDNR
2051.0212	2050.0139	2050.0384	-0.0245	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1089	2473.1016	2473.1371	-0.0355	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1111.5560, 1120.5461, 1149.6095, 1425.6030, 1464.5890, 1481.6079, 1547.7476, 1614.7950, 1638.7993, 1658.8304, 1691.7700, 1770.8900, 1984.8745, 2099.9451, 2273.1528, 2530.3464, 2613.1572, 3069.3582, 3154.4604, 3199.4026, 3227.4558, 3303.4529, 3316.6902, 3455.5583

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 40

Protein View

Match to: **gi|47933675** Score: **100** Expect: **8.7e-008**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **40**
Number of mass values matched: **11**
Sequence Coverage: **30%**

Matched peptides shown in **Bold Red**

```
    1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
   51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
  101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
  151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
  201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
  251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
  301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
```

```
351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6079	1480.6006	1480.6000	0.0006	0	QGGEENECQFQR
35 - 43	1083.5582	1082.5509	1082.5581	-0.0071	0	LNAQRPDNR
44 - 70	3069.3582	3068.3509	3068.3933	-0.0424	0	IESEGGYIETWNPNNQEFQCAGVALSR
120 - 128	1149.6095	1148.6022	1148.6050	-0.0028	1	YQSQKPSRR
129 - 146	2099.9451	2098.9378	2098.9304	0.0074	0	FQVGQDDPSQQQQDSHQK
195 - 208	1770.8900	1769.8827	1769.8848	-0.0021	1	RFYLAGNQEQEFLR
196 - 208	1614.7950	1613.7877	1613.7837	0.0040	0	FYLAGNQEQEFLR
209 - 220	1547.7476	1546.7403	1546.7389	0.0014	0	YQQQQGSRPHYR
228 - 255	3199.4026	3198.3953	3198.4277	-0.0324	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR
263 - 277	1658.8304	1657.8231	1657.8270	-0.0039	1	GENEREEQGAIVTVK
300 - 312	1691.7700	1690.7627	1690.7659	-0.0031	1	EEFDEDRSRPQQR

No match to: 805.4429, 815.4255, 816.5836, 840.4349, 860.6141, 872.4407, 904.6465, 932.4471, 948.6750, 949.4723, 992.7075, 1036.7257, 1080.5308, 1111.5560, 1120.5461, 1425.6030, 1464.5890, 1638.7993, 1984.8745, 2051.0212, 2273.1528, 2474.1089, 2530.3464, 2613.1572, 3154.4604, 3227.4558, 3303.4529, 3316.6902, 3455.5583

Spot 51

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:36:08 GMT
Top Score : 138 for gi|47933675, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	138	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	138	iso-Ara h3 [Arachis hypogaea]
3.	gi|230338	23975	21	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
4.	gi|28194657	13874	17	putative caffeic acid methyl transferase [Arachis hypogaea]
5.	gi|62177385	14731	16	resistance protein Cre [Arachis hypogaea]
6.	gi|2498261	2416	13	33.0 kDa cold shock protein (AHCSP33)
7.	gi|62177393	21055	12	resistance protein Cre [Arachis hypogaea]
8.	gi|62177626	19671	12	resistance protein PRG [Arachis hypogaea]
9.	gi|60594911	28600	12	N-acetylglucosaminyl-transferase [Rhizobium sp. NET30]
10.	gi|60594909	28570	12	N-acetylglucosaminyl-transferase [Rhizobium sp. NCHA22]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 138 **Expect:** 1.4e-011 **Queries matched:** 16
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
859.4807	858.4734	858.4559	0.0175	256	262	0	QTVENLR
993.5130	992.5057	992.5039	0.0018	120	127	0	YQSQKPSR
1083.5750	1082.5677	1082.5581	0.0097	35	43	0	LNAQRPDNR
1095.4679	1094.4606	1094.4628	-0.0022	299	306	1	REEFDEDR
1149.6213	1148.6140	1148.6050	0.0090	120	128	1	YQSQKPSRR
1481.6130	1480.6057	1480.6000	0.0057	23	34	0	QGGEENECQFQR
1547.7567	1546.7494	1546.7389	0.0105	209	220	0	YQQQQGSRPHYR
1614.7960	1613.7887	1613.7837	0.0050	196	208	0	FYLAGNQEQEFLR
1658.8499	1657.8426	1657.8270	0.0156	263	277	1	GENEREEQGAIVTVK
1691.7894	1690.7821	1690.7659	0.0163	300	312	1	EEFDEDRSRPQQR
1770.8993	1769.8920	1769.8848	0.0072	195	208	1	RFYLAGNQEQEFLR

2099.9412	2098.9339	2098.9304	0.0035	129 - 146	0	FQVGQDDPSQQQQDSHQK
2256.0696	2255.0623	2255.0315	0.0308	128 - 146	1	RFQVGQDDPSQQQQDSHQK
2492.1494	2491.1421	2491.1588	-0.0167	129 - 149	1	FQVGQDDPSQQQQDSHQKVHR
3069.3899	3068.3826	3068.3933	-0.0107	44 - 70	0	IESEGGYIETWNPNNQEFQCAGVALSR
3199.4573	3198.4500	3198.4277	0.0223	228 - 255	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 805.4572, 845.1028, 855.0690, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1307.6849, 1464.5979, 1475.7537, 1638.8511, 1754.4689, 1832.8914, 1984.8966, 2088.9976, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2499.2644, 2514.3379, 2613.1792, 3211.5134, 3228.4553, 3300.7080, 3455.6265

2. gi|112380623 **Mass:** 58570 **Score:** 138 **Expect:** 1.4e-011 **Queries matched:** 16

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
859.4807	858.4734	858.4559	0.0175	258 - 264		0	QTVENLR
993.5130	992.5057	992.5039	0.0018	122 - 129		0	YQSQKPSR
1083.5750	1082.5677	1082.5581	0.0097	37 - 45		0	LNAQRPDNR
1095.4679	1094.4606	1094.4628	-0.0022	301 - 308		1	REEFDEDR
1149.6213	1148.6140	1148.6050	0.0090	122 - 130		1	YQSQKPSRR
1481.6130	1480.6057	1480.6000	0.0057	25 - 36		0	QGGEENECQFQR
1547.7567	1546.7494	1546.7389	0.0105	211 - 222		0	YQQQQGSRPHYR
1614.7960	1613.7887	1613.7837	0.0050	198 - 210		0	FYLAGNQEQEFLR
1658.8499	1657.8426	1657.8270	0.0156	265 - 279		1	GENEREEQGAIVTVK
1691.7894	1690.7821	1690.7659	0.0163	302 - 314		1	EEFDEDRSRPQQR
1770.8993	1769.8920	1769.8848	0.0072	197 - 210		1	RFYLAGNQEQEFLR
2099.9412	2098.9339	2098.9304	0.0035	131 - 148		0	FQVGQDDPSQQQQDSHQK
2256.0696	2255.0623	2255.0315	0.0308	130 - 148		1	RFQVGQDDPSQQQQDSHQK
2492.1494	2491.1421	2491.1588	-0.0167	131 - 151		1	FQVGQDDPSQQQQDSHQKVHR
3069.3899	3068.3826	3068.3933	-0.0107	46 - 72		0	IESEGGYIETWNPNNQEFQCAGVALSR
3199.4573	3198.4500	3198.4277	0.0223	230 - 257		0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 805.4572, 845.1028, 855.0690, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1307.6849, 1464.5979, 1475.7537, 1638.8511, 1754.4689, 1832.8914, 1984.8966, 2088.9976, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2499.2644, 2514.3379, 2613.1792, 3211.5134, 3228.4553, 3300.7080, 3455.6265

3. gi|230338 **Mass:** 23975 **Score:** 21 **Expect:** 7.1 **Queries matched:** 3

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.6045	1045.5972	1045.5880	0.0093	90 - 99		1	LKSAASLNSR
2273.1533	2272.1460	2272.1521	-0.0061	70 - 89		0	SIVHPSYNSNTLNNDIMLIK
2514.3379	2513.3306	2513.3311	-0.0005	70 - 91		1	SIVHPSYNSNTLNNDIMLIKLK

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

4. gi|28194657 **Mass:** 13874 **Score:** 17 **Expect:** 18 **Queries matched:** 2

putative caffeic acid methyl transferase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1658.8499	1657.8426	1657.8133	0.0293	1	-	16	0	DGITHVGGDMFVSVPK
2483.2200	2482.2127	2482.1871	0.0256	1	-	23	1	DGITHVGGDMFVSVPKADAIYMK + 2 Oxidation (M)

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

5. gi|62177385 **Mass:** 14731 **Score:** 16 **Expect:** 21 **Queries matched:** 2

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
2088.9976	2087.9903	2087.9979	-0.0076	72	-	89	1	NCPPELESIGRSIVETCK
2295.1426	2294.1353	2294.1147	0.0207	15	-	34	1	TIKNCFPENNNGGMILVTTR + Oxidation (M)

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2273.1533, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

6. gi|2498261 **Mass:** 2416 **Score:** 13 **Expect:** 46 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1547.7567	1546.7494	1546.7263	0.0231	9	-	24	0	ASYTVTPPAQANAADA

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

7. gi|62177393 **Mass:** 21055 **Score:** 12 **Expect:** 54 **Queries matched:** 3

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1691.7894	1690.7821	1690.7991	-0.0169	112 -	124	1	SDWIYFRDVEFSK
2295.1426	2294.1353	2294.1326	0.0027	42 -	61	1	IMGTEPPLFLKGMDVETSWK + Oxidation (M)
2311.1426	2310.1353	2310.1275	0.0078	42 -	61	1	IMGTEPPLFLKGMDVETSWK + 2 Oxidation (M)

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2273.1533, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

8. gi|62177626 **Mass:** 19671 **Score:** 12 **Expect:** 56 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1145.5767	1144.5694	1144.5724	-0.0029	32 -	41	0	ISDQEEGLVR
2335.1172	2334.1099	2334.1280	-0.0181	151 -	171	0	ANYEDLSNQAIHYAQGLPFAL

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2256.0696, 2273.1533, 2295.1426, 2311.1426, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

9. gi|60594911 **Mass:** 28600 **Score:** 12 **Expect:** 59 **Queries matched:** 2

N-acetylglucosaminyl-transferase [Rhizobium sp. NET30]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2162.0383	2161.0310	2161.0547	-0.0237	135 -	152	1	TALTMLLDQYETQMFRGK + Oxidation (M)
2227.1443	2226.1370	2226.1612	-0.0242	71 -	92	1	LALKMQDPAIGAAMGQLAASNR

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2185.0366, 2226.0540, 2256.0696, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

10. gi|60594909 **Mass:** 28570 **Score:** 12 **Expect:** 61 **Queries matched:** 2

N-acetylglucosaminyl-transferase [Rhizobium sp. NCHA22]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2162.0383	2161.0310	2161.0547	-0.0237	135 -	152	1	TALTMLLDQYETQMFRGK + Oxidation (M)
2227.1443	2226.1370	2226.1612	-0.0242	71 -	92	1	LALKMQDPAIGAAMGQLAASNR

No match to: 805.4572, 845.1028, 855.0690, 859.4807, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 993.5130, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1083.5750, 1095.4679, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1149.6213, 1307.6849, 1464.5979, 1475.7537, 1481.6130, 1547.7567, 1614.7960, 1638.8511, 1658.8499, 1691.7894, 1754.4689, 1770.8993, 1832.8914, 1984.8966, 2088.9976, 2099.9412, 2145.0542, 2185.0366, 2226.0540,

2256.0696, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2492.1494, 2499.2644, 2514.3379, 2613.1792, 3069.3899, 3199.4573, 3211.5134, 3228.4553, 3300.7080, 3455.6265

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 59

Protein View

Match to: **gi|47933675** Score: **138** Expect: **1.4e-011**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **59**
Number of mass values matched: **16**
Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

```
   1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
  51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
 101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
 151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
 201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
 251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
 301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
 351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
 401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
 451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
 501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6130	1480.6057	1480.6000	0.0057	0	QGGEENECQFQR
35 - 43	1083.5750	1082.5677	1082.5581	0.0097	0	LNAQRPDNR
44 - 70	3069.3899	3068.3826	3068.3933	-0.0107	0	IESEGGYIETWNPNNQEFQCAGVALSR
120 - 127	993.5130	992.5057	992.5039	0.0018	0	YQSQKPSR
120 - 128	1149.6213	1148.6140	1148.6050	0.0090	1	YQSQKPSRR
128 - 146	2256.0696	2255.0623	2255.0315	0.0308	1	RFQVGQDDPSQQQQDSHQK
129 - 146	2099.9412	2098.9339	2098.9304	0.0035	0	FQVGQDDPSQQQQDSHQK
129 - 149	2492.1494	2491.1421	2491.1588	-0.0167	1	FQVGQDDPSQQQQDSHQKVHR
195 - 208	1770.8993	1769.8920	1769.8848	0.0072	1	RFYLAGNQEQEFLR
196 - 208	1614.7960	1613.7887	1613.7837	0.0050	0	FYLAGNQEQEFLR
209 - 220	1547.7567	1546.7494	1546.7389	0.0105	0	YQQQQGSRPHYR
228 - 255	3199.4573	3198.4500	3198.4277	0.0223	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR
256 - 262	859.4807	858.4734	858.4559	0.0175	0	QTVENLR
263 - 277	1658.8499	1657.8426	1657.8270	0.0156	1	GENEREEQGAIVTVK
299 - 306	1095.4679	1094.4606	1094.4628	-0.0022	1	REEFDEDR
300 - 312	1691.7894	1690.7821	1690.7659	0.0163	1	EEFDEDRSRPQQR

No match to: 805.4572, 845.1028, 855.0690, 861.0842, 871.0406, 877.0588, 885.9771, 886.4592, 939.3989, 1046.6045, 1066.0743, 1080.5345, 1082.5496, 1137.0652, 1137.5834, 1145.1086, 1145.5767, 1307.6849, 1464.5979, 1475.7537, 1638.8511, 1754.4689, 1832.8914, 1984.8966, 2088.9976, 2145.0542, 2162.0383, 2185.0366, 2226.0540, 2227.1443, 2273.1533, 2295.1426, 2311.1426, 2335.1172, 2352.0938, 2483.2200, 2499.2644, 2514.3379, 2613.1792, 3211.5134, 3228.4553, 3300.7080, 3455.6265

Spot 52

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 4 May 2007 at 11:32:51 GMT
Top Score : 127 for gi|47933675, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	127	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	127	iso-Ara h3 [Arachis hypogaea]
3.	gi|288487	4881	26	chitinase [Arachis hypogaea]
4.	gi|2498261	2416	14	33.0 kDa cold shock protein (AHCSP33)
5.	gi|288485	4783	12	chitinase [Arachis hypogaea]
6.	gi|288481	4811	12	chitinase [Arachis hypogaea]
7.	gi|62361120	20068	11	resistance protein PLTR [Arachis hypogaea]
8.	gi|544001	4824	11	Endochitinase 3 (CHIT 3)
9.	gi|3335563	36849	11	polyprotein [Peanut stripe virus]
10.	gi|62177393	21055	11	resistance protein Cre [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 127 **Expect:** 1.7e-010 **Queries matched:** 15
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
771.4174	770.4101	770.4147	-0.0046	307	312	0	SRPQQR
859.4546	858.4473	858.4559	-0.0086	256	262	0	QTVENLR
939.3694	938.3621	938.3617	0.0004	300	306	0	EEFDEDR
993.5042	992.4969	992.5039	-0.0070	120	127	0	YQSQKPSR
1083.5654	1082.5581	1082.5581	0.0001	35	43	0	LNAQRPDNR
1095.4717	1094.4644	1094.4628	0.0016	299	306	1	REEFDEDR
1149.6182	1148.6109	1148.6050	0.0059	120	128	1	YQSQKPSRR
1481.6180	1480.6107	1480.6000	0.0107	23	34	0	QGGEENECQFQR

1547.7592	1546.7519	1546.7389	0.0130	209 - 220	0	YQQQQGSRPHYR
1614.7999	1613.7926	1613.7837	0.0089	196 - 208	0	FYLAGNQEQEFLR
1658.8452	1657.8379	1657.8270	0.0109	263 - 277	1	GENEREEQGAIVTVK
1691.7874	1690.7801	1690.7659	0.0143	300 - 312	1	EEFDEDRSRPQQR
1770.9001	1769.8928	1769.8848	0.0080	195 - 208	1	RFYLAGNQEQEFLR
2099.9385	2098.9312	2098.9304	0.0008	129 - 146	0	FQVGQDDPSQQQQDSHQK
2256.0510	2255.0437	2255.0315	0.0122	128 - 146	1	RFQVGQDDPSQQQQDSHQK

No match to: 885.9687, 949.4672, 956.4603, 988.6172, 1111.5602, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1543.6776, 1588.7975, 1727.8352, 1728.3342, 1744.8959, 1754.4480, 1792.8781, 1824.9312, 2213.0583, 2213.5417, 2214.0647, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462, 2956.2939, 3069.3254, 3084.3347, 3153.3770, 3199.3442, 3211.4417, 3240.4126, 3438.0537, 3454.4990

2. gi|112380623 **Mass:** 58570 **Score:** 127 **Expect:** 1.7e-010 **Queries matched:** 15

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
771.4174	770.4101	770.4147	-0.0046	309 - 314		0	SRPQQR
859.4546	858.4473	858.4559	-0.0086	258 - 264		0	QTVENLR
939.3694	938.3621	938.3617	0.0004	302 - 308		0	EEFDEDR
993.5042	992.4969	992.5039	-0.0070	122 - 129		0	YQSQKPSR
1083.5654	1082.5581	1082.5581	0.0001	37 - 45		0	LNAQRPDNR
1095.4717	1094.4644	1094.4628	0.0016	301 - 308		1	REEFDEDR
1149.6182	1148.6109	1148.6050	0.0059	122 - 130		1	YQSQKPSRR
1481.6180	1480.6107	1480.6000	0.0107	25 - 36		0	QGGEENECQFQR
1547.7592	1546.7519	1546.7389	0.0130	211 - 222		0	YQQQQGSRPHYR
1614.7999	1613.7926	1613.7837	0.0089	198 - 210		0	FYLAGNQEQEFLR
1658.8452	1657.8379	1657.8270	0.0109	265 - 279		1	GENEREEQGAIVTVK
1691.7874	1690.7801	1690.7659	0.0143	302 - 314		1	EEFDEDRSRPQQR
1770.9001	1769.8928	1769.8848	0.0080	197 - 210		1	RFYLAGNQEQEFLR
2099.9385	2098.9312	2098.9304	0.0008	131 - 148		0	FQVGQDDPSQQQQDSHQK
2256.0510	2255.0437	2255.0315	0.0122	130 - 148		1	RFQVGQDDPSQQQQDSHQK

No match to: 885.9687, 949.4672, 956.4603, 988.6172, 1111.5602, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1543.6776, 1588.7975, 1727.8352, 1728.3342, 1744.8959, 1754.4480, 1792.8781, 1824.9312, 2213.0583, 2213.5417, 2214.0647, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462, 2956.2939, 3069.3254, 3084.3347, 3153.3770, 3199.3442, 3211.4417, 3240.4126, 3438.0537, 3454.4990

3. gi|288487 **Mass:** 4881 **Score:** 26 **Expect:** 2.5 **Queries matched:** 2

chitinase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1792.8781	1791.8708	1791.8824	-0.0116	30 - 47		0	VSGFGVITNIINGGLDCG
1824.9312	1823.9239	1823.8948	0.0291	1 - 17		0	MTPQGNKPSSHDVITGR

No match to: 771.4174, 859.4546, 885.9687, 939.3694, 949.4672, 956.4603, 988.6172, 993.5042, 1083.5654,

1095.4717, 1111.5602, 1149.6182, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1481.6180, 1543.6776, 1547.7592, 1588.7975, 1614.7999, 1658.8452, 1691.7874, 1727.8352, 1728.3342, 1744.8959, 1754.4480, 1770.9001, 2099.9385, 2213.0583, 2213.5417, 2214.0647, 2256.0510, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462, 2956.2939, 3069.3254, 3084.3347, 3153.3770, 3199.3442, 3211.4417, 3240.4126, 3438.0537, 3454.4990

4. gi|2498261 **Mass:** 2416 **Score:** 14 **Expect:** 38 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1547.7592	1546.7519	1546.7263	0.0256	9 -	24	0	ASYTVTPPAQANAADA

No match to: 771.4174, 859.4546, 885.9687, 939.3694, 949.4672, 956.4603, 988.6172, 993.5042, 1083.5654, 1095.4717, 1111.5602, 1149.6182, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1481.6180, 1543.6776, 1588.7975, 1614.7999, 1658.8452, 1691.7874, 1727.8352, 1728.3342, 1744.8959, 1754.4480, 1770.9001, 1792.8781, 1824.9312, 2099.9385, 2213.0583, 2213.5417, 2214.0647, 2256.0510, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462, 2956.2939, 3069.3254, 3084.3347, 3153.3770, 3199.3442, 3211.4417, 3240.4126, 3438.0537, 3454.4990

5. gi|288485 **Mass:** 4783 **Score:** 12 **Expect:** 62 **Queries matched:** 1

chitinase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1792.8781	1791.8708	1791.8824	-0.0116	30 -	47	0	VSGFGVITNIINGGLDCG

No match to: 771.4174, 859.4546, 885.9687, 939.3694, 949.4672, 956.4603, 988.6172, 993.5042, 1083.5654, 1095.4717, 1111.5602, 1149.6182, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1481.6180, 1543.6776, 1547.7592, 1588.7975, 1614.7999, 1658.8452, 1691.7874, 1727.8352, 1728.3342, 1744.8959, 1754.4480, 1770.9001, 1824.9312, 2099.9385, 2213.0583, 2213.5417, 2214.0647, 2256.0510, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462, 2956.2939, 3069.3254, 3084.3347, 3153.3770, 3199.3442, 3211.4417, 3240.4126, 3438.0537, 3454.4990

6. gi|288481 **Mass:** 4811 **Score:** 12 **Expect:** 62 **Queries matched:** 1

chitinase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1792.8781	1791.8708	1791.8824	-0.0116	30 -	47	0	VSGFGVITNIINGGLDCG

No match to: 771.4174, 859.4546, 885.9687, 939.3694, 949.4672, 956.4603, 988.6172, 993.5042, 1083.5654, 1095.4717, 1111.5602, 1149.6182, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1481.6180, 1543.6776, 1547.7592, 1588.7975, 1614.7999, 1658.8452, 1691.7874, 1727.8352, 1728.3342, 1744.8959, 1754.4480, 1770.9001, 1824.9312, 2099.9385, 2213.0583, 2213.5417, 2214.0647, 2256.0510, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462, 2956.2939, 3069.3254, 3084.3347, 3153.3770, 3199.3442, 3211.4417, 3240.4126, 3438.0537, 3454.4990

7. gi|62361120 **Mass:** 20068 **Score:** 11 **Expect:** 63 **Queries matched:** 2

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
988.6172	987.6099	987.6076	0.0023	103 -	111	1	GSKILITTR
1727.8352	1726.8279	1726.8420	-0.0141	142 -	156	1	HARLSTDSMENPTLR

No match to: 771.4174, 859.4546, 885.9687, 939.3694, 949.4672, 956.4603, 993.5042, 1083.5654, 1095.4717, 1111.5602, 1149.6182, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1481.6180, 1543.6776, 1547.7592, 1588.7975, 1614.7999, 1658.8452, 1691.7874, 1728.3342, 1744.8959, 1754.4480, 1770.9001, 1792.8781, 1824.9312, 2099.9385, 2213.0583, 2213.5417, 2214.0647, 2256.0510, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462,

2956.2939, 3069.3254, 3084.3347, 3153.3770, 3199.3442, 3211.4417, 3240.4126, 3438.0537, 3454.4990

8. gi|544001 **Mass:** 4824 **Score:** 11 **Expect:** 65 **Queries matched:** 1

Endochitinase 3 (CHIT 3)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1824.9312	1823.9239	1823.8948	0.0291	1 -	17	0	MTPQGNKPSSHDVITGR

No match to: 771.4174, 859.4546, 885.9687, 939.3694, 949.4672, 956.4603, 988.6172, 993.5042, 1083.5654, 1095.4717, 1111.5602, 1149.6182, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1481.6180, 1543.6776, 1547.7592, 1588.7975, 1614.7999, 1658.8452, 1691.7874, 1727.8352, 1728.3342, 1744.8959, 1754.4480, 1770.9001, 1792.8781, 2099.9385, 2213.0583, 2213.5417, 2214.0647, 2256.0510, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462, 2956.2939, 3069.3254, 3084.3347, 3153.3770, 3199.3442, 3211.4417, 3240.4126, 3438.0537, 3454.4990

9. gi|3335563 **Mass:** 36849 **Score:** 11 **Expect:** 68 **Queries matched:** 2

polyprotein [Peanut stripe virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2213.0583	2212.0510	2212.0113	0.0397	310 -	329	1	HTARDVNQNMHTLLGMGSAQ + 2 Oxidation (M)
3199.3442	3198.3369	3198.3957	-0.0587	219 -	244	1	QIMHHFSDAAEAYIEMRNSEQPYMPR + 3 Oxidation (M)

No match to: 771.4174, 859.4546, 885.9687, 939.3694, 949.4672, 956.4603, 988.6172, 993.5042, 1083.5654, 1095.4717, 1111.5602, 1149.6182, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1481.6180, 1543.6776, 1547.7592, 1588.7975, 1614.7999, 1658.8452, 1691.7874, 1727.8352, 1728.3342, 1744.8959, 1754.4480, 1770.9001, 1792.8781, 1824.9312, 2099.9385, 2213.5417, 2214.0647, 2256.0510, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462, 2956.2939, 3069.3254, 3084.3347, 3153.3770, 3211.4417, 3240.4126, 3438.0537, 3454.4990

10. gi|62177393 **Mass:** 21055 **Score:** 11 **Expect:** 70 **Queries matched:** 2

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1691.7874	1690.7801	1690.7991	-0.0189	112 -	124	1	SDWIYFRDVEFSK
1744.8959	1743.8886	1743.9229	-0.0343	12 -	26	0	ELWLQLNSLLMEGAK

No match to: 771.4174, 859.4546, 885.9687, 939.3694, 949.4672, 956.4603, 988.6172, 993.5042, 1083.5654, 1095.4717, 1111.5602, 1149.6182, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1481.6180, 1543.6776, 1547.7592, 1588.7975, 1614.7999, 1658.8452, 1727.8352, 1728.3342, 1754.4480, 1770.9001, 1792.8781, 1824.9312, 2099.9385, 2213.0583, 2213.5417, 2214.0647, 2256.0510, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462, 2956.2939, 3069.3254, 3084.3347, 3153.3770, 3199.3442, 3211.4417, 3240.4126, 3438.0537, 3454.4990

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)

Mass values : **MONOISOTOPIC**
Protein Mass : **Unrestricted**
Peptide Mass Tolerance : **± 20 ppm**
Peptide Charge State : **1+**
Max Missed Cleavages : **1**
Number of queries : **50**
gi|47933675 Score: **127** Expect: **1.7e-010**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **15**
Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

```
    1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
   51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
  101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
  151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
  201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
  251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
  301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
  351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
  401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
  451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
  501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6180	1480.6107	1480.6000	0.0107	0	QGGEENECQFQR
35 - 43	1083.5654	1082.5581	1082.5581	0.0001	0	LNAQRPDNR
120 - 127	993.5042	992.4969	992.5039	-0.0070	0	YQSQKPSR
120 - 128	1149.6182	1148.6109	1148.6050	0.0059	1	YQSQKPSRR
128 - 146	2256.0510	2255.0437	2255.0315	0.0122	1	RFQVGQDDPSQQQQDSHQK
129 - 146	2099.9385	2098.9312	2098.9304	0.0008	0	FQVGQDDPSQQQQDSHQK
195 - 208	1770.9001	1769.8928	1769.8848	0.0080	1	RFYLAGNQEQEFLR
196 - 208	1614.7999	1613.7926	1613.7837	0.0089	0	FYLAGNQEQEFLR

209 - 220	1547.7592	1546.7519	1546.7389	0.0130	0	YQQQQGSRPHYR
256 - 262	859.4546	858.4473	858.4559	-0.0086	0	QTVENLR
263 - 277	1658.8452	1657.8379	1657.8270	0.0109	1	GENEREEQGAIVTVK
299 - 306	1095.4717	1094.4644	1094.4628	0.0016	1	REEFDEDR
300 - 306	939.3694	938.3621	938.3617	0.0004	0	EEFDEDR
300 - 312	1691.7874	1690.7801	1690.7659	0.0143	1	EEFDEDRSRPQQR
307 - 312	771.4174	770.4101	770.4147	-0.0046	0	SRPQQR

No match to: 885.9687, 949.4672, 956.4603, 988.6172, 1111.5602, 1159.4824, 1260.6686, 1354.6973, 1387.5757, 1464.5908, 1543.6776, 1588.7975, 1727.8352, 1728.3342, 1744.8959, 1754.4480, 1792.8781, 1824.9312, 2213.0583, 2213.5417, 2214.0647, 2273.1594, 2482.2263, 2499.2703, 2612.1631, 2613.1462, 2956.2939, 3069.3254, 3084.3347, 3153.3770, 3199.3442, 3211.4417, 3240.4126, 3438.0537, 3454.4990

Spot 53

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 4 May 2007 at 11:32:47 GMT
Top Score : 133 for gi|47933675, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	133	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	133	iso-Ara h3 [Arachis hypogaea]
3.	gi|22135348	25768	42	trypsin inhibitor [Arachis hypogaea]
4.	gi|118776570	60681	42	arachin 6 [Arachis hypogaea]
5.	gi|9864777	60754	32	Gly1 [Arachis hypogaea]
6.	gi|57669861	61041	32	arachin Ahy-4 [Arachis hypogaea]
7.	gi|108595573	61041	32	arachin Ahy-4 [Arachis hypogaea]
8.	gi|5712199	61430	26	glycinin [Arachis hypogaea]
9.	gi|52001219	61810	25	arachin Ahy-1 [Arachis hypogaea]
10.	gi|52001221	61836	25	arachin Ahy-2 [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 133 **Expect:** 4.4e-011 **Queries matched:** 15
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
771.4106	770.4033	770.4147	-0.0114	307	312	0	SRPQQR
859.4589	858.4516	858.4559	-0.0043	256	262	0	QTVENLR
939.3743	938.3670	938.3617	0.0053	300	306	0	EEFDEDR
993.5161	992.5088	992.5039	0.0049	120	127	0	YQSQKPSR
1083.5593	1082.5520	1082.5581	-0.0060	35	43	0	LNAQRPDNR
1095.4620	1094.4547	1094.4628	-0.0081	299	306	1	REEFDEDR
1149.6111	1148.6038	1148.6050	-0.0012	120	128	1	YQSQKPSRR
1481.6086	1480.6013	1480.6000	0.0013	23	34	0	QGGEENECQFQR

1547.7461	1546.7388	1546.7389	-0.0001	209 - 220	0	YQQQQGSRPHYR
1614.7938	1613.7865	1613.7837	0.0028	196 - 208	0	FYLAGNQEQEFLR
1658.8362	1657.8289	1657.8270	0.0019	263 - 277	1	GENEREEQGAIVTVK
1770.8909	1769.8836	1769.8848	-0.0012	195 - 208	1	RFYLAGNQEQEFLR
2099.9351	2098.9278	2098.9304	-0.0026	129 - 146	0	FQVGQDDPSQQQQDSHQK
3069.3513	3068.3440	3068.3933	-0.0493	44 - 70	0	IESEGGYIETWNPNNQEFQCAGVALSR
3199.3982	3198.3909	3198.4277	-0.0368	228 - 255	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 870.5054, 949.4722, 1080.5397, 1111.5620, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1534.6819, 1543.6725, 1588.7896, 1687.8256, 1730.8862, 1744.8862, 1756.8502, 1774.8656, 1957.8564, 2051.0259, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2474.1631, 2612.1738, 2927.3223, 3153.4253, 3211.4666, 3240.3916, 3300.7048

2. gi|112380623 **Mass:** 58570 **Score:** 133 **Expect:** 4.4e-011 **Queries matched:** 15

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
771.4106	770.4033	770.4147	-0.0114	309 - 314		0	SRPQQR
859.4589	858.4516	858.4559	-0.0043	258 - 264		0	QTVENLR
939.3743	938.3670	938.3617	0.0053	302 - 308		0	EEFDEDR
993.5161	992.5088	992.5039	0.0049	122 - 129		0	YQSQKPSR
1083.5593	1082.5520	1082.5581	-0.0060	37 - 45		0	LNAQRPDNR
1095.4620	1094.4547	1094.4628	-0.0081	301 - 308		1	REEFDEDR
1149.6111	1148.6038	1148.6050	-0.0012	122 - 130		1	YQSQKPSRR
1481.6086	1480.6013	1480.6000	0.0013	25 - 36		0	QGGEENECQFQR
1547.7461	1546.7388	1546.7389	-0.0001	211 - 222		0	YQQQQGSRPHYR
1614.7938	1613.7865	1613.7837	0.0028	198 - 210		0	FYLAGNQEQEFLR
1658.8362	1657.8289	1657.8270	0.0019	265 - 279		1	GENEREEQGAIVTVK
1770.8909	1769.8836	1769.8848	-0.0012	197 - 210		1	RFYLAGNQEQEFLR
2099.9351	2098.9278	2098.9304	-0.0026	131 - 148		0	FQVGQDDPSQQQQDSHQK
3069.3513	3068.3440	3068.3933	-0.0493	46 - 72		0	IESEGGYIETWNPNNQEFQCAGVALSR
3199.3982	3198.3909	3198.4277	-0.0368	230 - 257		0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 870.5054, 949.4722, 1080.5397, 1111.5620, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1534.6819, 1543.6725, 1588.7896, 1687.8256, 1730.8862, 1744.8862, 1756.8502, 1774.8656, 1957.8564, 2051.0259, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2474.1631, 2612.1738, 2927.3223, 3153.4253, 3211.4666, 3240.3916, 3300.7048

3. gi|22135348 **Mass:** 25768 **Score:** 42 **Expect:** 0.052 **Queries matched:** 5

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5593	1082.5520	1082.5581	-0.0060	39 - 47		0	LNAQRPDNR
1534.6819	1533.6746	1533.6630	0.0116	27 - 38		0	QQPEENACQFQR
1730.8862	1729.8789	1729.8648	0.0142	197 - 210		1	RFNLAGNHEQEFLR

2051.0259	2050.0186	2050.0384	-0.0198	84 - 100	0	RPFYSNAPQEIFIQQGR
2474.1631	2473.1558	2473.1371	0.0187	101 - 122	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 771.4106, 859.4589, 870.5054, 939.3743, 949.4722, 993.5161, 1080.5397, 1095.4620, 1111.5620, 1149.6111, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1481.6086, 1543.6725, 1547.7461, 1588.7896, 1614.7938, 1658.8362, 1687.8256, 1744.8862, 1756.8502, 1770.8909, 1774.8656, 1957.8564, 2099.9351, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2612.1738, 2927.3223, 3069.3513, 3153.4253, 3199.3982, 3211.4666, 3240.3916, 3300.7048

4. gi|118776570 **Mass:** 60681 **Score:** 42 **Expect:** 0.062 **Queries matched:** 7

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5054	869.4981	869.5083	-0.0101	279 -	285	0	QIVQNLR
1083.5593	1082.5520	1082.5581	-0.0060	37 -	45	0	LNAQRPDNR
1534.6819	1533.6746	1533.6630	0.0116	25 -	36	0	QQPEENACQFQR
1730.8862	1729.8789	1729.8648	0.0142	195 -	208	1	RFNLAGNHEQEFLR
1770.8909	1769.8836	1769.8584	0.0252	220 -	235	0	SLPLSPYSPQPGQEDR
2051.0259	2050.0186	2050.0384	-0.0198	82 -	98	0	RPFYSNAPQEIFIQQGR
2474.1631	2473.1558	2473.1371	0.0187	99 -	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 771.4106, 859.4589, 939.3743, 949.4722, 993.5161, 1080.5397, 1095.4620, 1111.5620, 1149.6111, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1481.6086, 1543.6725, 1547.7461, 1588.7896, 1614.7938, 1658.8362, 1687.8256, 1744.8862, 1756.8502, 1774.8656, 1957.8564, 2099.9351, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2612.1738, 2927.3223, 3069.3513, 3153.4253, 3199.3982, 3211.4666, 3240.3916, 3300.7048

5. gi|9864777 **Mass:** 60754 **Score:** 32 **Expect:** 0.5 **Queries matched:** 6

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5054	869.4981	869.5083	-0.0101	280 -	286	0	QIVQNLR
1083.5593	1082.5520	1082.5581	-0.0060	38 -	46	0	LNAQRPDNR
1534.6819	1533.6746	1533.6630	0.0116	26 -	37	0	QQPEENACQFQR
1730.8862	1729.8789	1729.8648	0.0142	197 -	210	1	RFNLAGNHEQEFLR
2051.0259	2050.0186	2050.0384	-0.0198	83 -	99	0	RPFYSNAPQEIFIQQGR
2474.1631	2473.1558	2473.1371	0.0187	100 -	121	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 771.4106, 859.4589, 939.3743, 949.4722, 993.5161, 1080.5397, 1095.4620, 1111.5620, 1149.6111, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1481.6086, 1543.6725, 1547.7461, 1588.7896, 1614.7938, 1658.8362, 1687.8256, 1744.8862, 1756.8502, 1770.8909, 1774.8656, 1957.8564, 2099.9351, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2612.1738, 2927.3223, 3069.3513, 3153.4253, 3199.3982, 3211.4666, 3240.3916, 3300.7048

6. gi|57669861 **Mass:** 61041 **Score:** 32 **Expect:** 0.52 **Queries matched:** 6

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

870.5054	869.4981	869.5083	-0.0101	281 - 287	0	QIVQNLR
1083.5593	1082.5520	1082.5581	-0.0060	37 - 45	0	LNAQRPDNR
1534.6819	1533.6746	1533.6630	0.0116	25 - 36	0	QQPEENACQFQR
1730.8862	1729.8789	1729.8648	0.0142	195 - 208	1	RFNLAGNHEQEFLR
2051.0259	2050.0186	2050.0384	-0.0198	82 - 98	0	RPFYSNAPQEIFIQQGR
2474.1631	2473.1558	2473.1371	0.0187	99 - 120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 771.4106, 859.4589, 939.3743, 949.4722, 993.5161, 1080.5397, 1095.4620, 1111.5620, 1149.6111, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1481.6086, 1543.6725, 1547.7461, 1588.7896, 1614.7938, 1658.8362, 1687.8256, 1744.8862, 1756.8502, 1770.8909, 1774.8656, 1957.8564, 2099.9351, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2612.1738, 2927.3223, 3069.3513, 3153.4253, 3199.3982, 3211.4666, 3240.3916, 3300.7048

7. gi|108595573 **Mass:** 61041 **Score:** 32 **Expect:** 0.52 **Queries matched:** 6

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
870.5054	869.4981	869.5083	-0.0101	281 - 287		0	QIVQNLR
1083.5593	1082.5520	1082.5581	-0.0060	37 - 45		0	LNAQRPDNR
1534.6819	1533.6746	1533.6630	0.0116	25 - 36		0	QQPEENACQFQR
1730.8862	1729.8789	1729.8648	0.0142	195 - 208		1	RFNLAGNHEQEFLR
2051.0259	2050.0186	2050.0384	-0.0198	82 - 98		0	RPFYSNAPQEIFIQQGR
2474.1631	2473.1558	2473.1371	0.0187	99 - 120		0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 771.4106, 859.4589, 939.3743, 949.4722, 993.5161, 1080.5397, 1095.4620, 1111.5620, 1149.6111, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1481.6086, 1543.6725, 1547.7461, 1588.7896, 1614.7938, 1658.8362, 1687.8256, 1744.8862, 1756.8502, 1770.8909, 1774.8656, 1957.8564, 2099.9351, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2612.1738, 2927.3223, 3069.3513, 3153.4253, 3199.3982, 3211.4666, 3240.3916, 3300.7048

8. gi|5712199 **Mass:** 61430 **Score:** 26 **Expect:** 2.4 **Queries matched:** 5

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5593	1082.5520	1082.5581	-0.0060	37 - 45		0	LNAQRPDNR
1534.6819	1533.6746	1533.6630	0.0116	25 - 36		0	QQPEENACQFQR
1730.8862	1729.8789	1729.8648	0.0142	195 - 208		1	RFNLAGNHEQEFLR
2051.0259	2050.0186	2050.0384	-0.0198	82 - 98		0	RPFYSNAPQEIFIQQGR
2474.1631	2473.1558	2473.1371	0.0187	99 - 120		0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 771.4106, 859.4589, 870.5054, 939.3743, 949.4722, 993.5161, 1080.5397, 1095.4620, 1111.5620, 1149.6111, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1481.6086, 1543.6725, 1547.7461, 1588.7896, 1614.7938, 1658.8362, 1687.8256, 1744.8862, 1756.8502, 1770.8909, 1774.8656, 1957.8564, 2099.9351, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2612.1738, 2927.3223, 3069.3513, 3153.4253, 3199.3982, 3211.4666, 3240.3916, 3300.7048

9. gi|52001219 **Mass:** 61810 **Score:** 25 **Expect:** 2.5 **Queries matched:** 5

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5593	1082.5520	1082.5581	-0.0060	37	45	0	LNAQRPDNR
1534.6819	1533.6746	1533.6630	0.0116	25	36	0	QQPEENACQFQR
1730.8862	1729.8789	1729.8648	0.0142	195	208	1	RFNLAGNHEQEFLR
2051.0259	2050.0186	2050.0384	-0.0198	82	98	0	RPFYSNAPQEIFIQQGR
2474.1631	2473.1558	2473.1371	0.0187	99	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 771.4106, 859.4589, 870.5054, 939.3743, 949.4722, 993.5161, 1080.5397, 1095.4620, 1111.5620, 1149.6111, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1481.6086, 1543.6725, 1547.7461, 1588.7896, 1614.7938, 1658.8362, 1687.8256, 1744.8862, 1756.8502, 1770.8909, 1774.8656, 1957.8564, 2099.9351, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2612.1738, 2927.3223, 3069.3513, 3153.4253, 3199.3982, 3211.4666, 3240.3916, 3300.7048

10. gi|52001221 **Mass:** 61836 **Score:** 25 **Expect:** 2.6 **Queries matched:** 5

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5593	1082.5520	1082.5581	-0.0060	37	45	0	LNAQRPDNR
1534.6819	1533.6746	1533.6630	0.0116	25	36	0	QQPEENACQFQR
1730.8862	1729.8789	1729.8648	0.0142	196	209	1	RFNLAGNHEQEFLR
2051.0259	2050.0186	2050.0384	-0.0198	82	98	0	RPFYSNAPQEIFIQQGR
2474.1631	2473.1558	2473.1371	0.0187	99	120	0	GYFGLIFPGCPSTYEEPAQQGR

No match to: 771.4106, 859.4589, 870.5054, 939.3743, 949.4722, 993.5161, 1080.5397, 1095.4620, 1111.5620, 1149.6111, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1481.6086, 1543.6725, 1547.7461, 1588.7896, 1614.7938, 1658.8362, 1687.8256, 1744.8862, 1756.8502, 1770.8909, 1774.8656, 1957.8564, 2099.9351, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2612.1738, 2927.3223, 3069.3513, 3153.4253, 3199.3982, 3211.4666, 3240.3916, 3300.7048

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|47933675** Score: **133** Expect: **4.4e-011**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **15**
Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

```
     1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
    51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
   101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
   201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
   251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
   301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
   351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
   401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
   451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
   501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6086	1480.6013	1480.6000	0.0013	0	QGGEENECQFQR
35 - 43	1083.5593	1082.5520	1082.5581	-0.0060	0	LNAQRPDNR
44 - 70	3069.3513	3068.3440	3068.3933	-0.0493	0	IESEGGYIETWNPNNQEFQCAGVALSR
120 - 127	993.5161	992.5088	992.5039	0.0049	0	YQSQKPSR
120 - 128	1149.6111	1148.6038	1148.6050	-0.0012	1	YQSQKPSRR
129 - 146	2099.9351	2098.9278	2098.9304	-0.0026	0	FQVGQDDPSQQQQDSHQK
195 - 208	1770.8909	1769.8836	1769.8848	-0.0012	1	RFYLAGNQEQEFLR
196 - 208	1614.7938	1613.7865	1613.7837	0.0028	0	FYLAGNQEQEFLR
209 - 220	1547.7461	1546.7388	1546.7389	-0.0001	0	YQQQQGSRPHYR
228 - 255	3199.3982	3198.3909	3198.4277	-0.0368	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

256 - 262	859.4589	858.4516	858.4559	-0.0043	0	QTVENLR
263 - 277	1658.8362	1657.8289	1657.8270	0.0019	1	GENEREEQGAIVTVK
299 - 306	1095.4620	1094.4547	1094.4628	-0.0081	1	REEFDEDR
300 - 306	939.3743	938.3670	938.3617	0.0053	0	EEFDEDR
307 - 312	771.4106	770.4033	770.4147	-0.0114	0	SRPQQR

No match to: 870.5054, 949.4722, 1080.5397, 1111.5620, 1174.6385, 1228.5920, 1260.6586, 1323.7468, 1375.7233, 1387.5784, 1464.5864, 1534.6819, 1543.6725, 1588.7896, 1687.8256, 1730.8862, 1744.8862, 1756.8502, 1774.8656, 1957.8564, 2051.0259, 2185.0288, 2192.9988, 2256.0916, 2256.7156, 2273.1587, 2295.1299, 2311.1323, 2474.1631, 2612.1738, 2927.3223, 3153.4253, 3211.4666, 3240.3916, 3300.7048

Spot 54

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 4 May 2007 at 11:32:54 GMT
Top Score : 161 for gi|47933675, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	161	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	161	iso-Ara h3 [Arachis hypogaea]
3.	gi|95100501	15302	16	Cu-Zn superoxide dismutase [Arachis hypogaea]
4.	gi|2498261	2416	14	33.0 kDa cold shock protein (AHCSP33)
5.	gi|110676574	16915	13	pathogenesis-related protein 10 [Arachis hypogaea]
6.	gi|544001	4824	11	Endochitinase 3 (CHIT 3)
7.	gi|288487	4881	11	chitinase [Arachis hypogaea]
8.	gi|1834333	4154	11	unknown [Arachis hypogaea]
9.	gi|1709314	4568	10	Chitooligosaccharide deacetylase (Nodulation protein B)
10.	gi|988275	4568	10	NodB

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 161 **Expect:** 7e-014 **Queries matched:** 17
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
771.4211	770.4138	770.4147	-0.0009	307	312	0	SRPQQR
859.4658	858.4585	858.4559	0.0026	256	262	0	QTVENLR
939.3750	938.3677	938.3617	0.0060	300	306	0	EEFDEDR
993.5092	992.5019	992.5039	-0.0020	120	127	0	YQSQKPSR
1083.5654	1082.5581	1082.5581	0.0001	35	43	0	LNAQRPDNR
1095.4728	1094.4655	1094.4628	0.0027	299	306	1	REEFDEDR
1149.6134	1148.6061	1148.6050	0.0011	120	128	1	YQSQKPSRR
1376.6356	1375.6283	1375.6103	0.0180	282	293	0	ILSPDEEDESSR

1481.6078	1480.6005	1480.6000	0.0005	23 - 34	0	QGGEENECQFQR
1547.7479	1546.7406	1546.7389	0.0017	209 - 220	0	YQQQQGSRPHYR
1614.7899	1613.7826	1613.7837	-0.0011	196 - 208	0	FYLAGNQEQEFLR
1658.8328	1657.8255	1657.8270	-0.0015	263 - 277	1	GENEREEQGAIVTVK
1770.8904	1769.8831	1769.8848	-0.0017	195 - 208	1	RFYLAGNQEQEFLR
2099.9412	2098.9339	2098.9304	0.0035	129 - 146	0	FQVGQDDPSQQQQDSHQK
2256.0623	2255.0550	2255.0315	0.0235	128 - 146	1	RFQVGQDDPSQQQQDSHQK
3069.3621	3068.3548	3068.3933	-0.0385	44 - 70	0	IESEGGYIETWNPNNQEFQCAGVALSR
3199.4016	3198.3943	3198.4277	-0.0334	228 - 255	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 949.4753, 956.4700, 1101.5591, 1111.5609, 1120.5508, 1159.4773, 1260.6552, 1354.6819, 1370.1681, 1387.5765, 1403.6327, 1427.6738, 1464.5875, 1543.6783, 1588.7876, 1687.8257, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1775.8575, 1824.9338, 1957.8634, 2113.9651, 2192.9907, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3153.4338, 3211.4988, 3240.4324, 3496.6272

2. gi|112380623 **Mass:** 58570 **Score:** 161 **Expect:** 7e-014 **Queries matched:** 17

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
771.4211	770.4138	770.4147	-0.0009	309 - 314	0	SRPQQR
859.4658	858.4585	858.4559	0.0026	258 - 264	0	QTVENLR
939.3750	938.3677	938.3617	0.0060	302 - 308	0	EEFDEDR
993.5092	992.5019	992.5039	-0.0020	122 - 129	0	YQSQKPSR
1083.5654	1082.5581	1082.5581	0.0001	37 - 45	0	LNAQRPDNR
1095.4728	1094.4655	1094.4628	0.0027	301 - 308	1	REEFDEDR
1149.6134	1148.6061	1148.6050	0.0011	122 - 130	1	YQSQKPSRR
1376.6356	1375.6283	1375.6103	0.0180	284 - 295	0	ILSPDEEDESSR
1481.6078	1480.6005	1480.6000	0.0005	25 - 36	0	QGGEENECQFQR
1547.7479	1546.7406	1546.7389	0.0017	211 - 222	0	YQQQQGSRPHYR
1614.7899	1613.7826	1613.7837	-0.0011	198 - 210	0	FYLAGNQEQEFLR
1658.8328	1657.8255	1657.8270	-0.0015	265 - 279	1	GENEREEQGAIVTVK
1770.8904	1769.8831	1769.8848	-0.0017	197 - 210	1	RFYLAGNQEQEFLR
2099.9412	2098.9339	2098.9304	0.0035	131 - 148	0	FQVGQDDPSQQQQDSHQK
2256.0623	2255.0550	2255.0315	0.0235	130 - 148	1	RFQVGQDDPSQQQQDSHQK
3069.3621	3068.3548	3068.3933	-0.0385	46 - 72	0	IESEGGYIETWNPNNQEFQCAGVALSR
3199.4016	3198.3943	3198.4277	-0.0334	230 - 257	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 949.4753, 956.4700, 1101.5591, 1111.5609, 1120.5508, 1159.4773, 1260.6552, 1354.6819, 1370.1681, 1387.5765, 1403.6327, 1427.6738, 1464.5875, 1543.6783, 1588.7876, 1687.8257, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1775.8575, 1824.9338, 1957.8634, 2113.9651, 2192.9907, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3153.4338, 3211.4988, 3240.4324, 3496.6272

3. gi|95100501 **Mass:** 15302 **Score:** 16 **Expect:** 24 **Queries matched:** 2

Cu-Zn superoxide dismutase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1427.6738	1426.6665	1426.6912	-0.0247	128 -	142	1	GGHELSKSTGNAGGR
1687.8257	1686.8184	1686.8470	-0.0286	135 -	152	1	STGNAGGRVACGIIGLQG

No match to: 771.4211, 859.4658, 939.3750, 949.4753, 956.4700, 993.5092, 1083.5654, 1095.4728, 1101.5591, 1111.5609, 1120.5508, 1149.6134, 1159.4773, 1260.6552, 1354.6819, 1370.1681, 1376.6356, 1387.5765, 1403.6327, 1464.5875, 1481.6078, 1543.6783, 1547.7479, 1588.7876, 1614.7899, 1658.8328, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1770.8904, 1775.8575, 1824.9338, 1957.8634, 2099.9412, 2113.9651, 2192.9907, 2256.0623, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3069.3621, 3153.4338, 3199.4016, 3211.4988, 3240.4324, 3496.6272

4. gi|2498261 **Mass:** 2416 **Score:** 14 **Expect:** 38 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1547.7479	1546.7406	1546.7263	0.0143	9 -	24	0	ASYTVTPPAQANAADA

No match to: 771.4211, 859.4658, 939.3750, 949.4753, 956.4700, 993.5092, 1083.5654, 1095.4728, 1101.5591, 1111.5609, 1120.5508, 1149.6134, 1159.4773, 1260.6552, 1354.6819, 1370.1681, 1376.6356, 1387.5765, 1403.6327, 1427.6738, 1464.5875, 1481.6078, 1543.6783, 1588.7876, 1614.7899, 1658.8328, 1687.8257, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1770.8904, 1775.8575, 1824.9338, 1957.8634, 2099.9412, 2113.9651, 2192.9907, 2256.0623, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3069.3621, 3153.4338, 3199.4016, 3211.4988, 3240.4324, 3496.6272

5. gi|110676574 **Mass:** 16915 **Score:** 13 **Expect:** 43 **Queries matched:** 2

pathogenesis-related protein 10 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1260.6552	1259.6479	1259.6721	-0.0241	54 -	64	1	KLTIVEDGETR
1376.6356	1375.6283	1375.6289	-0.0006	123 -	134	1	GDAKPEEEDMKK

No match to: 771.4211, 859.4658, 939.3750, 949.4753, 956.4700, 993.5092, 1083.5654, 1095.4728, 1101.5591, 1111.5609, 1120.5508, 1149.6134, 1159.4773, 1354.6819, 1370.1681, 1387.5765, 1403.6327, 1427.6738, 1464.5875, 1481.6078, 1543.6783, 1547.7479, 1588.7876, 1614.7899, 1658.8328, 1687.8257, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1770.8904, 1775.8575, 1824.9338, 1957.8634, 2099.9412, 2113.9651, 2192.9907, 2256.0623, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3069.3621, 3153.4338, 3199.4016, 3211.4988, 3240.4324, 3496.6272

6. gi|544001 **Mass:** 4824 **Score:** 11 **Expect:** 65 **Queries matched:** 1

Endochitinase 3 (CHIT 3)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1824.9338	1823.9265	1823.8948	0.0317	1 -	17	0	MTPQGNKPSSHDVITGR

No match to: 771.4211, 859.4658, 939.3750, 949.4753, 956.4700, 993.5092, 1083.5654, 1095.4728, 1101.5591, 1111.5609, 1120.5508, 1149.6134, 1159.4773, 1260.6552, 1354.6819, 1370.1681, 1376.6356, 1387.5765, 1403.6327, 1427.6738, 1464.5875, 1481.6078, 1543.6783, 1547.7479, 1588.7876, 1614.7899, 1658.8328, 1687.8257, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1770.8904, 1775.8575, 1957.8634, 2099.9412, 2113.9651, 2192.9907, 2256.0623, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3069.3621, 3153.4338, 3199.4016, 3211.4988, 3240.4324, 3496.6272

7. gi|288487 **Mass:** 4881 **Score:** 11 **Expect:** 66 **Queries matched:** 1

chitinase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1824.9338	1823.9265	1823.8948	0.0317	1 -	17	0	MTPQGNKPSSHDVITGR

No match to: 771.4211, 859.4658, 939.3750, 949.4753, 956.4700, 993.5092, 1083.5654, 1095.4728, 1101.5591, 1111.5609, 1120.5508, 1149.6134, 1159.4773, 1260.6552, 1354.6819, 1370.1681, 1376.6356, 1387.5765, 1403.6327, 1427.6738, 1464.5875, 1481.6078, 1543.6783, 1547.7479, 1588.7876, 1614.7899, 1658.8328, 1687.8257, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1770.8904, 1775.8575, 1957.8634, 2099.9412, 2113.9651, 2192.9907, 2256.0623, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3069.3621, 3153.4338, 3199.4016, 3211.4988, 3240.4324, 3496.6272

8. gi|1834333 **Mass:** 4154 **Score:** 11 **Expect:** 70 **Queries matched:** 1

unknown [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1658.8328	1657.8255	1657.8034	0.0221	4 -	17	1	KFDDSFMRPVFGGR

No match to: 771.4211, 859.4658, 939.3750, 949.4753, 956.4700, 993.5092, 1083.5654, 1095.4728, 1101.5591, 1111.5609, 1120.5508, 1149.6134, 1159.4773, 1260.6552, 1354.6819, 1370.1681, 1376.6356, 1387.5765, 1403.6327, 1427.6738, 1464.5875, 1481.6078, 1543.6783, 1547.7479, 1588.7876, 1614.7899, 1687.8257, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1770.8904, 1775.8575, 1824.9338, 1957.8634, 2099.9412, 2113.9651, 2192.9907, 2256.0623, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3069.3621, 3153.4338, 3199.4016, 3211.4988, 3240.4324, 3496.6272

9. gi|1709314 **Mass:** 4568 **Score:** 10 **Expect:** 96 **Queries matched:** 1

Chitooligosaccharide deacetylase (Nodulation protein B)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5654	1082.5581	1082.5581	0.0001	3 -	11	1	HSDNLRSVR

No match to: 771.4211, 859.4658, 939.3750, 949.4753, 956.4700, 993.5092, 1095.4728, 1101.5591, 1111.5609, 1120.5508, 1149.6134, 1159.4773, 1260.6552, 1354.6819, 1370.1681, 1376.6356, 1387.5765, 1403.6327, 1427.6738, 1464.5875, 1481.6078, 1543.6783, 1547.7479, 1588.7876, 1614.7899, 1658.8328, 1687.8257, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1770.8904, 1775.8575, 1824.9338, 1957.8634, 2099.9412, 2113.9651, 2192.9907, 2256.0623, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3069.3621, 3153.4338, 3199.4016, 3211.4988, 3240.4324, 3496.6272

10. gi|988275 **Mass:** 4568 **Score:** 10 **Expect:** 96 **Queries matched:** 1

NodB

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5654	1082.5581	1082.5581	0.0001	3 -	11	1	HSDNLRSVR

No match to: 771.4211, 859.4658, 939.3750, 949.4753, 956.4700, 993.5092, 1095.4728, 1101.5591, 1111.5609, 1120.5508, 1149.6134, 1159.4773, 1260.6552, 1354.6819, 1370.1681, 1376.6356, 1387.5765, 1403.6327, 1427.6738, 1464.5875, 1481.6078, 1543.6783, 1547.7479, 1588.7876, 1614.7899, 1658.8328, 1687.8257, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1770.8904, 1775.8575, 1824.9338, 1957.8634, 2099.9412, 2113.9651, 2192.9907, 2256.0623, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3069.3621, 3153.4338, 3199.4016, 3211.4988, 3240.4324, 3496.6272

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC

Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|47933675** Score: **161** Expect: **7e-014**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **17**
Sequence Coverage: **34%**

Matched peptides shown in **Bold Red**

```
     1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
    51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
   101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
   201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
   251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
   301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
   351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
   401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
   451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
   501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6078	1480.6005	1480.6000	0.0005	0	QGGEENECQFQR
35 - 43	1083.5654	1082.5581	1082.5581	0.0001	0	LNAQRPDNR
44 - 70	3069.3621	3068.3548	3068.3933	-0.0385	0	IESEGGYIETWNPNNQEFQCAGVALSR

120 - 127	993.5092	992.5019	992.5039	-0.0020	0	YQSQKPSR
120 - 128	1149.6134	1148.6061	1148.6050	0.0011	1	YQSQKPSRR
128 - 146	2256.0623	2255.0550	2255.0315	0.0235	1	RFQVGQDDPSQQQQDSHQK
129 - 146	2099.9412	2098.9339	2098.9304	0.0035	0	FQVGQDDPSQQQQDSHQK
195 - 208	1770.8904	1769.8831	1769.8848	-0.0017	1	RFYLAGNQEQEFLR
196 - 208	1614.7899	1613.7826	1613.7837	-0.0011	0	FYLAGNQEQEFLR
209 - 220	1547.7479	1546.7406	1546.7389	0.0017	0	YQQQQGSRPHYR
228 - 255	3199.4016	3198.3943	3198.4277	-0.0334	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR
256 - 262	859.4658	858.4585	858.4559	0.0026	0	QTVENLR
263 - 277	1658.8328	1657.8255	1657.8270	-0.0015	1	GENEREEQGAIVTVK
282 - 293	1376.6356	1375.6283	1375.6103	0.0180	0	ILSPDEEDESSR
299 - 306	1095.4728	1094.4655	1094.4628	0.0027	1	REEFDEDR
300 - 306	939.3750	938.3677	938.3617	0.0060	0	EEFDEDR
307 - 312	771.4211	770.4138	770.4147	-0.0009	0	SRPQQR

No match to: 949.4753, 956.4700, 1101.5591, 1111.5609, 1120.5508, 1159.4773, 1260.6552, 1354.6819, 1370.1681, 1387.5765, 1403.6327, 1427.6738, 1464.5875, 1543.6783, 1588.7876, 1687.8257, 1728.4342, 1743.8721, 1744.8860, 1756.8413, 1775.8575, 1824.9338, 1957.8634, 2113.9651, 2192.9907, 2273.1572, 2499.2783, 2612.1694, 2997.3660, 3153.4338, 3211.4988, 3240.4324, 3496.6272

Spot 55

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 09:59:58 GMT**
Top Score : **58 for gi|46560474, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560474	33641	58	conarachin [Arachis hypogaea]
2.	gi|16612200	71701	37	major allergen Arah1 [Arachis hypogaea]
3.	gi|1168391	71701	37	Allergen Ara h 1, clone P41B precursor (Ara h I)
4.	gi|602436	71701	37	Ara h I
5.	gi|46560472	34169	30	conarachin [Arachis hypogaea]
6.	gi|46560476	48122	29	conarachin [Arachis hypogaea]
7.	gi|52001225	76343	22	conarachin [Arachis hypogaea]
8.	gi|47933675	58368	20	glycinin [Arachis hypogaea]
9.	gi|112380623	58570	20	iso-Ara h3 [Arachis hypogaea]
10.	gi|46560478	66934	18	conarachin [Arachis hypogaea]

Results List

1. gi|46560474 **Mass:** 33641 **Score:** 58 **Expect:** 0.0015 **Queries matched:** 9
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1175.5720	1174.5647	1174.5829	-0.0182	37	47	0	SSENNEGVIVK
1359.6830	1358.6757	1358.6652	0.0105	120	131	0	EGALMLPHFNSK + Oxidation (M)
1376.6890	1375.6817	1375.6619	0.0198	240	252	0	DLAFPGSGEQVEK
1643.8191	1642.8118	1642.7798	0.0321	67	81	0	GSEEEGDITNPINLR
1730.9030	1729.8957	1729.9250	-0.0292	240	255	1	DLAFPGSGEQVEKLIK
1771.9091	1770.9018	1770.8747	0.0271	66	81	1	KGSEEEGDITNPINLR
1817.9731	1816.9658	1816.9570	0.0088	221	236	1	IFLAGDKDNVIDQIEK
2082.2095	2081.2022	2081.2030	-0.0007	132	151	1	AMVIVVVNKGTGNLELVAVR
2098.2197	2097.2124	2097.1979	0.0146	132	151	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1013.5283, 1016.5552, 1017.5815, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1279.5548, 1315.2766, 1331.7214, 1353.6981, 1392.1868,

1392.6868, 1481.6340, 1540.8300, 1546.8605, 1547.7734, 1614.8105, 1618.8126, 1639.8101, 1744.9131, 1770.9098, 1778.9957, 1795.7706, 1796.8157, 1800.9716, 1916.8895, 1943.0593, 2044.9410, 2145.1431, 2168.0261, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049

2. gi|16612200 **Mass:** 71701 **Score:** 37 **Expect:** 0.16 **Queries matched:** 9

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1175.5720	1174.5647	1174.5829	-0.0182	357	367	0	SSENNEGVIVK
1359.6830	1358.6757	1358.6652	0.0105	440	451	0	EGALMLPHFNSK + Oxidation (M)
1376.6890	1375.6817	1375.6619	0.0198	560	572	0	DLAFPGSGEQVEK
1643.8191	1642.8118	1642.7798	0.0321	387	401	0	GSEEEGDITNPINLR
1730.9030	1729.8957	1729.9250	-0.0292	560	575	1	DLAFPGSGEQVEKLIK
1771.9091	1770.9018	1770.8747	0.0271	386	401	1	KGSEEEGDITNPINLR
1817.9731	1816.9658	1816.9570	0.0088	541	556	1	IFLAGDKDNVIDQIEK
2082.2095	2081.2022	2081.2030	-0.0007	452	471	1	AMVIVVVNKGTGNLELVAVR
2098.2197	2097.2124	2097.1979	0.0146	452	471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1013.5283, 1016.5552, 1017.5815, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1279.5548, 1315.2766, 1331.7214, 1353.6981, 1392.1868, 1392.6868, 1481.6340, 1540.8300, 1546.8605, 1547.7734, 1614.8105, 1618.8126, 1639.8101, 1744.9131, 1770.9098, 1778.9957, 1795.7706, 1796.8157, 1800.9716, 1916.8895, 1943.0593, 2044.9410, 2145.1431, 2168.0261, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049

3. gi|1168391 **Mass:** 71701 **Score:** 37 **Expect:** 0.16 **Queries matched:** 9

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1175.5720	1174.5647	1174.5829	-0.0182	357	367	0	SSENNEGVIVK
1359.6830	1358.6757	1358.6652	0.0105	440	451	0	EGALMLPHFNSK + Oxidation (M)
1376.6890	1375.6817	1375.6619	0.0198	560	572	0	DLAFPGSGEQVEK
1643.8191	1642.8118	1642.7798	0.0321	387	401	0	GSEEEGDITNPINLR
1730.9030	1729.8957	1729.9250	-0.0292	560	575	1	DLAFPGSGEQVEKLIK
1771.9091	1770.9018	1770.8747	0.0271	386	401	1	KGSEEEGDITNPINLR
1817.9731	1816.9658	1816.9570	0.0088	541	556	1	IFLAGDKDNVIDQIEK
2082.2095	2081.2022	2081.2030	-0.0007	452	471	1	AMVIVVVNKGTGNLELVAVR
2098.2197	2097.2124	2097.1979	0.0146	452	471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1013.5283, 1016.5552, 1017.5815, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1279.5548, 1315.2766, 1331.7214, 1353.6981, 1392.1868, 1392.6868, 1481.6340, 1540.8300, 1546.8605, 1547.7734, 1614.8105, 1618.8126, 1639.8101, 1744.9131, 1770.9098, 1778.9957, 1795.7706, 1796.8157, 1800.9716, 1916.8895, 1943.0593, 2044.9410, 2145.1431, 2168.0261, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049

4. gi|602436 **Mass:** 71701 **Score:** 37 **Expect:** 0.16 **Queries matched:** 9

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1175.5720	1174.5647	1174.5829	-0.0182	357	-	367	0	SSENNEGVIVK
1359.6830	1358.6757	1358.6652	0.0105	440	-	451	0	EGALMLPHFNSK + Oxidation (M)
1376.6890	1375.6817	1375.6619	0.0198	560	-	572	0	DLAFPGSGEQVEK
1643.8191	1642.8118	1642.7798	0.0321	387	-	401	0	GSEEEGDITNPINLR
1730.9030	1729.8957	1729.9250	-0.0292	560	-	575	1	DLAFPGSGEQVEKLIK
1771.9091	1770.9018	1770.8747	0.0271	386	-	401	1	KGSEEEGDITNPINLR
1817.9731	1816.9658	1816.9570	0.0088	541	-	556	1	IFLAGDKDNVIDQIEK
2082.2095	2081.2022	2081.2030	-0.0007	452	-	471	1	AMVIVVVNKGTGNLELVAVR
2098.2197	2097.2124	2097.1979	0.0146	452	-	471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1013.5283, 1016.5552, 1017.5815, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1279.5548, 1315.2766, 1331.7214, 1353.6981, 1392.1868, 1392.6868, 1481.6340, 1540.8300, 1546.8605, 1547.7734, 1614.8105, 1618.8126, 1639.8101, 1744.9131, 1770.9098, 1778.9957, 1795.7706, 1796.8157, 1800.9716, 1916.8895, 1943.0593, 2044.9410, 2145.1431, 2168.0261, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049

5. gi|46560472 **Mass:** 34169 **Score:** 30 **Expect:** 0.86 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1359.6830	1358.6757	1358.6652	0.0105	121	-	132	0	EGALMLPHFNSK + Oxidation (M)
1376.6890	1375.6817	1375.6619	0.0198	244	-	256	0	DLAFPGSGEQVEK
1730.9030	1729.8957	1729.9250	-0.0292	244	-	259	1	DLAFPGSGEQVEKLIK
1817.9731	1816.9658	1816.9570	0.0088	225	-	240	1	IFLAGDKDNVIDQIEK
2082.2095	2081.2022	2081.2030	-0.0007	133	-	152	1	AMVIVVVNKGTGNLELVAVR
2098.2197	2097.2124	2097.1979	0.0146	133	-	152	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1013.5283, 1016.5552, 1017.5815, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1175.5720, 1279.5548, 1315.2766, 1331.7214, 1353.6981, 1392.1868, 1392.6868, 1481.6340, 1540.8300, 1546.8605, 1547.7734, 1614.8105, 1618.8126, 1639.8101, 1643.8191, 1744.9131, 1770.9098, 1771.9091, 1778.9957, 1795.7706, 1796.8157, 1800.9716, 1916.8895, 1943.0593, 2044.9410, 2145.1431, 2168.0261, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049

6. gi|46560476 **Mass:** 48122 **Score:** 29 **Expect:** 1.1 **Queries matched:** 7

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1175.5720	1174.5647	1174.5829	-0.0182	160	-	170	0	SSENNEGVIVK
1359.6830	1358.6757	1358.6652	0.0105	242	-	253	0	EGALMLPHFNSK + Oxidation (M)
1376.6890	1375.6817	1375.6619	0.0198	362	-	374	0	DLAFPGSGEQVEK
1730.9030	1729.8957	1729.9250	-0.0292	362	-	377	1	DLAFPGSGEQVEKLIK

1817.9731	1816.9658	1816.9570	0.0088	343 - 358	1	IFLAGDKDNVIDQIEK
2082.2095	2081.2022	2081.2030	-0.0007	254 - 273	1	AMVIVVVNKGTGNLELVAVR
2098.2197	2097.2124	2097.1979	0.0146	254 - 273	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1013.5283, 1016.5552, 1017.5815, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1279.5548, 1315.2766, 1331.7214, 1353.6981, 1392.1868, 1392.6868, 1481.6340, 1540.8300, 1546.8605, 1547.7734, 1614.8105, 1618.8126, 1639.8101, 1643.8191, 1744.9131, 1770.9098, 1771.9091, 1778.9957, 1795.7706, 1796.8157, 1800.9716, 1916.8895, 1943.0593, 2044.9410, 2145.1431, 2168.0261, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049

7. gi|52001225 **Mass:** 76343 **Score:** 22 **Expect:** 6.2 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1013.5283	1012.5210	1012.5301	-0.0091	38 -	46	0	LNALTPDNR
1017.5815	1016.5742	1016.5800	-0.0058	66 -	74	1	CAGVTLLKR
1331.7214	1330.7141	1330.6993	0.0149	277 -	288	1	VEGGFRDVISPR
1778.9957	1777.9884	1777.9686	0.0198	262 -	276	1	ILQNPPEQTKDQIVR
1795.7706	1794.7633	1794.7404	0.0229	133 -	147	0	ESEQEQEQQGDSHHK
2168.0261	2167.0188	2167.0293	-0.0105	47 -	65	0	IESQGGITETWNSNHPELR

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1016.5552, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1175.5720, 1279.5548, 1315.2766, 1353.6981, 1359.6830, 1376.6890, 1392.1868, 1392.6868, 1481.6340, 1540.8300, 1546.8605, 1547.7734, 1614.8105, 1618.8126, 1639.8101, 1643.8191, 1730.9030, 1744.9131, 1770.9098, 1771.9091, 1796.8157, 1800.9716, 1817.9731, 1916.8895, 1943.0593, 2044.9410, 2082.2095, 2098.2197, 2145.1431, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049

8. gi|47933675 **Mass:** 58368 **Score:** 20 **Expect:** 9.6 **Queries matched:** 5

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1481.6340	1480.6267	1480.6000	0.0267	23 -	34	0	QGGEENECQFQR
1547.7734	1546.7661	1546.7389	0.0272	209 -	220	0	YQQQQGSRPHYR
1614.8105	1613.8032	1613.7837	0.0195	196 -	208	0	FYLAGNQEQEFLR
1618.8126	1617.8053	1617.7746	0.0307	342 -	356	0	SSNPDIYNPQAGSLR
1770.9098	1769.9025	1769.8848	0.0177	195 -	208	1	RFYLAGNQEQEFLR

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1013.5283, 1016.5552, 1017.5815, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1175.5720, 1279.5548, 1315.2766, 1331.7214, 1353.6981, 1359.6830, 1376.6890, 1392.1868, 1392.6868, 1540.8300, 1546.8605, 1639.8101, 1643.8191, 1730.9030, 1744.9131, 1771.9091, 1778.9957, 1795.7706, 1796.8157, 1800.9716, 1817.9731, 1916.8895, 1943.0593, 2044.9410, 2082.2095, 2098.2197, 2145.1431, 2168.0261, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049

9. gi|112380623 **Mass:** 58570 **Score:** 20 **Expect:** 9.6 **Queries matched:** 5

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1481.6340	1480.6267	1480.6000	0.0267	25	36	0	QGGEENECQFQR
1547.7734	1546.7661	1546.7389	0.0272	211	222	0	YQQQQGSRPHYR
1614.8105	1613.8032	1613.7837	0.0195	198	210	0	FYLAGNQEQEFLR
1618.8126	1617.8053	1617.7746	0.0307	344	358	0	SSNPDIYNPQAGSLR
1770.9098	1769.9025	1769.8848	0.0177	197	210	1	RFYLAGNQEQEFLR

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1013.5283, 1016.5552, 1017.5815, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1175.5720, 1279.5548, 1315.2766, 1331.7214, 1353.6981, 1359.6830, 1376.6890, 1392.1868, 1392.6868, 1540.8300, 1546.8605, 1639.8101, 1643.8191, 1730.9030, 1744.9131, 1771.9091, 1778.9957, 1795.7706, 1796.8157, 1800.9716, 1817.9731, 1916.8895, 1943.0593, 2044.9410, 2082.2095, 2098.2197, 2145.1431, 2168.0261, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049

10. gi|46560478 **Mass:** 66934 **Score:** 18 **Expect:** 15 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1359.6830	1358.6757	1358.6652	0.0105	432	443	0	EGALMLPHFNSK + Oxidation (M)
1376.6890	1375.6817	1375.6619	0.0198	555	567	0	DLAFPGSGEQVEK
1730.9030	1729.8957	1729.9250	-0.0292	555	570	1	DLAFPGSGEQVEKLIK
1817.9731	1816.9658	1816.9570	0.0088	536	551	1	IFLAGDKDNVIDQIEK
2082.2095	2081.2022	2081.2030	-0.0007	444	463	1	AMVIVVVNKGTGNLELVAVR
2098.2197	2097.2124	2097.1979	0.0146	444	463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1013.5283, 1016.5552, 1017.5815, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1175.5720, 1279.5548, 1315.2766, 1331.7214, 1353.6981, 1392.1868, 1392.6868, 1481.6340, 1540.8300, 1546.8605, 1547.7734, 1614.8105, 1618.8126, 1639.8101, 1643.8191, 1744.9131, 1770.9098, 1771.9091, 1778.9957, 1795.7706, 1796.8157, 1800.9716, 1916.8895, 1943.0593, 2044.9410, 2145.1431, 2168.0261, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 65

Protein View

Match to: **gi|46560474** Score: **58** Expect: **0.0015**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **33641**; Calculated pI value: **5.07**
NCBI BLAST search of gi|46560474 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **65**
Number of mass values matched: **9**
Sequence Coverage: **30%**

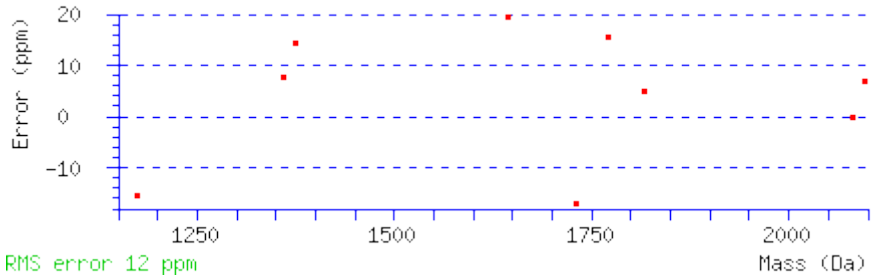
Matched peptides shown in **Bold Red**

```
     1 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK
    51 EHVEELTKHA KSVSKKGSEE EGDITNPINL REGEPDLSNN FGKLFEVKPD
   101 KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV
   151 RKEQQQRGRR EEEEDEDQEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI
   201 NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD LAFPGSGEQV
   251 EKLIKNQRES HFVSARPQSQ SPSSPEKEDQ EEENQGGKGP LLSILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
37 - 47	1175.5720	1174.5647	1174.5829	-0.0182	0	SSENNEGVIVK	
66 - 81	1771.9091	1770.9018	1770.8747	0.0271	1	KGSEEEGDITNPINLR	
67 - 81	1643.8191	1642.8118	1642.7798	0.0321	0	GSEEEGDITNPINLR	
120 - 131	1359.6830	1358.6757	1358.6652	0.0105	0	EGALMLPHFNSK	Oxidation (M)
132 - 151	2082.2095	2081.2022	2081.2030	-0.0007	1	AMVIVVVNKGTGNLELVAVR	
132 - 151	2098.2197	2097.2124	2097.1979	0.0146	1	AMVIVVVNKGTGNLELVAVR	Oxidation (M)
221 - 236	1817.9731	1816.9658	1816.9570	0.0088	1	IFLAGDKDNVIDQIEK	
240 - 252	1376.6890	1375.6817	1375.6619	0.0198	0	DLAFPGSGEQVEK	
240 - 255	1730.9030	1729.8957	1729.9250	-0.0292	1	DLAFPGSGEQVEKLIK	

No match to: 805.3895, 816.4063, 855.0400, 861.0482, 877.0272, 906.4750, 912.5915, 1000.5528, 1013.5283, 1016.5552, 1017.5815, 1046.5941, 1066.0758, 1106.5480, 1111.4662, 1133.4680, 1279.5548, 1315.2766, 1331.7214, 1353.6981, 1392.1868, 1392.6868, 1481.6340, 1540.8300, 1546.8605, 1547.7734, 1614.8105, 1618.8126, 1639.8101, 1744.9131, 1770.9098, 1778.9957, 1795.7706, 1796.8157, 1800.9716, 1916.8895, 1943.0593, 2044.9410, 2145.1431, 2168.0261, 2172.0229, 2173.0576, 2185.0295, 2200.0154, 2273.1489, 2311.1184, 2424.2705, 2512.0693, 2627.1372, 2766.7522, 2783.2227, 2791.2722, 2939.2913, 3075.0850, 3091.5342, 3154.3049



Ara h 1 sequence

```
  1 MRGRVSPLML LLGILVLASV SATHAKSSPY QKKTENPCAQ RCLQSCQQEP
 51 DDLKQKACES RCTKLEYDPR CVYDPRGHTG TTNQRSPPGE RTRGRQPGDY
101 DDDRRQPRRE EGGRWGPAGP RERERREEDWR QPREDWRRPS HQQPRKIRPE
151 GREGEQEWGT PGSHVREETS RNNPFYFPSR RFSTRYGNQN GRIRVLQRFD
201 QRSRQFQNLQ NHRIVQIEAK PNTLVLPKHA DADNILVIQQ GQATVTVANG
251 NNRKSFNLDE GHALRIPSGF ISYILNRHDN QNLRVAKISM PVNTPGQFED
301 FFPASSRDQS SYLQGFSRNT LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ
351 RRWSTRSSEN NEGVIVKVSK EHVEELTKHA KSVSKKGSEE EGDITNPINL
401 REGEPDLSNN FGKLFEVKPD KKNPQLQDLD MMLTCVEIKE GALMLPHFNS
451 KAMVIVVVNK GTGNLELVAV RKEQQQRGRR EEEEDEDEEE EGSNREVRRY
501 TARLKEGDVF IMPAAHPVAI NASSELHLLG FGINAENNHR IFLAGDKDNV
551 IDQIEKQAKD LAFPGSGEQV EKLIKNQKES HFVSARPQSQ SQSPSSPEKE
601 SPEKEDQEEE NQGGKGPLLS ILKAFN
```

Spot 56

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 10:00:04 GMT**
Top Score : **52 for gi|46560474, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560474	33641	52	conarachin [Arachis hypogaea]
2.	gi|16612200	71701	32	major allergen Arah1 [Arachis hypogaea]
3.	gi|1168391	71701	32	Allergen Ara h 1, clone P41B precursor (Ara h I)
4.	gi|602436	71701	32	Ara h I
5.	gi|46560472	34169	32	conarachin [Arachis hypogaea]
6.	gi|52001225	76343	27	conarachin [Arachis hypogaea]
7.	gi|46560476	48122	25	conarachin [Arachis hypogaea]
8.	gi|46560478	66934	19	conarachin [Arachis hypogaea]
9.	gi|620025	70639	19	Ara h I
10.	gi|1168390	70639	19	Allergen Ara h 1, clone P17 precursor (Ara h I)

Results List

1. gi|46560474 **Mass:** 33641 **Score:** 52 **Expect:** 0.0054 **Queries matched:** 8
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6442	1127.6369	1127.6298	0.0071	141	151	0	GTGNLELVAVR
1359.6851	1358.6778	1358.6652	0.0126	120	131	0	EGALMLPHFNSK + Oxidation (M)
1643.8147	1642.8074	1642.7798	0.0277	67	81	0	GSEEEGDITNPINLR
1730.9055	1729.8982	1729.9250	-0.0267	240	255	1	DLAFPGSGEQVEKLIK
1771.9038	1770.8965	1770.8747	0.0218	66	81	1	KGSEEEGDITNPINLR
1817.9780	1816.9707	1816.9570	0.0137	221	236	1	IFLAGDKDNVIDQIEK
2082.2109	2081.2036	2081.2030	0.0007	132	151	1	AMVIVVVNKGTGNLELVAVR
2098.2092	2097.2019	2097.1979	0.0041	132	151	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1017.5856, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1133.4653, 1315.2750, 1320.6125, 1331.7201, 1353.7078, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1744.9048,

1770.9138, 1778.9946, 1795.7709, 1796.8254, 1800.9735, 1916.8849, 1943.0618, 2044.9382, 2146.1396, 2168.0266, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2512.0789, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572

2. gi|16612200 **Mass:** 71701 **Score:** 32 **Expect:** 0.54 **Queries matched:** 8

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6442	1127.6369	1127.6298	0.0071	461	471	0	GTGNLELVAVR
1359.6851	1358.6778	1358.6652	0.0126	440	451	0	EGALMLPHFNSK + Oxidation (M)
1643.8147	1642.8074	1642.7798	0.0277	387	401	0	GSEEEGDITNPINLR
1730.9055	1729.8982	1729.9250	-0.0267	560	575	1	DLAFPGSGEQVEKLIK
1771.9038	1770.8965	1770.8747	0.0218	386	401	1	KGSEEEGDITNPINLR
1817.9780	1816.9707	1816.9570	0.0137	541	556	1	IFLAGDKDNVIDQIEK
2082.2109	2081.2036	2081.2030	0.0007	452	471	1	AMVIVVVNKGTGNLELVAVR
2098.2092	2097.2019	2097.1979	0.0041	452	471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1017.5856, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1133.4653, 1315.2750, 1320.6125, 1331.7201, 1353.7078, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1744.9048, 1770.9138, 1778.9946, 1795.7709, 1796.8254, 1800.9735, 1916.8849, 1943.0618, 2044.9382, 2146.1396, 2168.0266, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2512.0789, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572

3. gi|1168391 **Mass:** 71701 **Score:** 32 **Expect:** 0.54 **Queries matched:** 8

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6442	1127.6369	1127.6298	0.0071	461	471	0	GTGNLELVAVR
1359.6851	1358.6778	1358.6652	0.0126	440	451	0	EGALMLPHFNSK + Oxidation (M)
1643.8147	1642.8074	1642.7798	0.0277	387	401	0	GSEEEGDITNPINLR
1730.9055	1729.8982	1729.9250	-0.0267	560	575	1	DLAFPGSGEQVEKLIK
1771.9038	1770.8965	1770.8747	0.0218	386	401	1	KGSEEEGDITNPINLR
1817.9780	1816.9707	1816.9570	0.0137	541	556	1	IFLAGDKDNVIDQIEK
2082.2109	2081.2036	2081.2030	0.0007	452	471	1	AMVIVVVNKGTGNLELVAVR
2098.2092	2097.2019	2097.1979	0.0041	452	471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1017.5856, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1133.4653, 1315.2750, 1320.6125, 1331.7201, 1353.7078, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1744.9048, 1770.9138, 1778.9946, 1795.7709, 1796.8254, 1800.9735, 1916.8849, 1943.0618, 2044.9382, 2146.1396, 2168.0266, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2512.0789, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572

4. gi|602436 **Mass:** 71701 **Score:** 32 **Expect:** 0.54 **Queries matched:** 8

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6442	1127.6369	1127.6298	0.0071	461	471	0	GTGNLELVAVR

1359.6851	1358.6778	1358.6652	0.0126	440 - 451	0	EGALMLPHFNSK + Oxidation (M)
1643.8147	1642.8074	1642.7798	0.0277	387 - 401	0	GSEEEGDITNPINLR
1730.9055	1729.8982	1729.9250	-0.0267	560 - 575	1	DLAFPGSGEQVEKLIK
1771.9038	1770.8965	1770.8747	0.0218	386 - 401	1	KGSEEEGDITNPINLR
1817.9780	1816.9707	1816.9570	0.0137	541 - 556	1	IFLAGDKDNVIDQIEK
2082.2109	2081.2036	2081.2030	0.0007	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2098.2092	2097.2019	2097.1979	0.0041	452 - 471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1017.5856, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1133.4653, 1315.2750, 1320.6125, 1331.7201, 1353.7078, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1744.9048, 1770.9138, 1778.9946, 1795.7709, 1796.8254, 1800.9735, 1916.8849, 1943.0618, 2044.9382, 2146.1396, 2168.0266, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2512.0789, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572

5. gi|46560472 **Mass:** 34169 **Score:** 32 **Expect:** 0.56 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6442	1127.6369	1127.6298	0.0071	142 - 152		0	GTGNLELVAVR
1359.6851	1358.6778	1358.6652	0.0126	121 - 132		0	EGALMLPHFNSK + Oxidation (M)
1730.9055	1729.8982	1729.9250	-0.0267	244 - 259		1	DLAFPGSGEQVEKLIK
1817.9780	1816.9707	1816.9570	0.0137	225 - 240		1	IFLAGDKDNVIDQIEK
2082.2109	2081.2036	2081.2030	0.0007	133 - 152		1	AMVIVVVNKGTGNLELVAVR
2098.2092	2097.2019	2097.1979	0.0041	133 - 152		1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1017.5856, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1133.4653, 1315.2750, 1320.6125, 1331.7201, 1353.7078, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1643.8147, 1744.9048, 1770.9138, 1771.9038, 1778.9946, 1795.7709, 1796.8254, 1800.9735, 1916.8849, 1943.0618, 2044.9382, 2146.1396, 2168.0266, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2512.0789, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572

6. gi|52001225 **Mass:** 76343 **Score:** 27 **Expect:** 1.9 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1017.5856	1016.5783	1016.5800	-0.0017	66 - 74		1	CAGVTLLKR
1331.7201	1330.7128	1330.6993	0.0136	277 - 288		1	VEGGFRDVISPR
1778.9946	1777.9873	1777.9686	0.0187	262 - 276		1	ILQNPPEQTKDQIVR
1795.7709	1794.7636	1794.7404	0.0232	133 - 147		0	ESEQEQEQQGDSHHK
2168.0266	2167.0193	2167.0293	-0.0100	47 - 65		0	IESQGGITETWNSNHPELR
2512.0789	2511.0716	2511.1163	-0.0446	133 - 152		1	ESEQEQEQQGDSHHKIYHFR

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1128.6442, 1133.4653, 1315.2750, 1320.6125, 1353.7078, 1359.6851, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1643.8147, 1730.9055, 1744.9048, 1770.9138, 1771.9038, 1796.8254, 1800.9735, 1817.9780, 1916.8849, 1943.0618, 2044.9382, 2082.2109, 2098.2092, 2146.1396, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572

7. gi|46560476 **Mass:** 48122 **Score:** 25 **Expect:** 2.8 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6442	1127.6369	1127.6298	0.0071	263	273	0	GTGNLELVAVR
1359.6851	1358.6778	1358.6652	0.0126	242	253	0	EGALMLPHFNSK + Oxidation (M)
1730.9055	1729.8982	1729.9250	-0.0267	362	377	1	DLAFPGSGEQVEKLIK
1817.9780	1816.9707	1816.9570	0.0137	343	358	1	IFLAGDKDNVIDQIEK
2082.2109	2081.2036	2081.2030	0.0007	254	273	1	AMVIVVVNKGTGNLELVAVR
2098.2092	2097.2019	2097.1979	0.0041	254	273	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1017.5856, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1133.4653, 1315.2750, 1320.6125, 1331.7201, 1353.7078, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1643.8147, 1744.9048, 1770.9138, 1771.9038, 1778.9946, 1795.7709, 1796.8254, 1800.9735, 1916.8849, 1943.0618, 2044.9382, 2146.1396, 2168.0266, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2512.0789, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572

8. gi|46560478 **Mass:** 66934 **Score:** 19 **Expect:** 11 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6442	1127.6369	1127.6298	0.0071	453	463	0	GTGNLELVAVR
1359.6851	1358.6778	1358.6652	0.0126	432	443	0	EGALMLPHFNSK + Oxidation (M)
1730.9055	1729.8982	1729.9250	-0.0267	555	570	1	DLAFPGSGEQVEKLIK
1817.9780	1816.9707	1816.9570	0.0137	536	551	1	IFLAGDKDNVIDQIEK
2082.2109	2081.2036	2081.2030	0.0007	444	463	1	AMVIVVVNKGTGNLELVAVR
2098.2092	2097.2019	2097.1979	0.0041	444	463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1017.5856, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1133.4653, 1315.2750, 1320.6125, 1331.7201, 1353.7078, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1643.8147, 1744.9048, 1770.9138, 1771.9038, 1778.9946, 1795.7709, 1796.8254, 1800.9735, 1916.8849, 1943.0618, 2044.9382, 2146.1396, 2168.0266, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2512.0789, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572

9. gi|620025 **Mass:** 70639 **Score:** 19 **Expect:** 12 **Queries matched:** 6

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6442	1127.6369	1127.6298	0.0071	453	463	0	GTGNLELVAVR
1359.6851	1358.6778	1358.6652	0.0126	432	443	0	EGALMLPHFNSK + Oxidation (M)
1730.9055	1729.8982	1729.9250	-0.0267	555	570	1	DLAFPGSGEQVEKLIK
1817.9780	1816.9707	1816.9570	0.0137	536	551	1	IFLAGDKDNVIDQIEK
2082.2109	2081.2036	2081.2030	0.0007	444	463	1	AMVIVVVNKGTGNLELVAVR
2098.2092	2097.2019	2097.1979	0.0041	444	463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1017.5856, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1133.4653, 1315.2750, 1320.6125, 1331.7201, 1353.7078, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1643.8147,

1744.9048, 1770.9138, 1771.9038, 1778.9946, 1795.7709, 1796.8254, 1800.9735, 1916.8849, 1943.0618, 2044.9382, 2146.1396, 2168.0266, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2512.0789, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572

10. gi|1168390 **Mass:** 70639 **Score:** 19 **Expect:** 12 **Queries matched:** 6

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6442	1127.6369	1127.6298	0.0071	453	463	0	GTGNLELVAVR
1359.6851	1358.6778	1358.6652	0.0126	432	443	0	EGALMLPHFNSK + Oxidation (M)
1730.9055	1729.8982	1729.9250	-0.0267	555	570	1	DLAFPGSGEQVEKLIK
1817.9780	1816.9707	1816.9570	0.0137	536	551	1	IFLAGDKDNVIDQIEK
2082.2109	2081.2036	2081.2030	0.0007	444	463	1	AMVIVVVNKGTGNLELVAVR
2098.2092	2097.2019	2097.1979	0.0041	444	463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1017.5856, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1133.4653, 1315.2750, 1320.6125, 1331.7201, 1353.7078, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1643.8147, 1744.9048, 1770.9138, 1771.9038, 1778.9946, 1795.7709, 1796.8254, 1800.9735, 1916.8849, 1943.0618, 2044.9382, 2146.1396, 2168.0266, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2512.0789, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 56

Protein View

Match to: **gi|46560474** Score: **52** Expect: **0.0054**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **33641**; Calculated pI value: **5.07**
NCBI BLAST search of gi|46560474 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **56**
Number of mass values matched: **8**
Sequence Coverage: **26%**

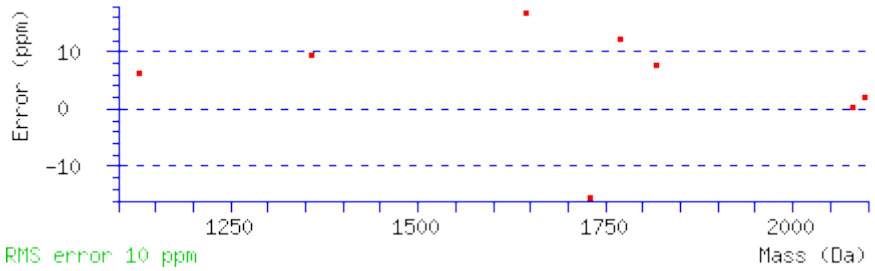
Matched peptides shown in **Bold Red**

```
     1 LEAAFNAEFN EIRRVLLEEN AGGEQEERGQ RRWSTRSSEN NEGVIVKVSK
    51 EHVEELTKHA KSVSKKGSEE EGDITNPINL REGEPDLSNN FGKLFEVKPD
   101 KKNPQLQDLD MMLTCVEIKE GALMLPHFNS KAMVIVVVNK GTGNLELVAV
   151 RKEQQQRGRR EEEEDEDQEE EGSNREVRRY TARLKEGDVF IMPAAHPVAI
   201 NASSELHLLG FGINAENNHR IFLAGDKDNV IDQIEKQAKD LAFPGSGEQV
   251 EKLIKNQRES HFVSARPQSQ SPSSPEKEDQ EEENQGGKGP LLSILKAFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
66 - 81	1771.9038	1770.8965	1770.8747	0.0218	1	KGSEEEGDITNPINLR
67 - 81	1643.8147	1642.8074	1642.7798	0.0277	0	GSEEEGDITNPINLR
120 - 131	1359.6851	1358.6778	1358.6652	0.0126	0	EGALMLPHFNSK Oxidation (M)
132 - 151	2082.2109	2081.2036	2081.2030	0.0007	1	AMVIVVVNKGTGNLELVAVR
132 - 151	2098.2092	2097.2019	2097.1979	0.0041	1	AMVIVVVNKGTGNLELVAVR Oxidation (M)
141 - 151	1128.6442	1127.6369	1127.6298	0.0071	0	GTGNLELVAVR
221 - 236	1817.9780	1816.9707	1816.9570	0.0137	1	IFLAGDKDNVIDQIEK
240 - 255	1730.9055	1729.8982	1729.9250	-0.0267	1	DLAFPGSGEQVEKLIK

No match to: 805.3957, 816.4066, 861.0479, 906.4855, 1000.5548, 1017.5856, 1020.5650, 1046.5981, 1106.5464, 1111.4700, 1133.4653, 1315.2750, 1320.6125, 1331.7201, 1353.7078, 1392.1888, 1392.6913, 1481.6376, 1547.7729, 1638.8818, 1744.9048, 1770.9138, 1778.9946, 1795.7709, 1796.8254, 1800.9735, 1916.8849, 1943.0618, 2044.9382, 2146.1396, 2168.0266, 2173.0688, 2185.0327, 2200.0144, 2273.1506, 2311.1223, 2424.2800, 2512.0789, 2531.3093, 2627.1465, 2766.7214, 2783.2383, 2791.2949, 2940.3274, 3075.1038, 3091.5535, 3154.3279, 3228.3572



Spot 57

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 16:07:01 GMT**
Top Score : **139 for gi|46560472, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560472	34169	139	conarachin [Arachis hypogaea]
2.	gi|46560478	66934	102	conarachin [Arachis hypogaea]
3.	gi|620025	70639	100	Ara h I
4.	gi|1168390	70639	100	Allergen Ara h 1, clone P17 precursor (Ara h I)
5.	gi|46560474	33641	72	conarachin [Arachis hypogaea]
6.	gi|46560476	48122	59	conarachin [Arachis hypogaea]
7.	gi|16612200	71701	45	major allergen Arah1 [Arachis hypogaea]
8.	gi|1168391	71701	45	Allergen Ara h 1, clone P41B precursor (Ara h I)
9.	gi|602436	71701	45	Ara h I
10.	gi|40738310	112681	21	1a protein [Cucumber mosaic virus]

Results List

1. gi|46560472 **Mass:** 34169 **Score:** 139 **Expect:** 1.1e-011 **Queries matched:** 15
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4374	815.4301	815.4249	0.0052	153	158	1	KEQQQR
1103.6445	1102.6372	1102.6386	-0.0014	95	103	1	LFEVKPDKK
1128.6459	1127.6386	1127.6298	0.0088	142	152	0	GTGNLELVAVR
1256.7512	1255.7439	1255.7247	0.0192	142	153	1	GTGNLELVAVRK
1297.6836	1296.6763	1296.7037	-0.0274	50	60	1	VSKEHVQELTK
1320.5961	1319.5888	1319.5741	0.0147	83	94	0	DGEPDLSNNFGR
1359.6807	1358.6734	1358.6652	0.0082	121	132	0	EGALMLPHFNSK + Oxidation (M)
1376.6733	1375.6660	1375.6619	0.0041	244	256	0	DLAFPGSGEQVEK
1586.7810	1585.7737	1585.7583	0.0154	69	82	0	GSEEEDITNPINLR

1714.8729	1713.8656	1713.8533	0.0124	68 - 82	1	KGSEEEDITNPINLR
1730.9363	1729.9290	1729.9250	0.0041	244 - 259	1	DLAFPGSGEQVEKLIK
1817.9706	1816.9633	1816.9570	0.0063	225 - 240	1	IFLAGDKDNVIDQIEK
2082.2017	2081.1944	2081.2030	-0.0085	133 - 152	1	AMVIVVVNKGTGNLELVAVR
2098.2214	2097.2141	2097.1979	0.0163	133 - 152	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2281.8386	2280.8313	2280.8414	-0.0100	162 - 179	0	EQEWEEEEEDEEEEGSNR

No match to: 805.4625, 807.4455, 876.4714, 940.5633, 944.3936, 1035.5770, 1080.5309, 1157.5867, 1205.5789, 1228.5895, 1288.6295, 1696.9608, 1787.9515, 1799.9559, 1825.0439, 1826.8732, 1976.9471, 2036.2742, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2273.1563, 2297.8303, 2326.2178, 2514.3215, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

2. gi|46560478 **Mass:** 66934 **Score:** 102 **Expect:** 5.5e-008 **Queries matched:** 15

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
816.4374	815.4301	815.4249	0.0052	464 - 469	1	KEQQQR
1103.6445	1102.6372	1102.6386	-0.0014	406 - 414	1	LFEVKPDKK
1128.6459	1127.6386	1127.6298	0.0088	453 - 463	0	GTGNLELVAVR
1256.7512	1255.7439	1255.7247	0.0192	453 - 464	1	GTGNLELVAVRK
1297.6836	1296.6763	1296.7037	-0.0274	361 - 371	1	VSKEHVQELTK
1320.5961	1319.5888	1319.5741	0.0147	394 - 405	0	DGEPDLSNNFGR
1359.6807	1358.6734	1358.6652	0.0082	432 - 443	0	EGALMLPHFNSK + Oxidation (M)
1376.6733	1375.6660	1375.6619	0.0041	555 - 567	0	DLAFPGSGEQVEK
1586.7810	1585.7737	1585.7583	0.0154	380 - 393	0	GSEEEDITNPINLR
1714.8729	1713.8656	1713.8533	0.0124	379 - 393	1	KGSEEEDITNPINLR
1730.9363	1729.9290	1729.9250	0.0041	555 - 570	1	DLAFPGSGEQVEKLIK
1817.9706	1816.9633	1816.9570	0.0063	536 - 551	1	IFLAGDKDNVIDQIEK
2082.2017	2081.1944	2081.2030	-0.0085	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2098.2214	2097.2141	2097.1979	0.0163	444 - 463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2281.8386	2280.8313	2280.8414	-0.0100	473 - 490	0	EQEWEEEEEDEEEEGSNR

No match to: 805.4625, 807.4455, 876.4714, 940.5633, 944.3936, 1035.5770, 1080.5309, 1157.5867, 1205.5789, 1228.5895, 1288.6295, 1696.9608, 1787.9515, 1799.9559, 1825.0439, 1826.8732, 1976.9471, 2036.2742, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2273.1563, 2297.8303, 2326.2178, 2514.3215, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

3. gi|620025 **Mass:** 70639 **Score:** 100 **Expect:** 8.7e-008 **Queries matched:** 15

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
816.4374	815.4301	815.4249	0.0052	464 - 469	1	KEQQQR
1103.6445	1102.6372	1102.6386	-0.0014	406 - 414	1	LFEVKPDKK
1128.6459	1127.6386	1127.6298	0.0088	453 - 463	0	GTGNLELVAVR
1256.7512	1255.7439	1255.7247	0.0192	453 - 464	1	GTGNLELVAVRK

1297.6836	1296.6763	1296.7037	-0.0274	361 - 371	1	VSKEHVQELTK
1320.5961	1319.5888	1319.5741	0.0147	394 - 405	0	DGEPDLSNNFGR
1359.6807	1358.6734	1358.6652	0.0082	432 - 443	0	EGALMLPHFNSK + Oxidation (M)
1376.6733	1375.6660	1375.6619	0.0041	555 - 567	0	DLAFPGSGEQVEK
1586.7810	1585.7737	1585.7583	0.0154	380 - 393	0	GSEEEDITNPINLR
1714.8729	1713.8656	1713.8533	0.0124	379 - 393	1	KGSEEEDITNPINLR
1730.9363	1729.9290	1729.9250	0.0041	555 - 570	1	DLAFPGSGEQVEKLIK
1817.9706	1816.9633	1816.9570	0.0063	536 - 551	1	IFLAGDKDNVIDQIEK
2082.2017	2081.1944	2081.2030	-0.0085	444 - 463	1	AMVIVVVNKGTGNLELVAVR
2098.2214	2097.2141	2097.1979	0.0163	444 - 463	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2281.8386	2280.8313	2280.8414	-0.0100	473 - 490	0	EQEWEEEEEDEEEEGSNR

No match to: 805.4625, 807.4455, 876.4714, 940.5633, 944.3936, 1035.5770, 1080.5309, 1157.5867, 1205.5789, 1228.5895, 1288.6295, 1696.9608, 1787.9515, 1799.9559, 1825.0439, 1826.8732, 1976.9471, 2036.2742, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2273.1563, 2297.8303, 2326.2178, 2514.3215, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

4. gi|1168390 **Mass:** 70639 **Score:** 100 **Expect:** 8.7e-008 **Queries matched:** 15

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4374	815.4301	815.4249	0.0052	464 - 469		1	KEQQQR
1103.6445	1102.6372	1102.6386	-0.0014	406 - 414		1	LFEVKPDKK
1128.6459	1127.6386	1127.6298	0.0088	453 - 463		0	GTGNLELVAVR
1256.7512	1255.7439	1255.7247	0.0192	453 - 464		1	GTGNLELVAVRK
1297.6836	1296.6763	1296.7037	-0.0274	361 - 371		1	VSKEHVQELTK
1320.5961	1319.5888	1319.5741	0.0147	394 - 405		0	DGEPDLSNNFGR
1359.6807	1358.6734	1358.6652	0.0082	432 - 443		0	EGALMLPHFNSK + Oxidation (M)
1376.6733	1375.6660	1375.6619	0.0041	555 - 567		0	DLAFPGSGEQVEK
1586.7810	1585.7737	1585.7583	0.0154	380 - 393		0	GSEEEDITNPINLR
1714.8729	1713.8656	1713.8533	0.0124	379 - 393		1	KGSEEEDITNPINLR
1730.9363	1729.9290	1729.9250	0.0041	555 - 570		1	DLAFPGSGEQVEKLIK
1817.9706	1816.9633	1816.9570	0.0063	536 - 551		1	IFLAGDKDNVIDQIEK
2082.2017	2081.1944	2081.2030	-0.0085	444 - 463		1	AMVIVVVNKGTGNLELVAVR
2098.2214	2097.2141	2097.1979	0.0163	444 - 463		1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)
2281.8386	2280.8313	2280.8414	-0.0100	473 - 490		0	EQEWEEEEEDEEEEGSNR

No match to: 805.4625, 807.4455, 876.4714, 940.5633, 944.3936, 1035.5770, 1080.5309, 1157.5867, 1205.5789, 1228.5895, 1288.6295, 1696.9608, 1787.9515, 1799.9559, 1825.0439, 1826.8732, 1976.9471, 2036.2742, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2273.1563, 2297.8303, 2326.2178, 2514.3215, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

5. gi|46560474 **Mass:** 33641 **Score:** 72 **Expect:** 5.6e-005 **Queries matched:** 10

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4374	815.4301	815.4249	0.0052	152	157	1	KEQQQR
1103.6445	1102.6372	1102.6386	-0.0014	94	102	1	LFEVKPDKK
1128.6459	1127.6386	1127.6298	0.0088	141	151	0	GTGNLELVAVR
1256.7512	1255.7439	1255.7247	0.0192	141	152	1	GTGNLELVAVRK
1359.6807	1358.6734	1358.6652	0.0082	120	131	0	EGALMLPHFNSK + Oxidation (M)
1376.6733	1375.6660	1375.6619	0.0041	240	252	0	DLAFPGSGEQVEK
1730.9363	1729.9290	1729.9250	0.0041	240	255	1	DLAFPGSGEQVEKLIK
1817.9706	1816.9633	1816.9570	0.0063	221	236	1	IFLAGDKDNVIDQIEK
2082.2017	2081.1944	2081.2030	-0.0085	132	151	1	AMVIVVVNKGTGNLELVAVR
2098.2214	2097.2141	2097.1979	0.0163	132	151	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.4625, 807.4455, 876.4714, 940.5633, 944.3936, 1035.5770, 1080.5309, 1157.5867, 1205.5789, 1228.5895, 1288.6295, 1297.6836, 1320.5961, 1586.7810, 1696.9608, 1714.8729, 1787.9515, 1799.9559, 1825.0439, 1826.8732, 1976.9471, 2036.2742, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2273.1563, 2281.8386, 2297.8303, 2326.2178, 2514.3215, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

6. gi|46560476 **Mass:** 48122 **Score:** 59 **Expect:** 0.0012 **Queries matched:** 10

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4374	815.4301	815.4249	0.0052	274	279	1	KEQQQR
1103.6445	1102.6372	1102.6386	-0.0014	216	224	1	LFEVKPDKK
1128.6459	1127.6386	1127.6298	0.0088	263	273	0	GTGNLELVAVR
1256.7512	1255.7439	1255.7247	0.0192	263	274	1	GTGNLELVAVRK
1359.6807	1358.6734	1358.6652	0.0082	242	253	0	EGALMLPHFNSK + Oxidation (M)
1376.6733	1375.6660	1375.6619	0.0041	362	374	0	DLAFPGSGEQVEK
1730.9363	1729.9290	1729.9250	0.0041	362	377	1	DLAFPGSGEQVEKLIK
1817.9706	1816.9633	1816.9570	0.0063	343	358	1	IFLAGDKDNVIDQIEK
2082.2017	2081.1944	2081.2030	-0.0085	254	273	1	AMVIVVVNKGTGNLELVAVR
2098.2214	2097.2141	2097.1979	0.0163	254	273	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.4625, 807.4455, 876.4714, 940.5633, 944.3936, 1035.5770, 1080.5309, 1157.5867, 1205.5789, 1228.5895, 1288.6295, 1297.6836, 1320.5961, 1586.7810, 1696.9608, 1714.8729, 1787.9515, 1799.9559, 1825.0439, 1826.8732, 1976.9471, 2036.2742, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2273.1563, 2281.8386, 2297.8303, 2326.2178, 2514.3215, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

7. gi|16612200 **Mass:** 71701 **Score:** 45 **Expect:** 0.028 **Queries matched:** 10

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4374	815.4301	815.4249	0.0052	472	477	1	KEQQQR
1103.6445	1102.6372	1102.6386	-0.0014	414	422	1	LFEVKPDKK
1128.6459	1127.6386	1127.6298	0.0088	461	471	0	GTGNLELVAVR
1256.7512	1255.7439	1255.7247	0.0192	461	472	1	GTGNLELVAVRK

1359.6807	1358.6734	1358.6652	0.0082	440 - 451	0	EGALMLPHFNSK + Oxidation (M)
1376.6733	1375.6660	1375.6619	0.0041	560 - 572	0	DLAFPGSGEQVEK
1730.9363	1729.9290	1729.9250	0.0041	560 - 575	1	DLAFPGSGEQVEKLIK
1817.9706	1816.9633	1816.9570	0.0063	541 - 556	1	IFLAGDKDNVIDQIEK
2082.2017	2081.1944	2081.2030	-0.0085	452 - 471	1	AMVIVVVNKGTGNLELVAVR
2098.2214	2097.2141	2097.1979	0.0163	452 - 471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.4625, 807.4455, 876.4714, 940.5633, 944.3936, 1035.5770, 1080.5309, 1157.5867, 1205.5789, 1228.5895, 1288.6295, 1297.6836, 1320.5961, 1586.7810, 1696.9608, 1714.8729, 1787.9515, 1799.9559, 1825.0439, 1826.8732, 1976.9471, 2036.2742, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2273.1563, 2281.8386, 2297.8303, 2326.2178, 2514.3215, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

8. gi|1168391 **Mass:** 71701 **Score:** 45 **Expect:** 0.028 **Queries matched:** 10

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4374	815.4301	815.4249	0.0052	472 - 477		1	KEQQQR
1103.6445	1102.6372	1102.6386	-0.0014	414 - 422		1	LFEVKPDKK
1128.6459	1127.6386	1127.6298	0.0088	461 - 471		0	GTGNLELVAVR
1256.7512	1255.7439	1255.7247	0.0192	461 - 472		1	GTGNLELVAVRK
1359.6807	1358.6734	1358.6652	0.0082	440 - 451		0	EGALMLPHFNSK + Oxidation (M)
1376.6733	1375.6660	1375.6619	0.0041	560 - 572		0	DLAFPGSGEQVEK
1730.9363	1729.9290	1729.9250	0.0041	560 - 575		1	DLAFPGSGEQVEKLIK
1817.9706	1816.9633	1816.9570	0.0063	541 - 556		1	IFLAGDKDNVIDQIEK
2082.2017	2081.1944	2081.2030	-0.0085	452 - 471		1	AMVIVVVNKGTGNLELVAVR
2098.2214	2097.2141	2097.1979	0.0163	452 - 471		1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.4625, 807.4455, 876.4714, 940.5633, 944.3936, 1035.5770, 1080.5309, 1157.5867, 1205.5789, 1228.5895, 1288.6295, 1297.6836, 1320.5961, 1586.7810, 1696.9608, 1714.8729, 1787.9515, 1799.9559, 1825.0439, 1826.8732, 1976.9471, 2036.2742, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2273.1563, 2281.8386, 2297.8303, 2326.2178, 2514.3215, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

9. gi|602436 **Mass:** 71701 **Score:** 45 **Expect:** 0.028 **Queries matched:** 10

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
816.4374	815.4301	815.4249	0.0052	472 - 477		1	KEQQQR
1103.6445	1102.6372	1102.6386	-0.0014	414 - 422		1	LFEVKPDKK
1128.6459	1127.6386	1127.6298	0.0088	461 - 471		0	GTGNLELVAVR
1256.7512	1255.7439	1255.7247	0.0192	461 - 472		1	GTGNLELVAVRK
1359.6807	1358.6734	1358.6652	0.0082	440 - 451		0	EGALMLPHFNSK + Oxidation (M)
1376.6733	1375.6660	1375.6619	0.0041	560 - 572		0	DLAFPGSGEQVEK
1730.9363	1729.9290	1729.9250	0.0041	560 - 575		1	DLAFPGSGEQVEKLIK
1817.9706	1816.9633	1816.9570	0.0063	541 - 556		1	IFLAGDKDNVIDQIEK
2082.2017	2081.1944	2081.2030	-0.0085	452 - 471		1	AMVIVVVNKGTGNLELVAVR

2098.2214	2097.2141	2097.1979	0.0163	452 - 471	1	AMVIVVVNKGTGNLELVAVR + Oxidation (M)

No match to: 805.4625, 807.4455, 876.4714, 940.5633, 944.3936, 1035.5770, 1080.5309, 1157.5867, 1205.5789, 1228.5895, 1288.6295, 1297.6836, 1320.5961, 1586.7810, 1696.9608, 1714.8729, 1787.9515, 1799.9559, 1825.0439, 1826.8732, 1976.9471, 2036.2742, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2273.1563, 2281.8386, 2297.8303, 2326.2178, 2514.3215, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

10. gi|40738310 **Mass:** 112681 **Score:** 21 **Expect:** 7.1 **Queries matched:** 6

1a protein [Cucumber mosaic virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1035.5770	1034.5697	1034.5647	0.0050	479 -	486	1	EEKEFLIK
1157.5867	1156.5794	1156.5593	0.0201	141 -	149	1	HAERLMNMR
1376.6733	1375.6660	1375.6329	0.0331	589 -	600	0	ATAMLEYAAYEK + Oxidation (M)
1976.9471	1975.9398	1975.9131	0.0267	748 -	764	1	MALFQSSDSKEACTFVR
2273.1563	2272.1490	2272.1958	-0.0468	780 -	799	0	VLVDEVVLLHFGQLCAVMSK + Oxidation (M)
2514.3215	2513.3142	2513.3749	-0.0606	780 -	801	1	VLVDEVVLLHFGQLCAVMSKLK + Oxidation (M)

No match to: 805.4625, 807.4455, 816.4374, 876.4714, 940.5633, 944.3936, 1080.5309, 1103.6445, 1128.6459, 1205.5789, 1228.5895, 1256.7512, 1288.6295, 1297.6836, 1320.5961, 1359.6807, 1586.7810, 1696.9608, 1714.8729, 1730.9363, 1787.9515, 1799.9559, 1817.9706, 1825.0439, 1826.8732, 2036.2742, 2082.2017, 2098.2214, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2281.8386, 2297.8303, 2326.2178, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|46560472** Score: **139** Expect: **1.1e-011**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **34169**; Calculated pI value: **5.07**
NCBI BLAST search of gi|46560472 against nr

Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **15**
Sequence Coverage: **44%**

Matched peptides shown in **Bold Red**

```
     1 GNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRRSTRS SDNEGVIVKV
    51 SKEHVQELTK HAKSVSKKGS EEEDITNPIN LRDGEPDLSN NFGRLFEVKP
   101 DKKNPQLQDL DMMLTCVEIK EGALMLPHFN SKAMVIVVVN KGTGNLELVA
   151 VRKEQQQRGR REQEWEEEEE DEEEEGSNRE VRRYTARLKE GDVFIMPAAH
   201 PVAINASSEL HLLGFGINAE NNHRIFLAGD KDNVIDQIEK QAKDLAFPGS
   251 GEQVEKLIKN QRESHFVSAR PQSQSPSSPE KEDQEEENQG GKGPLLSILK
   301 AFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
50 - 60	1297.6836	1296.6763	1296.7037	-0.0274	1	VSKEHVQELTK
68 - 82	1714.8729	1713.8656	1713.8533	0.0124	1	KGSEEEDITNPINLR
69 - 82	1586.7810	1585.7737	1585.7583	0.0154	0	GSEEEDITNPINLR
83 - 94	1320.5961	1319.5888	1319.5741	0.0147	0	DGEPDLSNNFGR
95 - 103	1103.6445	1102.6372	1102.6386	-0.0014	1	LFEVKPDKK
121 - 132	1359.6807	1358.6734	1358.6652	0.0082	0	EGALMLPHFNSK Oxidation (M)
133 - 152	2082.2017	2081.1944	2081.2030	-0.0085	1	AMVIVVVNKGTGNLELVAVR
133 - 152	2098.2214	2097.2141	2097.1979	0.0163	1	AMVIVVVNKGTGNLELVAVR Oxidation (M)
142 - 152	1128.6459	1127.6386	1127.6298	0.0088	0	GTGNLELVAVR
142 - 153	1256.7512	1255.7439	1255.7247	0.0192	1	GTGNLELVAVRK
153 - 158	816.4374	815.4301	815.4249	0.0052	1	KEQQQR
162 - 179	2281.8386	2280.8313	2280.8414	-0.0100	0	EQEWEEEEEDEEEEGSNR
225 - 240	1817.9706	1816.9633	1816.9570	0.0063	1	IFLAGDKDNVIDQIEK
244 - 256	1376.6733	1375.6660	1375.6619	0.0041	0	DLAFPGSGEQVEK
244 - 259	1730.9363	1729.9290	1729.9250	0.0041	1	DLAFPGSGEQVEKLIK

No match to: 805.4625, 807.4455, 876.4714, 940.5633, 944.3936, 1035.5770, 1080.5309, 1157.5867, 1205.5789, 1228.5895, 1288.6295, 1696.9608, 1787.9515, 1799.9559, 1825.0439, 1826.8732, 1976.9471, 2036.2742, 2116.0828, 2129.1270, 2145.1501, 2210.2930, 2273.1563, 2297.8303, 2326.2178, 2514.3215, 2530.3389, 2662.3806, 2860.2029, 2974.2388, 2990.2234, 3132.5222, 3211.4443, 3228.4294, 3300.6292

Related to full length ara h 1:

Matched peptides shown in **Bold Red**

```
     1 MRGRVSPLML LLGILVLASV SATQAKSPYR KTENPCAQRC LQSCQQEPDD
    51 LKQKACESRC TKLEYDPRCV YDTGATNQRH PPGERTRGRQ PGDYDDDRRQ
   101 PRREEGGRWG PAEPRERERE EDWRQPREDW RRPSHQQPRK IRPEGREGEQ
   151 EWGTPGSEVR EETSRNNPFY FPSRRFSTRY GNQNGRIRVL QRFDQRSKQF
   201 QNLQNHRIVQ IEARPNTLVL PKHADADNIL VIQQGQATVT VANGNNRKSF
   251 NLDEGHALRI PSGFISYILN RHDNQNLRVA KISMPVNTPG QFEDFFPASS
   301 RDQSSYLQGF SRNTLEAAFN AEFNEIRRVL LEENAGGEQE ERGQRRRSTR
   351 SSDNEGVIVK VSKEHVQELT KHAKSVSKKG SEEEDITNPI NLRDGEPDLS
   401 NNFGRLFEVK PDKKNPQLQD LDMMLTCVEI KEGALMLPHF NSKAMVIVVV
   451 NKGTGNLELV AVRKEQQQRG RREQEWEEEE EDEEEEGSNR EVRRYTARLK
   501 EGDVFIMPAA HPVAINASSE LHLLGFGINA ENNHRIFLAG DKDNVIDQIE
   551 KQAKDLAFPG SGEQVEKLIK NQRESHFVSA RPQSQSPSSP EKEDQEEENQ
   601 GGKGPLLSIL KAFN
```

Spot 58

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:50:52 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **116 for gi|47933675, glycinin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	116	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	116	iso-Ara h3 [Arachis hypogaea]
3.	gi|40738308	112559	21	1a protein [Cucumber mosaic virus]
4.	gi|40738310	112681	21	1a protein [Cucumber mosaic virus]
5.	gi|31558995	91467	19	phospholipase D [Arachis hypogaea]
6.	gi|88193699	91214	19	phospholipase D alpha 1 [Arachis hypogaea]
7.	gi|88193695	91214	19	phospholipase D alpha 1 [Arachis hypogaea]
8.	gi|2498261	2416	17	33.0 kDa cold shock protein (AHCSP33)
9.	gi|28194649	4642	15	secretory protein [Arachis hypogaea]
10.	gi|110617834	4438	13	drought-responsive protein [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 116 **Expect:** 2.2e-009 **Queries matched:** 5
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1083.5552	1082.5479	1082.5581	-0.0101	35	-	43	0	---	LNAQRPDNR
1481.5951	1480.5878	1480.6000	-0.0122	23	-	34	0	---	QGGEENECQFQR
1481.5951	1480.5878	1480.6000	-0.0122	23	-	34	0	63	QGGEENECQFQR
1547.7329	1546.7256	1546.7389	-0.0133	209	-	220	0	---	YQQQQGSRPHYR
1547.7329	1546.7256	1546.7389	-0.0133	209	-	220	0	32	YQQQQGSRPHYR

No match to: 1151.7059, 1464.5687, 1588.7748, 1588.7748, 1687.8113, 1692.8776, 1744.8738, 1744.8738, 1787.9309, 1957.8513, 1957.8513, 1976.9329, 2113.9541, 3074.3782, 3241.4128

2. gi|112380623 **Mass:** 58570 **Score:** 116 **Expect:** 2.2e-009 **Queries matched:** 5

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5552	1082.5479	1082.5581	-0.0101	37	45	0	---	LNAQRPDNR
1481.5951	1480.5878	1480.6000	-0.0122	25	36	0	---	QGGEENECQFQR
1481.5951	1480.5878	1480.6000	-0.0122	25	36	0	63	QGGEENECQFQR
1547.7329	1546.7256	1546.7389	-0.0133	211	222	0	---	YQQQQGSRPHYR
1547.7329	1546.7256	1546.7389	-0.0133	211	222	0	32	YQQQQGSRPHYR

No match to: 1151.7059, 1464.5687, 1588.7748, 1588.7748, 1687.8113, 1692.8776, 1744.8738, 1744.8738, 1787.9309, 1957.8513, 1957.8513, 1976.9329, 2113.9541, 3074.3782, 3241.4128

3. gi|40738308 **Mass:** 112559 **Score:** 21 **Expect:** 7.8 **Queries matched:** 4

1a protein [Cucumber mosaic virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5552	1082.5479	1082.5219	0.0261	381	388	1	---	KAWMEQFK + Oxidation (M)
1464.5687	1463.5614	1463.6061	-0.0446	440	451	0	---	MYDMWNASSISK + 2 Oxidation (M)
1687.8113	1686.8040	1686.7671	0.0369	805	819	0	---	AICFGDSEQIAFSSR
1976.9329	1975.9256	1975.9131	0.0125	748	764	1	---	MALFQSSDSKEACTFVR

No match to: 1151.7059, 1481.5951, 1481.5951, 1547.7329, 1547.7329, 1588.7748, 1588.7748, 1692.8776, 1744.8738, 1744.8738, 1787.9309, 1957.8513, 1957.8513, 2113.9541, 3074.3782, 3241.4128

4. gi|40738310 **Mass:** 112681 **Score:** 21 **Expect:** 7.8 **Queries matched:** 4

1a protein [Cucumber mosaic virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5552	1082.5479	1082.5219	0.0261	381	388	1	---	KAWMEQFK + Oxidation (M)
1464.5687	1463.5614	1463.6061	-0.0446	440	451	0	---	MYDMWNASSISK + 2 Oxidation (M)
1687.8113	1686.8040	1686.7671	0.0369	805	819	0	---	AICFGDSEQIAFSSR
1976.9329	1975.9256	1975.9131	0.0125	748	764	1	---	MALFQSSDSKEACTFVR

No match to: 1151.7059, 1481.5951, 1481.5951, 1547.7329, 1547.7329, 1588.7748, 1588.7748, 1692.8776, 1744.8738, 1744.8738, 1787.9309, 1957.8513, 1957.8513, 2113.9541, 3074.3782, 3241.4128

5. gi|31558995 **Mass:** 91467 **Score:** 19 **Expect:** 12 **Queries matched:** 4

phospholipase D [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1588.7748	1587.7675	1587.7364	0.0311	371	383	1	---	GGPREPWHDIHCK
1588.7748	1587.7675	1587.7364	0.0311	371	383	1	---	GGPREPWHDIHCK
1692.8776	1691.8703	1691.8399	0.0304	403	417	1	---	QGTDQGMLLSEEKLK + Oxidation (M)
3241.4128	3240.4055	3240.3838	0.0218	692	717	0	---	MSIWYEHLGMHEDTFLNPESEECINK + 2 Oxidation (M)

No match to: 1083.5552, 1151.7059, 1464.5687, 1481.5951, 1481.5951, 1547.7329, 1547.7329, 1687.8113, 1744.8738, 1744.8738, 1787.9309, 1957.8513, 1957.8513, 1976.9329, 2113.9541, 3074.3782

6. gi|88193699 **Mass:** 91214 **Score:** 19 **Expect:** 12 **Queries matched:** 4

phospholipase D alpha 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1588.7748	1587.7675	1587.7364	0.0311	371 -	383	1	---	GGPREPWHDIHCK
1588.7748	1587.7675	1587.7364	0.0311	371 -	383	1	---	GGPREPWHDIHCK
1692.8776	1691.8703	1691.8399	0.0304	403 -	417	1	---	QGTDQGMLLSEEKLK + Oxidation (M)
3241.4128	3240.4055	3240.3838	0.0218	692 -	717	0	---	MSLWYEHLGMHEDTFLNPESEECINK + 2 Oxidation (M)

No match to: 1083.5552, 1151.7059, 1464.5687, 1481.5951, 1481.5951, 1547.7329, 1547.7329, 1687.8113, 1744.8738, 1744.8738, 1787.9309, 1957.8513, 1957.8513, 1976.9329, 2113.9541, 3074.3782

7. gi|88193695 **Mass:** 91214 **Score:** 19 **Expect:** 12 **Queries matched:** 4

phospholipase D alpha 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1588.7748	1587.7675	1587.7364	0.0311	371 -	383	1	---	GGPREPWHDIHCK
1588.7748	1587.7675	1587.7364	0.0311	371 -	383	1	---	GGPREPWHDIHCK
1692.8776	1691.8703	1691.8399	0.0304	403 -	417	1	---	QGTDQGMLLSEEKLK + Oxidation (M)
3241.4128	3240.4055	3240.3838	0.0218	692 -	717	0	---	MSLWYEHLGMHEDTFLNPESEECINK + 2 Oxidation (M)

No match to: 1083.5552, 1151.7059, 1464.5687, 1481.5951, 1481.5951, 1547.7329, 1547.7329, 1687.8113, 1744.8738, 1744.8738, 1787.9309, 1957.8513, 1957.8513, 1976.9329, 2113.9541, 3074.3782

8. gi|2498261 **Mass:** 2416 **Score:** 17 **Expect:** 17 **Queries matched:** 2

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1547.7329	1546.7256	1546.7263	-0.0007	9 -	24	0	---	ASYTVTPPAQANAADA
1547.7329	1546.7256	1546.7263	-0.0007	9 -	24	0	---	ASYTVTPPAQANAADA

No match to: 1083.5552, 1151.7059, 1464.5687, 1481.5951, 1481.5951, 1588.7748, 1588.7748, 1687.8113, 1692.8776, 1744.8738, 1744.8738, 1787.9309, 1957.8513, 1957.8513, 1976.9329, 2113.9541, 3074.3782, 3241.4128

9. gi|28194649 **Mass:** 4642 **Score:** 15 **Expect:** 27 **Queries matched:** 1

secretory protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2113.9541	2112.9468	2113.0852	-0.1384	1 -	19	1	---	MKLDPFPWAAVAPMPVVGR + 2 Oxidation (M)

No match to: 1083.5552, 1151.7059, 1464.5687, 1481.5951, 1481.5951, 1547.7329, 1547.7329, 1588.7748, 1588.7748, 1687.8113, 1692.8776, 1744.8738, 1744.8738, 1787.9309, 1957.8513, 1957.8513, 1976.9329, 3074.3782, 3241.4128

10. gi|110617834 **Mass:** 4438 **Score:** 13 **Expect:** 40 **Queries matched:** 2

drought-responsive protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1481.5951	1480.5878	1480.6591	-0.0713	18 -	28	1	---	FRTGLCYYCNK
1481.5951	1480.5878	1480.6591	-0.0713	18 -	28	1	---	FRTGLCYYCNK

No match to: 1083.5552, 1151.7059, 1464.5687, 1547.7329, 1547.7329, 1588.7748, 1588.7748, 1687.8113, 1692.8776, 1744.8738, 1744.8738, 1787.9309, 1957.8513, 1957.8513, 1976.9329, 2113.9541, 3074.3782, 3241.4128

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Number of Queries: 20

Protein View

Match to: **gi|47933675** Score: **116** Expect: **2.2e-009**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

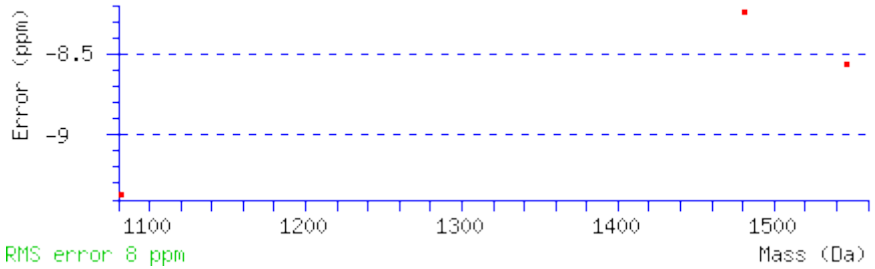
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **6%**

Matched peptides shown in **Bold Red**

```
     1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
    51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
   101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
   201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
   251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
   301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
   351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
   401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
   451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
   501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
23 - 34	1481.5951	1480.5878	1480.6000	-0.0122	0	QGGEENECQFQR	(No match)
23 - 34	1481.5951	1480.5878	1480.6000	-0.0122	0	QGGEENECQFQR	(Ions score 63)
35 - 43	1083.5552	1082.5479	1082.5581	-0.0101	0	LNAQRPDNR	(No match)
209 - 220	1547.7329	1546.7256	1546.7389	-0.0133	0	YQQQQGSRPHYR	(No match)
209 - 220	1547.7329	1546.7256	1546.7389	-0.0133	0	YQQQQGSRPHYR	(Ions score 32)



Spot 59

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:33:42 GMT**
Top Score : **52 for gi|46560472, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560472	34169	52	conarachin [Arachis hypogaea]
2.	gi|46560474	33641	42	conarachin [Arachis hypogaea]
3.	gi|46560478	66934	37	conarachin [Arachis hypogaea]
4.	gi|620025	70639	36	Ara h I
5.	gi|1168390	70639	36	Allergen Ara h 1, clone P17 precursor (Ara h I)
6.	gi|16612200	71701	28	major allergen Arah1 [Arachis hypogaea]
7.	gi|1168391	71701	28	Allergen Ara h 1, clone P41B precursor (Ara h I)
8.	gi|602436	71701	28	Ara h I
9.	gi|46560476	48122	25	conarachin [Arachis hypogaea]
10.	gi|47933675	58368	23	glycinin [Arachis hypogaea]

Results List

1. gi|46560472 **Mass:** 34169 **Score:** 52 **Expect:** 0.0052 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6396	1127.6323	1127.6298	0.0025	142	152	0	GTGNLELVAVR
1320.5831	1319.5758	1319.5741	0.0017	83	94	0	DGEPDLSNNFGR
1343.6906	1342.6833	1342.6703	0.0130	121	132	0	EGALMLPHFNSK
1586.7627	1585.7554	1585.7583	-0.0029	69	82	0	GSEEEDITNPINLR
1817.9672	1816.9599	1816.9570	0.0029	225	240	1	IFLAGDKDNVIDQIEK
2082.2012	2081.1939	2081.2030	-0.0090	133	152	1	AMVIVVVNKGTGNLELVAVR

No match to: 816.4039, 906.4887, 928.3976, 1073.6003, 1080.5358, 1111.5623, 1174.6729, 1547.7588, 1614.8127, 1730.8807, 1756.8564, 1770.8993, 1771.8958, 1774.8628, 1787.9502, 1976.9391, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

2. gi|46560474 **Mass:** 33641 **Score:** 42 **Expect:** 0.053 **Queries matched:** 5

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6396	1127.6323	1127.6298	0.0025	141	151	0	GTGNLELVAVR
1343.6906	1342.6833	1342.6703	0.0130	120	131	0	EGALMLPHFNSK
1771.8958	1770.8885	1770.8747	0.0138	66	81	1	KGSEEEGDITNPINLR
1817.9672	1816.9599	1816.9570	0.0029	221	236	1	IFLAGDKDNVIDQIEK
2082.2012	2081.1939	2081.2030	-0.0090	132	151	1	AMVIVVVNKGTGNLELVAVR

No match to: 816.4039, 906.4887, 928.3976, 1073.6003, 1080.5358, 1111.5623, 1174.6729, 1320.5831, 1547.7588, 1586.7627, 1614.8127, 1730.8807, 1756.8564, 1770.8993, 1774.8628, 1787.9502, 1976.9391, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

3. gi|46560478 **Mass:** 66934 **Score:** 37 **Expect:** 0.17 **Queries matched:** 6

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6396	1127.6323	1127.6298	0.0025	453	463	0	GTGNLELVAVR
1320.5831	1319.5758	1319.5741	0.0017	394	405	0	DGEPDLSNNFGR
1343.6906	1342.6833	1342.6703	0.0130	432	443	0	EGALMLPHFNSK
1586.7627	1585.7554	1585.7583	-0.0029	380	393	0	GSEEEDITNPINLR
1817.9672	1816.9599	1816.9570	0.0029	536	551	1	IFLAGDKDNVIDQIEK
2082.2012	2081.1939	2081.2030	-0.0090	444	463	1	AMVIVVVNKGTGNLELVAVR

No match to: 816.4039, 906.4887, 928.3976, 1073.6003, 1080.5358, 1111.5623, 1174.6729, 1547.7588, 1614.8127, 1730.8807, 1756.8564, 1770.8993, 1771.8958, 1774.8628, 1787.9502, 1976.9391, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

4. gi|620025 **Mass:** 70639 **Score:** 36 **Expect:** 0.21 **Queries matched:** 6

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6396	1127.6323	1127.6298	0.0025	453	463	0	GTGNLELVAVR
1320.5831	1319.5758	1319.5741	0.0017	394	405	0	DGEPDLSNNFGR
1343.6906	1342.6833	1342.6703	0.0130	432	443	0	EGALMLPHFNSK
1586.7627	1585.7554	1585.7583	-0.0029	380	393	0	GSEEEDITNPINLR
1817.9672	1816.9599	1816.9570	0.0029	536	551	1	IFLAGDKDNVIDQIEK
2082.2012	2081.1939	2081.2030	-0.0090	444	463	1	AMVIVVVNKGTGNLELVAVR

No match to: 816.4039, 906.4887, 928.3976, 1073.6003, 1080.5358, 1111.5623, 1174.6729, 1547.7588, 1614.8127, 1730.8807, 1756.8564, 1770.8993, 1771.8958, 1774.8628, 1787.9502, 1976.9391, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

5. gi|1168390 **Mass:** 70639 **Score:** 36 **Expect:** 0.21 **Queries matched:** 6

Allergen Ara h 1, clone P17 precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6396	1127.6323	1127.6298	0.0025	453	463	0	GTGNLELVAVR

1320.5831	1319.5758	1319.5741	0.0017	394 - 405	0	DGEPDLSNNFGR
1343.6906	1342.6833	1342.6703	0.0130	432 - 443	0	EGALMLPHFNSK
1586.7627	1585.7554	1585.7583	-0.0029	380 - 393	0	GSEEEDITNPINLR
1817.9672	1816.9599	1816.9570	0.0029	536 - 551	1	IFLAGDKDNVIDQIEK
2082.2012	2081.1939	2081.2030	-0.0090	444 - 463	1	AMVIVVVNKGTGNLELVAVR

No match to: 816.4039, 906.4887, 928.3976, 1073.6003, 1080.5358, 1111.5623, 1174.6729, 1547.7588, 1614.8127, 1730.8807, 1756.8564, 1770.8993, 1771.8958, 1774.8628, 1787.9502, 1976.9391, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

6. gi|16612200 **Mass:** 71701 **Score:** 28 **Expect:** 1.6 **Queries matched:** 5

major allergen Arah1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6396	1127.6323	1127.6298	0.0025	461 - 471		0	GTGNLELVAVR
1343.6906	1342.6833	1342.6703	0.0130	440 - 451		0	EGALMLPHFNSK
1771.8958	1770.8885	1770.8747	0.0138	386 - 401		1	KGSEEEGDITNPINLR
1817.9672	1816.9599	1816.9570	0.0029	541 - 556		1	IFLAGDKDNVIDQIEK
2082.2012	2081.1939	2081.2030	-0.0090	452 - 471		1	AMVIVVVNKGTGNLELVAVR

No match to: 816.4039, 906.4887, 928.3976, 1073.6003, 1080.5358, 1111.5623, 1174.6729, 1320.5831, 1547.7588, 1586.7627, 1614.8127, 1730.8807, 1756.8564, 1770.8993, 1774.8628, 1787.9502, 1976.9391, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

7. gi|1168391 **Mass:** 71701 **Score:** 28 **Expect:** 1.6 **Queries matched:** 5

Allergen Ara h 1, clone P41B precursor (Ara h I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6396	1127.6323	1127.6298	0.0025	461 - 471		0	GTGNLELVAVR
1343.6906	1342.6833	1342.6703	0.0130	440 - 451		0	EGALMLPHFNSK
1771.8958	1770.8885	1770.8747	0.0138	386 - 401		1	KGSEEEGDITNPINLR
1817.9672	1816.9599	1816.9570	0.0029	541 - 556		1	IFLAGDKDNVIDQIEK
2082.2012	2081.1939	2081.2030	-0.0090	452 - 471		1	AMVIVVVNKGTGNLELVAVR

No match to: 816.4039, 906.4887, 928.3976, 1073.6003, 1080.5358, 1111.5623, 1174.6729, 1320.5831, 1547.7588, 1586.7627, 1614.8127, 1730.8807, 1756.8564, 1770.8993, 1774.8628, 1787.9502, 1976.9391, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

8. gi|602436 **Mass:** 71701 **Score:** 28 **Expect:** 1.6 **Queries matched:** 5

Ara h I

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6396	1127.6323	1127.6298	0.0025	461 - 471		0	GTGNLELVAVR
1343.6906	1342.6833	1342.6703	0.0130	440 - 451		0	EGALMLPHFNSK
1771.8958	1770.8885	1770.8747	0.0138	386 - 401		1	KGSEEEGDITNPINLR
1817.9672	1816.9599	1816.9570	0.0029	541 - 556		1	IFLAGDKDNVIDQIEK
2082.2012	2081.1939	2081.2030	-0.0090	452 - 471		1	AMVIVVVNKGTGNLELVAVR

No match to: 816.4039, 906.4887, 928.3976, 1073.6003, 1080.5358, 1111.5623, 1174.6729, 1320.5831, 1547.7588, 1586.7627, 1614.8127, 1730.8807, 1756.8564, 1770.8993, 1774.8628, 1787.9502, 1976.9391, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

9. gi|46560476 **Mass:** 48122 **Score:** 25 **Expect:** 2.8 **Queries matched:** 4

conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1128.6396	1127.6323	1127.6298	0.0025	263 -	273	0	GTGNLELVAVR
1343.6906	1342.6833	1342.6703	0.0130	242 -	253	0	EGALMLPHFNSK
1817.9672	1816.9599	1816.9570	0.0029	343 -	358	1	IFLAGDKDNVIDQIEK
2082.2012	2081.1939	2081.2030	-0.0090	254 -	273	1	AMVIVVVNKGTGNLELVAVR

No match to: 816.4039, 906.4887, 928.3976, 1073.6003, 1080.5358, 1111.5623, 1174.6729, 1320.5831, 1547.7588, 1586.7627, 1614.8127, 1730.8807, 1756.8564, 1770.8993, 1771.8958, 1774.8628, 1787.9502, 1976.9391, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

10. gi|47933675 **Mass:** 58368 **Score:** 23 **Expect:** 4.9 **Queries matched:** 4

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1073.6003	1072.5930	1072.5764	0.0167	268 -	277	0	EEQGAIVTVK
1547.7588	1546.7515	1546.7389	0.0126	209 -	220	0	YQQQQGSRPHYR
1614.8127	1613.8054	1613.7837	0.0217	196 -	208	0	FYLAGNQEQEFLR
1770.8993	1769.8920	1769.8848	0.0072	195 -	208	1	RFYLAGNQEQEFLR

No match to: 816.4039, 906.4887, 928.3976, 1080.5358, 1111.5623, 1128.6396, 1174.6729, 1320.5831, 1343.6906, 1586.7627, 1730.8807, 1756.8564, 1771.8958, 1774.8628, 1787.9502, 1817.9672, 1976.9391, 2082.2012, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 33

Protein View

Match to: **gi|46560472** Score: **52** Expect: **0.0052**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **34169**; Calculated pI value: **5.07**
NCBI BLAST search of gi|46560472 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **33**
Number of mass values matched: **6**
Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

```
     1 GNTLEAAFNA EFNEIRRVLL EENAGGEQEE RGQRRRSTRS SDNEGVIVKV
    51 SKEHVQELTK HAKSVSKKGS EEEDITNPIN LRDGEPDLSN NFGRLFEVKP
   101 DKKNPQLQDL DMMLTCVEIK EGALMLPHFN SKAMVIVVVN KGTGNLELVA
   151 VRKEQQQRGR REQEWEEEEE DEEEEGSNRE VRRYTARLKE GDVFIMPAAH
   201 PVAINASSEL HLLGFGINAE NNHRIFLAGD KDNVIDQIEK QAKDLAFPGS
   251 GEQVEKLIKN QRESHFVSAR PQSQSPSSPE KEDQEEENQG GKGPLLSILK
   301 AFN
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
69 - 82	1586.7627	1585.7554	1585.7583	-0.0029	0	GSEEEDITNPINLR
83 - 94	1320.5831	1319.5758	1319.5741	0.0017	0	DGEPDLSNNFGR
121 - 132	1343.6906	1342.6833	1342.6703	0.0130	0	EGALMLPHFNSK
133 - 152	2082.2012	2081.1939	2081.2030	-0.0090	1	AMVIVVVNKGTGNLELVAVR
142 - 152	1128.6396	1127.6323	1127.6298	0.0025	0	GTGNLELVAVR
225 - 240	1817.9672	1816.9599	1816.9570	0.0029	1	IFLAGDKDNVIDQIEK

No match to: 816.4039, 906.4887, 928.3976, 1073.6003, 1080.5358, 1111.5623, 1174.6729, 1547.7588, 1614.8127, 1730.8807, 1756.8564, 1770.8993, 1771.8958, 1774.8628, 1787.9502, 1976.9391, 2185.0391, 2192.9827, 2226.1487, 2256.7104, 2273.1602, 2295.1221, 2612.1631, 3136.3569, 3153.3599, 3211.4182, 3301.6460

Spot 60

Database : Arachis 260207 (876 sequences; 195471 residues)
Timestamp : 31 Jul 2008 at 06:53:15 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 52 for gi|5712199, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|5712199	61430	52	glycinin [Arachis hypogaea]
2.	gi|22135348	25768	46	trypsin inhibitor [Arachis hypogaea]
3.	gi|118452819	33841	39	11S seed storage globulin precursor B1 [Arachis hypogaea]
4.	gi|118776570	60681	39	arachin 6 [Arachis hypogaea]
5.	gi|57669861	61041	39	arachin Ahy-4 [Arachis hypogaea]
6.	gi|108595573	61041	39	arachin Ahy-4 [Arachis hypogaea]
7.	gi|52001219	61810	39	arachin Ahy-1 [Arachis hypogaea]
8.	gi|37789212	61803	39	storage protein [Arachis hypogaea]
9.	gi|21314465	62042	39	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|9864777	60754	39	Gly1 [Arachis hypogaea]

Results List

1. gi|5712199 **Mass:** 61430 **Score:** 52 **Expect:** 0.0061 **Queries matched:** 5
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1574.7520	1573.7447	1573.7637	-0.0189	196	208	0	---	FNLAGNHEQEFLR
1574.7520	1573.7447	1573.7637	-0.0189	196	208	0	26	FNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195	208	1	---	RFNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195	208	1	---	RFNLAGNHEQEFLR
3361.4607	3360.4534	3360.4693	-0.0159	251	280	0	---	AGQEEEDEGGNIFSGFTPEFLEQAFQVDDR

No match to: 982.5580, 1017.6548, 1033.6791, 1151.7035, 1363.7703, 1363.7703, 1434.8843, 1618.0459, 1622.7643, 1622.7643, 1638.7567, 1638.7567, 1901.2360, 2454.2078

2. gi|22135348 **Mass:** 25768 **Score:** 46 **Expect:** 0.025 **Queries matched:** 4

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1574.7520	1573.7447	1573.7637	-0.0189	198	210	0	---	FNLAGNHEQEFLR
1574.7520	1573.7447	1573.7637	-0.0189	198	210	0	26	FNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	197	210	1	---	RFNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	197	210	1	---	RFNLAGNHEQEFLR

No match to: 982.5580, 1017.6548, 1033.6791, 1151.7035, 1363.7703, 1363.7703, 1434.8843, 1618.0459, 1622.7643, 1622.7643, 1638.7567, 1638.7567, 1901.2360, 2454.2078, 3361.4607

3. gi|118452819 **Mass:** 33841 **Score:** 39 **Expect:** 0.11 **Queries matched:** 2

11S seed storage globulin precursor B1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1363.7703	1362.7630	1362.7771	-0.0141	76	87	0	---	GLLLPHYINAPR
1363.7703	1362.7630	1362.7771	-0.0141	76	87	0	32	GLLLPHYINAPR

No match to: 982.5580, 1017.6548, 1033.6791, 1151.7035, 1434.8843, 1574.7520, 1574.7520, 1618.0459, 1622.7643, 1622.7643, 1638.7567, 1638.7567, 1730.8501, 1730.8501, 1901.2360, 2454.2078, 3361.4607

4. gi|118776570 **Mass:** 60681 **Score:** 39 **Expect:** 0.11 **Queries matched:** 4

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1574.7520	1573.7447	1573.7637	-0.0189	196	208	0	---	FNLAGNHEQEFLR
1574.7520	1573.7447	1573.7637	-0.0189	196	208	0	26	FNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195	208	1	---	RFNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195	208	1	---	RFNLAGNHEQEFLR

No match to: 982.5580, 1017.6548, 1033.6791, 1151.7035, 1363.7703, 1363.7703, 1434.8843, 1618.0459, 1622.7643, 1622.7643, 1638.7567, 1638.7567, 1901.2360, 2454.2078, 3361.4607

5. gi|57669861 **Mass:** 61041 **Score:** 39 **Expect:** 0.11 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1574.7520	1573.7447	1573.7637	-0.0189	196	208	0	---	FNLAGNHEQEFLR
1574.7520	1573.7447	1573.7637	-0.0189	196	208	0	26	FNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195	208	1	---	RFNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195	208	1	---	RFNLAGNHEQEFLR

No match to: 982.5580, 1017.6548, 1033.6791, 1151.7035, 1363.7703, 1363.7703, 1434.8843, 1618.0459, 1622.7643, 1622.7643, 1638.7567, 1638.7567, 1901.2360, 2454.2078, 3361.4607

6. gi|108595573 **Mass:** 61041 **Score:** 39 **Expect:** 0.11 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1574.7520	1573.7447	1573.7637	-0.0189	196 - 208	0	---	FNLAGNHEQEFLR
1574.7520	1573.7447	1573.7637	-0.0189	196 - 208	0	26	FNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195 - 208	1	---	RFNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195 - 208	1	---	RFNLAGNHEQEFLR

No match to: 982.5580, 1017.6548, 1033.6791, 1151.7035, 1363.7703, 1363.7703, 1434.8843, 1618.0459, 1622.7643, 1622.7643, 1638.7567, 1638.7567, 1901.2360, 2454.2078, 3361.4607

7. gi|52001219 **Mass:** 61810 **Score:** 39 **Expect:** 0.12 **Queries matched:** 4

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1574.7520	1573.7447	1573.7637	-0.0189	196 - 208	0	---	FNLAGNHEQEFLR
1574.7520	1573.7447	1573.7637	-0.0189	196 - 208	0	26	FNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195 - 208	1	---	RFNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195 - 208	1	---	RFNLAGNHEQEFLR

No match to: 982.5580, 1017.6548, 1033.6791, 1151.7035, 1363.7703, 1363.7703, 1434.8843, 1618.0459, 1622.7643, 1622.7643, 1638.7567, 1638.7567, 1901.2360, 2454.2078, 3361.4607

8. gi|37789212 **Mass:** 61803 **Score:** 39 **Expect:** 0.12 **Queries matched:** 4

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1574.7520	1573.7447	1573.7637	-0.0189	196 - 208	0	---	FNLAGNHEQEFLR
1574.7520	1573.7447	1573.7637	-0.0189	196 - 208	0	26	FNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195 - 208	1	---	RFNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195 - 208	1	---	RFNLAGNHEQEFLR

No match to: 982.5580, 1017.6548, 1033.6791, 1151.7035, 1363.7703, 1363.7703, 1434.8843, 1618.0459, 1622.7643, 1622.7643, 1638.7567, 1638.7567, 1901.2360, 2454.2078, 3361.4607

9. gi|21314465 **Mass:** 62042 **Score:** 39 **Expect:** 0.12 **Queries matched:** 4

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1574.7520	1573.7447	1573.7637	-0.0189	196 - 208	0	---	FNLAGNHEQEFLR
1574.7520	1573.7447	1573.7637	-0.0189	196 - 208	0	26	FNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195 - 208	1	---	RFNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	195 - 208	1	---	RFNLAGNHEQEFLR

No match to: 982.5580, 1017.6548, 1033.6791, 1151.7035, 1363.7703, 1363.7703, 1434.8843, 1618.0459, 1622.7643, 1622.7643, 1638.7567, 1638.7567, 1901.2360, 2454.2078, 3361.4607

10. gi|9864777 **Mass:** 60754 **Score:** 39 **Expect:** 0.12 **Queries matched:** 4

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1574.7520	1573.7447	1573.7637	-0.0189	198 - 210	0	---	FNLAGNHEQEFLR

1574.7520	1573.7447	1573.7637	-0.0189	198 - 210	0	26	FNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	197 - 210	1	---	RFNLAGNHEQEFLR
1730.8501	1729.8428	1729.8648	-0.0219	197 - 210	1	---	RFNLAGNHEQEFLR

No match to: 982.5580, 1017.6548, 1033.6791, 1151.7035, 1363.7703, 1363.7703, 1434.8843, 1618.0459, 1622.7643, 1622.7643, 1638.7567, 1638.7567, 1901.2360, 2454.2078, 3361.4607

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Number of Queries: 19

Protein View

Match to: **gi|5712199** Score: **52** Expect: **0.0061**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **61430**; Calculated pI value: **5.48**
NCBI BLAST search of gi|5712199 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **8%**

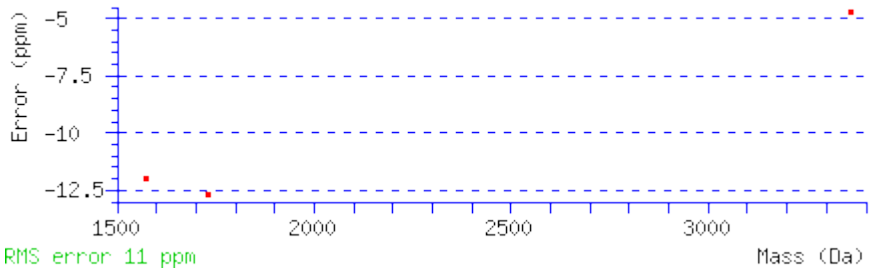
Matched peptides shown in **Bold Red**

```
   1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
  51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
 101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
 151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
 201 NHEQEFLRYQ QQSRQSRRRS LPYSPYSPHS RPRREEREFR PRGQHSRRER
 251 AGQEEEDEGG NIFSGFTPEF LEQAFQVDDR QIVQNLWGEN ESEEEGAIVT
 301 VRGGLRILSP DGTRGADEEE EYDEDQYEYH EQDGRRGRGS RGGGNGIEET
```

```
351 ICTACVKKNI GGNRSPHIYD PQRWFTQNCH DLNLLILRWL GLSAEYGNLY
401 RNALFVPHYN TNAHSIIYAL RGRAHVQVVD SNGNRVYDEE LQEGHVLVVP
451 QNFAVAGKSQ SENFEYVAFK TDSRPSIANF AGENSFIDNL PEEVVANSYG
501 LPREQARQLK NNNPFKFFVP PFQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
195 - 208	1730.8501	1729.8428	1729.8648	-0.0219	1	**RFNLAGNHEQEFLR**	(No match)
195 - 208	1730.8501	1729.8428	1729.8648	-0.0219	1	**RFNLAGNHEQEFLR**	(No match)
196 - 208	1574.7520	1573.7447	1573.7637	-0.0189	0	**FNLAGNHEQEFLR**	(No match)
196 - 208	1574.7520	1573.7447	1573.7637	-0.0189	0	**FNLAGNHEQEFLR**	(Ions score 26)
251 - 280	3361.4607	3360.4534	3360.4693	-0.0159	0	**AGQEEEDEGGNIFSGFTPEFLEQAFQVDDR**	(No match)



Spot 61

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:36:33 GMT**
Top Score : **44 for gi|118776570, arachin 6 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	44	arachin 6 [Arachis hypogaea]
2.	gi|52001219	61810	44	arachin Ahy-1 [Arachis hypogaea]
3.	gi|37789212	61803	44	storage protein [Arachis hypogaea]
4.	gi|47933675	58368	36	glycinin [Arachis hypogaea]
5.	gi|112380623	58570	36	iso-Ara h3 [Arachis hypogaea]
6.	gi|21314465	62042	34	allergen Arah3/Arah4 [Arachis hypogaea]
7.	gi|57669861	61041	26	arachin Ahy-4 [Arachis hypogaea]
8.	gi|108595573	61041	26	arachin Ahy-4 [Arachis hypogaea]
9.	gi|5712199	61430	25	glycinin [Arachis hypogaea]
10.	gi|9864777	60754	17	Gly1 [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** **44** **Expect:** 0.033 **Queries matched:** 6

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1269.7498	1268.7425	1268.7452	-0.0027	377	387	0	TANELNLLILR
1349.6793	1348.6720	1348.6927	-0.0207	516	526	0	FFVPPFQQSPR
1541.7705	1540.7632	1540.7673	-0.0041	388	400	0	WLGLSAEYGNLYR
1730.8652	1729.8579	1729.8648	-0.0068	195	208	1	RFNLAGNHEQEFLR
1770.8910	1769.8837	1769.8584	0.0253	220	235	0	SLPLSPYSPQPGQEDR
2314.1948	2313.1875	2313.2018	-0.0142	401	420	0	NALFVPHYNTNAHSIIYALR

No match to: 835.5038, 881.2703, 1043.5951, 1080.5375, 1306.6755, 1377.7125, 1547.7399, 1614.7760, 1618.7830, 1861.9690, 1923.9835, 2021.0145, 2092.0503, 2273.1396, 2311.1255, 2373.2302, 2390.2534, 2444.2651, 2461.2737, 2613.1990, 2652.3992, 3137.4402, 3153.4272, 3546.7510, 3803.9207

2. gi|52001219 **Mass:** 61810 **Score:** 44 **Expect:** 0.033 **Queries matched:** 6

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1269.7498	1268.7425	1268.7452	-0.0027	384	394	0	TANELNLLILR
1306.6755	1305.6682	1305.6717	-0.0035	523	533	0	FFVPPSEQSLR
1541.7705	1540.7632	1540.7673	-0.0041	395	407	0	WLGLSAEYGNLYR
1730.8652	1729.8579	1729.8648	-0.0068	195	208	1	RFNLAGNHEQEFLR
2021.0145	2020.0072	2020.0166	-0.0093	517	533	1	NNNPFKFFVPPSEQSLR
2314.1948	2313.1875	2313.2018	-0.0142	408	427	0	NALFVPHYNTNAHSIIYALR

No match to: 835.5038, 881.2703, 1043.5951, 1080.5375, 1349.6793, 1377.7125, 1547.7399, 1614.7760, 1618.7830, 1770.8910, 1861.9690, 1923.9835, 2092.0503, 2273.1396, 2311.1255, 2373.2302, 2390.2534, 2444.2651, 2461.2737, 2613.1990, 2652.3992, 3137.4402, 3153.4272, 3546.7510, 3803.9207

3. gi|37789212 **Mass:** 61803 **Score:** 44 **Expect:** 0.033 **Queries matched:** 6

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1269.7498	1268.7425	1268.7452	-0.0027	384	394	0	TANELNLLILR
1306.6755	1305.6682	1305.6717	-0.0035	523	533	0	FFVPPSEQSLR
1541.7705	1540.7632	1540.7673	-0.0041	395	407	0	WLGLSAEYGNLYR
1730.8652	1729.8579	1729.8648	-0.0068	195	208	1	RFNLAGNHEQEFLR
2021.0145	2020.0072	2020.0166	-0.0093	517	533	1	NNNPFKFFVPPSEQSLR
2314.1948	2313.1875	2313.2018	-0.0142	408	427	0	NALFVPHYNTNAHSIIYALR

No match to: 835.5038, 881.2703, 1043.5951, 1080.5375, 1349.6793, 1377.7125, 1547.7399, 1614.7760, 1618.7830, 1770.8910, 1861.9690, 1923.9835, 2092.0503, 2273.1396, 2311.1255, 2373.2302, 2390.2534, 2444.2651, 2461.2737, 2613.1990, 2652.3992, 3137.4402, 3153.4272, 3546.7510, 3803.9207

4. gi|47933675 **Mass:** 58368 **Score:** 36 **Expect:** 0.21 **Queries matched:** 5

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1547.7399	1546.7326	1546.7389	-0.0063	209	220	0	YQQQQGSRPHYR
1614.7760	1613.7687	1613.7837	-0.0150	196	208	0	FYLAGNQEQEFLR
1618.7830	1617.7757	1617.7746	0.0011	342	356	0	SSNPDIYNPQAGSLR
1770.8910	1769.8837	1769.8848	-0.0011	195	208	1	RFYLAGNQEQEFLR
2652.3992	2651.3919	2651.4070	-0.0151	357	380	0	SVNELDLPILGWLGLSAQHGTIYR

No match to: 835.5038, 881.2703, 1043.5951, 1080.5375, 1269.7498, 1306.6755, 1349.6793, 1377.7125, 1541.7705, 1730.8652, 1861.9690, 1923.9835, 2021.0145, 2092.0503, 2273.1396, 2311.1255, 2314.1948, 2373.2302, 2390.2534, 2444.2651, 2461.2737, 2613.1990, 3137.4402, 3153.4272, 3546.7510, 3803.9207

5. gi|112380623 **Mass:** 58570 **Score:** 36 **Expect:** 0.21 **Queries matched:** 5

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1547.7399	1546.7326	1546.7389	-0.0063	211	222	0	YQQQQGSRPHYR

1614.7760	1613.7687	1613.7837	-0.0150	198 - 210	0	FYLAGNQEQEFLR
1618.7830	1617.7757	1617.7746	0.0011	344 - 358	0	SSNPDIYNPQAGSLR
1770.8910	1769.8837	1769.8848	-0.0011	197 - 210	1	RFYLAGNQEQEFLR
2652.3992	2651.3919	2651.4070	-0.0151	359 - 382	0	SVNELDLPILGWLGLSAQHGTIYR

No match to: 835.5038, 881.2703, 1043.5951, 1080.5375, 1269.7498, 1306.6755, 1349.6793, 1377.7125, 1541.7705, 1730.8652, 1861.9690, 1923.9835, 2021.0145, 2092.0503, 2273.1396, 2311.1255, 2314.1948, 2373.2302, 2390.2534, 2444.2651, 2461.2737, 2613.1990, 3137.4402, 3153.4272, 3546.7510, 3803.9207

6. gi|21314465 **Mass:** 62042 **Score:** 34 **Expect:** 0.32 **Queries matched:** 5

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1306.6755	1305.6682	1305.6717	-0.0035	525 - 535		0	FFVPPSEQSLR
1541.7705	1540.7632	1540.7673	-0.0041	397 - 409		0	WLGLSAEYGNLYR
1730.8652	1729.8579	1729.8648	-0.0068	195 - 208		1	RFNLAGNHEQEFLR
2021.0145	2020.0072	2020.0166	-0.0093	519 - 535		1	NNNPFKFFVPPSEQSLR
2314.1948	2313.1875	2313.2018	-0.0142	410 - 429		0	NALFVPHYNTNAHSIIYALR

No match to: 835.5038, 881.2703, 1043.5951, 1080.5375, 1269.7498, 1349.6793, 1377.7125, 1547.7399, 1614.7760, 1618.7830, 1770.8910, 1861.9690, 1923.9835, 2092.0503, 2273.1396, 2311.1255, 2373.2302, 2390.2534, 2444.2651, 2461.2737, 2613.1990, 2652.3992, 3137.4402, 3153.4272, 3546.7510, 3803.9207

7. gi|57669861 **Mass:** 61041 **Score:** 26 **Expect:** 2.5 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1541.7705	1540.7632	1540.7673	-0.0041	389 - 401		0	WLGLSAEYGNLYR
1618.7830	1617.7757	1617.7481	0.0276	288 - 302		0	GENESEEEGAIVTVR
1730.8652	1729.8579	1729.8648	-0.0068	195 - 208		1	RFNLAGNHEQEFLR
2314.1948	2313.1875	2313.2018	-0.0142	402 - 421		0	NALFVPHYNTNAHSIIYALR

No match to: 835.5038, 881.2703, 1043.5951, 1080.5375, 1269.7498, 1306.6755, 1349.6793, 1377.7125, 1547.7399, 1614.7760, 1770.8910, 1861.9690, 1923.9835, 2021.0145, 2092.0503, 2273.1396, 2311.1255, 2373.2302, 2390.2534, 2444.2651, 2461.2737, 2613.1990, 2652.3992, 3137.4402, 3153.4272, 3546.7510, 3803.9207

8. gi|108595573 **Mass:** 61041 **Score:** 26 **Expect:** 2.5 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1541.7705	1540.7632	1540.7673	-0.0041	389 - 401		0	WLGLSAEYGNLYR
1618.7830	1617.7757	1617.7481	0.0276	288 - 302		0	GENESEEEGAIVTVR
1730.8652	1729.8579	1729.8648	-0.0068	195 - 208		1	RFNLAGNHEQEFLR
2314.1948	2313.1875	2313.2018	-0.0142	402 - 421		0	NALFVPHYNTNAHSIIYALR

No match to: 835.5038, 881.2703, 1043.5951, 1080.5375, 1269.7498, 1306.6755, 1349.6793, 1377.7125, 1547.7399, 1614.7760, 1770.8910, 1861.9690, 1923.9835, 2021.0145, 2092.0503, 2273.1396, 2311.1255, 2373.2302, 2390.2534, 2444.2651, 2461.2737, 2613.1990, 2652.3992, 3137.4402, 3153.4272, 3546.7510, 3803.9207

9. gi|5712199 **Mass:** 61430 **Score:** 25 **Expect:** 3 **Queries matched:** 4

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1349.6793	1348.6720	1348.6927	-0.0207	517	527	0	FFVPPFQQSPR
1541.7705	1540.7632	1540.7673	-0.0041	389	401	0	WLGLSAEYGNLYR
1730.8652	1729.8579	1729.8648	-0.0068	195	208	1	RFNLAGNHEQEFLR
2314.1948	2313.1875	2313.2018	-0.0142	402	421	0	NALFVPHYNTNAHSIIYALR

No match to: 835.5038, 881.2703, 1043.5951, 1080.5375, 1269.7498, 1306.6755, 1377.7125, 1547.7399, 1614.7760, 1618.7830, 1770.8910, 1861.9690, 1923.9835, 2021.0145, 2092.0503, 2273.1396, 2311.1255, 2373.2302, 2390.2534, 2444.2651, 2461.2737, 2613.1990, 2652.3992, 3137.4402, 3153.4272, 3546.7510, 3803.9207

10. gi|9864777 **Mass:** 60754 **Score:** 17 **Expect:** 17 **Queries matched:** 3

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1541.7705	1540.7632	1540.7673	-0.0041	388	400	0	WLGLSAEYGNLYR
1730.8652	1729.8579	1729.8648	-0.0068	197	210	1	RFNLAGNHEQEFLR
2314.1948	2313.1875	2313.2018	-0.0142	401	420	0	NALFVPHYNTNAHSIIYALR

No match to: 835.5038, 881.2703, 1043.5951, 1080.5375, 1269.7498, 1306.6755, 1349.6793, 1377.7125, 1547.7399, 1614.7760, 1618.7830, 1770.8910, 1861.9690, 1923.9835, 2021.0145, 2092.0503, 2273.1396, 2311.1255, 2373.2302, 2390.2534, 2444.2651, 2461.2737, 2613.1990, 2652.3992, 3137.4402, 3153.4272, 3546.7510, 3803.9207

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 31

Protein View

Match to: **gi|47933675** Score: **47** Expect: **0.019**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **40**
Number of mass values matched: **7**
Sequence Coverage: **12%**

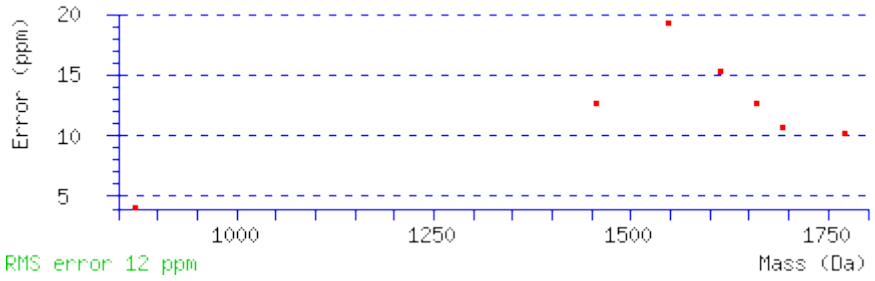
Matched peptides shown in **Bold Red**

```
    1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
   51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
  101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
  151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
  201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
  251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
  301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
  351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
  401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
  451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
  501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
195 - 208	1770.9102	1769.9029	1769.8848	0.0181	1	RFYLAGNQEQEFLR
196 - 208	1614.8156	1613.8083	1613.7837	0.0246	0	FYLAGNQEQEFLR
209 - 220	1547.7760	1546.7687	1546.7389	0.0298	0	YQQQQGSRPHYR
263 - 277	1658.8553	1657.8480	1657.8270	0.0210	1	GENEREEQGAIVTVK
268 - 281	1456.8302	1455.8229	1455.8044	0.0185	1	EEQGAIVTVKGGLR
300 - 312	1691.7911	1690.7838	1690.7659	0.0180	1	EEFDEDRSRPQQR
483 - 489	872.4983	871.4910	871.4875	0.0035	1	EQARQLK

No match to: 815.4954, 840.4911, 851.4652, 859.5150, 886.5195, 927.5779, 932.5036, 949.5270, 1095.5164, 1120.5905, 1225.6344, 1260.6891, 1354.7123, 1391.6947, 1531.3109, 1618.8313, 1754.4377, 1792.8812, 1824.8120, 1847.8862, 1935.8650, 2042.0664, 2217.0273, 2273.1375, 2328.0740, 2499.2583, 2601.1440, 2882.4717, 3144.3884, 3200.3325, 3438.0784, 3454.4915, 3762.7612



Spot 62

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 4 May 2007 at 11:34:04 GMT
Top Score : 62 for gi|118776570, arachin 6 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	62	arachin 6 [Arachis hypogaea]
2.	gi|57669861	61041	40	arachin Ahy-4 [Arachis hypogaea]
3.	gi|108595573	61041	40	arachin Ahy-4 [Arachis hypogaea]
4.	gi|5712199	61430	23	glycinin [Arachis hypogaea]
5.	gi|22135348	25768	21	trypsin inhibitor [Arachis hypogaea]
6.	gi|230338	23975	17	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
7.	gi|3703107	58543	15	glycinin [Arachis hypogaea]
8.	gi|9864777	60754	14	Gly1 [Arachis hypogaea]
9.	gi|2498261	2416	14	33.0 kDa cold shock protein (AHCSP33)
10.	gi|62177385	14731	14	resistance protein Cre [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 62 **Expect:** 0.00056 **Queries matched:** 8
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3951	808.3878	808.3827	0.0051	209 -	214	0	YQQQSR
870.5159	869.5086	869.5083	0.0004	279 -	285	0	QIVQNLR
1574.7744	1573.7671	1573.7637	0.0035	196 -	208	0	FNLAGNHEQEFLR
1730.8706	1729.8633	1729.8648	-0.0014	195 -	208	1	RFNLAGNHEQEFLR
1770.8855	1769.8782	1769.8584	0.0198	220 -	235	0	SLPLSPYSPQPGQEDR
2262.8311	2261.8238	2261.8243	-0.0005	312 -	329	0	SPDEEEEYDEDEYAEEER
2441.2703	2440.2630	2440.2557	0.0074	279 -	300	1	QIVQNLRGENESEEQGAIVTVK

3291.4973	3290.4900	3290.4751	0.0149	249 - 278	0	AGQEQENEGGNIFSGFTSEFLAQAFQVDDR

No match to: 861.0674, 865.9564, 866.4420, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758, 1137.5931, 1176.5369, 1193.5507, 1314.6268, 1547.7520, 1622.7782, 1638.7759, 1714.4231, 1753.7415, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2273.1560, 2407.0896, 2453.2393, 2470.2620, 2514.3203, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3300.6667, 3360.4644, 3646.6411

2. gi|57669861 **Mass:** 61041 **Score:** 40 **Expect:** 0.08 **Queries matched:** 6

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3951	808.3878	808.3827	0.0051	209 -	214	0	YQQQSR
870.5159	869.5086	869.5083	0.0004	281 -	287	0	QIVQNLR
1574.7744	1573.7671	1573.7637	0.0035	196 -	208	0	FNLAGNHEQEFLR
1730.8706	1729.8633	1729.8648	-0.0014	195 -	208	1	RFNLAGNHEQEFLR
2470.2620	2469.2547	2469.2458	0.0089	281 -	302	1	QIVQNLRGENESEEEGAIVTVR
3360.4644	3359.4571	3359.4853	-0.0282	251 -	280	0	AGQEEENEGGNIFSGFTPEFLEQAFQVDDR

No match to: 861.0674, 865.9564, 866.4420, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758, 1137.5931, 1176.5369, 1193.5507, 1314.6268, 1547.7520, 1622.7782, 1638.7759, 1714.4231, 1753.7415, 1770.8855, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2262.8311, 2273.1560, 2407.0896, 2441.2703, 2453.2393, 2514.3203, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3291.4973, 3300.6667, 3646.6411

3. gi|108595573 **Mass:** 61041 **Score:** 40 **Expect:** 0.08 **Queries matched:** 6

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3951	808.3878	808.3827	0.0051	209 -	214	0	YQQQSR
870.5159	869.5086	869.5083	0.0004	281 -	287	0	QIVQNLR
1574.7744	1573.7671	1573.7637	0.0035	196 -	208	0	FNLAGNHEQEFLR
1730.8706	1729.8633	1729.8648	-0.0014	195 -	208	1	RFNLAGNHEQEFLR
2470.2620	2469.2547	2469.2458	0.0089	281 -	302	1	QIVQNLRGENESEEEGAIVTVR
3360.4644	3359.4571	3359.4853	-0.0282	251 -	280	0	AGQEEENEGGNIFSGFTPEFLEQAFQVDDR

No match to: 861.0674, 865.9564, 866.4420, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758, 1137.5931, 1176.5369, 1193.5507, 1314.6268, 1547.7520, 1622.7782, 1638.7759, 1714.4231, 1753.7415, 1770.8855, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2262.8311, 2273.1560, 2407.0896, 2441.2703, 2453.2393, 2514.3203, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3291.4973, 3300.6667, 3646.6411

4. gi|5712199 **Mass:** 61430 **Score:** 23 **Expect:** 4 **Queries matched:** 4

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3951	808.3878	808.3827	0.0051	209 -	214	0	YQQQSR
1574.7744	1573.7671	1573.7637	0.0035	196 -	208	0	FNLAGNHEQEFLR
1730.8706	1729.8633	1729.8648	-0.0014	195 -	208	1	RFNLAGNHEQEFLR
3646.6411	3645.6338	3645.6130	0.0208	249 -	280	1	ERAGQEEEDEGGNIFSGFTPEFLEQAFQVDDR

No match to: 861.0674, 865.9564, 866.4420, 870.5159, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758,

1137.5931, 1176.5369, 1193.5507, 1314.6268, 1547.7520, 1622.7782, 1638.7759, 1714.4231, 1753.7415, 1770.8855, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2262.8311, 2273.1560, 2407.0896, 2441.2703, 2453.2393, 2470.2620, 2514.3203, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3291.4973, 3300.6667, 3360.4644

5. gi|22135348 **Mass:** 25768 **Score:** 21 **Expect:** 7 **Queries matched:** 3

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3951	808.3878	808.3827	0.0051	211 -	216	0	YQQQSR
1574.7744	1573.7671	1573.7637	0.0035	198 -	210	0	FNLAGNHEQEFLR
1730.8706	1729.8633	1729.8648	-0.0014	197 -	210	1	RFNLAGNHEQEFLR

No match to: 861.0674, 865.9564, 866.4420, 870.5159, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758, 1137.5931, 1176.5369, 1193.5507, 1314.6268, 1547.7520, 1622.7782, 1638.7759, 1714.4231, 1753.7415, 1770.8855, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2262.8311, 2273.1560, 2407.0896, 2441.2703, 2453.2393, 2470.2620, 2514.3203, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3291.4973, 3300.6667, 3360.4644, 3646.6411

6. gi|230338 **Mass:** 23975 **Score:** 17 **Expect:** 19 **Queries matched:** 2

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2273.1560	2272.1487	2272.1521	-0.0034	70 -	89	0	SIVHPSYNSNTLNNDIMLIK
2514.3203	2513.3130	2513.3311	-0.0181	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK

No match to: 809.3951, 861.0674, 865.9564, 866.4420, 870.5159, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758, 1137.5931, 1176.5369, 1193.5507, 1314.6268, 1547.7520, 1574.7744, 1622.7782, 1638.7759, 1714.4231, 1730.8706, 1753.7415, 1770.8855, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2262.8311, 2407.0896, 2441.2703, 2453.2393, 2470.2620, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3291.4973, 3300.6667, 3360.4644, 3646.6411

7. gi|3703107 **Mass:** 58543 **Score:** 15 **Expect:** 25 **Queries matched:** 3

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3951	808.3878	808.3827	0.0051	186 -	191	0	YQQQSR
870.5159	869.5086	869.5083	0.0004	258 -	264	0	QIVQNLR
3360.4644	3359.4571	3359.4853	-0.0282	228 -	257	0	AGQEEENEGGNIFSGFTPEFLEQAFQVDDR

No match to: 861.0674, 865.9564, 866.4420, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758, 1137.5931, 1176.5369, 1193.5507, 1314.6268, 1547.7520, 1574.7744, 1622.7782, 1638.7759, 1714.4231, 1730.8706, 1753.7415, 1770.8855, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2262.8311, 2273.1560, 2407.0896, 2441.2703, 2453.2393, 2470.2620, 2514.3203, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3291.4973, 3300.6667, 3646.6411

8. gi|9864777 **Mass:** 60754 **Score:** 14 **Expect:** 32 **Queries matched:** 4

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
809.3951	808.3878	808.3827	0.0051	211 -	216	0	YQQQSR
870.5159	869.5086	869.5083	0.0004	280 -	286	0	QIVQNLR
1574.7744	1573.7671	1573.7637	0.0035	198 -	210	0	FNLAGNHEQEFLR
1730.8706	1729.8633	1729.8648	-0.0014	197 -	210	1	RFNLAGNHEQEFLR

No match to: 861.0674, 865.9564, 866.4420, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758, 1137.5931, 1176.5369, 1193.5507, 1314.6268, 1547.7520, 1622.7782, 1638.7759, 1714.4231, 1753.7415, 1770.8855, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2262.8311, 2273.1560, 2407.0896, 2441.2703, 2453.2393, 2470.2620, 2514.3203, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3291.4973, 3300.6667, 3360.4644, 3646.6411

9. gi|2498261 **Mass:** 2416 **Score:** 14 **Expect:** 32 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1547.7520	1546.7447	1546.7263	0.0184	9	-	24	0	ASYTVTPPAQANAADA

No match to: 809.3951, 861.0674, 865.9564, 866.4420, 870.5159, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758, 1137.5931, 1176.5369, 1193.5507, 1314.6268, 1574.7744, 1622.7782, 1638.7759, 1714.4231, 1730.8706, 1753.7415, 1770.8855, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2262.8311, 2273.1560, 2407.0896, 2441.2703, 2453.2393, 2470.2620, 2514.3203, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3291.4973, 3300.6667, 3360.4644, 3646.6411

10. gi|62177385 **Mass:** 14731 **Score:** 14 **Expect:** 39 **Queries matched:** 2

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
866.4420	865.4347	865.4228	0.0119	66	-	71	1	EVFCRR
1730.8706	1729.8633	1729.8787	-0.0154	1	-	14	1	NLILDDVWDSKAWR

No match to: 809.3951, 861.0674, 865.9564, 870.5159, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758, 1137.5931, 1176.5369, 1193.5507, 1314.6268, 1547.7520, 1574.7744, 1622.7782, 1638.7759, 1714.4231, 1753.7415, 1770.8855, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2262.8311, 2273.1560, 2407.0896, 2441.2703, 2453.2393, 2470.2620, 2514.3203, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3291.4973, 3300.6667, 3360.4644, 3646.6411

Protein View

Match to: **gi|118776570** Score: **62** Expect: **0.00056**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **41**
Number of mass values matched: **8**
Sequence Coverage: **20%**

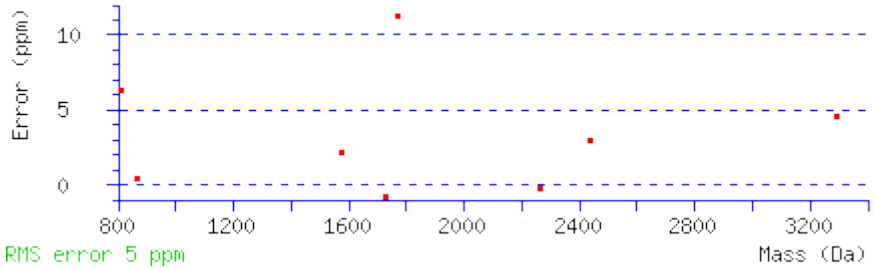
Matched peptides shown in **Bold Red**

```
   1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
  51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
 101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
 151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
 201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
 251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
 301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
 351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
 401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
 451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
 501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
195 - 208	1730.8706	1729.8633	1729.8648	-0.0014	1	RFNLAGNHEQEFLR
196 - 208	1574.7744	1573.7671	1573.7637	0.0035	0	FNLAGNHEQEFLR
209 - 214	809.3951	808.3878	808.3827	0.0051	0	YQQQSR
220 - 235	1770.8855	1769.8782	1769.8584	0.0198	0	SLPLSPYSPQPGQEDR
249 - 278	3291.4973	3290.4900	3290.4751	0.0149	0	AGQEQENEGGNIFSGFTSEFLAQAFQVDDR
279 - 285	870.5159	869.5086	869.5083	0.0004	0	QIVQNLR
279 - 300	2441.2703	2440.2630	2440.2557	0.0074	1	QIVQNLRGENESEEQGAIVTVK
312 - 329	2262.8311	2261.8238	2261.8243	-0.0005	0	SPDEEEEYDEDEYAEEER

No match to: 861.0674, 865.9564, 866.4420, 958.4737, 1080.5277, 1111.5596, 1129.5439, 1137.0758, 1137.5931, 1176.5369, 1193.5507, 1314.6268, 1547.7520, 1622.7782, 1638.7759, 1714.4231, 1753.7415, 1774.8248, 1784.8071, 1794.8717, 2256.6790, 2273.1560, 2407.0896, 2453.2393, 2470.2620, 2514.3203, 2612.1877, 3136.4150, 3153.4500, 3211.4846, 3300.6667, 3360.4644, 3646.6411



Spot 63

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:54:58 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **100 for gi|52001223, arachin Ahy-3 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|52001223	54991	100	arachin Ahy-3 [Arachis hypogaea]
2.	gi|47933675	58368	95	glycinin [Arachis hypogaea]
3.	gi|112380623	58570	83	iso-Ara h3 [Arachis hypogaea]
4.	gi|115187491	12957	29	aux/IAA protein [Arachis hypogaea]
5.	gi|40738310	112681	17	1a protein [Cucumber mosaic virus]
6.	gi|544001	4824	14	Endochitinase 3 (CHIT 3)
7.	gi|288487	4881	14	chitinase [Arachis hypogaea]
8.	gi|90819614	13067	13	putative 11 kDa protein [Cowpea mild mottle virus]
9.	gi|55736071	7998	13	auxin-induced putative tetratricopeptide-containing protein [Arachis hypogaea]
10.	gi|37221925	17814	12	resistance protein [Arachis stenosperma]

Results List

1. gi|52001223 **Mass:** 54991 **Score:** 100 **Expect:** 9e-008 **Queries matched:** 8
arachin Ahy-3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1302.6509	1301.6436	1301.6727	-0.0291	343	354	0	8	LGLSAEYGSIHR
1302.6509	1301.6436	1301.6727	-0.0291	343	354	0	---	LGLSAEYGSIHR
1396.7432	1395.7359	1395.7721	-0.0362	331	342	0	---	TVNELDLPILNR
1396.7432	1395.7359	1395.7721	-0.0362	331	342	0	36	TVNELDLPILNR
1455.6895	1454.6822	1454.7193	-0.0371	412	423	0	---	SQSEHFLYVAFK
1565.7175	1564.7102	1564.7481	-0.0379	316	330	0	---	STSADIYNPQAGSVR
2133.9890	2132.9817	2133.0313	-0.0495	464	481	0	5	NNNPFTFLVPPQDSQMIR + Oxidation (M)
2133.9890	2132.9817	2133.0313	-0.0495	464	481	0	---	NNNPFTFLVPPQDSQMIR + Oxidation (M)

No match to: 886.9603, 1151.6882, 1307.6095, 1462.6439, 1618.7415, 1618.7415, 1652.7146, 2454.2173, 2454.2173

2. gi|47933675 **Mass:** 58368 **Score:** 95 **Expect:** 2.8e-007 **Queries matched:** 5

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1462.6439	1461.6366	1461.6775	-0.0409	438 -	449	0	---	AQSENYEYLAFK
1618.7415	1617.7342	1617.7746	-0.0404	342 -	356	0	57	SSNPDIYNPQAGSLR
1618.7415	1617.7342	1617.7746	-0.0404	342 -	356	0	---	SSNPDIYNPQAGSLR
2454.2173	2453.2100	2453.2637	-0.0537	381 -	402	0	---	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)
2454.2173	2453.2100	2453.3537	-0.1437	1 -	22	1	---	KLLALSLCFCVLVLGASSVTFR

No match to: 886.9603, 1151.6882, 1302.6509, 1302.6509, 1307.6095, 1396.7432, 1396.7432, 1455.6895, 1565.7175, 1652.7146, 2133.9890, 2133.9890

3. gi|112380623 **Mass:** 58570 **Score:** 83 **Expect:** 4.6e-006 **Queries matched:** 5

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1462.6439	1461.6366	1461.6775	-0.0409	440 -	451	0	---	AQSENYEYLAFK
1618.7415	1617.7342	1617.7746	-0.0404	344 -	358	0	57	SSNPDIYNPQAGSLR
1618.7415	1617.7342	1617.7746	-0.0404	344 -	358	0	---	SSNPDIYNPQAGSLR
2454.2173	2453.2100	2453.2637	-0.0537	383 -	404	0	---	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)
2454.2173	2453.2100	2453.2637	-0.0537	383 -	404	0	---	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)

No match to: 886.9603, 1151.6882, 1302.6509, 1302.6509, 1307.6095, 1396.7432, 1396.7432, 1455.6895, 1565.7175, 1652.7146, 2133.9890, 2133.9890

4. gi|115187491 **Mass:** 12957 **Score:** 29 **Expect:** 1.2 **Queries matched:** 2

aux/IAA protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1396.7432	1395.7359	1395.7106	0.0253	89 -	103	0	---	NGGAAAPTSTPPVTR
1396.7432	1395.7359	1395.7106	0.0253	89 -	103	0	17	NGGAAAPTSTPPVTR

No match to: 886.9603, 1151.6882, 1302.6509, 1302.6509, 1307.6095, 1455.6895, 1462.6439, 1565.7175, 1618.7415, 1618.7415, 1652.7146, 2133.9890, 2133.9890, 2454.2173, 2454.2173

5. gi|40738310 **Mass:** 112681 **Score:** 17 **Expect:** 18 **Queries matched:** 4

1a protein [Cucumber mosaic virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1565.7175	1564.7102	1564.7344	-0.0242	917 -	928	1	---	EMNLPKTFWDER
1652.7146	1651.7073	1651.8127	-0.1054	726 -	740	0	---	SIFEPSTDMIVTANK
2133.9890	2132.9817	2133.0894	-0.1077	414 -	431	0	---	IDINDYHYIGFATLLHTK
2133.9890	2132.9817	2133.0894	-0.1077	414 -	431	0	---	IDINDYHYIGFATLLHTK

No match to: 886.9603, 1151.6882, 1302.6509, 1302.6509, 1307.6095, 1396.7432, 1396.7432, 1455.6895, 1462.6439, 1618.7415, 1618.7415, 2454.2173, 2454.2173

6. gi|544001 **Mass:** 4824 **Score:** 14 **Expect:** 33 **Queries matched:** 2

Endochitinase 3 (CHIT 3)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1302.6509	1301.6436	1301.6112	0.0324	18 -	29	1	---	WTPSDADRAAGR
1302.6509	1301.6436	1301.6112	0.0324	18 -	29	1	---	WTPSDADRAAGR

No match to: 886.9603, 1151.6882, 1307.6095, 1396.7432, 1396.7432, 1455.6895, 1462.6439, 1565.7175, 1618.7415, 1618.7415, 1652.7146, 2133.9890, 2133.9890, 2454.2173, 2454.2173

7. gi|288487 **Mass:** 4881 **Score:** 14 **Expect:** 33 **Queries matched:** 2

chitinase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1302.6509	1301.6436	1301.6112	0.0324	18 -	29	1	---	WTPSDADRAAGR
1302.6509	1301.6436	1301.6112	0.0324	18 -	29	1	---	WTPSDADRAAGR

No match to: 886.9603, 1151.6882, 1307.6095, 1396.7432, 1396.7432, 1455.6895, 1462.6439, 1565.7175, 1618.7415, 1618.7415, 1652.7146, 2133.9890, 2133.9890, 2454.2173, 2454.2173

8. gi|90819614 **Mass:** 13067 **Score:** 13 **Expect:** 46 **Queries matched:** 2

putative 11 kDa protein [Cowpea mild mottle virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2454.2173	2453.2100	2453.1255	0.0845	74 -	94	0	---	CNGVDCKPGLNYPSWVGDFIR
2454.2173	2453.2100	2453.1255	0.0845	74 -	94	0	---	CNGVDCKPGLNYPSWVGDFIR

No match to: 886.9603, 1151.6882, 1302.6509, 1302.6509, 1307.6095, 1396.7432, 1396.7432, 1455.6895, 1462.6439, 1565.7175, 1618.7415, 1618.7415, 1652.7146, 2133.9890, 2133.9890

9. gi|55736071 **Mass:** 7998 **Score:** 13 **Expect:** 49 **Queries matched:** 1

auxin-induced putative tetratricopeptide-containing protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1462.6439	1461.6366	1461.6807	-0.0441	43 -	55	1	---	SNVTKGENSNQER

No match to: 886.9603, 1151.6882, 1302.6509, 1302.6509, 1307.6095, 1396.7432, 1396.7432, 1455.6895, 1565.7175, 1618.7415, 1618.7415, 1652.7146, 2133.9890, 2133.9890, 2454.2173, 2454.2173

10. gi|37221925 **Mass:** 17814 **Score:** 12 **Expect:** 59 **Queries matched:** 2

resistance protein [Arachis stenosperma]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2454.2173	2453.2100	2453.2775	-0.0674	24 -	45	1	---	ENSATHDHGHLIRILLNTLGDK
2454.2173	2453.2100	2453.2775	-0.0674	24 -	45	1	---	ENSATHDHGHLIRILLNTLGDK

No match to: 886.9603, 1151.6882, 1302.6509, 1302.6509, 1307.6095, 1396.7432, 1396.7432, 1455.6895, 1462.6439, 1565.7175, 1618.7415, 1618.7415, 1652.7146, 2133.9890, 2133.9890

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of Queries: 17

Protein View

Match to: **gi|52001223** Score: **100** Expect: **9e-008**
arachin Ahy-3 [Arachis hypogaea]

Nominal mass (M_r): **54991**; Calculated pI value: **5.40**
NCBI BLAST search of gi|52001223 against nr
Unformatted sequence string for pasting into other applications

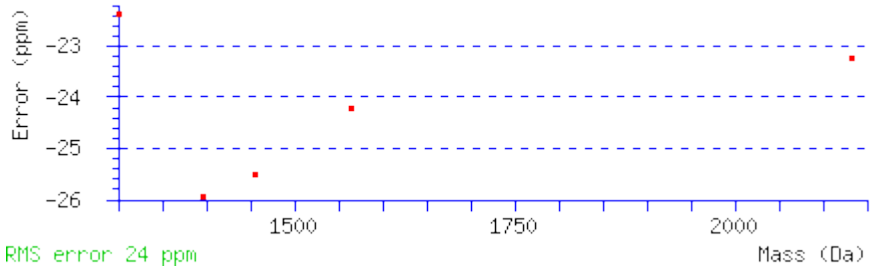
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **14%**

Matched peptides shown in **Bold Red**

```
     1 MAKLLALSVC FCFLVLGASS VTFRQQGEEN ECQFQRLNAQ RPDNCIESEG
    51 GYIETWNPNN QEFQCAGVAL SRFVLRRNAL RRPFYSNAPQ EIFIYQGSGY
   101 FGLIFPGCPG TFEEPIQGSE QFQRPSRHFQ GQDQSQRPLD THQKVHGFRE
   151 GDLIAVPHGV AFWIYNDQDT DVVAISVLHT NSLHNQLDQF PRRFNLAGKQ
   201 EQEFLRYQQR SGRQSPKGEE QEQEQENEGG NVFSGFSTEF LSHGFQVNED
   251 IVRNLRGENE REEQGAIVTV KGGLSILVPP EWRQSYQQPG RGDKDFNNGI
   301 EETICTATVK MNIGKSTSAD IYNPQAGSVR TVNELDLPIL NRLGLSAEYG
   351 SIHRDAMFVP HYNMNANSMI YALHGGAHVQ VVDCNGNRVF DEELQEGQSL
   401 VVPQNFAVAA KSQSEHFLYV AFKTNSRASI SNLAGKNSYM WNLPEDVVAN
   451 SYGLQYEQAR QLKNNNPFTF LVPPQDSQMI RTVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
316 - 330	1565.7175	1564.7102	1564.7481	-0.0379	0	**STSADIYNPQAGSVR** (No match)
331 - 342	1396.7432	1395.7359	1395.7721	-0.0362	0	**TVNELDLPILNR** (No match)
331 - 342	1396.7432	1395.7359	1395.7721	-0.0362	0	**TVNELDLPILNR** (Ions score 36)
343 - 354	1302.6509	1301.6436	1301.6727	-0.0291	0	**LGLSAEYGSIHR** (Ions score 8)
343 - 354	1302.6509	1301.6436	1301.6727	-0.0291	0	**LGLSAEYGSIHR** (No match)
412 - 423	1455.6895	1454.6822	1454.7193	-0.0371	0	**SQSEHFLYVAFK** (No match)
464 - 481	2133.9890	2132.9817	2133.0313	-0.0495	0	**NNNPFTFLVPPQDSQMIR** Oxidation (M) (Ions score 5)
464 - 481	2133.9890	2132.9817	2133.0313	-0.0495	0	**NNNPFTFLVPPQDSQMIR** Oxidation (M) (No match)



Spot 64

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:10:32 GMT
Top Score : 62 for gi|47933675, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	62	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	62	iso-Ara h3 [Arachis hypogaea]
3.	gi|62177433	15552	29	resistance protein PNTR [Arachis hypogaea]
4.	gi|62177648	7475	23	resistance protein PRG [Arachis hypogaea]
5.	gi|62177463	9663	23	resistance protein PNTR [Arachis hypogaea]
6.	gi|62177626	19671	22	resistance protein PRG [Arachis hypogaea]
7.	gi|62177534	19717	21	resistance protein PRG [Arachis hypogaea]
8.	gi|62177578	19703	21	resistance protein PRG [Arachis hypogaea]
9.	gi|62177628	19986	21	resistance protein PRG [Arachis hypogaea]
10.	gi|62177574	20142	21	resistance protein PRG [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 62 **Expect:** 0.00058 **Queries matched:** 11
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5865	1101.5792	1101.5930	-0.0138	487	495	1	QLKNNNPFK
1462.6786	1461.6713	1461.6775	-0.0062	438	449	0	AQSENYEYLAFK
1507.7019	1506.6946	1506.7078	-0.0131	496	507	0	FFVPPFDHQSMR
1523.7008	1522.6935	1522.7027	-0.0091	496	507	0	FFVPPFDHQSMR + Oxidation (M)
1618.7762	1617.7689	1617.7746	-0.0057	342	356	0	SSNPDIYNPQAGSLR
2438.2778	2437.2705	2437.2688	0.0017	381	402	0	NAMFVPHYTLNAHTIVVALNGR
2454.2830	2453.2757	2453.2637	0.0120	381	402	0	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)
2555.3342	2554.3269	2554.3066	0.0203	415	437	0	VYDEELQEGHVLVVPQNFAVAAK
2652.4292	2651.4219	2651.4070	0.0149	357	380	0	SVNELDLPILGWLGLSAQHGTIYR
3244.6440	3243.6367	3243.6006	0.0361	450	479	0	TDSRPSIANLAGENSIIDNLPEEVVANSYR

3831.9758	3830.9685	3830.9338	0.0347	403 - 437	1	AHVQVVDSNGNRVYDEELQEGHVLVVPQNFAVAAK

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1137.5557, 1145.0549, 1145.5597, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1565.7437, 1590.7750, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679, 1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2305.1426, 2311.1431, 2335.0967, 2351.0886, 2354.0974, 2530.3059, 2737.3567, 2785.4136, 2838.4014, 3136.5081, 3154.4890, 3211.5364, 3301.7947, 3612.9944, 3833.0142

2. gi|112380623 **Mass:** 58570 **Score:** 62 **Expect:** 0.00059 **Queries matched:** 11

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5865	1101.5792	1101.5930	-0.0138	489 - 497		1	QLKNNNPFK
1462.6786	1461.6713	1461.6775	-0.0062	440 - 451		0	AQSENYEYLAFK
1507.7019	1506.6946	1506.7078	-0.0131	498 - 509		0	FFVPPFDHQSMR
1523.7008	1522.6935	1522.7027	-0.0091	498 - 509		0	FFVPPFDHQSMR + Oxidation (M)
1618.7762	1617.7689	1617.7746	-0.0057	344 - 358		0	SSNPDIYNPQAGSLR
2438.2778	2437.2705	2437.2688	0.0017	383 - 404		0	NAMFVPHYTLNAHTIVVALNGR
2454.2830	2453.2757	2453.2637	0.0120	383 - 404		0	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)
2555.3342	2554.3269	2554.3066	0.0203	417 - 439		0	VYDEELQEGHVLVVPQNFAVAAK
2652.4292	2651.4219	2651.4070	0.0149	359 - 382		0	SVNELDLPILGWLGLSAQHGTIYR
3244.6440	3243.6367	3243.6006	0.0361	452 - 481		0	TDSRPSIANLAGENSIIDNLPEEVVANSYR
3831.9758	3830.9685	3830.9338	0.0347	405 - 439		1	AHVQVVDSNGNRVYDEELQEGHVLVVPQNFAVAAK

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1137.5557, 1145.0549, 1145.5597, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1565.7437, 1590.7750, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679, 1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2305.1426, 2311.1431, 2335.0967, 2351.0886, 2354.0974, 2530.3059, 2737.3567, 2785.4136, 2838.4014, 3136.5081, 3154.4890, 3211.5364, 3301.7947, 3612.9944, 3833.0142

3. gi|62177433 **Mass:** 15552 **Score:** 29 **Expect:** 1.1 **Queries matched:** 3

resistance protein PNTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2305.1426	2304.1353	2304.1749	-0.0396	6 -	25	1	TTLAQLVYNDNKVEEHFGVK
2785.4136	2784.4063	2784.3870	0.0193	18 -	41	1	VEEHFGVKAWIDVSQQFDVSHVTK
3136.5081	3135.5008	3135.5777	-0.0768	110 - 138		0	HETVAWEGVEPVQVLGHLLPQVFEGGHTA

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1102.5865, 1137.5557, 1145.0549, 1145.5597, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1462.6786, 1507.7019, 1523.7008, 1565.7437, 1590.7750, 1618.7762, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679, 1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2311.1431, 2335.0967, 2351.0886, 2354.0974, 2438.2778,

2454.2830, 2530.3059, 2555.3342, 2652.4292, 2737.3567, 2838.4014, 3154.4890, 3211.5364, 3244.6440, 3301.7947, 3612.9944, 3831.9758, 3833.0142

4. gi|62177648 **Mass:** 7475 **Score:** 23 **Expect:** 4.3 **Queries matched:** 3

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1145.5597	1144.5524	1144.5724	-0.0199	34	-	43	0	ISDQEEGLVR
1462.6786	1461.6713	1461.6533	0.0181	22	-	32	0	FECACFLFNVR
1590.7750	1589.7677	1589.7482	0.0195	22	-	33	1	FECACFLFNVRK

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1102.5865, 1137.5557, 1145.0549, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1507.7019, 1523.7008, 1565.7437, 1618.7762, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679, 1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2305.1426, 2311.1431, 2335.0967, 2351.0886, 2354.0974, 2438.2778, 2454.2830, 2530.3059, 2555.3342, 2652.4292, 2737.3567, 2785.4136, 2838.4014, 3136.5081, 3154.4890, 3211.5364, 3244.6440, 3301.7947, 3612.9944, 3831.9758, 3833.0142

5. gi|62177463 **Mass:** 9663 **Score:** 23 **Expect:** 4.7 **Queries matched:** 3

resistance protein PNTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1145.5597	1144.5524	1144.5724	-0.0199	32	-	41	0	ISDQEEGLVR
1462.6786	1461.6713	1461.6533	0.0181	20	-	30	0	FECACFLFNVR
1590.7750	1589.7677	1589.7482	0.0195	20	-	31	1	FECACFLFNVRK

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1102.5865, 1137.5557, 1145.0549, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1507.7019, 1523.7008, 1565.7437, 1618.7762, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679, 1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2305.1426, 2311.1431, 2335.0967, 2351.0886, 2354.0974, 2438.2778, 2454.2830, 2530.3059, 2555.3342, 2652.4292, 2737.3567, 2785.4136, 2838.4014, 3136.5081, 3154.4890, 3211.5364, 3244.6440, 3301.7947, 3612.9944, 3831.9758, 3833.0142

6. gi|62177626 **Mass:** 19671 **Score:** 22 **Expect:** 5.5 **Queries matched:** 4

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1145.5597	1144.5524	1144.5724	-0.0199	32	-	41	0	ISDQEEGLVR
1462.6786	1461.6713	1461.6533	0.0181	20	-	30	0	FECACFLFNVR
1590.7750	1589.7677	1589.7482	0.0195	20	-	31	1	FECACFLFNVRK
2335.0967	2334.0894	2334.1280	-0.0386	151	-	171	0	ANYEDLSNQAIHYAQGLPFAL

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1102.5865, 1137.5557, 1145.0549, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1507.7019, 1523.7008, 1565.7437, 1618.7762, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679,

1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2305.1426, 2311.1431, 2351.0886, 2354.0974, 2438.2778, 2454.2830, 2530.3059, 2555.3342, 2652.4292, 2737.3567, 2785.4136, 2838.4014, 3136.5081, 3154.4890, 3211.5364, 3244.6440, 3301.7947, 3612.9944, 3831.9758, 3833.0142

7. gi|62177534 **Mass:** 19717 **Score:** 21 **Expect:** 6.8 **Queries matched:** 4

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1145.5597	1144.5524	1144.5724	-0.0199	32	-	41	0	ISDQEEGLVR
1462.6786	1461.6713	1461.6533	0.0181	20	-	30	0	FECACFLFNVR
1590.7750	1589.7677	1589.7482	0.0195	20	-	31	1	FECACFLFNVRK
2335.0967	2334.0894	2334.1280	-0.0386	151	-	171	0	ANYEDLSNQAIHYAQGLPFAL

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1102.5865, 1137.5557, 1145.0549, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1507.7019, 1523.7008, 1565.7437, 1618.7762, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679, 1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2305.1426, 2311.1431, 2351.0886, 2354.0974, 2438.2778, 2454.2830, 2530.3059, 2555.3342, 2652.4292, 2737.3567, 2785.4136, 2838.4014, 3136.5081, 3154.4890, 3211.5364, 3244.6440, 3301.7947, 3612.9944, 3831.9758, 3833.0142

8. gi|62177578 **Mass:** 19703 **Score:** 21 **Expect:** 6.8 **Queries matched:** 4

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1145.5597	1144.5524	1144.5724	-0.0199	32	-	41	0	ISDQEEGLVR
1462.6786	1461.6713	1461.6533	0.0181	20	-	30	0	FECACFLFNVR
1590.7750	1589.7677	1589.7482	0.0195	20	-	31	1	FECACFLFNVRK
2335.0967	2334.0894	2334.1280	-0.0386	151	-	171	0	ANYEDLSNQAIHYAQGLPFAL

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1102.5865, 1137.5557, 1145.0549, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1507.7019, 1523.7008, 1565.7437, 1618.7762, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679, 1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2305.1426, 2311.1431, 2351.0886, 2354.0974, 2438.2778, 2454.2830, 2530.3059, 2555.3342, 2652.4292, 2737.3567, 2785.4136, 2838.4014, 3136.5081, 3154.4890, 3211.5364, 3244.6440, 3301.7947, 3612.9944, 3831.9758, 3833.0142

9. gi|62177628 **Mass:** 19986 **Score:** 21 **Expect:** 6.8 **Queries matched:** 4

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1145.5597	1144.5524	1144.5724	-0.0199	34	-	43	0	ISDQEEGLVR
1462.6786	1461.6713	1461.6533	0.0181	22	-	32	0	FECACFLFNVR
1590.7750	1589.7677	1589.7482	0.0195	22	-	33	1	FECACFLFNVRK

2335.0967	2334.0894	2334.1280	-0.0386	153 - 173	0	ANYEDLSNQAIHYAQGLPFAL

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1102.5865, 1137.5557, 1145.0549, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1507.7019, 1523.7008, 1565.7437, 1618.7762, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679, 1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2305.1426, 2311.1431, 2351.0886, 2354.0974, 2438.2778, 2454.2830, 2530.3059, 2555.3342, 2652.4292, 2737.3567, 2785.4136, 2838.4014, 3136.5081, 3154.4890, 3211.5364, 3244.6440, 3301.7947, 3612.9944, 3831.9758, 3833.0142

10. gi|62177574 **Mass:** 20142 **Score:** 21 **Expect:** 7.1 **Queries matched:** 4

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1145.5597	1144.5524	1144.5724	-0.0199	36 -	45	0	ISDQEEGLVR
1462.6786	1461.6713	1461.6533	0.0181	24 -	34	0	FECACFLFNVR
1590.7750	1589.7677	1589.7482	0.0195	24 -	35	1	FECACFLFNVRK
2335.0967	2334.0894	2334.1280	-0.0386	155 -	175	0	ANYEDLSNQAIHYAQGLPFAL

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1102.5865, 1137.5557, 1145.0549, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1507.7019, 1523.7008, 1565.7437, 1618.7762, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679, 1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2305.1426, 2311.1431, 2351.0886, 2354.0974, 2438.2778, 2454.2830, 2530.3059, 2555.3342, 2652.4292, 2737.3567, 2785.4136, 2838.4014, 3136.5081, 3154.4890, 3211.5364, 3244.6440, 3301.7947, 3612.9944, 3831.9758, 3833.0142

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 76

Protein View

Match to: **gi|47933675** Score: **62** Expect: **0.00058**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**

NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **76**
Number of mass values matched: **11**
Sequence Coverage: **31%**

Matched peptides shown in **Bold Red**

```
    1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
   51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
  101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
  151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
  201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
  251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
  301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
  351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
  401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
  451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
  501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
342 - 356	1618.7762	1617.7689	1617.7746	-0.0057	0	SSNPDIYNPQAGSLR
357 - 380	2652.4292	2651.4219	2651.4070	0.0149	0	SVNELDLPILGWLGLSAQHGTIYR
381 - 402	2438.2778	2437.2705	2437.2688	0.0017	0	NAMFVPHYTLNAHTIVVALNGR
381 - 402	2454.2830	2453.2757	2453.2637	0.0120	0	NAMFVPHYTLNAHTIVVALNGR Oxidation (M)
403 - 437	3831.9758	3830.9685	3830.9338	0.0347	1	AHVQVVDSNGNRVYDEELQEGHVLVVPQNFAVAAK
415 - 437	2555.3342	2554.3269	2554.3066	0.0203	0	VYDEELQEGHVLVVPQNFAVAAK
438 - 449	1462.6786	1461.6713	1461.6775	-0.0062	0	AQSENYEYLAFK
450 - 479	3244.6440	3243.6367	3243.6006	0.0361	0	TDSRPSIANLAGENSIIDNLPEEVVANSYR
487 - 495	1102.5865	1101.5792	1101.5930	-0.0138	1	QLKNNNPFK
496 - 507	1507.7019	1506.6946	1506.7078	-0.0131	0	FFVPPFDHQSMR
496 - 507	1523.7008	1522.6935	1522.7027	-0.0091	0	FFVPPFDHQSMR Oxidation (M)

No match to: 805.4559, 855.0679, 861.0791, 877.0543, 1046.6019, 1066.0750, 1080.5132, 1082.0345, 1082.5220, 1085.5723, 1137.5557, 1145.0549, 1145.5597, 1175.5745, 1209.5509, 1217.5588, 1220.5699, 1293.6409, 1294.6299, 1295.6094, 1296.6237, 1302.6721, 1306.6440, 1330.6652, 1367.6158, 1396.7849, 1461.7266, 1565.7437, 1590.7750, 1634.7440, 1636.7494, 1640.7501, 1652.7439, 1668.7401, 1714.6631, 1756.8076, 1774.8214, 1861.9679, 1913.9403, 1918.9309, 1934.8951, 1993.9584, 2146.6243, 2185.0369, 2201.0225, 2207.0249, 2225.0095, 2227.1084, 2273.1602, 2295.1431, 2305.1426, 2311.1431, 2335.0967, 2351.0886, 2354.0974, 2530.3059, 2737.3567, 2785.4136, 2838.4014, 3136.5081, 3154.4890, 3211.5364, 3301.7947, 3612.9944, 3833.0142

Spot 65

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:53:52 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **83 for gi|47933675, glycinin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	83	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	83	iso-Ara h3 [Arachis hypogaea]
3.	gi|2498261	2416	17	33.0 kDa cold shock protein (AHCSP33)
4.	gi|110617834	4438	14	drought-responsive protein [Arachis hypogaea]
5.	gi|5923742	15489	11	allergen Arah6 [Arachis hypogaea]
6.	gi|37221937	18271	11	resistance protein [Arachis hypogaea]
7.	gi|71040665	15203	10	Cu-Zn superoxide dismutase [Arachis hypogaea]
8.	gi|5902968	14156	10	profilin [Arachis hypogaea]
9.	gi|14423864	14156	10	Profilin (Allergen Ara h 5)
10.	gi|62177363	18791	10	resistance protein Cre [Arachis hypogaea]LFSLEVFCGEKCPLELEPIGRSIAKSCKGLPLAIKTIAGFVLKRERSEDAWKEI

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 83 **Expect:** 4.6e-006 **Queries matched:** 4
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1481.5979	1480.5906	1480.6000	-0.0094	23	-	34	0	---	QGGEENECQFQR
1481.5979	1480.5906	1480.6000	-0.0094	23	-	34	0	55	QGGEENECQFQR
1547.7349	1546.7276	1546.7389	-0.0113	209	-	220	0	16	YQQQQGSRPHYR
1547.7349	1546.7276	1546.7389	-0.0113	209	-	220	0	---	YQQQQGSRPHYR

No match to: 982.5646, 1151.7123, 1434.8922, 1464.5709, 1588.7728, 1588.7728, 1618.0560, 1732.0957, 1744.8746, 1744.8746, 1902.2437, 1957.8473, 1957.8473, 2212.0930, 3074.3677

2. gi|112380623 **Mass:** 58570 **Score:** 83 **Expect:** 4.6e-006 **Queries matched:** 4

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1481.5979	1480.5906	1480.6000	-0.0094	25	-	36	0	---	QGGEENECQFQR
1481.5979	1480.5906	1480.6000	-0.0094	25	-	36	0	55	QGGEENECQFQR
1547.7349	1546.7276	1546.7389	-0.0113	211	-	222	0	16	YQQQQGSRPHYR
1547.7349	1546.7276	1546.7389	-0.0113	211	-	222	0	---	YQQQQGSRPHYR

No match to: 982.5646, 1151.7123, 1434.8922, 1464.5709, 1588.7728, 1588.7728, 1618.0560, 1732.0957, 1744.8746, 1744.8746, 1902.2437, 1957.8473, 1957.8473, 2212.0930, 3074.3677

3. gi|2498261 **Mass:** 2416 **Score:** 17 **Expect:** 16 **Queries matched:** 2

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1547.7349	1546.7276	1546.7263	0.0013	9	-	24	0	---	ASYTVTPPAQANAADA
1547.7349	1546.7276	1546.7263	0.0013	9	-	24	0	---	ASYTVTPPAQANAADA

No match to: 982.5646, 1151.7123, 1434.8922, 1464.5709, 1481.5979, 1481.5979, 1588.7728, 1588.7728, 1618.0560, 1732.0957, 1744.8746, 1744.8746, 1902.2437, 1957.8473, 1957.8473, 2212.0930, 3074.3677

4. gi|110617834 **Mass:** 4438 **Score:** 14 **Expect:** 38 **Queries matched:** 2

drought-responsive protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1481.5979	1480.5906	1480.6591	-0.0685	18	-	28	1	---	FRTGLCYYCNK
1481.5979	1480.5906	1480.6591	-0.0685	18	-	28	1	---	FRTGLCYYCNK

No match to: 982.5646, 1151.7123, 1434.8922, 1464.5709, 1547.7349, 1547.7349, 1588.7728, 1588.7728, 1618.0560, 1732.0957, 1744.8746, 1744.8746, 1902.2437, 1957.8473, 1957.8473, 2212.0930, 3074.3677

5. gi|5923742 **Mass:** 15489 **Score:** 11 **Expect:** 73 **Queries matched:** 1

allergen Arah6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
3074.3677	3073.3604	3073.3763	-0.0159	13	-	38	1	---	QGDSSSCERQVDGVNLKPCEQHIMQR + Oxidation (M)

No match to: 982.5646, 1151.7123, 1434.8922, 1464.5709, 1481.5979, 1481.5979, 1547.7349, 1547.7349, 1588.7728, 1588.7728, 1618.0560, 1732.0957, 1744.8746, 1744.8746, 1902.2437, 1957.8473, 1957.8473, 2212.0930

6. gi|37221937 **Mass:** 18271 **Score:** 11 **Expect:** 76 **Queries matched:** 1

resistance protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
2212.0930	2211.0857	2211.2110	-0.1252	68	-	87	1	---	VLLVLDDISERSQLENLAGK

No match to: 982.5646, 1151.7123, 1434.8922, 1464.5709, 1481.5979, 1481.5979, 1547.7349, 1547.7349, 1588.7728, 1588.7728, 1618.0560, 1732.0957, 1744.8746, 1744.8746, 1902.2437, 1957.8473, 1957.8473, 3074.3677

7. gi|71040665 **Mass:** 15203 **Score:** 10 **Expect:** 80 **Queries matched:** 2

Cu-Zn superoxide dismutase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1588.7728	1587.7655	1587.7674	-0.0019	135 - 152	0	---	STGNAGGGVACGIIGLQG
1588.7728	1587.7655	1587.7674	-0.0019	135 - 152	0	---	STGNAGGGVACGIIGLQG

No match to: 982.5646, 1151.7123, 1434.8922, 1464.5709, 1481.5979, 1481.5979, 1547.7349, 1547.7349, 1618.0560, 1732.0957, 1744.8746, 1744.8746, 1902.2437, 1957.8473, 1957.8473, 2212.0930, 3074.3677

8. gi|5902968 **Mass:** 14156 **Score:** 10 **Expect:** 80 **Queries matched:** 2

profilin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1588.7728	1587.7655	1587.8330	-0.0675	72 -	86	0	---	YMVIQGEPGAIIPGK + Oxidation (M)
1588.7728	1587.7655	1587.8330	-0.0675	72 -	86	0	---	YMVIQGEPGAIIPGK + Oxidation (M)

No match to: 982.5646, 1151.7123, 1434.8922, 1464.5709, 1481.5979, 1481.5979, 1547.7349, 1547.7349, 1618.0560, 1732.0957, 1744.8746, 1744.8746, 1902.2437, 1957.8473, 1957.8473, 2212.0930, 3074.3677

9. gi|14423864 **Mass:** 14156 **Score:** 10 **Expect:** 80 **Queries matched:** 2

Profilin (Allergen Ara h 5)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1588.7728	1587.7655	1587.8330	-0.0675	72 -	86	0	---	YMVIQGEPGAIIPGK + Oxidation (M)
1588.7728	1587.7655	1587.8330	-0.0675	72 -	86	0	---	YMVIQGEPGAIIPGK + Oxidation (M)

No match to: 982.5646, 1151.7123, 1434.8922, 1464.5709, 1481.5979, 1481.5979, 1547.7349, 1547.7349, 1618.0560, 1732.0957, 1744.8746, 1744.8746, 1902.2437, 1957.8473, 1957.8473, 2212.0930, 3074.3677

10. gi|62177363 **Mass:** 18791 **Score:** 10 **Expect:** 82 **Queries matched:** 1

resistance protein Cre [Arachis hypogaea]LFSLEVFCGEKCPLELEPIGRSIAKSCKGLPLAIKTIAGFVLKRERSEDAWKEIMNLL

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2212.0930	2211.0857	2211.0225	0.0632	112 -	131	1	---	KMISNDDGANSELSNIQFGR + Oxidation (M)

No match to: 982.5646, 1151.7123, 1434.8922, 1464.5709, 1481.5979, 1481.5979, 1547.7349, 1547.7349, 1588.7728, 1588.7728, 1618.0560, 1732.0957, 1744.8746, 1744.8746, 1902.2437, 1957.8473, 1957.8473, 3074.3677

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Number of Queries: 19

Protein View

Match to: **gi|112380623** Score: **83** Expect: **4.6e-006**
iso-Ara h3 [Arachis hypogaea]

Nominal mass (M_r): **58570**; Calculated pI value: **5.41**
NCBI BLAST search of gi|112380623 against nr
Unformatted sequence string for pasting into other applications

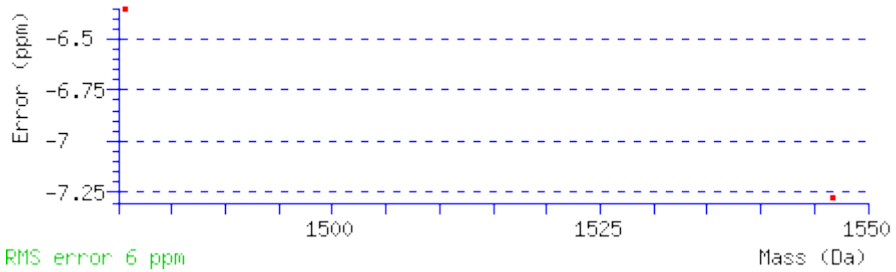
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **4%**

Matched peptides shown in **Bold Red**

```
    1 MAKLLALSLC FCVLVLGASS VTFRQGGEEN ECQFQRLNAQ RPDNRIESEG
   51 GYIETWNPNN QEFQCAGVAL SRTVLRRNAL RRPFYSNAPL EIYVQQGSGY
  101 FGLIFPGCPS TYEEPAQEGR RYQSQKPSRR FQVGQDDPSQ QQQDSHQKVH
  151 RFDEGDLIAV PTGVAFWMYN DEDTDVVTVT LSDTSSIHNQ LDQFPRRFYL
  201 AGNQEQEFLR YQQQQGSRPH YRQISPRVRG DEQENEGSNI FSGFAQEFLQ
  251 HAFQVDRQTV ENLRGENERE EQGAIVTVKG GLRILSPDEE DESSRSPPSR
  301 REEFDEDRSR PQQRGKYDEN RRGYKNGIEE TICSASVKKN LGRSSNPDIY
  351 NPQAGSLRSV NELDLPILGW LGLSAQHGTI YRNAMFVPHY TLNAHTIVVA
  401 LNGRAHVQVV DSNGNRVYDE ELQEGHVLVV PQNFAVAAKA QSENYEYLAF
  451 KTDSRPSIAN LAGENSIIDN LPEEVVANSY RLPREQARQL KNNNPFKFFV
  501 PPFDHQSMRE VA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
25 - 36	1481.5979	1480.5906	1480.6000	-0.0094	0	QGGEENECQFQR	(No match)
25 - 36	1481.5979	1480.5906	1480.6000	-0.0094	0	QGGEENECQFQR	(Ions score 55)
211 - 222	1547.7349	1546.7276	1546.7389	-0.0113	0	YQQQQGSRPHYR	(Ions score 16)
211 - 222	1547.7349	1546.7276	1546.7389	-0.0113	0	YQQQQGSRPHYR	(No match)


Error (ppm)
-6.5
-6.75
-7
-7.25
1500
1525
1550
Mass (Da)
RMS error 6 ppm

Spot 66

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:37:36 GMT**
Top Score : **74 for gi|47933675, glycinin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	74	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	74	iso-Ara h3 [Arachis hypogaea]
3.	gi|57669861	61041	18	arachin Ahy-4 [Arachis hypogaea]
4.	gi|108595573	61041	18	arachin Ahy-4 [Arachis hypogaea]
5.	gi|52001219	61810	17	arachin Ahy-1 [Arachis hypogaea]
6.	gi|37789212	61803	17	storage protein [Arachis hypogaea]
7.	gi|21314465	62042	17	allergen Arah3/Arah4 [Arachis hypogaea]
8.	gi|5712199	61430	17	glycinin [Arachis hypogaea]
9.	gi|62177598	17945	14	resistance protein PRG [Arachis hypogaea]
10.	gi|225546	5845	14	isolectine B alpha

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 74 **Expect:** 3.8e-005 **Queries matched:** 8
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1523.7008	1522.6935	1522.7027	-0.0091	496	507	0	FFVPPFDHQSMR + Oxidation (M)
1618.7781	1617.7708	1617.7746	-0.0038	342	356	0	SSNPDIYNPQAGSLR
2238.0444	2237.0371	2237.0476	-0.0104	490	507	1	NNNPFKFFVPPFDHQSMR + Oxidation (M)
2438.2620	2437.2547	2437.2688	-0.0141	381	402	0	NAMFVPHYTLNAHTIVVALNGR
2454.2734	2453.2661	2453.2637	0.0024	381	402	0	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)
2652.4084	2651.4011	2651.4070	-0.0059	357	380	0	SVNELDLPILGWLGLSAQHGTIYR
3244.6292	3243.6219	3243.6006	0.0213	450	479	0	TDSRPSIANLAGENSIIDNLPEEVVANSYR
3610.8665	3609.8592	3609.8386	0.0206	450	482	1	TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR

No match to: 1080.5240, 1111.5599, 1118.5892, 1133.5304, 1306.6792, 1541.7618, 1636.7426, 1652.7462, 1847.8944,

1861.9714, 2273.1643, 2305.1331, 2314.1997, 2367.0972, 2391.2581, 2392.3225, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3832.9614

2. gi|112380623 **Mass:** 58570 **Score:** 74 **Expect:** 3.9e-005 **Queries matched:** 8

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1523.7008	1522.6935	1522.7027	-0.0091	498	509	0	FFVPPFDHQSMR + Oxidation (M)
1618.7781	1617.7708	1617.7746	-0.0038	344	358	0	SSNPDIYNPQAGSLR
2238.0444	2237.0371	2237.0476	-0.0104	492	509	1	NNNPFKFFVPPFDHQSMR + Oxidation (M)
2438.2620	2437.2547	2437.2688	-0.0141	383	404	0	NAMFVPHYTLNAHTIVVALNGR
2454.2734	2453.2661	2453.2637	0.0024	383	404	0	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)
2652.4084	2651.4011	2651.4070	-0.0059	359	382	0	SVNELDLPILGWLGLSAQHGTIYR
3244.6292	3243.6219	3243.6006	0.0213	452	481	0	TDSRPSIANLAGENSIIDNLPEEVVANSYR
3610.8665	3609.8592	3609.8386	0.0206	452	484	1	TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR

No match to: 1080.5240, 1111.5599, 1118.5892, 1133.5304, 1306.6792, 1541.7618, 1636.7426, 1652.7462, 1847.8944, 1861.9714, 2273.1643, 2305.1331, 2314.1997, 2367.0972, 2391.2581, 2392.3225, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3832.9614

3. gi|57669861 **Mass:** 61041 **Score:** 18 **Expect:** 15 **Queries matched:** 3

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1541.7618	1540.7545	1540.7673	-0.0128	389	401	0	WLGLSAEYGNLYR
1618.7781	1617.7708	1617.7481	0.0227	288	302	0	GENESEEEGAIVTVR
2314.1997	2313.1924	2313.2018	-0.0093	402	421	0	NALFVPHYNTNAHSIIYALR

No match to: 1080.5240, 1111.5599, 1118.5892, 1133.5304, 1306.6792, 1523.7008, 1636.7426, 1652.7462, 1847.8944, 1861.9714, 2238.0444, 2273.1643, 2305.1331, 2367.0972, 2391.2581, 2392.3225, 2438.2620, 2454.2734, 2652.4084, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3244.6292, 3610.8665, 3832.9614

4. gi|108595573 **Mass:** 61041 **Score:** 18 **Expect:** 15 **Queries matched:** 3

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1541.7618	1540.7545	1540.7673	-0.0128	389	401	0	WLGLSAEYGNLYR
1618.7781	1617.7708	1617.7481	0.0227	288	302	0	GENESEEEGAIVTVR
2314.1997	2313.1924	2313.2018	-0.0093	402	421	0	NALFVPHYNTNAHSIIYALR

No match to: 1080.5240, 1111.5599, 1118.5892, 1133.5304, 1306.6792, 1523.7008, 1636.7426, 1652.7462, 1847.8944, 1861.9714, 2238.0444, 2273.1643, 2305.1331, 2367.0972, 2391.2581, 2392.3225, 2438.2620, 2454.2734, 2652.4084, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3244.6292, 3610.8665, 3832.9614

5. gi|52001219 **Mass:** 61810 **Score:** 17 **Expect:** 18 **Queries matched:** 3

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1306.6792	1305.6719	1305.6717	0.0002	523	533	0	FFVPPSEQSLR

1541.7618	1540.7545	1540.7673	-0.0128	395 - 407	0	WLGLSAEYGNLYR
2314.1997	2313.1924	2313.2018	-0.0093	408 - 427	0	NALFVPHYNTNAHSIIYALR

No match to: 1080.5240, 1111.5599, 1118.5892, 1133.5304, 1523.7008, 1618.7781, 1636.7426, 1652.7462, 1847.8944, 1861.9714, 2238.0444, 2273.1643, 2305.1331, 2367.0972, 2391.2581, 2392.3225, 2438.2620, 2454.2734, 2652.4084, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3244.6292, 3610.8665, 3832.9614

6. gi|37789212 **Mass:** 61803 **Score:** 17 **Expect:** 18 **Queries matched:** 3

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1306.6792	1305.6719	1305.6717	0.0002	523 - 533		0	FFVPPSEQSLR
1541.7618	1540.7545	1540.7673	-0.0128	395 - 407		0	WLGLSAEYGNLYR
2314.1997	2313.1924	2313.2018	-0.0093	408 - 427		0	NALFVPHYNTNAHSIIYALR

No match to: 1080.5240, 1111.5599, 1118.5892, 1133.5304, 1523.7008, 1618.7781, 1636.7426, 1652.7462, 1847.8944, 1861.9714, 2238.0444, 2273.1643, 2305.1331, 2367.0972, 2391.2581, 2392.3225, 2438.2620, 2454.2734, 2652.4084, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3244.6292, 3610.8665, 3832.9614

7. gi|21314465 **Mass:** 62042 **Score:** 17 **Expect:** 18 **Queries matched:** 3

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1306.6792	1305.6719	1305.6717	0.0002	525 - 535		0	FFVPPSEQSLR
1541.7618	1540.7545	1540.7673	-0.0128	397 - 409		0	WLGLSAEYGNLYR
2314.1997	2313.1924	2313.2018	-0.0093	410 - 429		0	NALFVPHYNTNAHSIIYALR

No match to: 1080.5240, 1111.5599, 1118.5892, 1133.5304, 1523.7008, 1618.7781, 1636.7426, 1652.7462, 1847.8944, 1861.9714, 2238.0444, 2273.1643, 2305.1331, 2367.0972, 2391.2581, 2392.3225, 2438.2620, 2454.2734, 2652.4084, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3244.6292, 3610.8665, 3832.9614

8. gi|5712199 **Mass:** 61430 **Score:** 17 **Expect:** 19 **Queries matched:** 3

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1118.5892	1117.5819	1117.5628	0.0191	235 - 242		1	EEREFRPR
1541.7618	1540.7545	1540.7673	-0.0128	389 - 401		0	WLGLSAEYGNLYR
2314.1997	2313.1924	2313.2018	-0.0093	402 - 421		0	NALFVPHYNTNAHSIIYALR

No match to: 1080.5240, 1111.5599, 1133.5304, 1306.6792, 1523.7008, 1618.7781, 1636.7426, 1652.7462, 1847.8944, 1861.9714, 2238.0444, 2273.1643, 2305.1331, 2367.0972, 2391.2581, 2392.3225, 2438.2620, 2454.2734, 2652.4084, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3244.6292, 3610.8665, 3832.9614

9. gi|62177598 **Mass:** 17945 **Score:** 14 **Expect:** 33 **Queries matched:** 1

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
3832.9614	3831.9541	3832.0158	-0.0617	76 - 110		1	VLLVLDDVHDGGLLENLAGEQDWFGPASRIIIITTR

No match to: 1080.5240, 1111.5599, 1118.5892, 1133.5304, 1306.6792, 1523.7008, 1541.7618, 1618.7781, 1636.7426, 1652.7462, 1847.8944, 1861.9714, 2238.0444, 2273.1643, 2305.1331, 2314.1997, 2367.0972, 2391.2581, 2392.3225,

2438.2620, 2454.2734, 2652.4084, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3244.6292, 3610.8665

10. gi|225546 **Mass:** 5845 **Score:** 14 **Expect:** 34 **Queries matched:** 1

isolectine B alpha

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2392.3225	2391.3152	2391.2685	0.0467	1 -	21	1	VTSYTLSDVVSLKDVVPEWVR

No match to: 1080.5240, 1111.5599, 1118.5892, 1133.5304, 1306.6792, 1523.7008, 1541.7618, 1618.7781, 1636.7426, 1652.7462, 1847.8944, 1861.9714, 2238.0444, 2273.1643, 2305.1331, 2314.1997, 2367.0972, 2391.2581, 2438.2620, 2454.2734, 2652.4084, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3244.6292, 3610.8665, 3832.9614

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 29

Protein View

Match to: **gi|47933675** Score: **74** Expect: **3.8e-005**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **29**
Number of mass values matched: **8**
Sequence Coverage: **21%**

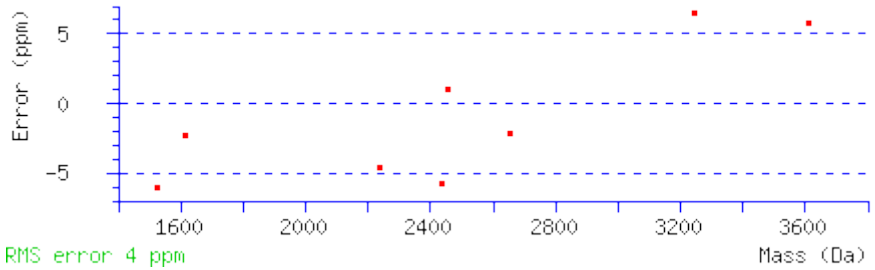
Matched peptides shown in **Bold Red**

```
   1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
  51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
 101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
 151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
 201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
 251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
 301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
 351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
 401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
 451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
 501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
342 - 356	1618.7781	1617.7708	1617.7746	-0.0038	0	SSNPDIYNPQAGSLR
357 - 380	2652.4084	2651.4011	2651.4070	-0.0059	0	SVNELDLPILGWLGLSAQHGTIYR
381 - 402	2438.2620	2437.2547	2437.2688	-0.0141	0	NAMFVPHYTLNAHTIVVALNGR
381 - 402	2454.2734	2453.2661	2453.2637	0.0024	0	NAMFVPHYTLNAHTIVVALNGR Oxidation (M)
450 - 479	3244.6292	3243.6219	3243.6006	0.0213	0	TDSRPSIANLAGENSIIDNLPEEVVANSYR
450 - 482	3610.8665	3609.8592	3609.8386	0.0206	1	TDSRPSIANLAGENSIIDNLPEEVVANSYRLPR
490 - 507	2238.0444	2237.0371	2237.0476	-0.0104	1	NNNPFKFFVPPFDHQSMR Oxidation (M)
496 - 507	1523.7008	1522.6935	1522.7027	-0.0091	0	FFVPPFDHQSMR Oxidation (M)

No match to: 1080.5240, 1111.5599, 1118.5892, 1133.5304, 1306.6792, 1541.7618, 1636.7426, 1652.7462, 1847.8944, 1861.9714, 2273.1643, 2305.1331, 2314.1997, 2367.0972, 2391.2581, 2392.3225, 2684.4128, 2719.3333, 2736.3655, 3228.5425, 3832.9614



Spot 67

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:11:34 GMT
Top Score : 82 for gi|47933675, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	82	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	82	iso-Ara h3 [Arachis hypogaea]
3.	gi|62177648	7475	21	resistance protein PRG [Arachis hypogaea]
4.	gi|62177463	9663	21	resistance protein PNTR [Arachis hypogaea]
5.	gi|50982245	17988	20	recombination protein A [Bradyrhizobium liaoningense]
6.	gi|62177598	17945	16	resistance protein PRG [Arachis hypogaea]
7.	gi|62177433	15552	15	resistance protein PNTR [Arachis hypogaea]
8.	gi|31558995	91467	15	phospholipase D [Arachis hypogaea]
9.	gi|88193699	91214	15	phospholipase D alpha 1 [Arachis hypogaea]
10.	gi|88193695	91214	15	phospholipase D alpha 1 [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 82 **Expect:** 5.5e-006 **Queries matched:** 14
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6006	1101.5933	1101.5930	0.0003	487	495	1	QLKNNNPFK
1295.6251	1294.6178	1294.6377	-0.0199	403	414	0	AHVQVVDSNGNR
1462.6781	1461.6708	1461.6775	-0.0067	438	449	0	AQSENYEYLAFK
1507.6960	1506.6887	1506.7078	-0.0190	496	507	0	FFVPPFDHQSMR
1523.6993	1522.6920	1522.7027	-0.0106	496	507	0	FFVPPFDHQSMR + Oxidation (M)
1618.7821	1617.7748	1617.7746	0.0002	342	356	0	SSNPDIYNPQAGSLR
2059.0532	2058.0459	2058.0242	0.0217	338	356	1	NLGRSSNPDIYNPQAGSLR
2238.0610	2237.0537	2237.0476	0.0062	490	507	1	NNNPFKFFVPPFDHQSMR + Oxidation (M)
2438.2747	2437.2674	2437.2688	-0.0014	381	402	0	NAMFVPHYTLNAHTIVVALNGR
2454.2864	2453.2791	2453.2637	0.0154	381	402	0	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)
2555.3364	2554.3291	2554.3066	0.0225	415	437	0	VYDEELQEGHVLVVPQNFAVAAK

2652.4341	2651.4268	2651.4070	0.0198	357 - 380	0	SVNELDLPILGWLGLSAQHGTIYR
3244.6750	3243.6677	3243.6006	0.0671	450 - 479	0	TDSRPSIANLAGENSIIDNLPEEVVANSYR
3832.0320	3831.0247	3830.9338	0.0909	403 - 437	1	AHVQVVDSNGNRVYDEELQEGHVLVVPQNFAVAAK

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1145.5698, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1278.6346, 1293.6327, 1294.6146, 1296.6315, 1330.6675, 1421.7242, 1443.7078, 1461.7192, 1484.6707, 1590.7668, 1600.7666, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1756.8306, 1774.8951, 1805.8672, 1861.9733, 1875.9479, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2185.0354, 2225.0134, 2227.1121, 2273.1592, 2305.1589, 2311.1433, 2351.0835, 2354.1011, 2367.1055, 2392.3469, 2437.2446, 2577.3105, 2617.2605, 2669.4180, 2719.3557, 2736.3557, 2785.4263, 2839.4922, 3211.5325, 3461.8926, 3610.9387, 3833.0439

2. gi|112380623 **Mass:** 58570 **Score:** 82 **Expect:** 5.6e-006 **Queries matched:** 14

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6006	1101.5933	1101.5930	0.0003	489 - 497		1	QLKNNNPFK
1295.6251	1294.6178	1294.6377	-0.0199	405 - 416		0	AHVQVVDSNGNR
1462.6781	1461.6708	1461.6775	-0.0067	440 - 451		0	AQSENYEYLAFK
1507.6960	1506.6887	1506.7078	-0.0190	498 - 509		0	FFVPPFDHQSMR
1523.6993	1522.6920	1522.7027	-0.0106	498 - 509		0	FFVPPFDHQSMR + Oxidation (M)
1618.7821	1617.7748	1617.7746	0.0002	344 - 358		0	SSNPDIYNPQAGSLR
2059.0532	2058.0459	2058.0242	0.0217	340 - 358		1	NLGRSSNPDIYNPQAGSLR
2238.0610	2237.0537	2237.0476	0.0062	492 - 509		1	NNNPFKFFVPPFDHQSMR + Oxidation (M)
2438.2747	2437.2674	2437.2688	-0.0014	383 - 404		0	NAMFVPHYTLNAHTIVVALNGR
2454.2864	2453.2791	2453.2637	0.0154	383 - 404		0	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)
2555.3364	2554.3291	2554.3066	0.0225	417 - 439		0	VYDEELQEGHVLVVPQNFAVAAK
2652.4341	2651.4268	2651.4070	0.0198	359 - 382		0	SVNELDLPILGWLGLSAQHGTIYR
3244.6750	3243.6677	3243.6006	0.0671	452 - 481		0	TDSRPSIANLAGENSIIDNLPEEVVANSYR
3832.0320	3831.0247	3830.9338	0.0909	405 - 439		1	AHVQVVDSNGNRVYDEELQEGHVLVVPQNFAVAAK

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1145.5698, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1278.6346, 1293.6327, 1294.6146, 1296.6315, 1330.6675, 1421.7242, 1443.7078, 1461.7192, 1484.6707, 1590.7668, 1600.7666, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1756.8306, 1774.8951, 1805.8672, 1861.9733, 1875.9479, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2185.0354, 2225.0134, 2227.1121, 2273.1592, 2305.1589, 2311.1433, 2351.0835, 2354.1011, 2367.1055, 2392.3469, 2437.2446, 2577.3105, 2617.2605, 2669.4180, 2719.3557, 2736.3557, 2785.4263, 2839.4922, 3211.5325, 3461.8926, 3610.9387, 3833.0439

3. gi|62177648 **Mass:** 7475 **Score:** 21 **Expect:** 7 **Queries matched:** 3

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1145.5698	1144.5625	1144.5724	-0.0098	34 - 43		0	ISDQEEGLVR
1462.6781	1461.6708	1461.6533	0.0176	22 - 32		0	FECACFLFNVR

1590.7668	1589.7595	1589.7482	0.0113	22 -	33	1	FECACFLFNVRK

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1102.6006, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1278.6346, 1293.6327, 1294.6146, 1295.6251, 1296.6315, 1330.6675, 1421.7242, 1443.7078, 1461.7192, 1484.6707, 1507.6960, 1523.6993, 1600.7666, 1618.7821, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1756.8306, 1774.8951, 1805.8672, 1861.9733, 1875.9479, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2059.0532, 2185.0354, 2225.0134, 2227.1121, 2238.0610, 2273.1592, 2305.1589, 2311.1433, 2351.0835, 2354.1011, 2367.1055, 2392.3469, 2437.2446, 2438.2747, 2454.2864, 2555.3364, 2577.3105, 2617.2605, 2652.4341, 2669.4180, 2719.3557, 2736.3557, 2785.4263, 2839.4922, 3211.5325, 3244.6750, 3461.8926, 3610.9387, 3832.0320, 3833.0439

4. gi|62177463 **Mass:** 9663 **Score:** 21 **Expect:** 7.6 **Queries matched:** 3

resistance protein PNTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1145.5698	1144.5625	1144.5724	-0.0098	32 -	41	0	ISDQEEGLVR
1462.6781	1461.6708	1461.6533	0.0176	20 -	30	0	FECACFLFNVR
1590.7668	1589.7595	1589.7482	0.0113	20 -	31	1	FECACFLFNVRK

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1102.6006, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1278.6346, 1293.6327, 1294.6146, 1295.6251, 1296.6315, 1330.6675, 1421.7242, 1443.7078, 1461.7192, 1484.6707, 1507.6960, 1523.6993, 1600.7666, 1618.7821, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1756.8306, 1774.8951, 1805.8672, 1861.9733, 1875.9479, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2059.0532, 2185.0354, 2225.0134, 2227.1121, 2238.0610, 2273.1592, 2305.1589, 2311.1433, 2351.0835, 2354.1011, 2367.1055, 2392.3469, 2437.2446, 2438.2747, 2454.2864, 2555.3364, 2577.3105, 2617.2605, 2652.4341, 2669.4180, 2719.3557, 2736.3557, 2785.4263, 2839.4922, 3211.5325, 3244.6750, 3461.8926, 3610.9387, 3832.0320, 3833.0439

5. gi|50982245 **Mass:** 17988 **Score:** 20 **Expect:** 9.6 **Queries matched:** 3

recombination protein A [Bradyrhizobium liaoningense]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1278.6346	1277.6273	1277.6503	-0.0229	36 -	47	0	IVEIYGPESSGK
1756.8306	1755.8233	1755.8461	-0.0227	128 -	144	0	AELEGEMGDALPGLQAR
2785.4263	2784.4190	2784.4326	-0.0136	6 -	33	1	NDRSMDIEAVSSGSLGLDIALGIGGLPK

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1102.6006, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1145.5698, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1293.6327, 1294.6146, 1295.6251, 1296.6315, 1330.6675, 1421.7242, 1443.7078, 1461.7192, 1462.6781, 1484.6707, 1507.6960, 1523.6993, 1590.7668, 1600.7666, 1618.7821, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1774.8951, 1805.8672, 1861.9733, 1875.9479, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2059.0532, 2185.0354, 2225.0134, 2227.1121, 2238.0610, 2273.1592, 2305.1589, 2311.1433, 2351.0835, 2354.1011, 2367.1055, 2392.3469, 2437.2446, 2438.2747, 2454.2864, 2555.3364, 2577.3105, 2617.2605, 2652.4341, 2669.4180, 2719.3557, 2736.3557, 2839.4922, 3211.5325, 3244.6750, 3461.8926, 3610.9387, 3832.0320, 3833.0439

6. gi|62177598 **Mass:** 17945 **Score:** 16 **Expect:** 24 **Queries matched:** 2

resistance protein PRG [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1330.6675	1329.6602	1329.6533	0.0069	65 -	75	1	GIICDSLCHKK
3833.0439	3832.0366	3832.0158	0.0208	76 -	110	1	VLLVLDDVHDGGLLENLAGEQDWFGPASRIIITTR

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1102.6006, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1145.5698, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1278.6346, 1293.6327, 1294.6146, 1295.6251, 1296.6315, 1421.7242, 1443.7078, 1461.7192, 1462.6781, 1484.6707, 1507.6960, 1523.6993, 1590.7668, 1600.7666, 1618.7821, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1756.8306, 1774.8951, 1805.8672, 1861.9733, 1875.9479, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2059.0532, 2185.0354, 2225.0134, 2227.1121, 2238.0610, 2273.1592, 2305.1589, 2311.1433, 2351.0835, 2354.1011, 2367.1055, 2392.3469, 2437.2446, 2438.2747, 2454.2864, 2555.3364, 2577.3105, 2617.2605, 2652.4341, 2669.4180, 2719.3557, 2736.3557, 2785.4263, 2839.4922, 3211.5325, 3244.6750, 3461.8926, 3610.9387, 3832.0320

7. gi|62177433 **Mass:** 15552 **Score:** 15 **Expect:** 28 **Queries matched:** 2

resistance protein PNTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2305.1589	2304.1516	2304.1749	-0.0233	6 -	25	1	TTLAQLVYNDNKVEEHFGVK
2785.4263	2784.4190	2784.3870	0.0320	18 -	41	1	VEEHFGVKAWIDVSQQFDVSHVTK

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1102.6006, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1145.5698, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1278.6346, 1293.6327, 1294.6146, 1295.6251, 1296.6315, 1330.6675, 1421.7242, 1443.7078, 1461.7192, 1462.6781, 1484.6707, 1507.6960, 1523.6993, 1590.7668, 1600.7666, 1618.7821, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1756.8306, 1774.8951, 1805.8672, 1861.9733, 1875.9479, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2059.0532, 2185.0354, 2225.0134, 2227.1121, 2238.0610, 2273.1592, 2311.1433, 2351.0835, 2354.1011, 2367.1055, 2392.3469, 2437.2446, 2438.2747, 2454.2864, 2555.3364, 2577.3105, 2617.2605, 2652.4341, 2669.4180, 2719.3557, 2736.3557, 2839.4922, 3211.5325, 3244.6750, 3461.8926, 3610.9387, 3832.0320, 3833.0439

8. gi|31558995 **Mass:** 91467 **Score:** 15 **Expect:** 28 **Queries matched:** 5

phospholipase D [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1875.9479	1874.9406	1874.9162	0.0244	163 -	178	0	VTLYQDAHVLDDFSPR
2059.0532	2058.0459	2058.0204	0.0256	2 -	19	0	AQFLLHGDINATICETQK
2227.1121	2226.1048	2226.0660	0.0388	638 -	656	0	MMIVDDEYIIIGSANINQR + 2 Oxidation (M)
2311.1433	2310.1360	2310.0811	0.0550	663 -	684	0	DTEIAMGAYQPHHLATSQGGAR
2354.1011	2353.0938	2353.1380	-0.0442	52 -	70	1	LEECFYIRCAHMASNIIVK

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1102.6006, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1145.5698, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1278.6346, 1293.6327, 1294.6146, 1295.6251, 1296.6315, 1330.6675, 1421.7242, 1443.7078, 1461.7192, 1462.6781, 1484.6707, 1507.6960, 1523.6993, 1590.7668, 1600.7666, 1618.7821, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1756.8306, 1774.8951, 1805.8672, 1861.9733, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2185.0354, 2225.0134, 2238.0610, 2273.1592, 2305.1589, 2351.0835, 2367.1055, 2392.3469, 2437.2446, 2438.2747, 2454.2864,

2555.3364, 2577.3105, 2617.2605, 2652.4341, 2669.4180, 2719.3557, 2736.3557, 2785.4263, 2839.4922, 3211.5325, 3244.6750, 3461.8926, 3610.9387, 3832.0320, 3833.0439

9. gi|88193699 **Mass:** 91214 **Score:** 15 **Expect:** 28 **Queries matched:** 5

phospholipase D alpha 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1875.9479	1874.9406	1874.9162	0.0244	163	-	178	0	VTLYQDAHVLDDFSPR
2059.0532	2058.0459	2058.0204	0.0256	2	-	19	0	AQFLLHGDINATICETQK
2227.1121	2226.1048	2226.0660	0.0388	638	-	656	0	MMIVDDEYIIIGSANINQR + 2 Oxidation (M)
2311.1433	2310.1360	2310.0811	0.0550	663	-	684	0	DTEIAMGAYQPHHLATSQGGAR
2354.1011	2353.0938	2353.1380	-0.0442	52	-	70	1	LEECFYIRCAHMASNIIVK

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1102.6006, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1145.5698, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1278.6346, 1293.6327, 1294.6146, 1295.6251, 1296.6315, 1330.6675, 1421.7242, 1443.7078, 1461.7192, 1462.6781, 1484.6707, 1507.6960, 1523.6993, 1590.7668, 1600.7666, 1618.7821, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1756.8306, 1774.8951, 1805.8672, 1861.9733, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2185.0354, 2225.0134, 2238.0610, 2273.1592, 2305.1589, 2351.0835, 2367.1055, 2392.3469, 2437.2446, 2438.2747, 2454.2864, 2555.3364, 2577.3105, 2617.2605, 2652.4341, 2669.4180, 2719.3557, 2736.3557, 2785.4263, 2839.4922, 3211.5325, 3244.6750, 3461.8926, 3610.9387, 3832.0320, 3833.0439

10. gi|88193695 **Mass:** 91214 **Score:** 15 **Expect:** 28 **Queries matched:** 5

phospholipase D alpha 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1875.9479	1874.9406	1874.9162	0.0244	163	-	178	0	VTLYQDAHVLDDFSPR
2059.0532	2058.0459	2058.0204	0.0256	2	-	19	0	AQFLLHGDINATICETQK
2227.1121	2226.1048	2226.0660	0.0388	638	-	656	0	MMIVDDEYIIIGSANINQR + 2 Oxidation (M)
2311.1433	2310.1360	2310.0811	0.0550	663	-	684	0	DTEIAMGAYQPHHLATSQGGAR
2354.1011	2353.0938	2353.1380	-0.0442	52	-	70	1	LEECFYIRCAHMASNIIVK

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1102.6006, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1145.5698, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1278.6346, 1293.6327, 1294.6146, 1295.6251, 1296.6315, 1330.6675, 1421.7242, 1443.7078, 1461.7192, 1462.6781, 1484.6707, 1507.6960, 1523.6993, 1590.7668, 1600.7666, 1618.7821, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1756.8306, 1774.8951, 1805.8672, 1861.9733, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2185.0354, 2225.0134, 2238.0610, 2273.1592, 2305.1589, 2351.0835, 2367.1055, 2392.3469, 2437.2446, 2438.2747, 2454.2864, 2555.3364, 2577.3105, 2617.2605, 2652.4341, 2669.4180, 2719.3557, 2736.3557, 2785.4263, 2839.4922, 3211.5325, 3244.6750, 3461.8926, 3610.9387, 3832.0320, 3833.0439

Search Parameters

Type of search : Peptide Mass Fingerprint

Enzyme : **Trypsin**
Fixed modifications : **Carbamidomethyl (C)**
Variable modifications : **Oxidation (M)**
Mass values : **MONOISOTOPIC**
Protein Mass : **Unrestricted**
Peptide Mass Tolerance : **± 25 ppm**
Peptide Charge State : **1+**
Max Missed Cleavages : **1**
Number of queries : **91**

Protein View

Match to: **gi|47933675** Score: **82** Expect: **5.5e-006**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **91**
Number of mass values matched: **14**
Sequence Coverage: **31%**

Matched peptides shown in **Bold Red**

```
     1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
    51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
   101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
   201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
   251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
   301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
   351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
   401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
   451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
   501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
338 - 356	2059.0532	2058.0459	2058.0242	0.0217	1	NLGRSSNPDIYNPQAGSLR
342 - 356	1618.7821	1617.7748	1617.7746	0.0002	0	SSNPDIYNPQAGSLR
357 - 380	2652.4341	2651.4268	2651.4070	0.0198	0	SVNELDLPILGWLGLSAQHGTIYR
381 - 402	2438.2747	2437.2674	2437.2688	-0.0014	0	NAMFVPHYTLNAHTIVVALNGR
381 - 402	2454.2864	2453.2791	2453.2637	0.0154	0	NAMFVPHYTLNAHTIVVALNGR Oxidation (M)
403 - 414	1295.6251	1294.6178	1294.6377	-0.0199	0	AHVQVVDSNGNR
403 - 437	3832.0320	3831.0247	3830.9338	0.0909	1	AHVQVVDSNGNRVYDEELQEGHVLVVPQNFAVAAK
415 - 437	2555.3364	2554.3291	2554.3066	0.0225	0	VYDEELQEGHVLVVPQNFAVAAK
438 - 449	1462.6781	1461.6708	1461.6775	-0.0067	0	AQSENYEYLAFK
450 - 479	3244.6750	3243.6677	3243.6006	0.0671	0	TDSRPSIANLAGENSIIDNLPEEVVANSYR
487 - 495	1102.6006	1101.5933	1101.5930	0.0003	1	QLKNNNPFK
490 - 507	2238.0610	2237.0537	2237.0476	0.0062	1	NNNPFKFFVPPFDHQSMR Oxidation (M)
496 - 507	1507.6960	1506.6887	1506.7078	-0.0190	0	FFVPPFDHQSMR
496 - 507	1523.6993	1522.6920	1522.7027	-0.0106	0	FFVPPFDHQSMR Oxidation (M)

No match to: 805.4468, 845.1039, 854.0810, 855.0682, 861.0785, 871.0317, 877.0432, 881.3223, 893.0249, 928.4832, 931.4897, 942.5690, 943.5330, 1046.5900, 1066.0673, 1080.5341, 1082.0471, 1085.5721, 1107.5607, 1118.5901, 1124.5768, 1145.0803, 1145.5698, 1175.5618, 1184.5413, 1218.5377, 1227.6285, 1228.1360, 1278.6346, 1293.6327, 1294.6146, 1296.6315, 1330.6675, 1421.7242, 1443.7078, 1461.7192, 1484.6707, 1590.7668, 1600.7666, 1634.7681, 1636.7543, 1640.7549, 1652.7389, 1751.8147, 1756.8306, 1774.8951, 1805.8672, 1861.9733, 1875.9479, 1883.9407, 1916.9662, 1917.4486, 1921.8939, 1923.8851, 2024.0220, 2185.0354, 2225.0134, 2227.1121, 2273.1592, 2305.1589, 2311.1433, 2351.0835, 2354.1011, 2367.1055, 2392.3469, 2437.2446, 2577.3105, 2617.2605, 2669.4180, 2719.3557, 2736.3557, 2785.4263, 2839.4922, 3211.5325, 3461.8926, 3610.9387, 3833.0439

Spot 68

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:11:50 GMT**
Top Score : **53 for gi|9864777, Gly1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|9864777	60754	53	Gly1 [Arachis hypogaea]
2.	gi|57669861	61041	45	arachin Ahy-4 [Arachis hypogaea]
3.	gi|108595573	61041	45	arachin Ahy-4 [Arachis hypogaea]
4.	gi|118776570	60681	44	arachin 6 [Arachis hypogaea]
5.	gi|47933675	58368	43	glycinin [Arachis hypogaea]
6.	gi|112380623	58570	43	iso-Ara h3 [Arachis hypogaea]
7.	gi|3703107	58543	37	glycinin [Arachis hypogaea]
8.	gi|52001221	61836	36	arachin Ahy-2 [Arachis hypogaea]
9.	gi|62177433	15552	29	resistance protein PNTR [Arachis hypogaea]
10.	gi|52001219	61810	27	arachin Ahy-1 [Arachis hypogaea]

Results List

1. gi|9864777 **Mass:** 60754 **Score:** 53 **Expect:** 0.0042 **Queries matched:** 10
Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1102.6042	1101.5969	1101.5930	0.0039	507	-	515	1	QLKNNNPFK
1255.7273	1254.7200	1254.7295	-0.0095	377	-	387	0	TANDLNLLILR
1295.6364	1294.6291	1294.6377	-0.0086	423	-	434	0	AHVQVVDSNGNR
1305.6934	1304.6861	1304.6877	-0.0015	516	-	526	0	FFVPPSQQSLR
1389.7028	1388.6955	1388.6935	0.0020	364	-	376	0	SPDIYNPQAGSLK
1434.6829	1433.6756	1433.6462	0.0294	458	-	469	0	SQSDNFEYVAFK
1541.7694	1540.7621	1540.7673	-0.0052	388	-	400	0	WLGLSAEYGNLYR
1659.8425	1658.8352	1658.8376	-0.0023	362	-	376	1	NRSPDIYNPQAGSLK
2020.0382	2019.0309	2019.0326	-0.0016	510	-	526	1	NNNPFKFFVPPSQQSLR
2541.3333	2540.3260	2540.2910	0.0351	435	-	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1103.5968, 1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1269.7480, 1277.6886, 1289.6444, 1293.6460, 1296.6310, 1307.6776, 1349.6824, 1365.6621, 1376.7214, 1421.7223, 1448.6655, 1461.6959, 1462.6747, 1475.7344, 1507.7168, 1523.6986, 1553.7611, 1618.7750, 1640.7638, 1652.7408, 1756.8340, 1774.8378, 1861.9741, 1875.9659, 1919.8722, 1924.9037, 1934.8833, 2145.0442, 2145.6316, 2162.0110, 2185.0391, 2224.9937, 2227.1091, 2273.1646, 2305.1414, 2311.1392, 2335.0933, 2351.0913, 2454.2805, 2530.3818, 2555.3315, 2613.2285, 2617.2307, 2652.4231, 2785.4053, 3136.5125, 3211.5283, 3300.7458, 3611.9275, 3819.0635

2. gi|57669861 **Mass:** 61041 **Score:** 45 **Expect:** 0.027 **Queries matched:** 9

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7273	1254.7200	1254.7295	-0.0095	378	388	0	TANDLNLLILR
1289.6444	1288.6371	1288.6564	-0.0192	518	528	0	FFVPPSQQSPR
1295.6364	1294.6291	1294.6377	-0.0086	424	435	0	AHVQVVDSNGNR
1389.7028	1388.6955	1388.6935	0.0020	365	377	0	SPDIYNPQAGSLK
1434.6829	1433.6756	1433.6462	0.0294	459	470	0	SQSDNFEYVAFK
1541.7694	1540.7621	1540.7673	-0.0052	389	401	0	WLGLSAEYGNLYR
1618.7750	1617.7677	1617.7481	0.0196	288	302	0	GENESEEEGAIVTVR
1659.8425	1658.8352	1658.8376	-0.0023	363	377	1	NRSPDIYNPQAGSLK
2541.3333	2540.3260	2540.2910	0.0351	436	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1102.6042, 1103.5968, 1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1269.7480, 1277.6886, 1293.6460, 1296.6310, 1305.6934, 1307.6776, 1349.6824, 1365.6621, 1376.7214, 1421.7223, 1448.6655, 1461.6959, 1462.6747, 1475.7344, 1507.7168, 1523.6986, 1553.7611, 1640.7638, 1652.7408, 1756.8340, 1774.8378, 1861.9741, 1875.9659, 1919.8722, 1924.9037, 1934.8833, 2020.0382, 2145.0442, 2145.6316, 2162.0110, 2185.0391, 2224.9937, 2227.1091, 2273.1646, 2305.1414, 2311.1392, 2335.0933, 2351.0913, 2454.2805, 2530.3818, 2555.3315, 2613.2285, 2617.2307, 2652.4231, 2785.4053, 3136.5125, 3211.5283, 3300.7458, 3611.9275, 3819.0635

3. gi|108595573 **Mass:** 61041 **Score:** 45 **Expect:** 0.027 **Queries matched:** 9

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7273	1254.7200	1254.7295	-0.0095	378	388	0	TANDLNLLILR
1289.6444	1288.6371	1288.6564	-0.0192	518	528	0	FFVPPSQQSPR
1295.6364	1294.6291	1294.6377	-0.0086	424	435	0	AHVQVVDSNGNR
1389.7028	1388.6955	1388.6935	0.0020	365	377	0	SPDIYNPQAGSLK
1434.6829	1433.6756	1433.6462	0.0294	459	470	0	SQSDNFEYVAFK
1541.7694	1540.7621	1540.7673	-0.0052	389	401	0	WLGLSAEYGNLYR
1618.7750	1617.7677	1617.7481	0.0196	288	302	0	GENESEEEGAIVTVR
1659.8425	1658.8352	1658.8376	-0.0023	363	377	1	NRSPDIYNPQAGSLK
2541.3333	2540.3260	2540.2910	0.0351	436	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1102.6042, 1103.5968, 1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1269.7480, 1277.6886, 1293.6460, 1296.6310, 1305.6934, 1307.6776, 1349.6824, 1365.6621, 1376.7214, 1421.7223, 1448.6655, 1461.6959, 1462.6747,

1475.7344, 1507.7168, 1523.6986, 1553.7611, 1640.7638, 1652.7408, 1756.8340, 1774.8378, 1861.9741, 1875.9659,
1919.8722, 1924.9037, 1934.8833, 2020.0382, 2145.0442, 2145.6316, 2162.0110, 2185.0391, 2224.9937, 2227.1091,
2273.1646, 2305.1414, 2311.1392, 2335.0933, 2351.0913, 2454.2805, 2530.3818, 2555.3315, 2613.2285, 2617.2307,
2652.4231, 2785.4053, 3136.5125, 3211.5283, 3300.7458, 3611.9275, 3819.0635

4. gi|118776570 **Mass:** 60681 **Score:** 44 **Expect:** 0.034 **Queries matched:** 9

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6042	1101.5969	1101.5930	0.0039	507	515	1	QLKNNNPFK
1269.7480	1268.7407	1268.7452	-0.0045	377	387	0	TANELNLLILR
1295.6364	1294.6291	1294.6377	-0.0086	423	434	0	AHVQVVDSNGNR
1349.6824	1348.6751	1348.6927	-0.0176	516	526	0	FFVPPFQQSPR
1389.7028	1388.6955	1388.6935	0.0020	364	376	0	SPDIYNPQAGSLK
1448.6655	1447.6582	1447.6619	-0.0037	458	469	0	SQSENFEYVAFK
1541.7694	1540.7621	1540.7673	-0.0052	388	400	0	WLGLSAEYGNLYR
1659.8425	1658.8352	1658.8376	-0.0023	362	376	1	NRSPDIYNPQAGSLK
2541.3333	2540.3260	2540.2910	0.0351	435	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1103.5968,
1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1255.7273, 1277.6886, 1289.6444, 1293.6460,
1296.6310, 1305.6934, 1307.6776, 1365.6621, 1376.7214, 1421.7223, 1434.6829, 1461.6959, 1462.6747, 1475.7344,
1507.7168, 1523.6986, 1553.7611, 1618.7750, 1640.7638, 1652.7408, 1756.8340, 1774.8378, 1861.9741, 1875.9659,
1919.8722, 1924.9037, 1934.8833, 2020.0382, 2145.0442, 2145.6316, 2162.0110, 2185.0391, 2224.9937, 2227.1091,
2273.1646, 2305.1414, 2311.1392, 2335.0933, 2351.0913, 2454.2805, 2530.3818, 2555.3315, 2613.2285, 2617.2307,
2652.4231, 2785.4053, 3136.5125, 3211.5283, 3300.7458, 3611.9275, 3819.0635

5. gi|47933675 **Mass:** 58368 **Score:** 43 **Expect:** 0.043 **Queries matched:** 9

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6042	1101.5969	1101.5930	0.0039	487	495	1	QLKNNNPFK
1295.6364	1294.6291	1294.6377	-0.0086	403	414	0	AHVQVVDSNGNR
1462.6747	1461.6674	1461.6775	-0.0101	438	449	0	AQSENYEYLAFK
1507.7168	1506.7095	1506.7078	0.0018	496	507	0	FFVPPFDHQSMR
1523.6986	1522.6913	1522.7027	-0.0113	496	507	0	FFVPPFDHQSMR + Oxidation (M)
1618.7750	1617.7677	1617.7746	-0.0069	342	356	0	SSNPDIYNPQAGSLR
2454.2805	2453.2732	2453.2637	0.0095	381	402	0	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)
2555.3315	2554.3242	2554.3066	0.0176	415	437	0	VYDEELQEGHVLVVPQNFAVAAK
2652.4231	2651.4158	2651.4070	0.0088	357	380	0	SVNELDLPILGWLGLSAQHGTIYR

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1103.5968,
1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1255.7273, 1269.7480, 1277.6886, 1289.6444,
1293.6460, 1296.6310, 1305.6934, 1307.6776, 1349.6824, 1365.6621, 1376.7214, 1389.7028, 1421.7223, 1434.6829,
1448.6655, 1461.6959, 1475.7344, 1541.7694, 1553.7611, 1640.7638, 1652.7408, 1659.8425, 1756.8340, 1774.8378,
1861.9741, 1875.9659, 1919.8722, 1924.9037, 1934.8833, 2020.0382, 2145.0442, 2145.6316, 2162.0110, 2185.0391,
2224.9937, 2227.1091, 2273.1646, 2305.1414, 2311.1392, 2335.0933, 2351.0913, 2530.3818, 2541.3333, 2613.2285,

2617.2307, 2785.4053, 3136.5125, 3211.5283, 3300.7458, 3611.9275, 3819.0635

6. gi|112380623 **Mass:** 58570 **Score:** 43 **Expect:** 0.044 **Queries matched:** 9

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6042	1101.5969	1101.5930	0.0039	489	497	1	QLKNNNPFK
1295.6364	1294.6291	1294.6377	-0.0086	405	416	0	AHVQVVDSNGNR
1462.6747	1461.6674	1461.6775	-0.0101	440	451	0	AQSENYEYLAFK
1507.7168	1506.7095	1506.7078	0.0018	498	509	0	FFVPPFDHQSMR
1523.6986	1522.6913	1522.7027	-0.0113	498	509	0	FFVPPFDHQSMR + Oxidation (M)
1618.7750	1617.7677	1617.7746	-0.0069	344	358	0	SSNPDIYNPQAGSLR
2454.2805	2453.2732	2453.2637	0.0095	383	404	0	NAMFVPHYTLNAHTIVVALNGR + Oxidation (M)
2555.3315	2554.3242	2554.3066	0.0176	417	439	0	VYDEELQEGHVLVVPQNFAVAAK
2652.4231	2651.4158	2651.4070	0.0088	359	382	0	SVNELDLPILGWLGLSAQHGTIYR

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1103.5968, 1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1255.7273, 1269.7480, 1277.6886, 1289.6444, 1293.6460, 1296.6310, 1305.6934, 1307.6776, 1349.6824, 1365.6621, 1376.7214, 1389.7028, 1421.7223, 1434.6829, 1448.6655, 1461.6959, 1475.7344, 1541.7694, 1553.7611, 1640.7638, 1652.7408, 1659.8425, 1756.8340, 1774.8378, 1861.9741, 1875.9659, 1919.8722, 1924.9037, 1934.8833, 2020.0382, 2145.0442, 2145.6316, 2162.0110, 2185.0391, 2224.9937, 2227.1091, 2273.1646, 2305.1414, 2311.1392, 2335.0933, 2351.0913, 2530.3818, 2541.3333, 2613.2285, 2617.2307, 2785.4053, 3136.5125, 3211.5283, 3300.7458, 3611.9275, 3819.0635

7. gi|3703107 **Mass:** 58543 **Score:** 37 **Expect:** 0.17 **Queries matched:** 8

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6042	1101.5969	1101.5930	0.0039	485	493	1	QLKNNNPFK
1255.7273	1254.7200	1254.7295	-0.0095	355	365	0	TANDLNLLILR
1289.6444	1288.6371	1288.6564	-0.0192	494	504	0	FFVPPSQQSPR
1295.6364	1294.6291	1294.6377	-0.0086	401	412	0	AHVQVVDSNGNR
1389.7028	1388.6955	1388.6935	0.0020	342	354	0	SPDIYNPQAGSLK
1448.6655	1447.6582	1447.6619	-0.0037	436	447	0	SQSENFEYVAFK
1659.8425	1658.8352	1658.8376	-0.0023	340	354	1	NRSPDIYNPQAGSLK
2541.3333	2540.3260	2540.2910	0.0351	413	435	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1103.5968, 1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1269.7480, 1277.6886, 1293.6460, 1296.6310, 1305.6934, 1307.6776, 1349.6824, 1365.6621, 1376.7214, 1421.7223, 1434.6829, 1461.6959, 1462.6747, 1475.7344, 1507.7168, 1523.6986, 1541.7694, 1553.7611, 1618.7750, 1640.7638, 1652.7408, 1756.8340, 1774.8378, 1861.9741, 1875.9659, 1919.8722, 1924.9037, 1934.8833, 2020.0382, 2145.0442, 2145.6316, 2162.0110, 2185.0391, 2224.9937, 2227.1091, 2273.1646, 2305.1414, 2311.1392, 2335.0933, 2351.0913, 2454.2805, 2530.3818, 2555.3315, 2613.2285, 2617.2307, 2652.4231, 2785.4053, 3136.5125, 3211.5283, 3300.7458, 3611.9275, 3819.0635

8. gi|52001221 **Mass:** 61836 **Score:** 36 **Expect:** 0.2 **Queries matched:** 8

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6042	1101.5969	1101.5930	0.0039	515	523	1	QLKNNNPFK
1255.7273	1254.7200	1254.7295	-0.0095	385	395	0	TANDLNLLILR
1295.6364	1294.6291	1294.6377	-0.0086	431	442	0	AHVQVVDSNGNR
1389.7028	1388.6955	1388.6935	0.0020	372	384	0	SPDIYNPQAGSLK
1434.6829	1433.6756	1433.6462	0.0294	466	477	0	SQSDNFEYVAFK
1541.7694	1540.7621	1540.7673	-0.0052	396	408	0	WLGLSAEYGNLYR
1659.8425	1658.8352	1658.8376	-0.0023	370	384	1	NRSPDIYNPQAGSLK
2541.3333	2540.3260	2540.2910	0.0351	443	465	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1103.5968, 1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1269.7480, 1277.6886, 1289.6444, 1293.6460, 1296.6310, 1305.6934, 1307.6776, 1349.6824, 1365.6621, 1376.7214, 1421.7223, 1448.6655, 1461.6959, 1462.6747, 1475.7344, 1507.7168, 1523.6986, 1553.7611, 1618.7750, 1640.7638, 1652.7408, 1756.8340, 1774.8378, 1861.9741, 1875.9659, 1919.8722, 1924.9037, 1934.8833, 2020.0382, 2145.0442, 2145.6316, 2162.0110, 2185.0391, 2224.9937, 2227.1091, 2273.1646, 2305.1414, 2311.1392, 2335.0933, 2351.0913, 2454.2805, 2530.3818, 2555.3315, 2613.2285, 2617.2307, 2652.4231, 2785.4053, 3136.5125, 3211.5283, 3300.7458, 3611.9275, 3819.0635

9. gi|62177433 **Mass:** 15552 **Score:** 29 **Expect:** 1.1 **Queries matched:** 3

resistance protein PNTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2305.1414	2304.1341	2304.1749	-0.0408	6	25	1	TTLAQLVYNDNKVEEHFGVK
2785.4053	2784.3980	2784.3870	0.0110	18	41	1	VEEHFGVKAWIDVSQQFDVSHVTK
3136.5125	3135.5052	3135.5777	-0.0724	110	138	0	HETVAWEGVEPVQVLGHLLPQVFEGGHTA

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1102.6042, 1103.5968, 1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1255.7273, 1269.7480, 1277.6886, 1289.6444, 1293.6460, 1295.6364, 1296.6310, 1305.6934, 1307.6776, 1349.6824, 1365.6621, 1376.7214, 1389.7028, 1421.7223, 1434.6829, 1448.6655, 1461.6959, 1462.6747, 1475.7344, 1507.7168, 1523.6986, 1541.7694, 1553.7611, 1618.7750, 1640.7638, 1652.7408, 1659.8425, 1756.8340, 1774.8378, 1861.9741, 1875.9659, 1919.8722, 1924.9037, 1934.8833, 2020.0382, 2145.0442, 2145.6316, 2162.0110, 2185.0391, 2224.9937, 2227.1091, 2273.1646, 2311.1392, 2335.0933, 2351.0913, 2454.2805, 2530.3818, 2541.3333, 2555.3315, 2613.2285, 2617.2307, 2652.4231, 3211.5283, 3300.7458, 3611.9275, 3819.0635

10. gi|52001219 **Mass:** 61810 **Score:** 27 **Expect:** 1.7 **Queries matched:** 7

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.6042	1101.5969	1101.5930	0.0039	514	522	1	QLKNNNPFK
1269.7480	1268.7407	1268.7452	-0.0045	384	394	0	TANELNLLILR
1296.6310	1295.6237	1295.6218	0.0020	430	441	0	AHVQVVDSNGDR
1389.7028	1388.6955	1388.6935	0.0020	371	383	0	SPDIYNPQAGSLK
1448.6655	1447.6582	1447.6619	-0.0037	465	476	0	SQSENFEYVAFK
1541.7694	1540.7621	1540.7673	-0.0052	395	407	0	WLGLSAEYGNLYR
1659.8425	1658.8352	1658.8376	-0.0023	369	383	1	NRSPDIYNPQAGSLK

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1103.5968, 1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1255.7273, 1277.6886, 1289.6444, 1293.6460, 1295.6364, 1305.6934, 1307.6776, 1349.6824, 1365.6621, 1376.7214, 1421.7223, 1434.6829, 1461.6959, 1462.6747, 1475.7344, 1507.7168, 1523.6986, 1553.7611, 1618.7750, 1640.7638, 1652.7408, 1756.8340, 1774.8378, 1861.9741, 1875.9659, 1919.8722, 1924.9037, 1934.8833, 2020.0382, 2145.0442, 2145.6316, 2162.0110, 2185.0391, 2224.9937, 2227.1091, 2273.1646, 2305.1414, 2311.1392, 2335.0933, 2351.0913, 2454.2805, 2530.3818, 2541.3333, 2555.3315, 2613.2285, 2617.2307, 2652.4231, 2785.4053, 3136.5125, 3211.5283, 3300.7458, 3611.9275, 3819.0635

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 76

Protein View

Match to: **gi|9864777** Score: **53** Expect: **0.0042**
Gly1 [Arachis hypogaea]

Nominal mass (M_r): **60754**; Calculated pI value: **5.48**
NCBI BLAST search of gi|9864777 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **76**
Number of mass values matched: **10**
Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

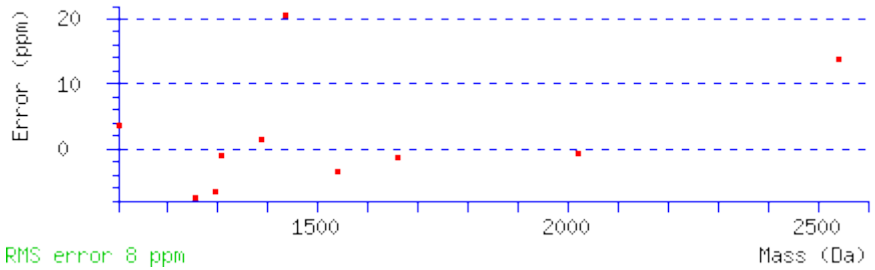
```
     1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE
    51 GGYIETWNPN NQEFECAGVA LSRLVLRRNA LRRPFYSNAP QEIFIQQGRG
   101 YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR
   151 RFDEGDLIAV PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
```

```
201 AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP RGQHSRRERA
251 GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV
301 KGGLRILSPD RKRGADEEEE YDEDEYEYDE EDRRRGRGSR GRGNGIEETI
351 CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
451 NFAVAGKSQS DNFEYVAFKT DSRPNIANFA GENSIIDNLP EEVVANSYGL
501 PREQARQLKN NNPFKFFVPP SQQSLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
362 - 376	1659.8425	1658.8352	1658.8376	-0.0023	1	NRSPDIYNPQAGSLK
364 - 376	1389.7028	1388.6955	1388.6935	0.0020	0	SPDIYNPQAGSLK
377 - 387	1255.7273	1254.7200	1254.7295	-0.0095	0	TANDLNLLILR
388 - 400	1541.7694	1540.7621	1540.7673	-0.0052	0	WLGLSAEYGNLYR
423 - 434	1295.6364	1294.6291	1294.6377	-0.0086	0	AHVQVVDSNGNR
435 - 457	2541.3333	2540.3260	2540.2910	0.0351	0	VYDEELQEGHVLVVPQNFAVAGK
458 - 469	1434.6829	1433.6756	1433.6462	0.0294	0	SQSDNFEYVAFK
507 - 515	1102.6042	1101.5969	1101.5930	0.0039	1	QLKNNNPFK
510 - 526	2020.0382	2019.0309	2019.0326	-0.0016	1	NNNPFKFFVPPSQQSLR
516 - 526	1305.6934	1304.6861	1304.6877	-0.0015	0	FFVPPSQQSLR

No match to: 805.4609, 861.1252, 877.0610, 881.2759, 1018.4543, 1046.6034, 1080.5157, 1082.5405, 1085.5710, 1103.5968, 1111.5579, 1116.6005, 1137.5774, 1145.0734, 1145.5636, 1175.5610, 1269.7480, 1277.6886, 1289.6444, 1293.6460, 1296.6310, 1307.6776, 1349.6824, 1365.6621, 1376.7214, 1421.7223, 1448.6655, 1461.6959, 1462.6747, 1475.7344, 1507.7168, 1523.6986, 1553.7611, 1618.7750, 1640.7638, 1652.7408, 1756.8340, 1774.8378, 1861.9741, 1875.9659, 1919.8722, 1924.9037, 1934.8833, 2145.0442, 2145.6316, 2162.0110, 2185.0391, 2224.9937, 2227.1091, 2273.1646, 2305.1414, 2311.1392, 2335.0933, 2351.0913, 2454.2805, 2530.3818, 2555.3315, 2613.2285, 2617.2307, 2652.4231, 2785.4053, 3136.5125, 3211.5283, 3300.7458, 3611.9275, 3819.0635



Spot 69

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:08:24 GMT**
Top Score : **67 for gi|118776570, arachin 6 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	67	arachin 6 [Arachis hypogaea]
2.	gi|18400528	46371	16	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [
3.	gi|230338	23975	16	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
4.	gi|31558995	91467	15	phospholipase D [Arachis hypogaea]
5.	gi|88193699	91214	15	phospholipase D alpha 1 [Arachis hypogaea]
6.	gi|88193695	91214	15	phospholipase D alpha 1 [Arachis hypogaea]
7.	gi|225836	26393	14	albumin
8.	gi|62177385	14731	12	resistance protein Cre [Arachis hypogaea]
9.	gi|88193701	92340	11	phospholipase D alpha 2 [Arachis hypogaea]
10.	gi|88193697	92340	11	phospholipase D alpha 2 [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 67 **Expect:** 0.00018 **Queries matched:** 11
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
828.4954	827.4881	827.4865	0.0017	305	311	1	ILSPDRK
870.5298	869.5225	869.5083	0.0143	279	285	0	QIVQNLR
1574.7596	1573.7523	1573.7637	-0.0113	196	208	0	FNLAGNHEQEFLR
1730.8662	1729.8589	1729.8648	-0.0058	195	208	1	RFNLAGNHEQEFLR
1770.8527	1769.8454	1769.8584	-0.0130	220	235	0	SLPLSPYSPQPGQEDR
1972.9457	1971.9384	1971.9860	-0.0476	286	304	1	GENESEEQGAIVTVKGGLR
2262.8364	2261.8291	2261.8243	0.0048	312	329	0	SPDEEEEYDEDEYAEEER
2441.2678	2440.2605	2440.2557	0.0049	279	300	1	QIVQNLRGENESEEQGAIVTVK
2790.1348	2789.1275	2789.0695	0.0580	312	333	1	SPDEEEEYDEDEYAEEERQQDR
3291.5110	3290.5037	3290.4751	0.0286	249	278	0	AGQEQENEGGNIFSGFTSEFLAQAFQVDDR
3576.6492	3575.6419	3575.6188	0.0232	247	278	1	ERAGQEQENEGGNIFSGFTSEFLAQAFQVDDR

No match to: 805.4614, 809.4212, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 866.4595, 871.0381, 877.0477, 887.0096, 893.0178, 1046.6017, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1129.5259, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1313.5920, 1314.6324, 1363.7734, 1376.5815, 1408.7146, 1445.7356, 1548.7200, 1622.7623, 1638.7499, 1696.6935, 1714.7303, 1752.8378, 1774.8386, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1918.9136, 1934.9191, 1958.9464, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2227.0676, 2273.1606, 2295.1548, 2305.1372, 2311.1335, 2335.0881, 2351.0864, 2354.0872, 2424.2249, 2514.3467, 2530.3330, 2612.2065, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3083.5071, 3098.4683, 3137.4019, 3211.5295, 3300.7749, 3316.7915, 3578.7915

2. gi|18400528 **Mass:** 46371 **Score:** 16 **Expect:** 20 **Queries matched:** 5

ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase [Ara

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1314.6324	1313.6251	1313.6009	0.0242	296 -	305	0	WMAPEMIQHR + Oxidation (M)
1408.7146	1407.7073	1407.6968	0.0105	130 -	143	0	LNMGPAFAQGAFGK
1918.9136	1917.9063	1917.8978	0.0086	296 -	310	1	WMAPEMIQHRAYNQK + Oxidation (M)
1934.9191	1933.9118	1933.8927	0.0192	296 -	310	1	WMAPEMIQHRAYNQK + 2 Oxidation (M)
3578.7915	3577.7842	3577.7544	0.0298	158 -	187	1	ILERPENSPEKAQFMEQQFQQEVSMLANLK + Oxidation (M)

No match to: 805.4614, 809.4212, 828.4954, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 866.4595, 870.5298, 871.0381, 877.0477, 887.0096, 893.0178, 1046.6017, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1129.5259, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1313.5920, 1363.7734, 1376.5815, 1445.7356, 1548.7200, 1574.7596, 1622.7623, 1638.7499, 1696.6935, 1714.7303, 1730.8662, 1752.8378, 1770.8527, 1774.8386, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1958.9464, 1972.9457, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2227.0676, 2262.8364, 2273.1606, 2295.1548, 2305.1372, 2311.1335, 2335.0881, 2351.0864, 2354.0872, 2424.2249, 2441.2678, 2514.3467, 2530.3330, 2612.2065, 2790.1348, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3083.5071, 3098.4683, 3137.4019, 3211.5295, 3291.5110, 3300.7749, 3316.7915, 3576.6492

3. gi|230338 **Mass:** 23975 **Score:** 16 **Expect:** 20 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.6017	1045.5944	1045.5880	0.0065	90 -	99	1	LKSAASLNSR
2273.1606	2272.1533	2272.1521	0.0012	70 -	89	0	SIVHPSYNSNTLNNDIMLIK
2514.3467	2513.3394	2513.3311	0.0083	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK
2530.3330	2529.3257	2529.3260	-0.0003	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4614, 809.4212, 828.4954, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 866.4595, 870.5298, 871.0381, 877.0477, 887.0096, 893.0178, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1129.5259, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1313.5920, 1314.6324, 1363.7734, 1376.5815, 1408.7146, 1445.7356, 1548.7200, 1574.7596, 1622.7623, 1638.7499, 1696.6935, 1714.7303, 1730.8662, 1752.8378, 1770.8527, 1774.8386, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1918.9136, 1934.9191, 1958.9464, 1972.9457, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2227.0676, 2262.8364, 2295.1548, 2305.1372, 2311.1335, 2335.0881, 2351.0864, 2354.0872, 2424.2249, 2441.2678, 2612.2065, 2790.1348, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3083.5071, 3098.4683, 3137.4019, 3211.5295, 3291.5110, 3300.7749, 3316.7915, 3576.6492, 3578.7915

4. gi|31558995 **Mass:** 91467 **Score:** 15 **Expect:** 27 **Queries matched:** 5

phospholipase D [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1129.5259	1128.5186	1128.5273	-0.0087	52	59	0	LEECFYIR
2227.0676	2226.0603	2226.0660	-0.0057	638	656	0	MMIVDDEYIIIGSANINQR + 2 Oxidation (M)
2311.1335	2310.1262	2310.0811	0.0452	663	684	0	DTEIAMGAYQPHHLATSQGGAR
2354.0872	2353.0799	2353.1380	-0.0581	52	70	1	LEECFYIRCAHMASNIIVK
3083.5071	3082.4998	3082.4759	0.0239	375	399	1	EPWHDIHCKLEGPIAWDVYSTFVQR

No match to: 805.4614, 809.4212, 828.4954, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 866.4595, 870.5298, 871.0381, 877.0477, 887.0096, 893.0178, 1046.6017, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1313.5920, 1314.6324, 1363.7734, 1376.5815, 1408.7146, 1445.7356, 1548.7200, 1574.7596, 1622.7623, 1638.7499, 1696.6935, 1714.7303, 1730.8662, 1752.8378, 1770.8527, 1774.8386, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1918.9136, 1934.9191, 1958.9464, 1972.9457, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2262.8364, 2273.1606, 2295.1548, 2305.1372, 2335.0881, 2351.0864, 2424.2249, 2441.2678, 2514.3467, 2530.3330, 2612.2065, 2790.1348, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3098.4683, 3137.4019, 3211.5295, 3291.5110, 3300.7749, 3316.7915, 3576.6492, 3578.7915

5. gi|88193699 **Mass:** 91214 **Score:** 15 **Expect:** 27 **Queries matched:** 5

phospholipase D alpha 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1129.5259	1128.5186	1128.5273	-0.0087	52	59	0	LEECFYIR
2227.0676	2226.0603	2226.0660	-0.0057	638	656	0	MMIVDDEYIIIGSANINQR + 2 Oxidation (M)
2311.1335	2310.1262	2310.0811	0.0452	663	684	0	DTEIAMGAYQPHHLATSQGGAR
2354.0872	2353.0799	2353.1380	-0.0581	52	70	1	LEECFYIRCAHMASNIIVK
3083.5071	3082.4998	3082.4759	0.0239	375	399	1	EPWHDIHCKLEGPIAWDVYSTFVQR

No match to: 805.4614, 809.4212, 828.4954, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 866.4595, 870.5298, 871.0381, 877.0477, 887.0096, 893.0178, 1046.6017, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1313.5920, 1314.6324, 1363.7734, 1376.5815, 1408.7146, 1445.7356, 1548.7200, 1574.7596, 1622.7623, 1638.7499, 1696.6935, 1714.7303, 1730.8662, 1752.8378, 1770.8527, 1774.8386, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1918.9136, 1934.9191, 1958.9464, 1972.9457, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2262.8364, 2273.1606, 2295.1548, 2305.1372, 2335.0881, 2351.0864, 2424.2249, 2441.2678, 2514.3467, 2530.3330, 2612.2065, 2790.1348, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3098.4683, 3137.4019, 3211.5295, 3291.5110, 3300.7749, 3316.7915, 3576.6492, 3578.7915

6. gi|88193695 **Mass:** 91214 **Score:** 15 **Expect:** 27 **Queries matched:** 5

phospholipase D alpha 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1129.5259	1128.5186	1128.5273	-0.0087	52	59	0	LEECFYIR
2227.0676	2226.0603	2226.0660	-0.0057	638	656	0	MMIVDDEYIIIGSANINQR + 2 Oxidation (M)
2311.1335	2310.1262	2310.0811	0.0452	663	684	0	DTEIAMGAYQPHHLATSQGGAR
2354.0872	2353.0799	2353.1380	-0.0581	52	70	1	LEECFYIRCAHMASNIIVK

3083.5071	3082.4998	3082.4759	0.0239	375 - 399	1	EPWHDIHCKLEGPIAWDVYSTFVQR	

No match to: 805.4614, 809.4212, 828.4954, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 866.4595, 870.5298, 871.0381, 877.0477, 887.0096, 893.0178, 1046.6017, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1313.5920, 1314.6324, 1363.7734, 1376.5815, 1408.7146, 1445.7356, 1548.7200, 1574.7596, 1622.7623, 1638.7499, 1696.6935, 1714.7303, 1730.8662, 1752.8378, 1770.8527, 1774.8386, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1918.9136, 1934.9191, 1958.9464, 1972.9457, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2262.8364, 2273.1606, 2295.1548, 2305.1372, 2335.0881, 2351.0864, 2424.2249, 2441.2678, 2514.3467, 2530.3330, 2612.2065, 2790.1348, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3098.4683, 3137.4019, 3211.5295, 3291.5110, 3300.7749, 3316.7915, 3576.6492, 3578.7915

7. gi|225836 **Mass:** 26393 **Score:** 14 **Expect:** 33 **Queries matched:** 3

albumin

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1313.5920	1312.5847	1312.5969	-0.0122	144 -	154	0	IDYETNSMVNK
1774.8386	1773.8313	1773.8567	-0.0254	198 -	214	0	VTVTPGATDDQIMDGVR
1918.9136	1917.9063	1917.9465	-0.0402	198 -	215	1	VTVTPGATDDQIMDGVRK + Oxidation (M)

No match to: 805.4614, 809.4212, 828.4954, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 866.4595, 870.5298, 871.0381, 877.0477, 887.0096, 893.0178, 1046.6017, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1129.5259, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1314.6324, 1363.7734, 1376.5815, 1408.7146, 1445.7356, 1548.7200, 1574.7596, 1622.7623, 1638.7499, 1696.6935, 1714.7303, 1730.8662, 1752.8378, 1770.8527, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1934.9191, 1958.9464, 1972.9457, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2227.0676, 2262.8364, 2273.1606, 2295.1548, 2305.1372, 2311.1335, 2335.0881, 2351.0864, 2354.0872, 2424.2249, 2441.2678, 2514.3467, 2530.3330, 2612.2065, 2790.1348, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3083.5071, 3098.4683, 3137.4019, 3211.5295, 3291.5110, 3300.7749, 3316.7915, 3576.6492, 3578.7915

8. gi|62177385 **Mass:** 14731 **Score:** 12 **Expect:** 58 **Queries matched:** 2

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1730.8662	1729.8589	1729.8787	-0.0198	1 -	14	1	NLILDDVWDSKAWR
2295.1548	2294.1475	2294.1147	0.0329	15 -	34	1	TIKNCFPENNNGGMILVTTR + Oxidation (M)

No match to: 805.4614, 809.4212, 828.4954, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 866.4595, 870.5298, 871.0381, 877.0477, 887.0096, 893.0178, 1046.6017, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1129.5259, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1313.5920, 1314.6324, 1363.7734, 1376.5815, 1408.7146, 1445.7356, 1548.7200, 1574.7596, 1622.7623, 1638.7499, 1696.6935, 1714.7303, 1752.8378, 1770.8527, 1774.8386, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1918.9136, 1934.9191, 1958.9464, 1972.9457, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2227.0676, 2262.8364, 2273.1606, 2305.1372, 2311.1335, 2335.0881, 2351.0864, 2354.0872, 2424.2249, 2441.2678, 2514.3467, 2530.3330, 2612.2065, 2790.1348, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3083.5071, 3098.4683, 3137.4019, 3211.5295, 3291.5110, 3300.7749, 3316.7915, 3576.6492, 3578.7915

9. gi|88193701 **Mass:** 92340 **Score:** 11 **Expect:** 74 **Queries matched:** 6

phospholipase D alpha 2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

866.4595	865.4522	865.4406	0.0117	132 - 139	0	NPIHGNSK
1445.7356	1444.7283	1444.7139	0.0145	164 - 175	0	FPGVPYTFFSQR
1638.7499	1637.7426	1637.7507	-0.0081	209 - 221	1	CWEDVFDAIEKAR
1918.9136	1917.9063	1917.8885	0.0178	591 - 606	1	TMEMMYKDIVEALNAK + 2 Oxidation (M)
1934.9191	1933.9118	1933.8880	0.0239	686 - 702	0	DSEIAMGAYQPYYLSAR
2227.0676	2226.0603	2226.0660	-0.0057	661 - 679	0	MMIVDDEYIIIGSANINQR + 2 Oxidation (M)

No match to: 805.4614, 809.4212, 828.4954, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 870.5298, 871.0381, 877.0477, 887.0096, 893.0178, 1046.6017, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1129.5259, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1313.5920, 1314.6324, 1363.7734, 1376.5815, 1408.7146, 1548.7200, 1574.7596, 1622.7623, 1696.6935, 1714.7303, 1730.8662, 1752.8378, 1770.8527, 1774.8386, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1958.9464, 1972.9457, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2262.8364, 2273.1606, 2295.1548, 2305.1372, 2311.1335, 2335.0881, 2351.0864, 2354.0872, 2424.2249, 2441.2678, 2514.3467, 2530.3330, 2612.2065, 2790.1348, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3083.5071, 3098.4683, 3137.4019, 3211.5295, 3291.5110, 3300.7749, 3316.7915, 3576.6492, 3578.7915

10. gi|88193697 **Mass:** 92340 **Score:** 11 **Expect:** 74 **Queries matched:** 6

phospholipase D alpha 2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
866.4595	865.4522	865.4406	0.0117	132 - 139	0	NPIHGNSK
1445.7356	1444.7283	1444.7139	0.0145	164 - 175	0	FPGVPYTFFSQR
1638.7499	1637.7426	1637.7507	-0.0081	209 - 221	1	CWEDVFDAIEKAR
1918.9136	1917.9063	1917.8885	0.0178	591 - 606	1	TMEMMYKDIVEALNAK + 2 Oxidation (M)
1934.9191	1933.9118	1933.8880	0.0239	686 - 702	0	DSEIAMGAYQPYYLSAR
2227.0676	2226.0603	2226.0660	-0.0057	661 - 679	0	MMIVDDEYIIIGSANINQR + 2 Oxidation (M)

No match to: 805.4614, 809.4212, 828.4954, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 870.5298, 871.0381, 877.0477, 887.0096, 893.0178, 1046.6017, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1129.5259, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1313.5920, 1314.6324, 1363.7734, 1376.5815, 1408.7146, 1548.7200, 1574.7596, 1622.7623, 1696.6935, 1714.7303, 1730.8662, 1752.8378, 1770.8527, 1774.8386, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1958.9464, 1972.9457, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2262.8364, 2273.1606, 2295.1548, 2305.1372, 2311.1335, 2335.0881, 2351.0864, 2354.0872, 2424.2249, 2441.2678, 2514.3467, 2530.3330, 2612.2065, 2790.1348, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3083.5071, 3098.4683, 3137.4019, 3211.5295, 3291.5110, 3300.7749, 3316.7915, 3576.6492, 3578.7915

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted

Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 91

Protein View

Match to: **gi|118776570** Score: **67** Expect: **0.00018**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **91**
Number of mass values matched: **11**
Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```
   1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
  51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
 101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
 151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
 201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
 251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
 301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
 351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
 401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
 451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
 501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
195 - 208	1730.8662	1729.8589	1729.8648	-0.0058	1	RFNLAGNHEQEFLR
196 - 208	1574.7596	1573.7523	1573.7637	-0.0113	0	FNLAGNHEQEFLR
220 - 235	1770.8527	1769.8454	1769.8584	-0.0130	0	SLPLSPYSPQPGQEDR
247 - 278	3576.6492	3575.6419	3575.6188	0.0232	1	ERAGQEQENEGGNIFSGFTSEFLAQAFQVDDR

249 - 278	3291.5110	3290.5037	3290.4751	0.0286	0	AGQEQENEGGNIFSGFTSEFLAQAFQVDDR
279 - 285	870.5298	869.5225	869.5083	0.0143	0	QIVQNLR
279 - 300	2441.2678	2440.2605	2440.2557	0.0049	1	QIVQNLRGENESEEQGAIVTVK
286 - 304	1972.9457	1971.9384	1971.9860	-0.0476	1	GENESEEQGAIVTVKGGLR
305 - 311	828.4954	827.4881	827.4865	0.0017	1	ILSPDRK
312 - 329	2262.8364	2261.8291	2261.8243	0.0048	0	SPDEEEEYDEDEYAEEER
312 - 333	2790.1348	2789.1275	2789.0695	0.0580	1	SPDEEEEYDEDEYAEEERQQDR

No match to: 805.4614, 809.4212, 853.4937, 854.0604, 855.0697, 861.0826, 865.9673, 866.4595, 871.0381, 877.0477, 887.0096, 893.0178, 1046.6017, 1066.0699, 1080.5073, 1082.0452, 1098.0103, 1111.5546, 1129.5259, 1137.0748, 1137.5667, 1145.0714, 1145.5708, 1156.5784, 1158.5433, 1175.5774, 1209.5659, 1215.4972, 1297.5702, 1313.5920, 1314.6324, 1363.7734, 1376.5815, 1408.7146, 1445.7356, 1548.7200, 1622.7623, 1638.7499, 1696.6935, 1714.7303, 1752.8378, 1774.8386, 1784.8109, 1786.8429, 1792.7863, 1794.7853, 1795.7946, 1802.8494, 1855.7346, 1918.9136, 1934.9191, 1958.9464, 2088.9443, 2106.9431, 2185.0361, 2224.9849, 2227.0676, 2273.1606, 2295.1548, 2305.1372, 2311.1335, 2335.0881, 2351.0864, 2354.0872, 2424.2249, 2514.3467, 2530.3330, 2612.2065, 2807.4902, 2824.5273, 2928.4138, 2939.3245, 2942.4583, 3083.5071, 3098.4683, 3137.4019, 3211.5295, 3300.7749, 3316.7915, 3578.7915

Spot 70

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:54:04 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **445 for gi|9864777, Gly1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|9864777	60754	445	Gly1 [Arachis hypogaea]
2.	gi|52001221	61836	445	arachin Ahy-2 [Arachis hypogaea]
3.	gi|22135348	25768	388	trypsin inhibitor [Arachis hypogaea]
4.	gi|118776570	60681	366	arachin 6 [Arachis hypogaea]
5.	gi|5712199	61430	366	glycinin [Arachis hypogaea]
6.	gi|57669861	61041	366	arachin Ahy-4 [Arachis hypogaea]
7.	gi|108595573	61041	366	arachin Ahy-4 [Arachis hypogaea]
8.	gi|52001219	61810	366	arachin Ahy-1 [Arachis hypogaea]
9.	gi|21314465	62042	366	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|37789212	61803	258	storage protein [Arachis hypogaea]

Results List

1. gi|9864777 **Mass:** 60754 **Score:** 445 **Expect:** 2.8e-042 **Queries matched:** 12
Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	38	-	46	0	---	LNAQRPDNR
1534.6555	1533.6482	1533.6630	-0.0148	26	-	37	0	---	QQPEENACQFQR
1574.7561	1573.7488	1573.7637	-0.0148	198	-	210	0	76	FNLAGNHEQEFLR
1574.7561	1573.7488	1573.7637	-0.0148	198	-	210	0	---	FNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	197	-	210	1	11	RFNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	197	-	210	1	---	RFNLAGNHEQEFLR
2051.0244	2050.0171	2050.0384	-0.0213	83	-	99	0	---	RPFYSNAPQEIFIQQGR
2051.0244	2050.0171	2050.0384	-0.0213	83	-	99	0	120	RPFYSNAPQEIFIQQGR

2202.9531	2201.9458	2201.9686	-0.0227	131 - 148	1	---	RFEGEDQSQQQQQDSHQK
2202.9531	2201.9458	2201.9686	-0.0227	131 - 148	1	58	RFEGEDQSQQQQQDSHQK
2474.1194	2473.1121	2473.1371	-0.0250	100 - 121	0	89	GYFGLIFPGCPSTYEEPAQQGR
2474.1194	2473.1121	2473.1371	-0.0250	100 - 121	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.5133, 1151.7085, 1517.6285, 3075.3518

2. gi|52001221 **Mass:** 61836 **Score:** 445 **Expect:** 2.8e-042 **Queries matched:** 12

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37 -	45	0	---	LNAQRPDNR
1534.6555	1533.6482	1533.6630	-0.0148	25 -	36	0	---	QQPEENACQFQR
1574.7561	1573.7488	1573.7637	-0.0148	197 -	209	0	76	FNLAGNHEQEFLR
1574.7561	1573.7488	1573.7637	-0.0148	197 -	209	0	---	FNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	196 -	209	1	11	RFNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	196 -	209	1	---	RFNLAGNHEQEFLR
2051.0244	2050.0171	2050.0384	-0.0213	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2051.0244	2050.0171	2050.0384	-0.0213	82 -	98	0	120	RPFYSNAPQEIFIQQGR
2202.9531	2201.9458	2201.9686	-0.0227	130 - 147	1	---	RFEGEDQSQQQQQDSHQK
2202.9531	2201.9458	2201.9686	-0.0227	130 - 147	1	58	RFEGEDQSQQQQQDSHQK
2474.1194	2473.1121	2473.1371	-0.0250	99 - 120	0	89	GYFGLIFPGCPSTYEEPAQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.5133, 1151.7085, 1517.6285, 3075.3518

3. gi|22135348 **Mass:** 25768 **Score:** 388 **Expect:** 1.4e-036 **Queries matched:** 10

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	39 -	47	0	---	LNAQRPDNR
1534.6555	1533.6482	1533.6630	-0.0148	27 -	38	0	---	QQPEENACQFQR
1574.7561	1573.7488	1573.7637	-0.0148	198 -	210	0	76	FNLAGNHEQEFLR
1574.7561	1573.7488	1573.7637	-0.0148	198 -	210	0	---	FNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	197 -	210	1	11	RFNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	197 -	210	1	---	RFNLAGNHEQEFLR
2051.0244	2050.0171	2050.0384	-0.0213	84 -	100	0	---	RPFYSNAPQEIFIQQGR
2051.0244	2050.0171	2050.0384	-0.0213	84 -	100	0	120	RPFYSNAPQEIFIQQGR
2474.1194	2473.1121	2473.1371	-0.0250	101 - 122	0	89	GYFGLIFPGCPSTYEEPAQQGR
2474.1194	2473.1121	2473.1371	-0.0250	101 - 122	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.5133, 1151.7085, 1517.6285, 2202.9531, 2202.9531, 3075.3518

4. gi|118776570 **Mass:** 60681 **Score:** 366 **Expect:** 2.2e-034 **Queries matched:** 10

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37	45	0	---	LNAQRPDNR
1534.6555	1533.6482	1533.6630	-0.0148	25	36	0	---	QQPEENACQFQR
1574.7561	1573.7488	1573.7637	-0.0148	196	208	0	76	FNLAGNHEQEFLR
1574.7561	1573.7488	1573.7637	-0.0148	196	208	0	---	FNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195	208	1	11	RFNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195	208	1	---	RFNLAGNHEQEFLR
2051.0244	2050.0171	2050.0384	-0.0213	82	98	0	---	RPFYSNAPQEIFIQQGR
2051.0244	2050.0171	2050.0384	-0.0213	82	98	0	120	RPFYSNAPQEIFIQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99	120	0	89	GYFGLIFPGCPSTYEEPAQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.5133, 1151.7085, 1517.6285, 2202.9531, 2202.9531, 3075.3518

5. gi|5712199 **Mass:** 61430 **Score:** 366 **Expect:** 2.2e-034 **Queries matched:** 10

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37	45	0	---	LNAQRPDNR
1534.6555	1533.6482	1533.6630	-0.0148	25	36	0	---	QQPEENACQFQR
1574.7561	1573.7488	1573.7637	-0.0148	196	208	0	76	FNLAGNHEQEFLR
1574.7561	1573.7488	1573.7637	-0.0148	196	208	0	---	FNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195	208	1	11	RFNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195	208	1	---	RFNLAGNHEQEFLR
2051.0244	2050.0171	2050.0384	-0.0213	82	98	0	---	RPFYSNAPQEIFIQQGR
2051.0244	2050.0171	2050.0384	-0.0213	82	98	0	120	RPFYSNAPQEIFIQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99	120	0	89	GYFGLIFPGCPSTYEEPAQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.5133, 1151.7085, 1517.6285, 2202.9531, 2202.9531, 3075.3518

6. gi|57669861 **Mass:** 61041 **Score:** 366 **Expect:** 2.2e-034 **Queries matched:** 10

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37	45	0	---	LNAQRPDNR
1534.6555	1533.6482	1533.6630	-0.0148	25	36	0	---	QQPEENACQFQR
1574.7561	1573.7488	1573.7637	-0.0148	196	208	0	76	FNLAGNHEQEFLR
1574.7561	1573.7488	1573.7637	-0.0148	196	208	0	---	FNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195	208	1	11	RFNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195	208	1	---	RFNLAGNHEQEFLR
2051.0244	2050.0171	2050.0384	-0.0213	82	98	0	---	RPFYSNAPQEIFIQQGR
2051.0244	2050.0171	2050.0384	-0.0213	82	98	0	120	RPFYSNAPQEIFIQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99	120	0	89	GYFGLIFPGCPSTYEEPAQQGR

2474.1194	2473.1121	2473.1371	-0.0250	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.5133, 1151.7085, 1517.6285, 2202.9531, 2202.9531, 3075.3518

7. gi|108595573 **Mass:** 61041 **Score:** 366 **Expect:** 2.2e-034 **Queries matched:** 10

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37 -	45	0	---	LNAQRPDNR
1534.6555	1533.6482	1533.6630	-0.0148	25 -	36	0	---	QQPEENACQFQR
1574.7561	1573.7488	1573.7637	-0.0148	196 -	208	0	76	FNLAGNHEQEFLR
1574.7561	1573.7488	1573.7637	-0.0148	196 -	208	0	---	FNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195 -	208	1	11	RFNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195 -	208	1	---	RFNLAGNHEQEFLR
2051.0244	2050.0171	2050.0384	-0.0213	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2051.0244	2050.0171	2050.0384	-0.0213	82 -	98	0	120	RPFYSNAPQEIFIQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99 -	120	0	89	GYFGLIFPGCPSTYEEPAQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99 -	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.5133, 1151.7085, 1517.6285, 2202.9531, 2202.9531, 3075.3518

8. gi|52001219 **Mass:** 61810 **Score:** 366 **Expect:** 2.2e-034 **Queries matched:** 10

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37 -	45	0	---	LNAQRPDNR
1534.6555	1533.6482	1533.6630	-0.0148	25 -	36	0	---	QQPEENACQFQR
1574.7561	1573.7488	1573.7637	-0.0148	196 -	208	0	76	FNLAGNHEQEFLR
1574.7561	1573.7488	1573.7637	-0.0148	196 -	208	0	---	FNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195 -	208	1	11	RFNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195 -	208	1	---	RFNLAGNHEQEFLR
2051.0244	2050.0171	2050.0384	-0.0213	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2051.0244	2050.0171	2050.0384	-0.0213	82 -	98	0	120	RPFYSNAPQEIFIQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99 -	120	0	89	GYFGLIFPGCPSTYEEPAQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99 -	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.5133, 1151.7085, 1517.6285, 2202.9531, 2202.9531, 3075.3518

9. gi|21314465 **Mass:** 62042 **Score:** 366 **Expect:** 2.2e-034 **Queries matched:** 10

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37 -	45	0	---	LNAQRPDNR
1534.6555	1533.6482	1533.6630	-0.0148	25 -	36	0	---	QQPEENACQFQR
1574.7561	1573.7488	1573.7637	-0.0148	196 -	208	0	76	FNLAGNHEQEFLR
1574.7561	1573.7488	1573.7637	-0.0148	196 -	208	0	---	FNLAGNHEQEFLR

1730.8558	1729.8485	1729.8648	-0.0162	195 - 208	1	11	RFNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195 - 208	1	---	RFNLAGNHEQEFLR
2051.0244	2050.0171	2050.0384	-0.0213	82 - 98	0	---	RPFYSNAPQEIFIQQGR
2051.0244	2050.0171	2050.0384	-0.0213	82 - 98	0	120	RPFYSNAPQEIFIQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99 - 120	0	89	GYFGLIFPGCPSTYEEPAQQGR
2474.1194	2473.1121	2473.1371	-0.0250	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.5133, 1151.7085, 1517.6285, 2202.9531, 2202.9531, 3075.3518

10. gi|37789212 **Mass:** 61803 **Score:** 258 **Expect:** 1.4e-023 **Queries matched:** 8

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5559	1082.5486	1082.5581	-0.0094	37 - 45		0	---	LNAQRPDNR
1534.6555	1533.6482	1533.6630	-0.0148	25 - 36		0	---	QQPEENACQFQR
1574.7561	1573.7488	1573.7637	-0.0148	196 - 208		0	76	FNLAGNHEQEFLR
1574.7561	1573.7488	1573.7637	-0.0148	196 - 208		0	---	FNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195 - 208		1	11	RFNLAGNHEQEFLR
1730.8558	1729.8485	1729.8648	-0.0162	195 - 208		1	---	RFNLAGNHEQEFLR
2051.0244	2050.0171	2050.0384	-0.0213	82 - 98		0	---	RPFYSNAPQEIFIQQGR
2051.0244	2050.0171	2050.0384	-0.0213	82 - 98		0	120	RPFYSNAPQEIFIQQGR

No match to: 1026.5133, 1151.7085, 1517.6285, 2202.9531, 2202.9531, 2474.1194, 2474.1194, 3075.3518

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Number of Queries: 16

Protein View

Match to: **gi|52001221** Score: **445** Expect: **2.8e-042**
arachin Ahy-2 [Arachis hypogaea]

Nominal mass (M_r): **61836**; Calculated pI value: **5.54**
NCBI BLAST search of gi|52001221 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```
    1 MAKLLALSVC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRLESEG
   51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
  101 FGLIFPGCPS TYEEPAQQGR RHQSQRAPRR FEGEDQSQQQ QQDSHQKVRR
  151 FDEGDLIAVP TGVALWMYND HDTDVVAVSL TDTNNNDNQL DQFPRRFNLA
  201 GNHEQEFLRY QQQSRRRSLP YSPYSPQSQP RQEEREFSPR GQHSRRERAG
  251 QEQENEGGNI FSGFTPEFLA QAFQVDDRQI LQNLRGENES DEQGAIVTVR
  301 GGLRILSPDR KRRQQYERPD EEEEYDEDEY EYDEEERQQD RRRGRGSRGR
  351 GNGIEETICT ASVKKNIGRN RSPDIYNPQA GSLKTANDLN LLILRWLGLS
  401 AEYGNLYRNA LFVPHYNTNA HSIIYALRGR AHVQVVDSNG NRVYDEELQE
  451 GHVLVVPQNF AVAGKSQSDN FEYVAFKTDS RPSIANLAGE NSIIDNLPEE
  501 VVANSYGLPR EQARQLKNNN PFKFFVPPSQ QSLGAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
25 - 36	1534.6555	1533.6482	1533.6630	-0.0148	0	QQPEENACQFQR	(No match)
37 - 45	1083.5559	1082.5486	1082.5581	-0.0094	0	LNAQRPDNR	(No match)
82 - 98	2051.0244	2050.0171	2050.0384	-0.0213	0	RPFYSNAPQEIFIQQGR	(No match)
82 - 98	2051.0244	2050.0171	2050.0384	-0.0213	0	RPFYSNAPQEIFIQQGR	(Ions score 120)
99 - 120	2474.1194	2473.1121	2473.1371	-0.0250	0	GYFGLIFPGCPSTYEEPAQQGR	(Ions score 89)
99 - 120	2474.1194	2473.1121	2473.1371	-0.0250	0	GYFGLIFPGCPSTYEEPAQQGR	(No match)
130 - 147	2202.9531	2201.9458	2201.9686	-0.0227	1	RFEGEDQSQQQQQDSHQK	(No match)
130 - 147	2202.9531	2201.9458	2201.9686	-0.0227	1	RFEGEDQSQQQQQDSHQK	(Ions score 58)
196 - 209	1730.8558	1729.8485	1729.8648	-0.0162	1	RFNLAGNHEQEFLR	(Ions score 11)
196 - 209	1730.8558	1729.8485	1729.8648	-0.0162	1	RFNLAGNHEQEFLR	(No match)
197 - 209	1574.7561	1573.7488	1573.7637	-0.0148	0	FNLAGNHEQEFLR	(Ions score 76)
197 - 209	1574.7561	1573.7488	1573.7637	-0.0148	0	FNLAGNHEQEFLR	(No match)

Spot 71

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:53:40 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **538 for gi|22135348, trypsin inhibitor [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|22135348	25768	538	trypsin inhibitor [Arachis hypogaea]
2.	gi|52001219	61810	497	arachin Ahy-1 [Arachis hypogaea]
3.	gi|21314465	62042	497	allergen Arah3/Arah4 [Arachis hypogaea]
4.	gi|9864777	60754	435	Gly1 [Arachis hypogaea]
5.	gi|118776570	60681	435	arachin 6 [Arachis hypogaea]
6.	gi|5712199	61430	435	glycinin [Arachis hypogaea]
7.	gi|57669861	61041	435	arachin Ahy-4 [Arachis hypogaea]
8.	gi|108595573	61041	435	arachin Ahy-4 [Arachis hypogaea]
9.	gi|52001221	61836	434	arachin Ahy-2 [Arachis hypogaea]
10.	gi|37789212	61803	364	storage protein [Arachis hypogaea]

Results List

1. gi|22135348 **Mass:** 25768 **Score:** 538 **Expect:** 1.4e-051 **Queries matched:** 16
trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
809.3835	808.3762	808.3827	-0.0065	211	216	0	---	YQQQSR
1005.5256	1004.5183	1004.5264	-0.0081	124	131	0	---	HQSQRPPR
1083.5590	1082.5517	1082.5581	-0.0063	39	47	0	---	LNAQRPDNR
1161.6249	1160.6176	1160.6275	-0.0099	124	132	1	---	HQSQRPPRR
1534.6571	1533.6498	1533.6630	-0.0132	27	38	0	---	QQPEENACQFQR
1534.6571	1533.6498	1533.6630	-0.0132	27	38	0	65	QQPEENACQFQR
1574.7592	1573.7519	1573.7637	-0.0117	198	210	0	85	FNLAGNHEQEFLR
1574.7592	1573.7519	1573.7637	-0.0117	198	210	0	---	FNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	197	210	1	---	RFNLAGNHEQEFLR

1730.8596	1729.8523	1729.8648	-0.0124	197 - 210	1	0	RFNLAGNHEQEFLR
1916.8376	1915.8303	1915.8409	-0.0105	133 - 148	0	---	FQGQDQSQQQQDSHQK
2051.0320	2050.0247	2050.0384	-0.0137	84 - 100	0	104	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	84 - 100	0	---	RPFYSNAPQEIFIQQGR
2072.9443	2071.9370	2071.9420	-0.0049	132 - 148	1	---	RFQGQDQSQQQQDSHQK
2474.1250	2473.1177	2473.1371	-0.0194	101 - 122	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1250	2473.1177	2473.1371	-0.0194	101 - 122	0	112	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5612, 1026.0187, 1026.5126, 1151.7098, 1517.6333, 1624.7750, 2491.1528, 3074.3574

2. gi|52001219 **Mass:** 61810 **Score:** 497 **Expect:** 1.7e-047 **Queries matched:** 16

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
809.3835	808.3762	808.3827	-0.0065	209 - 214	0	---	YQQQSR
1005.5256	1004.5183	1004.5264	-0.0081	122 - 129	0	---	HQSQRPPR
1083.5590	1082.5517	1082.5581	-0.0063	37 - 45	0	---	LNAQRPDNR
1161.6249	1160.6176	1160.6275	-0.0099	122 - 130	1	---	HQSQRPPRR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36	0	---	QQPEENACQFQR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36	0	65	QQPEENACQFQR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208	0	85	FNLAGNHEQEFLR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208	0	---	FNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208	1	---	RFNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208	1	0	RFNLAGNHEQEFLR
1916.8376	1915.8303	1915.8409	-0.0105	131 - 146	0	---	FQGQDQSQQQQDSHQK
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98	0	104	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98	0	---	RPFYSNAPQEIFIQQGR
2072.9443	2071.9370	2071.9420	-0.0049	130 - 146	1	---	RFQGQDQSQQQQDSHQK
2474.1250	2473.1177	2473.1371	-0.0194	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99 - 120	0	112	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5612, 1026.0187, 1026.5126, 1151.7098, 1517.6333, 1624.7750, 2491.1528, 3074.3574

3. gi|21314465 **Mass:** 62042 **Score:** 497 **Expect:** 1.7e-047 **Queries matched:** 16

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
809.3835	808.3762	808.3827	-0.0065	209 - 214	0	---	YQQQSR
1005.5256	1004.5183	1004.5264	-0.0081	122 - 129	0	---	HQSQRPPR
1083.5590	1082.5517	1082.5581	-0.0063	37 - 45	0	---	LNAQRPDNR
1161.6249	1160.6176	1160.6275	-0.0099	122 - 130	1	---	HQSQRPPRR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36	0	---	QQPEENACQFQR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36	0	65	QQPEENACQFQR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208	0	85	FNLAGNHEQEFLR

1574.7592	1573.7519	1573.7637	-0.0117	196 - 208	0	---	FNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208	1	---	RFNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208	1	0	RFNLAGNHEQEFLR
1916.8376	1915.8303	1915.8409	-0.0105	131 - 146	0	---	FQGQDQSQQQQDSHQK
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98	0	104	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98	0	---	RPFYSNAPQEIFIQQGR
2072.9443	2071.9370	2071.9420	-0.0049	130 - 146	1	---	RFQGQDQSQQQQDSHQK
2474.1250	2473.1177	2473.1371	-0.0194	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99 - 120	0	112	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5612, 1026.0187, 1026.5126, 1151.7098, 1517.6333, 1624.7750, 2491.1528, 3074.3574

4. gi|9864777 **Mass:** 60754 **Score:** 435 **Expect:** 2.8e-041 **Queries matched:** 12

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
809.3835	808.3762	808.3827	-0.0065	211 - 216		0	---	YQQQSR
1083.5590	1082.5517	1082.5581	-0.0063	38 - 46		0	---	LNAQRPDNR
1534.6571	1533.6498	1533.6630	-0.0132	26 - 37		0	---	QQPEENACQFQR
1534.6571	1533.6498	1533.6630	-0.0132	26 - 37		0	65	QQPEENACQFQR
1574.7592	1573.7519	1573.7637	-0.0117	198 - 210		0	85	FNLAGNHEQEFLR
1574.7592	1573.7519	1573.7637	-0.0117	198 - 210		0	---	FNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	197 - 210		1	---	RFNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	197 - 210		1	0	RFNLAGNHEQEFLR
2051.0320	2050.0247	2050.0384	-0.0137	83 - 99		0	104	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	83 - 99		0	---	RPFYSNAPQEIFIQQGR
2474.1250	2473.1177	2473.1371	-0.0194	100 - 121		0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1250	2473.1177	2473.1371	-0.0194	100 - 121		0	112	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5612, 1005.5256, 1026.0187, 1026.5126, 1151.7098, 1161.6249, 1517.6333, 1624.7750, 1916.8376, 2072.9443, 2491.1528, 3074.3574

5. gi|118776570 **Mass:** 60681 **Score:** 435 **Expect:** 2.8e-041 **Queries matched:** 12

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
809.3835	808.3762	808.3827	-0.0065	209 - 214		0	---	YQQQSR
1083.5590	1082.5517	1082.5581	-0.0063	37 - 45		0	---	LNAQRPDNR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36		0	---	QQPEENACQFQR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36		0	65	QQPEENACQFQR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208		0	85	FNLAGNHEQEFLR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208		0	---	FNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208		1	---	RFNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208		1	0	RFNLAGNHEQEFLR

2051.0320	2050.0247	2050.0384	-0.0137	82 - 98	0	104	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98	0	---	RPFYSNAPQEIFIQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99 - 120	0	112	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5612, 1005.5256, 1026.0187, 1026.5126, 1151.7098, 1161.6249, 1517.6333, 1624.7750, 1916.8376, 2072.9443, 2491.1528, 3074.3574

6. gi|5712199 **Mass:** 61430 **Score:** 435 **Expect:** 2.8e-041 **Queries matched:** 12

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
809.3835	808.3762	808.3827	-0.0065	209 - 214		0	---	YQQQSR
1083.5590	1082.5517	1082.5581	-0.0063	37 - 45		0	---	LNAQRPDNR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36		0	---	QQPEENACQFQR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36		0	65	QQPEENACQFQR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208		0	85	FNLAGNHEQEFLR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208		0	---	FNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208		1	---	RFNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208		1	0	RFNLAGNHEQEFLR
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98		0	104	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98		0	---	RPFYSNAPQEIFIQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99 - 120		0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99 - 120		0	112	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5612, 1005.5256, 1026.0187, 1026.5126, 1151.7098, 1161.6249, 1517.6333, 1624.7750, 1916.8376, 2072.9443, 2491.1528, 3074.3574

7. gi|57669861 **Mass:** 61041 **Score:** 435 **Expect:** 2.8e-041 **Queries matched:** 12

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
809.3835	808.3762	808.3827	-0.0065	209 - 214		0	---	YQQQSR
1083.5590	1082.5517	1082.5581	-0.0063	37 - 45		0	---	LNAQRPDNR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36		0	---	QQPEENACQFQR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36		0	65	QQPEENACQFQR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208		0	85	FNLAGNHEQEFLR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208		0	---	FNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208		1	---	RFNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208		1	0	RFNLAGNHEQEFLR
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98		0	104	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98		0	---	RPFYSNAPQEIFIQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99 - 120		0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99 - 120		0	112	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5612, 1005.5256, 1026.0187, 1026.5126, 1151.7098, 1161.6249, 1517.6333, 1624.7750, 1916.8376,

2072.9443, 2491.1528, 3074.3574

8. gi|108595573 **Mass:** 61041 **Score:** 435 **Expect:** 2.8e-041 **Queries matched:** 12

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
809.3835	808.3762	808.3827	-0.0065	209	214	0	---	YQQQSR
1083.5590	1082.5517	1082.5581	-0.0063	37	45	0	---	LNAQRPDNR
1534.6571	1533.6498	1533.6630	-0.0132	25	36	0	---	QQPEENACQFQR
1534.6571	1533.6498	1533.6630	-0.0132	25	36	0	65	QQPEENACQFQR
1574.7592	1573.7519	1573.7637	-0.0117	196	208	0	85	FNLAGNHEQEFLR
1574.7592	1573.7519	1573.7637	-0.0117	196	208	0	---	FNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195	208	1	---	RFNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195	208	1	0	RFNLAGNHEQEFLR
2051.0320	2050.0247	2050.0384	-0.0137	82	98	0	104	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82	98	0	---	RPFYSNAPQEIFIQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99	120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99	120	0	112	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5612, 1005.5256, 1026.0187, 1026.5126, 1151.7098, 1161.6249, 1517.6333, 1624.7750, 1916.8376, 2072.9443, 2491.1528, 3074.3574

9. gi|52001221 **Mass:** 61836 **Score:** 434 **Expect:** 3.5e-041 **Queries matched:** 12

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
809.3835	808.3762	808.3827	-0.0065	210	215	0	---	YQQQSR
1083.5590	1082.5517	1082.5581	-0.0063	37	45	0	---	LNAQRPDNR
1534.6571	1533.6498	1533.6630	-0.0132	25	36	0	---	QQPEENACQFQR
1534.6571	1533.6498	1533.6630	-0.0132	25	36	0	65	QQPEENACQFQR
1574.7592	1573.7519	1573.7637	-0.0117	197	209	0	85	FNLAGNHEQEFLR
1574.7592	1573.7519	1573.7637	-0.0117	197	209	0	---	FNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	196	209	1	---	RFNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	196	209	1	0	RFNLAGNHEQEFLR
2051.0320	2050.0247	2050.0384	-0.0137	82	98	0	104	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82	98	0	---	RPFYSNAPQEIFIQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99	120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1250	2473.1177	2473.1371	-0.0194	99	120	0	112	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5612, 1005.5256, 1026.0187, 1026.5126, 1151.7098, 1161.6249, 1517.6333, 1624.7750, 1916.8376, 2072.9443, 2491.1528, 3074.3574

10. gi|37789212 **Mass:** 61803 **Score:** 364 **Expect:** 3.5e-034 **Queries matched:** 14

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

809.3835	808.3762	808.3827	-0.0065	209 - 214	0	---	YQQQSR
1005.5256	1004.5183	1004.5264	-0.0081	122 - 129	0	---	HQSQRPPR
1083.5590	1082.5517	1082.5581	-0.0063	37 - 45	0	---	LNAQRPDNR
1161.6249	1160.6176	1160.6275	-0.0099	122 - 130	1	---	HQSQRPPRR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36	0	---	QQPEENACQFQR
1534.6571	1533.6498	1533.6630	-0.0132	25 - 36	0	65	QQPEENACQFQR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208	0	85	FNLAGNHEQEFLR
1574.7592	1573.7519	1573.7637	-0.0117	196 - 208	0	---	FNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208	1	---	RFNLAGNHEQEFLR
1730.8596	1729.8523	1729.8648	-0.0124	195 - 208	1	0	RFNLAGNHEQEFLR
1916.8376	1915.8303	1915.8409	-0.0105	131 - 146	0	---	FQGQDQSQQQQDSHQK
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98	0	104	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 - 98	0	---	RPFYSNAPQEIFIQQGR
2072.9443	2071.9370	2071.9420	-0.0049	130 - 146	1	---	RFQGQDQSQQQQDSHQK

No match to: 982.5612, 1026.0187, 1026.5126, 1151.7098, 1517.6333, 1624.7750, 2474.1250, 2474.1250, 2491.1528, 3074.3574

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1

Protein View

Match to: **gi|22135348** Score: **538** Expect: **1.4e-051**
trypsin inhibitor [Arachis hypogaea]

Nominal mass (M_r): **25768**; Calculated pI value: **6.66**
NCBI BLAST search of gi|22135348 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **47%**

Matched peptides shown in **Bold Red**

```
    1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES
   51 EGGYIETWNP NNQEFECAGV ALSRLVLRRN ALRRPFYSNA PQEIFIQQGR
  101 GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH
  151 RFDEGDLIAV PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
  201 AGNHEQEFLR YQQQSRRRS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
27 - 38	1534.6571	1533.6498	1533.6630	-0.0132	0	QQPEENACQFQR	(No match)
27 - 38	1534.6571	1533.6498	1533.6630	-0.0132	0	QQPEENACQFQR	(Ions score 65)
39 - 47	1083.5590	1082.5517	1082.5581	-0.0063	0	LNAQRPDNR	(No match)
84 - 100	2051.0320	2050.0247	2050.0384	-0.0137	0	RPFYSNAPQEIFIQQGR	(Ions score 104)
84 - 100	2051.0320	2050.0247	2050.0384	-0.0137	0	RPFYSNAPQEIFIQQGR	(No match)
101 - 122	2474.1250	2473.1177	2473.1371	-0.0194	0	GYFGLIFPGCPSTYEEPAQQGR	(No match)
101 - 122	2474.1250	2473.1177	2473.1371	-0.0194	0	GYFGLIFPGCPSTYEEPAQQGR	(Ions score 112)
124 - 131	1005.5256	1004.5183	1004.5264	-0.0081	0	HQSQRPPR	(No match)
124 - 132	1161.6249	1160.6176	1160.6275	-0.0099	1	HQSQRPPRR	(No match)
132 - 148	2072.9443	2071.9370	2071.9420	-0.0049	1	RFQGQDQSQQQQDSHQK	(No match)
133 - 148	1916.8376	1915.8303	1915.8409	-0.0105	0	FQGQDQSQQQQDSHQK	(No match)
197 - 210	1730.8596	1729.8523	1729.8648	-0.0124	1	RFNLAGNHEQEFLR	(No match)
197 - 210	1730.8596	1729.8523	1729.8648	-0.0124	1	RFNLAGNHEQEFLR	(Ions score 0)
198 - 210	1574.7592	1573.7519	1573.7637	-0.0117	0	FNLAGNHEQEFLR	(Ions score 85)
198 - 210	1574.7592	1573.7519	1573.7637	-0.0117	0	FNLAGNHEQEFLR	(No match)
211 - 216	809.3835	808.3762	808.3827	-0.0065	0	YQQQSR	(No match)

Spot 72

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:10:11 GMT
Top Score : 60 for gi|118776570, arachin 6 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	60	arachin 6 [Arachis hypogaea]
2.	gi|9864777	60754	60	Gly1 [Arachis hypogaea]
3.	gi|57669861	61041	52	arachin Ahy-4 [Arachis hypogaea]
4.	gi|108595573	61041	52	arachin Ahy-4 [Arachis hypogaea]
5.	gi|3703107	58543	43	glycinin [Arachis hypogaea]
6.	gi|52001221	61836	43	arachin Ahy-2 [Arachis hypogaea]
7.	gi|5712199	61430	36	glycinin [Arachis hypogaea]
8.	gi|52001219	61810	33	arachin Ahy-1 [Arachis hypogaea]
9.	gi|37789212	61803	33	storage protein [Arachis hypogaea]
10.	gi|21314465	62042	27	allergen Arah3/Arah4 [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 60 **Expect:** 0.00098 **Queries matched:** 11
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5889	1101.5816	1101.5930	-0.0114	507	515	1	QLKNNNPFK
1269.7455	1268.7382	1268.7452	-0.0070	377	387	0	TANELNLLILR
1295.6320	1294.6247	1294.6377	-0.0130	423	434	0	AHVQVVDSNGNR
1349.7026	1348.6953	1348.6927	0.0026	516	526	0	FFVPPFQQSPR
1389.6956	1388.6883	1388.6935	-0.0052	364	376	0	SPDIYNPQAGSLK
1448.6708	1447.6635	1447.6619	0.0016	458	469	0	SQSENFEYVAFK
1541.7695	1540.7622	1540.7673	-0.0051	388	400	0	WLGLSAEYGNLYR
1659.8462	1658.8389	1658.8376	0.0014	362	376	1	NRSPDIYNPQAGSLK
2064.0422	2063.0349	2063.0376	-0.0027	510	526	1	NNNPFKFFVPPFQQSPR
2314.1992	2313.1919	2313.2018	-0.0098	401	420	0	NALFVPHYNTNAHSIIYALR
2541.3167	2540.3094	2540.2910	0.0185	435	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1255.7354, 1289.6696, 1296.6212, 1305.6803, 1321.6842, 1360.6853, 1365.6960, 1376.7297, 1420.7325, 1434.6661, 1436.7208, 1496.7117, 1524.7596, 1549.7451, 1551.7480, 1553.7739, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2004.0283, 2020.0052, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

2. gi|9864777 **Mass:** 60754 **Score:** 60 **Expect:** 0.00098 **Queries matched:** 11

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5889	1101.5816	1101.5930	-0.0114	507	515	1	QLKNNNPFK
1255.7354	1254.7281	1254.7295	-0.0014	377	387	0	TANDLNLLILR
1295.6320	1294.6247	1294.6377	-0.0130	423	434	0	AHVQVVDSNGNR
1305.6803	1304.6730	1304.6877	-0.0146	516	526	0	FFVPPSQQSLR
1389.6956	1388.6883	1388.6935	-0.0052	364	376	0	SPDIYNPQAGSLK
1434.6661	1433.6588	1433.6462	0.0126	458	469	0	SQSDNFEYVAFK
1541.7695	1540.7622	1540.7673	-0.0051	388	400	0	WLGLSAEYGNLYR
1659.8462	1658.8389	1658.8376	0.0014	362	376	1	NRSPDIYNPQAGSLK
2020.0052	2018.9979	2019.0326	-0.0346	510	526	1	NNNPFKFFVPPSQQSLR
2314.1992	2313.1919	2313.2018	-0.0098	401	420	0	NALFVPHYNTNAHSIIYALR
2541.3167	2540.3094	2540.2910	0.0185	435	457	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1269.7455, 1289.6696, 1296.6212, 1321.6842, 1349.7026, 1360.6853, 1365.6960, 1376.7297, 1420.7325, 1436.7208, 1448.6708, 1496.7117, 1524.7596, 1549.7451, 1551.7480, 1553.7739, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2004.0283, 2064.0422, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

3. gi|57669861 **Mass:** 61041 **Score:** 52 **Expect:** 0.0058 **Queries matched:** 10

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7354	1254.7281	1254.7295	-0.0014	378	388	0	TANDLNLLILR
1289.6696	1288.6623	1288.6564	0.0060	518	528	0	FFVPPSQQSPR
1295.6320	1294.6247	1294.6377	-0.0130	424	435	0	AHVQVVDSNGNR
1389.6956	1388.6883	1388.6935	-0.0052	365	377	0	SPDIYNPQAGSLK
1434.6661	1433.6588	1433.6462	0.0126	459	470	0	SQSDNFEYVAFK
1541.7695	1540.7622	1540.7673	-0.0051	389	401	0	WLGLSAEYGNLYR
1659.8462	1658.8389	1658.8376	0.0014	363	377	1	NRSPDIYNPQAGSLK
2004.0283	2003.0210	2003.0013	0.0198	512	528	1	NNNPFKFFVPPSQQSPR

2314.1992	2313.1919	2313.2018	-0.0098	402 - 421	0	NALFVPHYNTNAHSIIYALR
2541.3167	2540.3094	2540.2910	0.0185	436 - 458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1102.5889, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1269.7455, 1296.6212, 1305.6803, 1321.6842, 1349.7026, 1360.6853, 1365.6960, 1376.7297, 1420.7325, 1436.7208, 1448.6708, 1496.7117, 1524.7596, 1549.7451, 1551.7480, 1553.7739, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2020.0052, 2064.0422, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

4. gi|108595573 **Mass:** 61041 **Score:** 52 **Expect:** 0.0058 **Queries matched:** 10

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.7354	1254.7281	1254.7295	-0.0014	378 -	388	0	TANDLNLLILR
1289.6696	1288.6623	1288.6564	0.0060	518 -	528	0	FFVPPSQQSPR
1295.6320	1294.6247	1294.6377	-0.0130	424 -	435	0	AHVQVVDSNGNR
1389.6956	1388.6883	1388.6935	-0.0052	365 -	377	0	SPDIYNPQAGSLK
1434.6661	1433.6588	1433.6462	0.0126	459 -	470	0	SQSDNFEYVAFK
1541.7695	1540.7622	1540.7673	-0.0051	389 -	401	0	WLGLSAEYGNLYR
1659.8462	1658.8389	1658.8376	0.0014	363 -	377	1	NRSPDIYNPQAGSLK
2004.0283	2003.0210	2003.0013	0.0198	512 -	528	1	NNNPFKFFVPPSQQSPR
2314.1992	2313.1919	2313.2018	-0.0098	402 -	421	0	NALFVPHYNTNAHSIIYALR
2541.3167	2540.3094	2540.2910	0.0185	436 -	458	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1102.5889, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1269.7455, 1296.6212, 1305.6803, 1321.6842, 1349.7026, 1360.6853, 1365.6960, 1376.7297, 1420.7325, 1436.7208, 1448.6708, 1496.7117, 1524.7596, 1549.7451, 1551.7480, 1553.7739, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2020.0052, 2064.0422, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

5. gi|3703107 **Mass:** 58543 **Score:** 43 **Expect:** 0.041 **Queries matched:** 9

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5889	1101.5816	1101.5930	-0.0114	485 -	493	1	QLKNNNPFK
1255.7354	1254.7281	1254.7295	-0.0014	355 -	365	0	TANDLNLLILR
1289.6696	1288.6623	1288.6564	0.0060	494 -	504	0	FFVPPSQQSPR
1295.6320	1294.6247	1294.6377	-0.0130	401 -	412	0	AHVQVVDSNGNR
1389.6956	1388.6883	1388.6935	-0.0052	342 -	354	0	SPDIYNPQAGSLK
1448.6708	1447.6635	1447.6619	0.0016	436 -	447	0	SQSENFEYVAFK
1659.8462	1658.8389	1658.8376	0.0014	340 -	354	1	NRSPDIYNPQAGSLK

2004.0283	2003.0210	2003.0013	0.0198	488 - 504	1	NNNPFKFFVPPSQQSPR
2541.3167	2540.3094	2540.2910	0.0185	413 - 435	0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1269.7455, 1296.6212, 1305.6803, 1321.6842, 1349.7026, 1360.6853, 1365.6960, 1376.7297, 1420.7325, 1434.6661, 1436.7208, 1496.7117, 1524.7596, 1541.7695, 1549.7451, 1551.7480, 1553.7739, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2020.0052, 2064.0422, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2314.1992, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

6. gi|52001221 **Mass:** 61836 **Score:** 43 **Expect:** 0.049 **Queries matched:** 9

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5889	1101.5816	1101.5930	-0.0114	515 - 523		1	QLKNNNPFK
1255.7354	1254.7281	1254.7295	-0.0014	385 - 395		0	TANDLNLLILR
1295.6320	1294.6247	1294.6377	-0.0130	431 - 442		0	AHVQVVDSNGNR
1389.6956	1388.6883	1388.6935	-0.0052	372 - 384		0	SPDIYNPQAGSLK
1434.6661	1433.6588	1433.6462	0.0126	466 - 477		0	SQSDNFEYVAFK
1541.7695	1540.7622	1540.7673	-0.0051	396 - 408		0	WLGLSAEYGNLYR
1659.8462	1658.8389	1658.8376	0.0014	370 - 384		1	NRSPDIYNPQAGSLK
2314.1992	2313.1919	2313.2018	-0.0098	409 - 428		0	NALFVPHYNTNAHSIIYALR
2541.3167	2540.3094	2540.2910	0.0185	443 - 465		0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1269.7455, 1289.6696, 1296.6212, 1305.6803, 1321.6842, 1349.7026, 1360.6853, 1365.6960, 1376.7297, 1420.7325, 1436.7208, 1448.6708, 1496.7117, 1524.7596, 1549.7451, 1551.7480, 1553.7739, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2004.0283, 2020.0052, 2064.0422, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

7. gi|5712199 **Mass:** 61430 **Score:** 36 **Expect:** 0.21 **Queries matched:** 8

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5889	1101.5816	1101.5930	-0.0114	508 - 516		1	QLKNNNPFK
1295.6320	1294.6247	1294.6377	-0.0130	424 - 435		0	AHVQVVDSNGNR
1349.7026	1348.6953	1348.6927	0.0026	517 - 527		0	FFVPPFQQSPR
1448.6708	1447.6635	1447.6619	0.0016	459 - 470		0	SQSENFEYVAFK
1541.7695	1540.7622	1540.7673	-0.0051	389 - 401		0	WLGLSAEYGNLYR
2064.0422	2063.0349	2063.0376	-0.0027	511 - 527		1	NNNPFKFFVPPFQQSPR
2314.1992	2313.1919	2313.2018	-0.0098	402 - 421		0	NALFVPHYNTNAHSIIYALR
2541.3167	2540.3094	2540.2910	0.0185	436 - 458		0	VYDEELQEGHVLVVPQNFAVAGK

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1255.7354, 1269.7455, 1289.6696, 1296.6212, 1305.6803, 1321.6842, 1360.6853, 1365.6960, 1376.7297, 1389.6956, 1420.7325, 1434.6661, 1436.7208, 1496.7117, 1524.7596, 1549.7451, 1551.7480, 1553.7739, 1659.8462, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2004.0283, 2020.0052, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

8. gi|52001219 **Mass:** 61810 **Score:** 33 **Expect:** 0.44 **Queries matched:** 8

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5889	1101.5816	1101.5930	-0.0114	514	522	1	QLKNNNPFK
1269.7455	1268.7382	1268.7452	-0.0070	384	394	0	TANELNLLILR
1296.6212	1295.6139	1295.6218	-0.0078	430	441	0	AHVQVVDSNGDR
1389.6956	1388.6883	1388.6935	-0.0052	371	383	0	SPDIYNPQAGSLK
1448.6708	1447.6635	1447.6619	0.0016	465	476	0	SQSENFEYVAFK
1541.7695	1540.7622	1540.7673	-0.0051	395	407	0	WLGLSAEYGNLYR
1659.8462	1658.8389	1658.8376	0.0014	369	383	1	NRSPDIYNPQAGSLK
2314.1992	2313.1919	2313.2018	-0.0098	408	427	0	NALFVPHYNTNAHSIIYALR

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1255.7354, 1289.6696, 1295.6320, 1305.6803, 1321.6842, 1349.7026, 1360.6853, 1365.6960, 1376.7297, 1420.7325, 1434.6661, 1436.7208, 1496.7117, 1524.7596, 1549.7451, 1551.7480, 1553.7739, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2004.0283, 2020.0052, 2064.0422, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2541.3167, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

9. gi|37789212 **Mass:** 61803 **Score:** 33 **Expect:** 0.44 **Queries matched:** 8

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5889	1101.5816	1101.5930	-0.0114	514	522	1	QLKNNNPFK
1269.7455	1268.7382	1268.7452	-0.0070	384	394	0	TANELNLLILR
1296.6212	1295.6139	1295.6218	-0.0078	430	441	0	AHVQVVDSNGDR
1389.6956	1388.6883	1388.6935	-0.0052	371	383	0	SPDIYNPQAGSLK
1448.6708	1447.6635	1447.6619	0.0016	465	476	0	SQSENFEYVAFK
1541.7695	1540.7622	1540.7673	-0.0051	395	407	0	WLGLSAEYGNLYR
1659.8462	1658.8389	1658.8376	0.0014	369	383	1	NRSPDIYNPQAGSLK
2314.1992	2313.1919	2313.2018	-0.0098	408	427	0	NALFVPHYNTNAHSIIYALR

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1255.7354, 1289.6696, 1295.6320, 1305.6803, 1321.6842, 1349.7026, 1360.6853, 1365.6960, 1376.7297,

1420.7325, 1434.6661, 1436.7208, 1496.7117, 1524.7596, 1549.7451, 1551.7480, 1553.7739, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2004.0283, 2020.0052, 2064.0422, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2541.3167, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

10. gi|21314465 **Mass:** 62042 **Score:** 27 **Expect:** 1.9 **Queries matched:** 7

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1102.5889	1101.5816	1101.5930	-0.0114	516	524	1	QLKNNNPFK
1296.6212	1295.6139	1295.6218	-0.0078	432	443	0	AHVQVVDSNGDR
1389.6956	1388.6883	1388.6935	-0.0052	371	383	0	SPDIYNPQAGSLK
1448.6708	1447.6635	1447.6619	0.0016	467	478	0	SQSENFEYVAFK
1541.7695	1540.7622	1540.7673	-0.0051	397	409	0	WLGLSAEYGNLYR
1659.8462	1658.8389	1658.8376	0.0014	369	383	1	NRSPDIYNPQAGSLK
2314.1992	2313.1919	2313.2018	-0.0098	410	429	0	NALFVPHYNTNAHSIIYALR

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1255.7354, 1269.7455, 1289.6696, 1295.6320, 1305.6803, 1321.6842, 1349.7026, 1360.6853, 1365.6960, 1376.7297, 1420.7325, 1434.6661, 1436.7208, 1496.7117, 1524.7596, 1549.7451, 1551.7480, 1553.7739, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2004.0283, 2020.0052, 2064.0422, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2541.3167, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 83

Protein View

Match to: **gi|9864777** Score: **60** Expect: **0.00098**
Gly1 [Arachis hypogaea]

Nominal mass (M_r): **60754**; Calculated pI value: **5.48**
NCBI BLAST search of gi|9864777 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **83**
Number of mass values matched: **11**
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
     1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE
    51 GGYIETWNPN NQEFECAGVA LSRLVLRRNA LRRPFYSNAP QEIFIQQGRG
   101 YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR
   151 RFDEGDLIAV PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
   201 AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP RGQHSRRERA
   251 GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV
   301 KGGLRILSPD RKRGADEEEE YDEDEYEYDE EDRRRGRGSR GRGNGIEETI
   351 CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR
   401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
   451 NFAVAGKSQS DNFEYVAFKT DSRPNIANFA GENSIIDNLP EEVVANSYGL
   501 PREQARQLKN NNPFKFFVPP SQQSLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
362 - 376	1659.8462	1658.8389	1658.8376	0.0014	1	NRSPDIYNPQAGSLK
364 - 376	1389.6956	1388.6883	1388.6935	-0.0052	0	SPDIYNPQAGSLK
377 - 387	1255.7354	1254.7281	1254.7295	-0.0014	0	TANDLNLLILR
388 - 400	1541.7695	1540.7622	1540.7673	-0.0051	0	WLGLSAEYGNLYR
401 - 420	2314.1992	2313.1919	2313.2018	-0.0098	0	NALFVPHYNTNAHSIIYALR
423 - 434	1295.6320	1294.6247	1294.6377	-0.0130	0	AHVQVVDSNGNR
435 - 457	2541.3167	2540.3094	2540.2910	0.0185	0	VYDEELQEGHVLVVPQNFAVAGK
458 - 469	1434.6661	1433.6588	1433.6462	0.0126	0	SQSDNFEYVAFK
507 - 515	1102.5889	1101.5816	1101.5930	-0.0114	1	QLKNNNPFK
510 - 526	2020.0052	2018.9979	2019.0326	-0.0346	1	NNNPFKFFVPPSQQSLR
516 - 526	1305.6803	1304.6730	1304.6877	-0.0146	0	FFVPPSQQSLR

No match to: 805.4618, 835.5098, 845.1089, 854.0661, 855.0568, 861.0768, 871.0389, 877.0496, 881.2755, 893.0228, 1022.5029, 1046.5879, 1066.0697, 1080.5294, 1082.0308, 1085.5494, 1137.0807, 1137.5703, 1145.0720, 1145.5741, 1175.5472, 1269.7455, 1289.6696, 1296.6212, 1321.6842, 1349.7026, 1360.6853, 1365.6960, 1376.7297, 1420.7325, 1436.7208, 1448.6708, 1496.7117, 1524.7596, 1549.7451, 1551.7480, 1553.7739, 1756.8521, 1758.8329, 1774.8456, 1786.8700, 1875.9987, 1889.9695, 1934.9120, 2004.0283, 2064.0422, 2091.0830, 2145.0388, 2162.0439, 2185.0347, 2224.9924, 2227.0522, 2273.1575, 2295.1528, 2311.1326, 2335.0996, 2351.0857, 2354.0945, 2508.3491, 2530.2336, 2532.3411, 2564.2825, 2604.2881, 2612.1599, 2765.2876, 3136.4712, 3154.4844, 3211.5427, 3301.7646, 3512.8350, 3547.8057, 3818.9358

Spot 73

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:55:15 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **348 for gi|118776570, arachin 6 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	348	arachin 6 [Arachis hypogaea]
2.	gi|5712199	61430	336	glycinin [Arachis hypogaea]
3.	gi|9864777	60754	332	Gly1 [Arachis hypogaea]
4.	gi|57669861	61041	271	arachin Ahy-4 [Arachis hypogaea]
5.	gi|108595573	61041	271	arachin Ahy-4 [Arachis hypogaea]
6.	gi|52001221	61836	260	arachin Ahy-2 [Arachis hypogaea]
7.	gi|52001219	61810	248	arachin Ahy-1 [Arachis hypogaea]
8.	gi|37789212	61803	248	storage protein [Arachis hypogaea]
9.	gi|21314465	62042	240	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|37221901	18557	30	resistance protein [Arachis stenosperma]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 348 **Expect:** 1.4e-032 **Queries matched:** 9
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1269.7354	1268.7281	1268.7452	-0.0171	377	387	0	---	TANELNLLILR
1349.6815	1348.6742	1348.6927	-0.0185	516	526	0	---	FFVPPFQQSPR
1349.6815	1348.6742	1348.6927	-0.0185	516	526	0	76	FFVPPFQQSPR
1541.7533	1540.7460	1540.7673	-0.0213	388	400	0	---	WLGLSAEYGNLYR
1541.7533	1540.7460	1540.7673	-0.0213	388	400	0	96	WLGLSAEYGNLYR
1659.8235	1658.8162	1658.8376	-0.0213	362	376	1	---	NRSPDIYNPQAGSLK
2314.1702	2313.1629	2313.2018	-0.0388	401	420	0	125	NALFVPHYNTNAHSIIYALR
2314.1702	2313.1629	2313.2018	-0.0388	401	420	0	---	NALFVPHYNTNAHSIIYALR

2541.2783	2540.2710	2540.2910	-0.0199	435 - 457	0	---	VYDEELQEGHVLVVPQNFAVAGK

No match to: 835.5054, 1255.7186, 1289.6459, 1305.6737, 1305.6737, 1365.6754, 1365.6754, 1376.7131, 1524.7313, 1545.7496, 1557.7451, 2296.1599, 2328.1589, 2346.1567, 2564.2368, 3053.4888, 3087.4849

2. gi|5712199 **Mass:** 61430 **Score:** 336 **Expect:** 2.2e-031 **Queries matched:** 8

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1269.7354	1268.7281	1268.6486	0.0795	238 -	247	1	---	EFRPRGQHSR
1349.6815	1348.6742	1348.6927	-0.0185	517 -	527	0	---	FFVPPFQQSPR
1349.6815	1348.6742	1348.6927	-0.0185	517 -	527	0	76	FFVPPFQQSPR
1541.7533	1540.7460	1540.7673	-0.0213	389 -	401	0	---	WLGLSAEYGNLYR
1541.7533	1540.7460	1540.7673	-0.0213	389 -	401	0	96	WLGLSAEYGNLYR
2314.1702	2313.1629	2313.2018	-0.0388	402 -	421	0	125	NALFVPHYNTNAHSIIYALR
2314.1702	2313.1629	2313.2018	-0.0388	402 -	421	0	---	NALFVPHYNTNAHSIIYALR
2541.2783	2540.2710	2540.2910	-0.0199	436 -	458	0	---	VYDEELQEGHVLVVPQNFAVAGK

No match to: 835.5054, 1255.7186, 1289.6459, 1305.6737, 1305.6737, 1365.6754, 1365.6754, 1376.7131, 1524.7313, 1545.7496, 1557.7451, 1659.8235, 2296.1599, 2328.1589, 2346.1567, 2564.2368, 3053.4888, 3087.4849

3. gi|9864777 **Mass:** 60754 **Score:** 332 **Expect:** 5.5e-031 **Queries matched:** 9

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1255.7186	1254.7113	1254.7295	-0.0182	377 -	387	0	---	TANDLNLLILR
1305.6737	1304.6664	1304.6877	-0.0212	516 -	526	0	59	FFVPPSQQSLR
1305.6737	1304.6664	1304.6877	-0.0212	516 -	526	0	---	FFVPPSQQSLR
1541.7533	1540.7460	1540.7673	-0.0213	388 -	400	0	---	WLGLSAEYGNLYR
1541.7533	1540.7460	1540.7673	-0.0213	388 -	400	0	96	WLGLSAEYGNLYR
1659.8235	1658.8162	1658.8376	-0.0213	362 -	376	1	---	NRSPDIYNPQAGSLK
2314.1702	2313.1629	2313.2018	-0.0388	401 -	420	0	125	NALFVPHYNTNAHSIIYALR
2314.1702	2313.1629	2313.2018	-0.0388	401 -	420	0	---	NALFVPHYNTNAHSIIYALR
2541.2783	2540.2710	2540.2910	-0.0199	435 -	457	0	---	VYDEELQEGHVLVVPQNFAVAGK

No match to: 835.5054, 1269.7354, 1289.6459, 1349.6815, 1349.6815, 1365.6754, 1365.6754, 1376.7131, 1524.7313, 1545.7496, 1557.7451, 2296.1599, 2328.1589, 2346.1567, 2564.2368, 3053.4888, 3087.4849

4. gi|57669861 **Mass:** 61041 **Score:** 271 **Expect:** 7e-025 **Queries matched:** 8

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1255.7186	1254.7113	1254.7295	-0.0182	378 -	388	0	---	TANDLNLLILR
1289.6459	1288.6386	1288.6564	-0.0177	518 -	528	0	---	FFVPPSQQSPR
1541.7533	1540.7460	1540.7673	-0.0213	389 -	401	0	---	WLGLSAEYGNLYR
1541.7533	1540.7460	1540.7673	-0.0213	389 -	401	0	96	WLGLSAEYGNLYR
1659.8235	1658.8162	1658.8376	-0.0213	363 -	377	1	---	NRSPDIYNPQAGSLK

2314.1702	2313.1629	2313.2018	-0.0388	402 - 421	0	125	NALFVPHYNTNAHSIIYALR
2314.1702	2313.1629	2313.2018	-0.0388	402 - 421	0	---	NALFVPHYNTNAHSIIYALR
2541.2783	2540.2710	2540.2910	-0.0199	436 - 458	0	---	VYDEELQEGHVLVVPQNFAVAGK

No match to: 835.5054, 1269.7354, 1305.6737, 1305.6737, 1349.6815, 1349.6815, 1365.6754, 1365.6754, 1376.7131, 1524.7313, 1545.7496, 1557.7451, 2296.1599, 2328.1589, 2346.1567, 2564.2368, 3053.4888, 3087.4849

5. gi|108595573 **Mass:** 61041 **Score:** 271 **Expect:** 7e-025 **Queries matched:** 8

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1255.7186	1254.7113	1254.7295	-0.0182	378 - 388		0	---	TANDLNLLILR
1289.6459	1288.6386	1288.6564	-0.0177	518 - 528		0	---	FFVPPSQQSPR
1541.7533	1540.7460	1540.7673	-0.0213	389 - 401		0	---	WLGLSAEYGNLYR
1541.7533	1540.7460	1540.7673	-0.0213	389 - 401		0	96	WLGLSAEYGNLYR
1659.8235	1658.8162	1658.8376	-0.0213	363 - 377		1	---	NRSPDIYNPQAGSLK
2314.1702	2313.1629	2313.2018	-0.0388	402 - 421		0	125	NALFVPHYNTNAHSIIYALR
2314.1702	2313.1629	2313.2018	-0.0388	402 - 421		0	---	NALFVPHYNTNAHSIIYALR
2541.2783	2540.2710	2540.2910	-0.0199	436 - 458		0	---	VYDEELQEGHVLVVPQNFAVAGK

No match to: 835.5054, 1269.7354, 1305.6737, 1305.6737, 1349.6815, 1349.6815, 1365.6754, 1365.6754, 1376.7131, 1524.7313, 1545.7496, 1557.7451, 2296.1599, 2328.1589, 2346.1567, 2564.2368, 3053.4888, 3087.4849

6. gi|52001221 **Mass:** 61836 **Score:** 260 **Expect:** 8.8e-024 **Queries matched:** 7

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1255.7186	1254.7113	1254.7295	-0.0182	385 - 395		0	---	TANDLNLLILR
1541.7533	1540.7460	1540.7673	-0.0213	396 - 408		0	---	WLGLSAEYGNLYR
1541.7533	1540.7460	1540.7673	-0.0213	396 - 408		0	96	WLGLSAEYGNLYR
1659.8235	1658.8162	1658.8376	-0.0213	370 - 384		1	---	NRSPDIYNPQAGSLK
2314.1702	2313.1629	2313.2018	-0.0388	409 - 428		0	125	NALFVPHYNTNAHSIIYALR
2314.1702	2313.1629	2313.2018	-0.0388	409 - 428		0	---	NALFVPHYNTNAHSIIYALR
2541.2783	2540.2710	2540.2910	-0.0199	443 - 465		0	---	VYDEELQEGHVLVVPQNFAVAGK

No match to: 835.5054, 1269.7354, 1289.6459, 1305.6737, 1305.6737, 1349.6815, 1349.6815, 1365.6754, 1365.6754, 1376.7131, 1524.7313, 1545.7496, 1557.7451, 2296.1599, 2328.1589, 2346.1567, 2564.2368, 3053.4888, 3087.4849

7. gi|52001219 **Mass:** 61810 **Score:** 248 **Expect:** 1.4e-022 **Queries matched:** 6

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1269.7354	1268.7281	1268.7452	-0.0171	384 - 394		0	---	TANELNLLILR
1541.7533	1540.7460	1540.7673	-0.0213	395 - 407		0	---	WLGLSAEYGNLYR
1541.7533	1540.7460	1540.7673	-0.0213	395 - 407		0	96	WLGLSAEYGNLYR
1659.8235	1658.8162	1658.8376	-0.0213	369 - 383		1	---	NRSPDIYNPQAGSLK
2314.1702	2313.1629	2313.2018	-0.0388	408 - 427		0	125	NALFVPHYNTNAHSIIYALR

2314.1702	2313.1629	2313.2018	-0.0388	408 - 427	0	---	NALFVPHYNTNAHSIIYALR

No match to: 835.5054, 1255.7186, 1289.6459, 1305.6737, 1305.6737, 1349.6815, 1349.6815, 1365.6754, 1365.6754, 1376.7131, 1524.7313, 1545.7496, 1557.7451, 2296.1599, 2328.1589, 2346.1567, 2541.2783, 2564.2368, 3053.4888, 3087.4849

8. gi|37789212 **Mass:** 61803 **Score:** 248 **Expect:** 1.4e-022 **Queries matched:** 6

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1269.7354	1268.7281	1268.7452	-0.0171	384 -	394	0	---	TANELNLLILR
1541.7533	1540.7460	1540.7673	-0.0213	395 -	407	0	---	WLGLSAEYGNLYR
1541.7533	1540.7460	1540.7673	-0.0213	395 -	407	0	96	WLGLSAEYGNLYR
1659.8235	1658.8162	1658.8376	-0.0213	369 -	383	1	---	NRSPDIYNPQAGSLK
2314.1702	2313.1629	2313.2018	-0.0388	408 -	427	0	125	NALFVPHYNTNAHSIIYALR
2314.1702	2313.1629	2313.2018	-0.0388	408 -	427	0	---	NALFVPHYNTNAHSIIYALR

No match to: 835.5054, 1255.7186, 1289.6459, 1305.6737, 1305.6737, 1349.6815, 1349.6815, 1365.6754, 1365.6754, 1376.7131, 1524.7313, 1545.7496, 1557.7451, 2296.1599, 2328.1589, 2346.1567, 2541.2783, 2564.2368, 3053.4888, 3087.4849

9. gi|21314465 **Mass:** 62042 **Score:** 240 **Expect:** 8.8e-022 **Queries matched:** 5

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1541.7533	1540.7460	1540.7673	-0.0213	397 -	409	0	---	WLGLSAEYGNLYR
1541.7533	1540.7460	1540.7673	-0.0213	397 -	409	0	96	WLGLSAEYGNLYR
1659.8235	1658.8162	1658.8376	-0.0213	369 -	383	1	---	NRSPDIYNPQAGSLK
2314.1702	2313.1629	2313.2018	-0.0388	410 -	429	0	125	NALFVPHYNTNAHSIIYALR
2314.1702	2313.1629	2313.2018	-0.0388	410 -	429	0	---	NALFVPHYNTNAHSIIYALR

No match to: 835.5054, 1255.7186, 1269.7354, 1289.6459, 1305.6737, 1305.6737, 1349.6815, 1349.6815, 1365.6754, 1365.6754, 1376.7131, 1524.7313, 1545.7496, 1557.7451, 2296.1599, 2328.1589, 2346.1567, 2541.2783, 2564.2368, 3053.4888, 3087.4849

10. gi|37221901 **Mass:** 18557 **Score:** 30 **Expect:** 0.8 **Queries matched:** 6

resistance protein [Arachis stenosperma]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1255.7186	1254.7113	1254.7295	-0.0182	69 -	79	1	---	RALIVLDDVNK
1349.6815	1348.6742	1348.6908	-0.0165	53 -	64	1	---	SVEEGISMIKEK
1349.6815	1348.6742	1348.6908	-0.0165	53 -	64	1	---	SVEEGISMIKEK
1365.6754	1364.6681	1364.6857	-0.0175	53 -	64	1	---	SVEEGISMIKEK + Oxidation (M)
1365.6754	1364.6681	1364.6857	-0.0175	53 -	64	1	---	SVEEGISMIKEK + Oxidation (M)
2328.1589	2327.1516	2327.1330	0.0187	119 -	137	1	---	MKLLSDPESLELFCWNAFK

No match to: 835.5054, 1269.7354, 1289.6459, 1305.6737, 1305.6737, 1376.7131, 1524.7313, 1541.7533, 1541.7533, 1545.7496, 1557.7451, 1659.8235, 2296.1599, 2314.1702, 2314.1702, 2346.1567, 2541.2783, 2564.2368, 3053.4888, 3087.4849

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Number of Queries: 26

Protein View

Match to: **gi|118776570** Score: **348** Expect: **1.4e-032**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

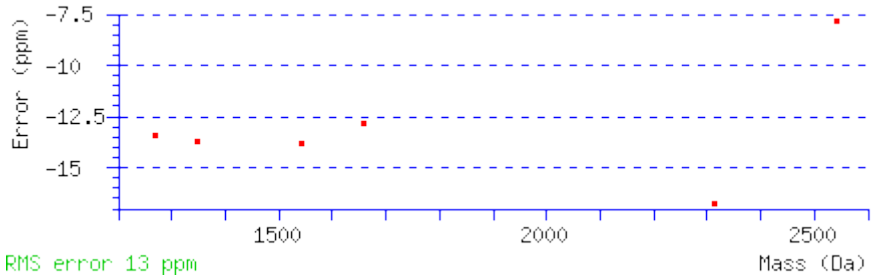
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```
     1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
    51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
   101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
   151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
   201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
   251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
   301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
   351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
   401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
   451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
   501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
362 - 376	1659.8235	1658.8162	1658.8376	-0.0213	1	NRSPDIYNPQAGSLK	(No match)
377 - 387	1269.7354	1268.7281	1268.7452	-0.0171	0	TANELNLLILR	(No match)
388 - 400	1541.7533	1540.7460	1540.7673	-0.0213	0	WLGLSAEYGNLYR	(No match)
388 - 400	1541.7533	1540.7460	1540.7673	-0.0213	0	WLGLSAEYGNLYR	(Ions score 96)
401 - 420	2314.1702	2313.1629	2313.2018	-0.0388	0	NALFVPHYNTNAHSIIYALR	(Ions score 125)
401 - 420	2314.1702	2313.1629	2313.2018	-0.0388	0	NALFVPHYNTNAHSIIYALR	(No match)
435 - 457	2541.2783	2540.2710	2540.2910	-0.0199	0	VYDEELQEGHVLVVPQNFAVAGK	(No match)
516 - 526	1349.6815	1348.6742	1348.6927	-0.0185	0	FFVPPFQQSPR	(No match)
516 - 526	1349.6815	1348.6742	1348.6927	-0.0185	0	FFVPPFQQSPR	(Ions score 76)



Spot 74

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:55:27 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **108 for gi|9864777, Gly1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|9864777	60754	108	Gly1 [Arachis hypogaea]
2.	gi|118776570	60681	98	arachin 6 [Arachis hypogaea]
3.	gi|5712199	61430	98	glycinin [Arachis hypogaea]
4.	gi|57669861	61041	80	arachin Ahy-4 [Arachis hypogaea]
5.	gi|108595573	61041	80	arachin Ahy-4 [Arachis hypogaea]
6.	gi|52001219	61810	80	arachin Ahy-1 [Arachis hypogaea]
7.	gi|37789212	61803	80	storage protein [Arachis hypogaea]
8.	gi|52001221	61836	80	arachin Ahy-2 [Arachis hypogaea]
9.	gi|21314465	62042	80	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|46560482	20907	24	seed storage protein SSP2 [Arachis hypogaea]

Results List

1. gi|9864777 **Mass:** 60754 **Score:** 108 **Expect:** 1.4e-008 **Queries matched:** 6
Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1305.6744	1304.6671	1304.6877	-0.0205	516	526	0	17	FFVPPSQQSLR
1305.6744	1304.6671	1304.6877	-0.0205	516	526	0	---	FFVPPSQQSLR
1541.7534	1540.7461	1540.7673	-0.0212	388	400	0	25	WLGLSAEYGNLYR
1541.7534	1540.7461	1540.7673	-0.0212	388	400	0	---	WLGLSAEYGNLYR
2314.1721	2313.1648	2313.2018	-0.0369	401	420	0	39	NALFVPHYNTNAHSIIYALR
2314.1721	2313.1648	2313.2018	-0.0369	401	420	0	---	NALFVPHYNTNAHSIIYALR

No match to: 886.9688, 1151.6973, 1349.6829, 1349.6829, 1365.6785, 1365.6785, 1545.7515, 1618.0433, 2542.2786

2. gi|118776570 **Mass:** 60681 **Score:** 98 **Expect:** 1.5e-007 **Queries matched:** 6

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1349.6829	1348.6756	1348.6927	-0.0171	516	526	0	7	FFVPPFQQSPR
1349.6829	1348.6756	1348.6927	-0.0171	516	526	0	---	FFVPPFQQSPR
1541.7534	1540.7461	1540.7673	-0.0212	388	400	0	25	WLGLSAEYGNLYR
1541.7534	1540.7461	1540.7673	-0.0212	388	400	0	---	WLGLSAEYGNLYR
2314.1721	2313.1648	2313.2018	-0.0369	401	420	0	39	NALFVPHYNTNAHSIIYALR
2314.1721	2313.1648	2313.2018	-0.0369	401	420	0	---	NALFVPHYNTNAHSIIYALR

No match to: 886.9688, 1151.6973, 1305.6744, 1305.6744, 1365.6785, 1365.6785, 1545.7515, 1618.0433, 2542.2786

3. gi|5712199 **Mass:** 61430 **Score:** 98 **Expect:** 1.5e-007 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1349.6829	1348.6756	1348.6927	-0.0171	517	527	0	7	FFVPPFQQSPR
1349.6829	1348.6756	1348.6927	-0.0171	517	527	0	---	FFVPPFQQSPR
1541.7534	1540.7461	1540.7673	-0.0212	389	401	0	25	WLGLSAEYGNLYR
1541.7534	1540.7461	1540.7673	-0.0212	389	401	0	---	WLGLSAEYGNLYR
2314.1721	2313.1648	2313.2018	-0.0369	402	421	0	39	NALFVPHYNTNAHSIIYALR
2314.1721	2313.1648	2313.2018	-0.0369	402	421	0	---	NALFVPHYNTNAHSIIYALR

No match to: 886.9688, 1151.6973, 1305.6744, 1305.6744, 1365.6785, 1365.6785, 1545.7515, 1618.0433, 2542.2786

4. gi|57669861 **Mass:** 61041 **Score:** 80 **Expect:** 9.4e-006 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1541.7534	1540.7461	1540.7673	-0.0212	389	401	0	25	WLGLSAEYGNLYR
1541.7534	1540.7461	1540.7673	-0.0212	389	401	0	---	WLGLSAEYGNLYR
2314.1721	2313.1648	2313.2018	-0.0369	402	421	0	39	NALFVPHYNTNAHSIIYALR
2314.1721	2313.1648	2313.2018	-0.0369	402	421	0	---	NALFVPHYNTNAHSIIYALR

No match to: 886.9688, 1151.6973, 1305.6744, 1305.6744, 1349.6829, 1349.6829, 1365.6785, 1365.6785, 1545.7515, 1618.0433, 2542.2786

5. gi|108595573 **Mass:** 61041 **Score:** 80 **Expect:** 9.4e-006 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1541.7534	1540.7461	1540.7673	-0.0212	389	401	0	25	WLGLSAEYGNLYR
1541.7534	1540.7461	1540.7673	-0.0212	389	401	0	---	WLGLSAEYGNLYR
2314.1721	2313.1648	2313.2018	-0.0369	402	421	0	39	NALFVPHYNTNAHSIIYALR
2314.1721	2313.1648	2313.2018	-0.0369	402	421	0	---	NALFVPHYNTNAHSIIYALR

No match to: 886.9688, 1151.6973, 1305.6744, 1305.6744, 1349.6829, 1349.6829, 1365.6785, 1365.6785, 1545.7515,

1618.0433, 2542.2786

6. gi|52001219 **Mass:** 61810 **Score:** 80 **Expect:** 9.4e-006 **Queries matched:** 4

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1541.7534	1540.7461	1540.7673	-0.0212	395	407	0	25	WLGLSAEYGNLYR
1541.7534	1540.7461	1540.7673	-0.0212	395	407	0	---	WLGLSAEYGNLYR
2314.1721	2313.1648	2313.2018	-0.0369	408	427	0	39	NALFVPHYNTNAHSIIYALR
2314.1721	2313.1648	2313.2018	-0.0369	408	427	0	---	NALFVPHYNTNAHSIIYALR

No match to: 886.9688, 1151.6973, 1305.6744, 1305.6744, 1349.6829, 1349.6829, 1365.6785, 1365.6785, 1545.7515, 1618.0433, 2542.2786

7. gi|37789212 **Mass:** 61803 **Score:** 80 **Expect:** 9.4e-006 **Queries matched:** 4

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1541.7534	1540.7461	1540.7673	-0.0212	395	407	0	25	WLGLSAEYGNLYR
1541.7534	1540.7461	1540.7673	-0.0212	395	407	0	---	WLGLSAEYGNLYR
2314.1721	2313.1648	2313.2018	-0.0369	408	427	0	39	NALFVPHYNTNAHSIIYALR
2314.1721	2313.1648	2313.2018	-0.0369	408	427	0	---	NALFVPHYNTNAHSIIYALR

No match to: 886.9688, 1151.6973, 1305.6744, 1305.6744, 1349.6829, 1349.6829, 1365.6785, 1365.6785, 1545.7515, 1618.0433, 2542.2786

8. gi|52001221 **Mass:** 61836 **Score:** 80 **Expect:** 9.6e-006 **Queries matched:** 4

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1541.7534	1540.7461	1540.7673	-0.0212	396	408	0	25	WLGLSAEYGNLYR
1541.7534	1540.7461	1540.7673	-0.0212	396	408	0	---	WLGLSAEYGNLYR
2314.1721	2313.1648	2313.2018	-0.0369	409	428	0	39	NALFVPHYNTNAHSIIYALR
2314.1721	2313.1648	2313.2018	-0.0369	409	428	0	---	NALFVPHYNTNAHSIIYALR

No match to: 886.9688, 1151.6973, 1305.6744, 1305.6744, 1349.6829, 1349.6829, 1365.6785, 1365.6785, 1545.7515, 1618.0433, 2542.2786

9. gi|21314465 **Mass:** 62042 **Score:** 80 **Expect:** 9.6e-006 **Queries matched:** 4

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1541.7534	1540.7461	1540.7673	-0.0212	397	409	0	25	WLGLSAEYGNLYR
1541.7534	1540.7461	1540.7673	-0.0212	397	409	0	---	WLGLSAEYGNLYR
2314.1721	2313.1648	2313.2018	-0.0369	410	429	0	39	NALFVPHYNTNAHSIIYALR
2314.1721	2313.1648	2313.2018	-0.0369	410	429	0	---	NALFVPHYNTNAHSIIYALR

No match to: 886.9688, 1151.6973, 1305.6744, 1305.6744, 1349.6829, 1349.6829, 1365.6785, 1365.6785, 1545.7515, 1618.0433, 2542.2786

10. gi|46560482 **Mass:** 20907 **Score:** 24 **Expect:** 3.8 **Queries matched:** 3

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1349.6829	1348.6756	1348.6272	0.0484	38	-	47	1	---	QQWEFQGDRR
1349.6829	1348.6756	1348.6272	0.0484	38	-	47	1	---	QQWEFQGDRR
2542.2786	2541.2713	2541.1998	0.0715	48	-	67	1	---	CQSQLERANLRPCEQHLMQK + Oxidation (M)

No match to: 886.9688, 1151.6973, 1305.6744, 1305.6744, 1365.6785, 1365.6785, 1541.7534, 1541.7534, 1545.7515, 1618.0433, 2314.1721, 2314.1721

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1

Number of Queries: 15

Protein View

Match to: **gi|9864777** Score: **108** Expect: **1.4e-008**
Gly1 [Arachis hypogaea]

Nominal mass (M_r): **60754;** Calculated pI value: **5.48**
NCBI BLAST search of gi|9864777 against nr
Unformatted sequence string for pasting into other applications

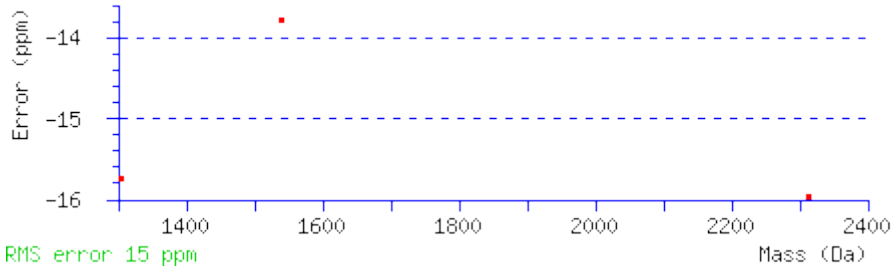
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **8%**

Matched peptides shown in **Bold Red**

```
   1 MIRGRLALSV CFCFLVLGAS SISFRQQPEE NACQFQRLNA QRPDNRLESE
  51 GGYIETWNPN NQEFECAGVA LSRLVLRRNA LRRPFYSNAP QEIFIQQGRG
 101 YFGLIFPGCP STYEEPAQQG RRHQSQRAPR RFEGEDQSQQ QQQDSHQKVR
 151 RFDEGDLIAV PTGVALWMFN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
 201 AGNHEQEFLR YQQQSRRRSL PYSPYSPQSQ PRQEEREFSP RGQHSRRERA
 251 GQEEENEGGN IFSGFTPEFL AQAFQVDDRQ IVQNLRGENE SEEEGAIVTV
 301 KGGLRILSPD RKRGADEEEE YDEDEYEYDE EDRRRGRGSR GRGNGIEETI
 351 CTASVKKNIG RNRSPDIYNP QAGSLKTAND LNLLILRWLG LSAEYGNLYR
 401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
 451 NFAVAGKSQS DNFEYVAFKT DSRPNIANFA GENSIIDNLP EEVVANSYGL
 501 PREQARQLKN NNPFKFFVPP SQQSLRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
388 - 400	1541.7534	1540.7461	1540.7673	-0.0212	0	**WLGLSAEYGNLYR**	(Ions score 25)
388 - 400	1541.7534	1540.7461	1540.7673	-0.0212	0	**WLGLSAEYGNLYR**	(No match)
401 - 420	2314.1721	2313.1648	2313.2018	-0.0369	0	**NALFVPHYNTNAHSIIYALR**	(Ions score 39)
401 - 420	2314.1721	2313.1648	2313.2018	-0.0369	0	**NALFVPHYNTNAHSIIYALR**	(No match)
516 - 526	1305.6744	1304.6671	1304.6877	-0.0205	0	**FFVPPSQQSLR**	(Ions score 17)
516 - 526	1305.6744	1304.6671	1304.6877	-0.0205	0	**FFVPPSQQSLR**	(No match)



Spot 75

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:34:31 GMT**
Top Score : **80 for gi|47933675, glycinin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	80	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	79	iso-Ara h3 [Arachis hypogaea]
3.	gi|62177385	14731	20	resistance protein Cre [Arachis hypogaea]
4.	gi|118776570	60681	16	arachin 6 [Arachis hypogaea]
5.	gi|2498261	2416	16	33.0 kDa cold shock protein (AHCSP33)
6.	gi|22135348	25768	15	trypsin inhibitor [Arachis hypogaea]
7.	gi|37221971	18241	11	resistance protein [Arachis cardenasii]
8.	gi|115187508	13067	11	triacylglycerol lipase [Arachis hypogaea]
9.	gi|71040679	22774	11	disease resistance-responsive family protein [Arachis hypogaea]
10.	gi|37221903	19440	11	resistance protein [Arachis stenosperma]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 80 **Expect:** 9.8e-006 **Queries matched:** 9
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
771.4117	770.4044	770.4147	-0.0103	307	312	0	SRPQQR
859.4534	858.4461	858.4559	-0.0098	256	262	0	QTVENLR
939.3539	938.3466	938.3617	-0.0151	300	306	0	EEFDEDR
1095.4667	1094.4594	1094.4628	-0.0034	299	306	1	REEFDEDR
1547.7544	1546.7471	1546.7389	0.0082	209	220	0	YQQQQGSRPHYR
1614.7999	1613.7926	1613.7837	0.0089	196	208	0	FYLAGNQEQEFLR
1658.8531	1657.8458	1657.8270	0.0188	263	277	1	GENEREEQGAIVTVK
1770.8954	1769.8881	1769.8848	0.0033	195	208	1	RFYLAGNQEQEFLR
3199.3879	3198.3806	3198.4277	-0.0471	228	255	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 1111.5643, 1191.6162, 1574.7885, 1730.8796, 1756.8488, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2295.1394, 2456.1565, 2612.1672, 2926.2771, 3153.4036,

3211.4390, 3228.4570, 3301.6743

2. gi|112380623 **Mass:** 58570 **Score:** 79 **Expect:** 1e-005 **Queries matched:** 9

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
771.4117	770.4044	770.4147	-0.0103	309	314	0	SRPQQR
859.4534	858.4461	858.4559	-0.0098	258	264	0	QTVENLR
939.3539	938.3466	938.3617	-0.0151	302	308	0	EEFDEDR
1095.4667	1094.4594	1094.4628	-0.0034	301	308	1	REEFDEDR
1547.7544	1546.7471	1546.7389	0.0082	211	222	0	YQQQQGSRPHYR
1614.7999	1613.7926	1613.7837	0.0089	198	210	0	FYLAGNQEQEFLR
1658.8531	1657.8458	1657.8270	0.0188	265	279	1	GENEREEQGAIVTVK
1770.8954	1769.8881	1769.8848	0.0033	197	210	1	RFYLAGNQEQEFLR
3199.3879	3198.3806	3198.4277	-0.0471	230	257	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR

No match to: 1111.5643, 1191.6162, 1574.7885, 1730.8796, 1756.8488, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2295.1394, 2456.1565, 2612.1672, 2926.2771, 3153.4036, 3211.4390, 3228.4570, 3301.6743

3. gi|62177385 **Mass:** 14731 **Score:** 20 **Expect:** 9.6 **Queries matched:** 2

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1730.8796	1729.8723	1729.8787	-0.0064	1	14	1	NLILDDVWDSKAWR
2295.1394	2294.1321	2294.1147	0.0175	15	34	1	TIKNCFPENNNGGMILVTTR + Oxidation (M)

No match to: 771.4117, 859.4534, 939.3539, 1095.4667, 1111.5643, 1191.6162, 1547.7544, 1574.7885, 1614.7999, 1658.8531, 1756.8488, 1770.8954, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2456.1565, 2612.1672, 2926.2771, 3153.4036, 3199.3879, 3211.4390, 3228.4570, 3301.6743

4. gi|118776570 **Mass:** 60681 **Score:** 16 **Expect:** 21 **Queries matched:** 3

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1574.7885	1573.7812	1573.7637	0.0176	196	208	0	FNLAGNHEQEFLR
1730.8796	1729.8723	1729.8648	0.0076	195	208	1	RFNLAGNHEQEFLR
1770.8954	1769.8881	1769.8584	0.0297	220	235	0	SLPLSPYSPQPGQEDR

No match to: 771.4117, 859.4534, 939.3539, 1095.4667, 1111.5643, 1191.6162, 1547.7544, 1614.7999, 1658.8531, 1756.8488, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2295.1394, 2456.1565, 2612.1672, 2926.2771, 3153.4036, 3199.3879, 3211.4390, 3228.4570, 3301.6743

5. gi|2498261 **Mass:** 2416 **Score:** 16 **Expect:** 25 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1547.7544	1546.7471	1546.7263	0.0208	9	24	0	ASYTVTPPAQANAADA

No match to: 771.4117, 859.4534, 939.3539, 1095.4667, 1111.5643, 1191.6162, 1574.7885, 1614.7999, 1658.8531,

1730.8796, 1756.8488, 1770.8954, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2295.1394, 2456.1565, 2612.1672, 2926.2771, 3153.4036, 3199.3879, 3211.4390, 3228.4570, 3301.6743

6. gi|22135348 **Mass:** 25768 **Score:** 15 **Expect:** 28 **Queries matched:** 2

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1574.7885	1573.7812	1573.7637	0.0176	198	210	0	FNLAGNHEQEFLR
1730.8796	1729.8723	1729.8648	0.0076	197	210	1	RFNLAGNHEQEFLR

No match to: 771.4117, 859.4534, 939.3539, 1095.4667, 1111.5643, 1191.6162, 1547.7544, 1614.7999, 1658.8531, 1756.8488, 1770.8954, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2295.1394, 2456.1565, 2612.1672, 2926.2771, 3153.4036, 3199.3879, 3211.4390, 3228.4570, 3301.6743

7. gi|37221971 **Mass:** 18241 **Score:** 11 **Expect:** 65 **Queries matched:** 1

resistance protein [Arachis cardenasii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
3211.4390	3210.4317	3210.4161	0.0157	9	35	1	EEEFMNGFDLKAWVCVSENFDIAESTK + Oxidation (M)

No match to: 771.4117, 859.4534, 939.3539, 1095.4667, 1111.5643, 1191.6162, 1547.7544, 1574.7885, 1614.7999, 1658.8531, 1730.8796, 1756.8488, 1770.8954, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2295.1394, 2456.1565, 2612.1672, 2926.2771, 3153.4036, 3199.3879, 3228.4570, 3301.6743

8. gi|115187508 **Mass:** 13067 **Score:** 11 **Expect:** 68 **Queries matched:** 1

triacylglycerol lipase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2612.1672	2611.1599	2611.2091	-0.0492	6	27	0	ESFDLSGPLYLTHVDWDNPNHR

No match to: 771.4117, 859.4534, 939.3539, 1095.4667, 1111.5643, 1191.6162, 1547.7544, 1574.7885, 1614.7999, 1658.8531, 1730.8796, 1756.8488, 1770.8954, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2295.1394, 2456.1565, 2926.2771, 3153.4036, 3199.3879, 3211.4390, 3228.4570, 3301.6743

9. gi|71040679 **Mass:** 22774 **Score:** 11 **Expect:** 73 **Queries matched:** 1

disease resistance-responsive family protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
3301.6743	3300.6670	3300.6191	0.0479	99	129	1	LVGKAQGIYASASQNDMGLLMVMNLEFSEGK

No match to: 771.4117, 859.4534, 939.3539, 1095.4667, 1111.5643, 1191.6162, 1547.7544, 1574.7885, 1614.7999, 1658.8531, 1730.8796, 1756.8488, 1770.8954, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2295.1394, 2456.1565, 2612.1672, 2926.2771, 3153.4036, 3199.3879, 3211.4390, 3228.4570

10. gi|37221903 **Mass:** 19440 **Score:** 11 **Expect:** 73 **Queries matched:** 1

resistance protein [Arachis stenosperma]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

3211.4390 3210.4317 3210.4062 0.0255 80 - 105 1 IEQLKALAGECDWFTGECDWFSYETR

No match to: 771.4117, 859.4534, 939.3539, 1095.4667, 1111.5643, 1191.6162, 1547.7544, 1574.7885, 1614.7999, 1658.8531, 1730.8796, 1756.8488, 1770.8954, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2295.1394, 2456.1565, 2612.1672, 2926.2771, 3153.4036, 3199.3879, 3228.4570, 3301.6743

Mascot Search Results

Protein View

Match to: **gi|47933675** Score: **80** Expect: **9.8e-006**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **31**
Number of mass values matched: **9**
Sequence Coverage: **17%**

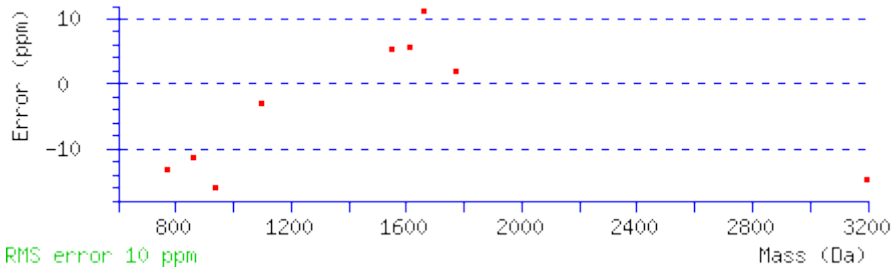
Matched peptides shown in **Bold Red**

```
     1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
    51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
   101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
   151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
   201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
   251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
   301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
   351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
   401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
   451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
   501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
195 - 208	1770.8954	1769.8881	1769.8848	0.0033	1	RFYLAGNQEQEFLR
196 - 208	1614.7999	1613.7926	1613.7837	0.0089	0	FYLAGNQEQEFLR
209 - 220	1547.7544	1546.7471	1546.7389	0.0082	0	YQQQQGSRPHYR
228 - 255	3199.3879	3198.3806	3198.4277	-0.0471	0	GDEQENEGSNIFSGFAQEFLQHAFQVDR
256 - 262	859.4534	858.4461	858.4559	-0.0098	0	QTVENLR
263 - 277	1658.8531	1657.8458	1657.8270	0.0188	1	GENEREEQGAIVTVK
299 - 306	1095.4667	1094.4594	1094.4628	-0.0034	1	REEFDEDR
300 - 306	939.3539	938.3466	938.3617	-0.0151	0	EEFDEDR
307 - 312	771.4117	770.4044	770.4147	-0.0103	0	SRPQQR

No match to: 1111.5643, 1191.6162, 1574.7885, 1730.8796, 1756.8488, 1774.8656, 1775.8636, 2192.9878, 2225.1643, 2255.7095, 2256.1541, 2256.7041, 2272.1711, 2273.1602, 2295.1394, 2456.1565, 2612.1672, 2926.2771, 3153.4036, 3211.4390, 3228.4570, 3301.6743



Spot 76

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 11:37:49 GMT**
Top Score : **47 for gi|47933675, glycinin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	47	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	47	iso-Ara h3 [Arachis hypogaea]
3.	gi|2498261	2416	15	33.0 kDa cold shock protein (AHCSP33)
4.	gi|37221923	17652	13	resistance protein [Arachis stenosperma]
5.	gi|6093763	353436	11	Genome polyprotein [Contains: P1 proteinase (N-terminal protein); Helper component proteinase
6.	gi|37222015	27514	11	resistance protein [Arachis cardenasii]
7.	gi|55736077	4575	10	auxin-induced hypothetical protein [Arachis hypogaea]
8.	gi|226557	9487	9	photosystem I 8kD protein
9.	gi|42760421	67322	9	9-cis-epoxycarotenoid dioxygenase [Arachis hypogaea]
10.	gi|62177385	14731	9	resistance protein Cre [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 47 **Expect:** 0.017 **Queries matched:** 7
glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1095.4672	1094.4599	1094.4628	-0.0029	299	306	1	REEFDEDR
1456.8173	1455.8100	1455.8044	0.0056	268	281	1	EEQGAIVTVKGGLR
1547.7643	1546.7570	1546.7389	0.0181	209	220	0	YQQQQGSRPHYR
1614.8014	1613.7941	1613.7837	0.0104	196	208	0	FYLAGNQEQEFLR
1658.8472	1657.8399	1657.8270	0.0129	263	277	1	GENEREEQGAIVTVK
1691.7885	1690.7812	1690.7659	0.0154	300	312	1	EEFDEDRSRPQQR
1770.9016	1769.8943	1769.8848	0.0095	195	208	1	RFYLAGNQEQEFLR

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 932.4416, 949.4646, 1080.5305, 1120.5417, 1171.5956, 1251.5839, 1310.6254, 1320.6080, 1354.6923, 1373.6454, 1391.6820, 1531.3116, 1702.8561, 1774.8921,

1847.8975, 2003.9799, 2042.0635, 2088.9851, 2272.6943, 2273.1450, 2499.2529, 2612.1262, 3137.2871, 3144.4338, 3153.3188, 3227.3691, 3454.4302

2. gi|112380623 **Mass:** 58570 **Score:** 47 **Expect:** 0.018 **Queries matched:** 7

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1095.4672	1094.4599	1094.4628	-0.0029	301	308	1	REEFDEDR
1456.8173	1455.8100	1455.8044	0.0056	270	283	1	EEQGAIVTVKGGLR
1547.7643	1546.7570	1546.7389	0.0181	211	222	0	YQQQQGSRPHYR
1614.8014	1613.7941	1613.7837	0.0104	198	210	0	FYLAGNQEQEFLR
1658.8472	1657.8399	1657.8270	0.0129	265	279	1	GENEREEQGAIVTVK
1691.7885	1690.7812	1690.7659	0.0154	302	314	1	EEFDEDRSRPQQR
1770.9016	1769.8943	1769.8848	0.0095	197	210	1	RFYLAGNQEQEFLR

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 932.4416, 949.4646, 1080.5305, 1120.5417, 1171.5956, 1251.5839, 1310.6254, 1320.6080, 1354.6923, 1373.6454, 1391.6820, 1531.3116, 1702.8561, 1774.8921, 1847.8975, 2003.9799, 2042.0635, 2088.9851, 2272.6943, 2273.1450, 2499.2529, 2612.1262, 3137.2871, 3144.4338, 3153.3188, 3227.3691, 3454.4302

3. gi|2498261 **Mass:** 2416 **Score:** 15 **Expect:** 31 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1547.7643	1546.7570	1546.7263	0.0307	9	24	0	ASYTVTPPAQANAADA

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 932.4416, 949.4646, 1080.5305, 1095.4672, 1120.5417, 1171.5956, 1251.5839, 1310.6254, 1320.6080, 1354.6923, 1373.6454, 1391.6820, 1456.8173, 1531.3116, 1614.8014, 1658.8472, 1691.7885, 1702.8561, 1770.9016, 1774.8921, 1847.8975, 2003.9799, 2042.0635, 2088.9851, 2272.6943, 2273.1450, 2499.2529, 2612.1262, 3137.2871, 3144.4338, 3153.3188, 3227.3691, 3454.4302

4. gi|37221923 **Mass:** 17652 **Score:** 13 **Expect:** 40 **Queries matched:** 2

resistance protein [Arachis stenosperma]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1391.6820	1390.6747	1390.6762	-0.0014	49	61	0	LGDVSEGVSMIER
1547.7643	1546.7570	1546.7773	-0.0202	49	62	1	LGDVSEGVSMIERR

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 932.4416, 949.4646, 1080.5305, 1095.4672, 1120.5417, 1171.5956, 1251.5839, 1310.6254, 1320.6080, 1354.6923, 1373.6454, 1456.8173, 1531.3116, 1614.8014, 1658.8472, 1691.7885, 1702.8561, 1770.9016, 1774.8921, 1847.8975, 2003.9799, 2042.0635, 2088.9851, 2272.6943, 2273.1450, 2499.2529, 2612.1262, 3137.2871, 3144.4338, 3153.3188, 3227.3691, 3454.4302

5. gi|6093763 **Mass:** 353436 **Score:** 11 **Expect:** 65 **Queries matched:** 6

Genome polyprotein [Contains: P1 proteinase (N-terminal protein); Helper component proteinase (HC-p

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
932.4416	931.4343	931.4255	0.0088	3047	3053	0	EIHMQMK + Oxidation (M)
1120.5417	1119.5344	1119.5342	0.0002	1245	1254	0	TAAEVVNNMR + Oxidation (M)

1847.8975	1846.8902	1846.8770	0.0132	919 - 934	1	TGFTGFSDTLLEMREK + Oxidation (M)
2003.9799	2002.9726	2002.9930	-0.0204	2138 - 2154	1	DMIIIKMPCDVPPFPSK + Oxidation (M)
2042.0635	2041.0562	2041.0587	-0.0025	844 - 861	1	KEMNIGLIFSMLSSLAQK + 2 Oxidation (M)
3144.4338	3143.4265	3143.4435	-0.0170	2608 - 2635	1	FKGNNSGQPSTVVDNTLMVMIAMFYGMK + 4 Oxidation (M)

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 949.4646, 1080.5305, 1095.4672, 1171.5956, 1251.5839, 1310.6254, 1320.6080, 1354.6923, 1373.6454, 1391.6820, 1456.8173, 1531.3116, 1547.7643, 1614.8014, 1658.8472, 1691.7885, 1702.8561, 1770.9016, 1774.8921, 2088.9851, 2272.6943, 2273.1450, 2499.2529, 2612.1262, 3137.2871, 3153.3188, 3227.3691, 3454.4302

6. gi|37222015 **Mass:** 27514 **Score:** 11 **Expect:** 78 **Queries matched:** 2

resistance protein [Arachis cardenasii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1251.5839	1250.5766	1250.5747	0.0019	35 -	44	1	SIVECACREK
1320.6080	1319.6007	1319.6040	-0.0033	136 -	146	1	AFSNMRHDTNK

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 932.4416, 949.4646, 1080.5305, 1095.4672, 1120.5417, 1171.5956, 1310.6254, 1354.6923, 1373.6454, 1391.6820, 1456.8173, 1531.3116, 1547.7643, 1614.8014, 1658.8472, 1691.7885, 1702.8561, 1770.9016, 1774.8921, 1847.8975, 2003.9799, 2042.0635, 2088.9851, 2272.6943, 2273.1450, 2499.2529, 2612.1262, 3137.2871, 3144.4338, 3153.3188, 3227.3691, 3454.4302

7. gi|55736077 **Mass:** 4575 **Score:** 10 **Expect:** 84 **Queries matched:** 1

auxin-induced hypothetical protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
949.4646	948.4573	948.4625	-0.0051	1 -	8	0	TTQNQTTR

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 932.4416, 1080.5305, 1095.4672, 1120.5417, 1171.5956, 1251.5839, 1310.6254, 1320.6080, 1354.6923, 1373.6454, 1391.6820, 1456.8173, 1531.3116, 1547.7643, 1614.8014, 1658.8472, 1691.7885, 1702.8561, 1770.9016, 1774.8921, 1847.8975, 2003.9799, 2042.0635, 2088.9851, 2272.6943, 2273.1450, 2499.2529, 2612.1262, 3137.2871, 3144.4338, 3153.3188, 3227.3691, 3454.4302

8. gi|226557 **Mass:** 9487 **Score:** 9 **Expect:** 98 **Queries matched:** 1

photosystem I 8kD protein

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1691.7885	1690.7812	1690.7766	0.0046	38 -	52	1	QIASAPRTEDCVGCK

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 932.4416, 949.4646, 1080.5305, 1095.4672, 1120.5417, 1171.5956, 1251.5839, 1310.6254, 1320.6080, 1354.6923, 1373.6454, 1391.6820, 1456.8173, 1531.3116, 1547.7643, 1614.8014, 1658.8472, 1702.8561, 1770.9016, 1774.8921, 1847.8975, 2003.9799, 2042.0635, 2088.9851, 2272.6943, 2273.1450, 2499.2529, 2612.1262, 3137.2871, 3144.4338, 3153.3188, 3227.3691, 3454.4302

9. gi|42760421 **Mass:** 67322 **Score:** 9 **Expect:** 1e+002 **Queries matched:** 2

9-cis-epoxycarotenoid dioxygenase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1658.8472	1657.8399	1657.8134	0.0266	260 -	273	0	LLAMSEDDLPYHVR
2499.2529	2498.2456	2498.2475	-0.0018	260 -	281	1	LLAMSEDDLPYHVRVTPNGDLK + Oxidation (M)

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 932.4416, 949.4646, 1080.5305, 1095.4672,

1120.5417, 1171.5956, 1251.5839, 1310.6254, 1320.6080, 1354.6923, 1373.6454, 1391.6820, 1456.8173, 1531.3116, 1547.7643, 1614.8014, 1691.7885, 1702.8561, 1770.9016, 1774.8921, 1847.8975, 2003.9799, 2042.0635, 2088.9851, 2272.6943, 2273.1450, 2612.1262, 3137.2871, 3144.4338, 3153.3188, 3227.3691, 3454.4302

10. gi|62177385 **Mass:** 14731 **Score:** 9 **Expect:** 1.2e+002 **Queries matched:** 1

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
2088.9851	2087.9778	2087.9979	-0.0201	72	-	89	1	NCPPELESIGRSIVETCK

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 932.4416, 949.4646, 1080.5305, 1095.4672, 1120.5417, 1171.5956, 1251.5839, 1310.6254, 1320.6080, 1354.6923, 1373.6454, 1391.6820, 1456.8173, 1531.3116, 1547.7643, 1614.8014, 1658.8472, 1691.7885, 1702.8561, 1770.9016, 1774.8921, 1847.8975, 2003.9799, 2042.0635, 2272.6943, 2273.1450, 2499.2529, 2612.1262, 3137.2871, 3144.4338, 3153.3188, 3227.3691, 3454.4302

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 40

Protein View

Match to: **gi|47933675** Score: **47** Expect: **0.017**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **40**
Number of mass values matched: **7**
Sequence Coverage: **11%**

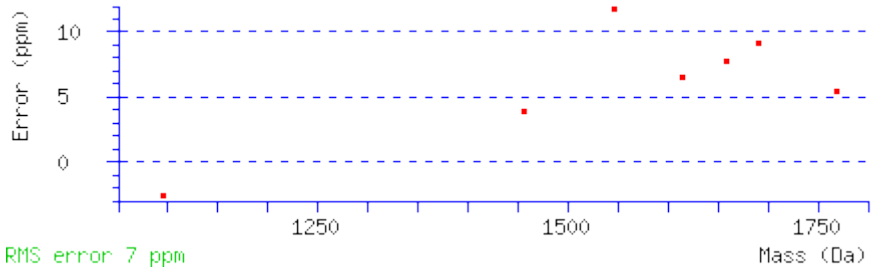
Matched peptides shown in **Bold Red**

```
   1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
  51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
 101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
 151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
 201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
 251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
 301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
 351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
 401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
 451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
 501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
195 - 208	1770.9016	1769.8943	1769.8848	0.0095	1	RFYLAGNQEQEFLR
196 - 208	1614.8014	1613.7941	1613.7837	0.0104	0	FYLAGNQEQEFLR
209 - 220	1547.7643	1546.7570	1546.7389	0.0181	0	YQQQQGSRPHYR
263 - 277	1658.8472	1657.8399	1657.8270	0.0129	1	GENEREEQGAIVTVK
268 - 281	1456.8173	1455.8100	1455.8044	0.0056	1	EEQGAIVTVKGGLR
299 - 306	1095.4672	1094.4599	1094.4628	-0.0029	1	REEFDEDR
300 - 312	1691.7885	1690.7812	1690.7659	0.0154	1	EEFDEDRSRPQQR

No match to: 815.4135, 840.4155, 851.3870, 872.4327, 881.2625, 927.5106, 932.4416, 949.4646, 1080.5305, 1120.5417, 1171.5956, 1251.5839, 1310.6254, 1320.6080, 1354.6923, 1373.6454, 1391.6820, 1531.3116, 1702.8561, 1774.8921, 1847.8975, 2003.9799, 2042.0635, 2088.9851, 2272.6943, 2273.1450, 2499.2529, 2612.1262, 3137.2871, 3144.4338, 3153.3188, 3227.3691, 3454.4302



Spot 77

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **20 Mar 2007 at 13:15:49 GMT**
Top Score : **108 for gi|31322017, allergen Ara h 2 isoform [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|31322017	20212	108	allergen Ara h 2 isoform [Arachis hypogaea]
2.	gi|46560480	22229	106	seed storage protein SSP1 [Arachis hypogaea]
3.	gi|26245447	20558	105	allergen Ara h 2.02 [Arachis hypogaea]
4.	gi|118776566	19009	101	conglutin 7 [Arachis hypogaea]
5.	gi|15418705	18612	97	allergen II [Arachis hypogaea]
6.	gi|28912768	19765	96	seed storage protein [Arachis hypogaea]
7.	gi|52001227	21293	91	2S protein 1 [Arachis hypogaea]
8.	gi|14347293	24390	86	unnamed protein product [Arachis hypogaea]
9.	gi|46560482	20907	83	seed storage protein SSP2 [Arachis hypogaea]
10.	gi|114309696	27933	12	MADS-box transcription factor [Arachis hypogaea]

Results List

1. gi|31322017 **Mass:** 20212 **Score:** 108 **Expect:** 1.4e-008 **Queries matched:** 13
allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4246	919.4173	919.4181	-0.0008	30	36	0	CQSQLER
935.4496	934.4423	934.4508	-0.0085	133	139	0	QQEQQFK
1056.4825	1055.4752	1055.4744	0.0008	90	99	0	GAGSSQHQER
1085.5518	1084.5445	1084.5447	-0.0002	144	152	0	NLPQQCGLR
1091.5582	1090.5509	1090.5519	-0.0010	133	140	1	QQEQQFKR
1121.4937	1120.4864	1120.4818	0.0046	157	166	0	CDLEVESGGR
1315.6439	1314.6366	1314.6429	-0.0062	20	29	1	QQWELQGDRR
1624.8035	1623.7962	1623.7973	-0.0011	37	49	0	ANLRPCEQHLMQK
1640.7972	1639.7899	1639.7922	-0.0023	37	49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6860	1725.6787	1725.6835	-0.0047	100	112	0	CCNELNEFENNQR

2012.8246	2011.8173	2011.8220	-0.0047	113 - 128	0	CMCEALQQIMENQSDR
2028.8208	2027.8135	2027.8169	-0.0034	113 - 128	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8306	2043.8233	2043.8118	0.0115	113 - 128	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 987.5052, 1045.5615, 1050.1021, 1066.0748, 1072.0846, 1074.5294, 1101.5438, 1104.4999, 1107.5338, 1212.5248, 1228.5151, 1277.0964, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1669.6752, 1709.6658, 1940.9348, 2211.1045, 2225.1191, 2239.0635, 2283.1733, 2299.1819, 2807.3171, 3061.3164, 3347.6819

2. gi|46560480 **Mass:** 22229 **Score:** 106 **Expect:** 2.2e-008 **Queries matched:** 13

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4246	919.4173	919.4181	-0.0008	48 -	54	0	CQSQLER
935.4496	934.4423	934.4508	-0.0085	151 -	157	0	QQEQQFK
1056.4825	1055.4752	1055.4744	0.0008	108 -	117	0	GAGSSQHQER
1085.5518	1084.5445	1084.5447	-0.0002	162 -	170	0	NLPQQCGLR
1091.5582	1090.5509	1090.5519	-0.0010	151 -	158	1	QQEQQFKR
1121.4937	1120.4864	1120.4818	0.0046	175 -	184	0	CDLEVESGGR
1315.6439	1314.6366	1314.6429	-0.0062	38 -	47	1	QQWELQGDRR
1624.8035	1623.7962	1623.7973	-0.0011	55 -	67	0	ANLRPCEQHLMQK
1640.7972	1639.7899	1639.7922	-0.0023	55 -	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6860	1725.6787	1725.6835	-0.0047	118 -	130	0	CCNELNEFENNQR
2012.8246	2011.8173	2011.8220	-0.0047	131 -	146	0	CMCEALQQIMENQSDR
2028.8208	2027.8135	2027.8169	-0.0034	131 -	146	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8306	2043.8233	2043.8118	0.0115	131 -	146	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 987.5052, 1045.5615, 1050.1021, 1066.0748, 1072.0846, 1074.5294, 1101.5438, 1104.4999, 1107.5338, 1212.5248, 1228.5151, 1277.0964, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1669.6752, 1709.6658, 1940.9348, 2211.1045, 2225.1191, 2239.0635, 2283.1733, 2299.1819, 2807.3171, 3061.3164, 3347.6819

3. gi|26245447 **Mass:** 20558 **Score:** 105 **Expect:** 2.8e-008 **Queries matched:** 13

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4246	919.4173	919.4181	-0.0008	33 -	39	0	CQSQLER
935.4496	934.4423	934.4508	-0.0085	136 -	142	0	QQEQQFK
1056.4825	1055.4752	1055.4744	0.0008	93 -	102	0	GAGSSQHQER
1085.5518	1084.5445	1084.5447	-0.0002	147 -	155	0	NLPQQCGLR
1091.5582	1090.5509	1090.5519	-0.0010	136 -	143	1	QQEQQFKR
1121.4937	1120.4864	1120.4818	0.0046	160 -	169	0	CDLEVESGGR
1315.6439	1314.6366	1314.6429	-0.0062	23 -	32	1	QQWELQGDRR
1624.8035	1623.7962	1623.7973	-0.0011	40 -	52	0	ANLRPCEQHLMQK
1640.7972	1639.7899	1639.7922	-0.0023	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)

1726.6860	1725.6787	1725.6835	-0.0047	103 - 115	0	CCNELNEFENNQR
2012.8246	2011.8173	2011.8220	-0.0047	116 - 131	0	CMCEALQQIMENQSDR
2028.8208	2027.8135	2027.8169	-0.0034	116 - 131	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8306	2043.8233	2043.8118	0.0115	116 - 131	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 987.5052, 1045.5615, 1050.1021, 1066.0748, 1072.0846, 1074.5294, 1101.5438, 1104.4999, 1107.5338, 1212.5248, 1228.5151, 1277.0964, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1669.6752, 1709.6658, 1940.9348, 2211.1045, 2225.1191, 2239.0635, 2283.1733, 2299.1819, 2807.3171, 3061.3164, 3347.6819

4. gi|118776566 **Mass:** 19009 **Score:** 101 **Expect:** 7e-008 **Queries matched:** 13

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4246	919.4173	919.4181	-0.0008	33 -	39	0	CQSQLER
935.4496	934.4423	934.4508	-0.0085	122 -	128	0	QQEQQFK
1056.4825	1055.4752	1055.4744	0.0008	79 -	88	0	GAGSSQHQER
1085.5518	1084.5445	1084.5447	-0.0002	133 -	141	0	NLPQQCGLR
1091.5582	1090.5509	1090.5519	-0.0010	122 -	129	1	QQEQQFKR
1121.4937	1120.4864	1120.4818	0.0046	146 -	155	0	CDLEVESGGR
1315.6439	1314.6366	1314.6429	-0.0062	23 -	32	1	QQWELQGDRR
1624.8035	1623.7962	1623.7973	-0.0011	40 -	52	0	ANLRPCEQHLMQK
1640.7972	1639.7899	1639.7922	-0.0023	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6860	1725.6787	1725.6835	-0.0047	89 -	101	0	CCNELNEFENNQR
2012.8246	2011.8173	2011.8220	-0.0047	102 -	117	0	CMCEALQQIMENQSDR
2028.8208	2027.8135	2027.8169	-0.0034	102 -	117	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8306	2043.8233	2043.8118	0.0115	102 -	117	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 987.5052, 1045.5615, 1050.1021, 1066.0748, 1072.0846, 1074.5294, 1101.5438, 1104.4999, 1107.5338, 1212.5248, 1228.5151, 1277.0964, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1669.6752, 1709.6658, 1940.9348, 2211.1045, 2225.1191, 2239.0635, 2283.1733, 2299.1819, 2807.3171, 3061.3164, 3347.6819

5. gi|15418705 **Mass:** 18612 **Score:** 97 **Expect:** 2e-007 **Queries matched:** 12

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4246	919.4173	919.4181	-0.0008	33 -	39	0	CQSQLER
935.4496	934.4423	934.4508	-0.0085	124 -	130	0	QQEQQFK
1056.4825	1055.4752	1055.4744	0.0008	81 -	90	0	GAGSSQHQER
1085.5518	1084.5445	1084.5447	-0.0002	135 -	143	0	NLPQQCGLR
1091.5582	1090.5509	1090.5519	-0.0010	124 -	131	1	QQEQQFKR
1315.6439	1314.6366	1314.6429	-0.0062	23 -	32	1	QQWELQGDRR
1624.8035	1623.7962	1623.7973	-0.0011	40 -	52	0	ANLRPCEQHLMQK
1640.7972	1639.7899	1639.7922	-0.0023	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)

1726.6860	1725.6787	1725.6835	-0.0047	91 - 103	0	CCNELNEFENNQR
2012.8246	2011.8173	2011.8220	-0.0047	104 - 119	0	CMCEALQQIMENQSDR
2028.8208	2027.8135	2027.8169	-0.0034	104 - 119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8306	2043.8233	2043.8118	0.0115	104 - 119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 987.5052, 1045.5615, 1050.1021, 1066.0748, 1072.0846, 1074.5294, 1101.5438, 1104.4999, 1107.5338, 1121.4937, 1212.5248, 1228.5151, 1277.0964, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1669.6752, 1709.6658, 1940.9348, 2211.1045, 2225.1191, 2239.0635, 2283.1733, 2299.1819, 2807.3171, 3061.3164, 3347.6819

6. gi|28912768 **Mass:** 19765 **Score:** 96 **Expect:** 2.4e-007 **Queries matched:** 12

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4246	919.4173	919.4181	-0.0008	31 -	37	0	CQSQLER
935.4496	934.4423	934.4508	-0.0085	134 -	140	0	QQEQQFK
1056.4825	1055.4752	1055.4744	0.0008	91 -	100	0	GAGSSQHQER
1085.5518	1084.5445	1084.5447	-0.0002	145 -	153	0	NLPQQCGLR
1091.5582	1090.5509	1090.5519	-0.0010	134 -	141	1	QQEQQFKR
1315.6439	1314.6366	1314.6429	-0.0062	21 -	30	1	QQWELQGDRR
1624.8035	1623.7962	1623.7973	-0.0011	38 -	50	0	ANLRPCEQHLMQK
1640.7972	1639.7899	1639.7922	-0.0023	38 -	50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6860	1725.6787	1725.6835	-0.0047	101 -	113	0	CCNELNEFENNQR
2012.8246	2011.8173	2011.8220	-0.0047	114 -	129	0	CMCEALQQIMENQSDR
2028.8208	2027.8135	2027.8169	-0.0034	114 -	129	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8306	2043.8233	2043.8118	0.0115	114 -	129	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 987.5052, 1045.5615, 1050.1021, 1066.0748, 1072.0846, 1074.5294, 1101.5438, 1104.4999, 1107.5338, 1121.4937, 1212.5248, 1228.5151, 1277.0964, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1669.6752, 1709.6658, 1940.9348, 2211.1045, 2225.1191, 2239.0635, 2283.1733, 2299.1819, 2807.3171, 3061.3164, 3347.6819

7. gi|52001227 **Mass:** 21293 **Score:** 91 **Expect:** 6.6e-007 **Queries matched:** 12

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4246	919.4173	919.4181	-0.0008	52 -	58	0	CQSQLER
935.4496	934.4423	934.4508	-0.0085	143 -	149	0	QQEQQFK
1056.4825	1055.4752	1055.4744	0.0008	100 -	109	0	GAGSSQHQER
1085.5518	1084.5445	1084.5447	-0.0002	154 -	162	0	NLPQQCGLR
1091.5582	1090.5509	1090.5519	-0.0010	143 -	150	1	QQEQQFKR
1315.6439	1314.6366	1314.6429	-0.0062	42 -	51	1	QQWELQGDRR
1624.8035	1623.7962	1623.7973	-0.0011	59 -	71	0	ANLRPCEQHLMQK
1640.7972	1639.7899	1639.7922	-0.0023	59 -	71	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6860	1725.6787	1725.6835	-0.0047	110 -	122	0	CCNELNEFENNQR

2012.8246	2011.8173	2011.8220	-0.0047	123 - 138	0	CMCEALQQIMENQSDR
2028.8208	2027.8135	2027.8169	-0.0034	123 - 138	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8306	2043.8233	2043.8118	0.0115	123 - 138	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 987.5052, 1045.5615, 1050.1021, 1066.0748, 1072.0846, 1074.5294, 1101.5438, 1104.4999, 1107.5338, 1121.4937, 1212.5248, 1228.5151, 1277.0964, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1669.6752, 1709.6658, 1940.9348, 2211.1045, 2225.1191, 2239.0635, 2283.1733, 2299.1819, 2807.3171, 3061.3164, 3347.6819

8. gi|14347293 **Mass:** 24390 **Score:** 86 **Expect:** 2.4e-006 **Queries matched:** 12

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4246	919.4173	919.4181	-0.0008	33 -	39	0	CQSQLER
935.4496	934.4423	934.4508	-0.0085	124 -	130	0	QQEQQFK
1056.4825	1055.4752	1055.4744	0.0008	81 -	90	0	GAGSSQHQER
1085.5518	1084.5445	1084.5447	-0.0002	135 -	143	0	NLPQQCGLR
1091.5582	1090.5509	1090.5519	-0.0010	124 -	131	1	QQEQQFKR
1315.6439	1314.6366	1314.6429	-0.0062	23 -	32	1	QQWELQGDRR
1624.8035	1623.7962	1623.7973	-0.0011	40 -	52	0	ANLRPCEQHLMQK
1640.7972	1639.7899	1639.7922	-0.0023	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6860	1725.6787	1725.6835	-0.0047	91 -	103	0	CCNELNEFENNQR
2012.8246	2011.8173	2011.8220	-0.0047	104 -	119	0	CMCEALQQIMENQSDR
2028.8208	2027.8135	2027.8169	-0.0034	104 -	119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8306	2043.8233	2043.8118	0.0115	104 -	119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 987.5052, 1045.5615, 1050.1021, 1066.0748, 1072.0846, 1074.5294, 1101.5438, 1104.4999, 1107.5338, 1121.4937, 1212.5248, 1228.5151, 1277.0964, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1669.6752, 1709.6658, 1940.9348, 2211.1045, 2225.1191, 2239.0635, 2283.1733, 2299.1819, 2807.3171, 3061.3164, 3347.6819

9. gi|46560482 **Mass:** 20907 **Score:** 83 **Expect:** 4.6e-006 **Queries matched:** 11

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4246	919.4173	919.4181	-0.0008	48 -	54	0	CQSQLER
935.4496	934.4423	934.4508	-0.0085	139 -	145	0	QQEQQFK
1056.4825	1055.4752	1055.4744	0.0008	96 -	105	0	GAGSSQHQER
1085.5518	1084.5445	1084.5447	-0.0002	150 -	158	0	NLPQQCGLR
1091.5582	1090.5509	1090.5519	-0.0010	139 -	146	1	QQEQQFKR
1624.8035	1623.7962	1623.7973	-0.0011	55 -	67	0	ANLRPCEQHLMQK
1640.7972	1639.7899	1639.7922	-0.0023	55 -	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6860	1725.6787	1725.6835	-0.0047	106 -	118	0	CCNELNEFENNQR
2012.8246	2011.8173	2011.8220	-0.0047	119 -	134	0	CMCEALQQIMENQSDR
2028.8208	2027.8135	2027.8169	-0.0034	119 -	134	0	CMCEALQQIMENQSDR + Oxidation (M)

2044.8306	2043.8233	2043.8118	0.0115	119 - 134	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 987.5052, 1045.5615, 1050.1021, 1066.0748, 1072.0846, 1074.5294, 1101.5438, 1104.4999, 1107.5338, 1121.4937, 1212.5248, 1228.5151, 1277.0964, 1315.6439, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1669.6752, 1709.6658, 1940.9348, 2211.1045, 2225.1191, 2239.0635, 2283.1733, 2299.1819, 2807.3171, 3061.3164, 3347.6819

10. gi|114309696 **Mass:** 27933 **Score:** 12 **Expect:** 54 **Queries matched:** 2

MADS-box transcription factor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1624.8035	1623.7962	1623.7926	0.0036	145 -	157	0	TQFMLDQLSELQR + Oxidation (M)
2283.1733	2282.1660	2282.1616	0.0044	32 -	51	0	AYELSVLCDAEVALIIFSNR

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 920.4246, 935.4496, 987.5052, 1045.5615, 1050.1021, 1056.4825, 1066.0748, 1072.0846, 1074.5294, 1085.5518, 1091.5582, 1101.5438, 1104.4999, 1107.5338, 1121.4937, 1212.5248, 1228.5151, 1277.0964, 1315.6439, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1640.7972, 1669.6752, 1709.6658, 1726.6860, 1940.9348, 2012.8246, 2028.8208, 2044.8306, 2211.1045, 2225.1191, 2239.0635, 2299.1819, 2807.3171, 3061.3164, 3347.6819

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|31322017** Score: **108** Expect: **1.4e-008**
allergen Ara h 2 isoform [Arachis hypogaea]

Nominal mass (M_r): **20212**; Calculated pI value: **5.69**
NCBI BLAST search of gi|31322017 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**

Number of mass values matched: **13**
Sequence Coverage: **56%**

Matched peptides shown in **Bold Red**

```
     1 LTILVAPALF LLAAHASARQ QWELQGDRRC QSQLERANLR PCEQHLMQKI
    51 QRDEDSYGRD PYSPSQDPYS PSQDPDRRDP YSPSPYDRRG AGSSQHQERC
   101 CNELNEFENN QRCMCEALQQ IMENQSDRLQ GRQQEQQFKR ELRNLPQQCG
   151 LRAPQRCDLE VESGGRDRY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
20 - 29	1315.6439	1314.6366	1314.6429	-0.0062	1	QQWELQGDRR	
30 - 36	920.4246	919.4173	919.4181	-0.0008	0	CQSQLER	
37 - 49	1624.8035	1623.7962	1623.7973	-0.0011	0	ANLRPCEQHLMQK	
37 - 49	1640.7972	1639.7899	1639.7922	-0.0023	0	ANLRPCEQHLMQK	Oxidation (M)
90 - 99	1056.4825	1055.4752	1055.4744	0.0008	0	GAGSSQHQER	
100 - 112	1726.6860	1725.6787	1725.6835	-0.0047	0	CCNELNEFENNQR	
113 - 128	2012.8246	2011.8173	2011.8220	-0.0047	0	CMCEALQQIMENQSDR	
113 - 128	2028.8208	2027.8135	2027.8169	-0.0034	0	CMCEALQQIMENQSDR	Oxidation (M)
113 - 128	2044.8306	2043.8233	2043.8118	0.0115	0	CMCEALQQIMENQSDR	2 Oxidation (M)
133 - 139	935.4496	934.4423	934.4508	-0.0085	0	QQEQQFK	
133 - 140	1091.5582	1090.5509	1090.5519	-0.0010	1	QQEQQFKR	
144 - 152	1085.5518	1084.5445	1084.5447	-0.0002	0	NLPQQCGLR	
157 - 166	1121.4937	1120.4864	1120.4818	0.0046	0	CDLEVESGGR	

No match to: 839.0862, 842.5092, 845.0936, 855.0577, 861.0731, 864.4918, 877.0438, 893.0159, 903.3978, 918.4277, 987.5052, 1045.5615, 1050.1021, 1066.0748, 1072.0846, 1074.5294, 1101.5438, 1104.4999, 1107.5338, 1212.5248, 1228.5151, 1277.0964, 1368.6111, 1384.6051, 1455.7091, 1471.7445, 1669.6752, 1709.6658, 1940.9348, 2211.1045, 2225.1191, 2239.0635, 2283.1733, 2299.1819, 2807.3171, 3061.3164, 3347.6819

Spot 78

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:14:00 GMT**
Top Score : **98 for gi|52001227, 2S protein 1 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|52001227	21293	98	2S protein 1 [Arachis hypogaea]
2.	gi|15418705	18612	89	allergen II [Arachis hypogaea]
3.	gi|28912768	19765	88	seed storage protein [Arachis hypogaea]
4.	gi|31322017	20212	87	allergen Ara h 2 isoform [Arachis hypogaea]
5.	gi|46560480	22229	84	seed storage protein SSP1 [Arachis hypogaea]
6.	gi|26245447	20558	84	allergen Ara h 2.02 [Arachis hypogaea]
7.	gi|118776566	19009	80	conglutin 7 [Arachis hypogaea]
8.	gi|14347293	24390	77	unnamed protein product [Arachis hypogaea]
9.	gi|46560482	20907	77	seed storage protein SSP2 [Arachis hypogaea]
10.	gi|230338	23975	17	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|52001227 **Mass:** 21293 **Score:** 98 **Expect:** 1.4e-007 **Queries matched:** 12
2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4376	919.4303	919.4181	0.0122	52	58	0	CQSQLER
1056.4918	1055.4845	1055.4744	0.0101	100	109	0	GAGSSQHQER
1085.5618	1084.5545	1084.5447	0.0098	154	162	0	NLPQQCGLR
1091.5657	1090.5584	1090.5519	0.0065	143	150	1	QQEQQFKR
1212.5620	1211.5547	1211.5755	-0.0208	99	109	1	RGAGSSQHQER
1315.6484	1314.6411	1314.6429	-0.0017	42	51	1	QQWELQGDRR
1537.7941	1536.7868	1536.7943	-0.0075	154	166	1	NLPQQCGLRAPQR
1624.8003	1623.7930	1623.7973	-0.0043	59	71	0	ANLRPCEQHLMQK
1640.7925	1639.7852	1639.7922	-0.0070	59	71	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6787	1725.6714	1725.6835	-0.0120	110	122	0	CCNELNEFENNQR

2227.1470	2226.1397	2226.1215	0.0182	3 -	22	1	GKHHTLFNTHSITTTTTMAK
2483.1008	2482.0935	2482.0821	0.0114	123 -	142	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

2. gi|15418705 **Mass:** 18612 **Score:** 89 **Expect:** 1.2e-006 **Queries matched:** 11

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4376	919.4303	919.4181	0.0122	33 -		39	0	CQSQLER
1056.4918	1055.4845	1055.4744	0.0101	81 -		90	0	GAGSSQHQER
1085.5618	1084.5545	1084.5447	0.0098	135 -		143	0	NLPQQCGLR
1091.5657	1090.5584	1090.5519	0.0065	124 -		131	1	QQEQQFKR
1212.5620	1211.5547	1211.5755	-0.0208	80 -		90	1	RGAGSSQHQER
1315.6484	1314.6411	1314.6429	-0.0017	23 -		32	1	QQWELQGDRR
1537.7941	1536.7868	1536.7943	-0.0075	135 -		147	1	NLPQQCGLRAPQR
1624.8003	1623.7930	1623.7973	-0.0043	40 -		52	0	ANLRPCEQHLMQK
1640.7925	1639.7852	1639.7922	-0.0070	40 -		52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6787	1725.6714	1725.6835	-0.0120	91 -		103	0	CCNELNEFENNQR
2483.1008	2482.0935	2482.0821	0.0114	104 -		123	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2227.1470, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

3. gi|28912768 **Mass:** 19765 **Score:** 88 **Expect:** 1.3e-006 **Queries matched:** 11

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4376	919.4303	919.4181	0.0122	31 -		37	0	CQSQLER
1056.4918	1055.4845	1055.4744	0.0101	91 -		100	0	GAGSSQHQER
1085.5618	1084.5545	1084.5447	0.0098	145 -		153	0	NLPQQCGLR
1091.5657	1090.5584	1090.5519	0.0065	134 -		141	1	QQEQQFKR
1212.5620	1211.5547	1211.5755	-0.0208	90 -		100	1	RGAGSSQHQER
1315.6484	1314.6411	1314.6429	-0.0017	21 -		30	1	QQWELQGDRR

1537.7941	1536.7868	1536.7943	-0.0075	145 - 157	1	NLPQQCGLRAPQR
1624.8003	1623.7930	1623.7973	-0.0043	38 - 50	0	ANLRPCEQHLMQK
1640.7925	1639.7852	1639.7922	-0.0070	38 - 50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6787	1725.6714	1725.6835	-0.0120	101 - 113	0	CCNELNEFENNQR
2483.1008	2482.0935	2482.0821	0.0114	114 - 133	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2227.1470, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

4. gi|31322017 **Mass:** 20212 **Score:** 87 **Expect:** 1.6e-006 **Queries matched:** 11

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4376	919.4303	919.4181	0.0122	30 -	36	0	CQSQLER
1056.4918	1055.4845	1055.4744	0.0101	90 -	99	0	GAGSSQHQER
1085.5618	1084.5545	1084.5447	0.0098	144 -	152	0	NLPQQCGLR
1091.5657	1090.5584	1090.5519	0.0065	133 -	140	1	QQEQQFKR
1212.5620	1211.5547	1211.5755	-0.0208	89 -	99	1	RGAGSSQHQER
1315.6484	1314.6411	1314.6429	-0.0017	20 -	29	1	QQWELQGDRR
1537.7941	1536.7868	1536.7943	-0.0075	144 -	156	1	NLPQQCGLRAPQR
1624.8003	1623.7930	1623.7973	-0.0043	37 -	49	0	ANLRPCEQHLMQK
1640.7925	1639.7852	1639.7922	-0.0070	37 -	49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6787	1725.6714	1725.6835	-0.0120	100 -	112	0	CCNELNEFENNQR
2483.1008	2482.0935	2482.0821	0.0114	113 -	132	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2227.1470, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

5. gi|46560480 **Mass:** 22229 **Score:** 84 **Expect:** 3.2e-006 **Queries matched:** 11

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4376	919.4303	919.4181	0.0122	48 -	54	0	CQSQLER
1056.4918	1055.4845	1055.4744	0.0101	108 -	117	0	GAGSSQHQER
1085.5618	1084.5545	1084.5447	0.0098	162 -	170	0	NLPQQCGLR

1091.5657	1090.5584	1090.5519	0.0065	151 - 158	1	QQEQQFKR
1212.5620	1211.5547	1211.5755	-0.0208	107 - 117	1	RGAGSSQHQER
1315.6484	1314.6411	1314.6429	-0.0017	38 - 47	1	QQWELQGDRR
1537.7941	1536.7868	1536.7943	-0.0075	162 - 174	1	NLPQQCGLRAPQR
1624.8003	1623.7930	1623.7973	-0.0043	55 - 67	0	ANLRPCEQHLMQK
1640.7925	1639.7852	1639.7922	-0.0070	55 - 67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6787	1725.6714	1725.6835	-0.0120	118 - 130	0	CCNELNEFENNQR
2483.1008	2482.0935	2482.0821	0.0114	131 - 150	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2227.1470, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

6. gi|26245447 **Mass:** 20558 **Score:** 84 **Expect:** 3.4e-006 **Queries matched:** 11

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4376	919.4303	919.4181	0.0122	33 -	39	0	CQSQLER
1056.4918	1055.4845	1055.4744	0.0101	93 -	102	0	GAGSSQHQER
1085.5618	1084.5545	1084.5447	0.0098	147 -	155	0	NLPQQCGLR
1091.5657	1090.5584	1090.5519	0.0065	136 -	143	1	QQEQQFKR
1212.5620	1211.5547	1211.5755	-0.0208	92 -	102	1	RGAGSSQHQER
1315.6484	1314.6411	1314.6429	-0.0017	23 -	32	1	QQWELQGDRR
1537.7941	1536.7868	1536.7943	-0.0075	147 -	159	1	NLPQQCGLRAPQR
1624.8003	1623.7930	1623.7973	-0.0043	40 -	52	0	ANLRPCEQHLMQK
1640.7925	1639.7852	1639.7922	-0.0070	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6787	1725.6714	1725.6835	-0.0120	103 -	115	0	CCNELNEFENNQR
2483.1008	2482.0935	2482.0821	0.0114	116 -	135	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2227.1470, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

7. gi|118776566 **Mass:** 19009 **Score:** 80 **Expect:** 9.8e-006 **Queries matched:** 11

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

920.4376	919.4303	919.4181	0.0122	33 - 39	0	CQSQLER
1056.4918	1055.4845	1055.4744	0.0101	79 - 88	0	GAGSSQHQER
1085.5618	1084.5545	1084.5447	0.0098	133 - 141	0	NLPQQCGLR
1091.5657	1090.5584	1090.5519	0.0065	122 - 129	1	QQEQQFKR
1212.5620	1211.5547	1211.5755	-0.0208	78 - 88	1	RGAGSSQHQER
1315.6484	1314.6411	1314.6429	-0.0017	23 - 32	1	QQWELQGDRR
1537.7941	1536.7868	1536.7943	-0.0075	133 - 145	1	NLPQQCGLRAPQR
1624.8003	1623.7930	1623.7973	-0.0043	40 - 52	0	ANLRPCEQHLMQK
1640.7925	1639.7852	1639.7922	-0.0070	40 - 52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6787	1725.6714	1725.6835	-0.0120	89 - 101	0	CCNELNEFENNQR
2483.1008	2482.0935	2482.0821	0.0114	102 - 121	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2227.1470, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

8. gi|14347293 **Mass:** 24390 **Score:** 77 **Expect:** 1.8e-005 **Queries matched:** 11

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4376	919.4303	919.4181	0.0122	33 -	39	0	CQSQLER
1056.4918	1055.4845	1055.4744	0.0101	81 -	90	0	GAGSSQHQER
1085.5618	1084.5545	1084.5447	0.0098	135 -	143	0	NLPQQCGLR
1091.5657	1090.5584	1090.5519	0.0065	124 -	131	1	QQEQQFKR
1212.5620	1211.5547	1211.5755	-0.0208	80 -	90	1	RGAGSSQHQER
1315.6484	1314.6411	1314.6429	-0.0017	23 -	32	1	QQWELQGDRR
1537.7941	1536.7868	1536.7943	-0.0075	135 -	147	1	NLPQQCGLRAPQR
1624.8003	1623.7930	1623.7973	-0.0043	40 -	52	0	ANLRPCEQHLMQK
1640.7925	1639.7852	1639.7922	-0.0070	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6787	1725.6714	1725.6835	-0.0120	91 -	103	0	CCNELNEFENNQR
2483.1008	2482.0935	2482.0821	0.0114	104 -	123	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2227.1470, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

9. gi|46560482 **Mass:** 20907 **Score:** 77 **Expect:** 1.9e-005 **Queries matched:** 10

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4376	919.4303	919.4181	0.0122	48	54	0	CQSQLER
1056.4918	1055.4845	1055.4744	0.0101	96	105	0	GAGSSQHQER
1085.5618	1084.5545	1084.5447	0.0098	150	158	0	NLPQQCGLR
1091.5657	1090.5584	1090.5519	0.0065	139	146	1	QQEQQFKR
1212.5620	1211.5547	1211.5755	-0.0208	95	105	1	RGAGSSQHQER
1537.7941	1536.7868	1536.7943	-0.0075	150	162	1	NLPQQCGLRAPQR
1624.8003	1623.7930	1623.7973	-0.0043	55	67	0	ANLRPCEQHLMQK
1640.7925	1639.7852	1639.7922	-0.0070	55	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6787	1725.6714	1725.6835	-0.0120	106	118	0	CCNELNEFENNQR
2483.1008	2482.0935	2482.0821	0.0114	119	138	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1315.6484, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2227.1470, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

10. gi|230338 **Mass:** 23975 **Score:** 17 **Expect:** 16 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.6017	1045.5944	1045.5880	0.0065	90	99	1	LKSAASLNSR
2273.1619	2272.1546	2272.1521	0.0025	70	89	0	SIVHPSYNSNTLNNDIMLIK
2514.3408	2513.3335	2513.3311	0.0024	70	91	1	SIVHPSYNSNTLNNDIMLIKLK
2530.3474	2529.3401	2529.3260	0.0141	70	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 920.4376, 1056.4918, 1074.5435, 1080.5256, 1085.5618, 1090.5458, 1091.5657, 1145.0708, 1145.5737, 1175.5419, 1212.5620, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1315.6484, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1537.7941, 1578.7919, 1624.8003, 1638.8394, 1640.7925, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1726.6787, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2227.1470, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2483.1008, 2501.1794, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 83

Protein View

Match to: **gi|52001227** Score: **98** Expect: **1.4e-007**
2S protein 1 [Arachis hypogaea]

Nominal mass (M_r): **21293**; Calculated pI value: **7.14**
NCBI BLAST search of gi|52001227 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **83**
Number of mass values matched: **12**
Sequence Coverage: **64%**

Matched peptides shown in **Bold Red**

```
     1 GR**GKHHTLFN THSITTTTTM AK**LTILVALA LFLLAAHASA R**QQWELQGDR**
    51 **RCQSQLERAN LRPCEQHLMQ K**IQRDEDSYE RDPYSPSQDP YSPSPYDR**RG**
   101 **AGSSQHQERC CNELNEFENN QRCMCEALQQ IMENQSDRLQ GRQQEQQFKR**
   151 ELR**NLPQQCG LRAPQR**CDLD VESGGRDRY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
3 - 22	2227.1470	2226.1397	2226.1215	0.0182	1	GKHHTLFNTHSITTTTTMAK
42 - 51	1315.6484	1314.6411	1314.6429	-0.0017	1	QQWELQGDRR
52 - 58	920.4376	919.4303	919.4181	0.0122	0	CQSQLER
59 - 71	1624.8003	1623.7930	1623.7973	-0.0043	0	ANLRPCEQHLMQK
59 - 71	1640.7925	1639.7852	1639.7922	-0.0070	0	ANLRPCEQHLMQK Oxidation (M)
99 - 109	1212.5620	1211.5547	1211.5755	-0.0208	1	RGAGSSQHQER
100 - 109	1056.4918	1055.4845	1055.4744	0.0101	0	GAGSSQHQER
110 - 122	1726.6787	1725.6714	1725.6835	-0.0120	0	CCNELNEFENNQR
123 - 142	2483.1008	2482.0935	2482.0821	0.0114	1	CMCEALQQIMENQSDRLQGR Oxidation (M)
143 - 150	1091.5657	1090.5584	1090.5519	0.0065	1	QQEQQFKR
154 - 162	1085.5618	1084.5545	1084.5447	0.0098	0	NLPQQCGLR
154 - 166	1537.7941	1536.7868	1536.7943	-0.0075	1	NLPQQCGLRAPQR

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

Spot 79

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 10:01:00 GMT**
Top Score : **98 for gi|15418705, allergen II [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|15418705	18612	98	allergen II [Arachis hypogaea]
2.	gi|28912768	19765	98	seed storage protein [Arachis hypogaea]
3.	gi|31322017	20212	97	allergen Ara h 2 isoform [Arachis hypogaea]
4.	gi|46560480	22229	94	seed storage protein SSP1 [Arachis hypogaea]
5.	gi|26245447	20558	94	allergen Ara h 2.02 [Arachis hypogaea]
6.	gi|52001227	21293	93	2S protein 1 [Arachis hypogaea]
7.	gi|118776566	19009	90	conglutin 7 [Arachis hypogaea]
8.	gi|14347293	24390	87	unnamed protein product [Arachis hypogaea]
9.	gi|46560482	20907	84	seed storage protein SSP2 [Arachis hypogaea]
10.	gi|83776779	16159	17	dessication protectant protein LEA 14 [Arachis hypogaea]

Results List

1. gi|15418705 **Mass:** 18612 **Score:** 98 **Expect:** 1.4e-007 **Queries matched:** 10
allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4131	919.4058	919.4181	-0.0123	33	39	0	CQSQLER
1056.4897	1055.4824	1055.4744	0.0080	81	90	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	135	143	0	NLPQQCGLR
1091.5646	1090.5573	1090.5519	0.0054	124	131	1	QQEQQFKR
1315.6709	1314.6636	1314.6429	0.0208	23	32	1	QQWELQGDRR
1537.8214	1536.8141	1536.7943	0.0198	135	147	1	NLPQQCGLRAPQR
1624.8292	1623.8219	1623.7973	0.0246	40	52	0	ANLRPCEQHLMQK
1640.8214	1639.8141	1639.7922	0.0219	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7123	1725.7050	1725.6835	0.0216	91	103	0	CCNELNEFENNQR
2483.0537	2482.0464	2482.0821	-0.0357	104	123	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 987.5001, 1046.6039, 1066.0782, 1074.5392, 1080.5353, 1113.5532, 1145.5479, 1194.5699, 1368.6439, 1454.3724, 1471.7714, 1487.7676, 1493.7489, 1525.6989, 1555.7037, 1578.8427, 1709.6881, 1725.6913, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2531.2986, 3138.2715, 3153.2842, 3228.3186

2. gi|28912768 **Mass:** 19765 **Score:** 98 **Expect:** 1.5e-007 **Queries matched:** 10

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4131	919.4058	919.4181	-0.0123	31	37	0	CQSQLER
1056.4897	1055.4824	1055.4744	0.0080	91	100	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	145	153	0	NLPQQCGLR
1091.5646	1090.5573	1090.5519	0.0054	134	141	1	QQEQQFKR
1315.6709	1314.6636	1314.6429	0.0208	21	30	1	QQWELQGDRR
1537.8214	1536.8141	1536.7943	0.0198	145	157	1	NLPQQCGLRAPQR
1624.8292	1623.8219	1623.7973	0.0246	38	50	0	ANLRPCEQHLMQK
1640.8214	1639.8141	1639.7922	0.0219	38	50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7123	1725.7050	1725.6835	0.0216	101	113	0	CCNELNEFENNQR
2483.0537	2482.0464	2482.0821	-0.0357	114	133	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 987.5001, 1046.6039, 1066.0782, 1074.5392, 1080.5353, 1113.5532, 1145.5479, 1194.5699, 1368.6439, 1454.3724, 1471.7714, 1487.7676, 1493.7489, 1525.6989, 1555.7037, 1578.8427, 1709.6881, 1725.6913, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2531.2986, 3138.2715, 3153.2842, 3228.3186

3. gi|31322017 **Mass:** 20212 **Score:** 97 **Expect:** 1.9e-007 **Queries matched:** 10

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4131	919.4058	919.4181	-0.0123	30	36	0	CQSQLER
1056.4897	1055.4824	1055.4744	0.0080	90	99	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	144	152	0	NLPQQCGLR
1091.5646	1090.5573	1090.5519	0.0054	133	140	1	QQEQQFKR
1315.6709	1314.6636	1314.6429	0.0208	20	29	1	QQWELQGDRR
1537.8214	1536.8141	1536.7943	0.0198	144	156	1	NLPQQCGLRAPQR
1624.8292	1623.8219	1623.7973	0.0246	37	49	0	ANLRPCEQHLMQK
1640.8214	1639.8141	1639.7922	0.0219	37	49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7123	1725.7050	1725.6835	0.0216	100	112	0	CCNELNEFENNQR
2483.0537	2482.0464	2482.0821	-0.0357	113	132	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 987.5001, 1046.6039, 1066.0782, 1074.5392, 1080.5353, 1113.5532, 1145.5479, 1194.5699, 1368.6439, 1454.3724, 1471.7714, 1487.7676, 1493.7489, 1525.6989, 1555.7037, 1578.8427, 1709.6881, 1725.6913, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2531.2986, 3138.2715, 3153.2842, 3228.3186

4. gi|46560480 **Mass:** 22229 **Score:** 94 **Expect:** 3.6e-007 **Queries matched:** 10

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4131	919.4058	919.4181	-0.0123	48	-	54	0	CQSQLER
1056.4897	1055.4824	1055.4744	0.0080	108	-	117	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	162	-	170	0	NLPQQCGLR
1091.5646	1090.5573	1090.5519	0.0054	151	-	158	1	QQEQQFKR
1315.6709	1314.6636	1314.6429	0.0208	38	-	47	1	QQWELQGDRR
1537.8214	1536.8141	1536.7943	0.0198	162	-	174	1	NLPQQCGLRAPQR
1624.8292	1623.8219	1623.7973	0.0246	55	-	67	0	ANLRPCEQHLMQK
1640.8214	1639.8141	1639.7922	0.0219	55	-	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7123	1725.7050	1725.6835	0.0216	118	-	130	0	CCNELNEFENNQR
2483.0537	2482.0464	2482.0821	-0.0357	131	-	150	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 987.5001, 1046.6039, 1066.0782, 1074.5392, 1080.5353, 1113.5532, 1145.5479, 1194.5699, 1368.6439, 1454.3724, 1471.7714, 1487.7676, 1493.7489, 1525.6989, 1555.7037, 1578.8427, 1709.6881, 1725.6913, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2531.2986, 3138.2715, 3153.2842, 3228.3186

5. gi|26245447 **Mass:** 20558 **Score:** 94 **Expect:** 3.7e-007 **Queries matched:** 10

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4131	919.4058	919.4181	-0.0123	33	-	39	0	CQSQLER
1056.4897	1055.4824	1055.4744	0.0080	93	-	102	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	147	-	155	0	NLPQQCGLR
1091.5646	1090.5573	1090.5519	0.0054	136	-	143	1	QQEQQFKR
1315.6709	1314.6636	1314.6429	0.0208	23	-	32	1	QQWELQGDRR
1537.8214	1536.8141	1536.7943	0.0198	147	-	159	1	NLPQQCGLRAPQR
1624.8292	1623.8219	1623.7973	0.0246	40	-	52	0	ANLRPCEQHLMQK
1640.8214	1639.8141	1639.7922	0.0219	40	-	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7123	1725.7050	1725.6835	0.0216	103	-	115	0	CCNELNEFENNQR
2483.0537	2482.0464	2482.0821	-0.0357	116	-	135	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 987.5001, 1046.6039, 1066.0782, 1074.5392, 1080.5353, 1113.5532, 1145.5479, 1194.5699, 1368.6439, 1454.3724, 1471.7714, 1487.7676, 1493.7489, 1525.6989, 1555.7037, 1578.8427, 1709.6881, 1725.6913, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2531.2986, 3138.2715, 3153.2842, 3228.3186

6. gi|52001227 **Mass:** 21293 **Score:** 93 **Expect:** 4.3e-007 **Queries matched:** 10

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4131	919.4058	919.4181	-0.0123	52	-	58	0	CQSQLER
1056.4897	1055.4824	1055.4744	0.0080	100	-	109	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	154	-	162	0	NLPQQCGLR

1091.5646	1090.5573	1090.5519	0.0054	143 - 150	1	QQEQQFKR
1315.6709	1314.6636	1314.6429	0.0208	42 - 51	1	QQWELQGDRR
1537.8214	1536.8141	1536.7943	0.0198	154 - 166	1	NLPQQCGLRAPQR
1624.8292	1623.8219	1623.7973	0.0246	59 - 71	0	ANLRPCEQHLMQK
1640.8214	1639.8141	1639.7922	0.0219	59 - 71	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7123	1725.7050	1725.6835	0.0216	110 - 122	0	CCNELNEFENNQR
2483.0537	2482.0464	2482.0821	-0.0357	123 - 142	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 987.5001, 1046.6039, 1066.0782, 1074.5392, 1080.5353, 1113.5532, 1145.5479, 1194.5699, 1368.6439, 1454.3724, 1471.7714, 1487.7676, 1493.7489, 1525.6989, 1555.7037, 1578.8427, 1709.6881, 1725.6913, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2531.2986, 3138.2715, 3153.2842, 3228.3186

7. gi|118776566 **Mass:** 19009 **Score:** 90 **Expect:** 9.2e-007 **Queries matched:** 10

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4131	919.4058	919.4181	-0.0123	33	39	0	CQSQLER
1056.4897	1055.4824	1055.4744	0.0080	79	88	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	133	141	0	NLPQQCGLR
1091.5646	1090.5573	1090.5519	0.0054	122	129	1	QQEQQFKR
1315.6709	1314.6636	1314.6429	0.0208	23	32	1	QQWELQGDRR
1537.8214	1536.8141	1536.7943	0.0198	133	145	1	NLPQQCGLRAPQR
1624.8292	1623.8219	1623.7973	0.0246	40	52	0	ANLRPCEQHLMQK
1640.8214	1639.8141	1639.7922	0.0219	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7123	1725.7050	1725.6835	0.0216	89	101	0	CCNELNEFENNQR
2483.0537	2482.0464	2482.0821	-0.0357	102	121	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 987.5001, 1046.6039, 1066.0782, 1074.5392, 1080.5353, 1113.5532, 1145.5479, 1194.5699, 1368.6439, 1454.3724, 1471.7714, 1487.7676, 1493.7489, 1525.6989, 1555.7037, 1578.8427, 1709.6881, 1725.6913, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2531.2986, 3138.2715, 3153.2842, 3228.3186

8. gi|14347293 **Mass:** 24390 **Score:** 87 **Expect:** 1.7e-006 **Queries matched:** 10

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4131	919.4058	919.4181	-0.0123	33	39	0	CQSQLER
1056.4897	1055.4824	1055.4744	0.0080	81	90	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	135	143	0	NLPQQCGLR
1091.5646	1090.5573	1090.5519	0.0054	124	131	1	QQEQQFKR
1315.6709	1314.6636	1314.6429	0.0208	23	32	1	QQWELQGDRR
1537.8214	1536.8141	1536.7943	0.0198	135	147	1	NLPQQCGLRAPQR
1624.8292	1623.8219	1623.7973	0.0246	40	52	0	ANLRPCEQHLMQK
1640.8214	1639.8141	1639.7922	0.0219	40	52	0	ANLRPCEQHLMQK + Oxidation (M)

1726.7123	1725.7050	1725.6835	0.0216	91 - 103	0	CCNELNEFENNQR
2483.0537	2482.0464	2482.0821	-0.0357	104 - 123	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 987.5001, 1046.6039, 1066.0782, 1074.5392, 1080.5353, 1113.5532, 1145.5479, 1194.5699, 1368.6439, 1454.3724, 1471.7714, 1487.7676, 1493.7489, 1525.6989, 1555.7037, 1578.8427, 1709.6881, 1725.6913, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2531.2986, 3138.2715, 3153.2842, 3228.3186

9. gi|46560482 **Mass:** 20907 **Score:** 84 **Expect:** 3.6e-006 **Queries matched:** 9

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4131	919.4058	919.4181	-0.0123	48 -	54	0	CQSQLER
1056.4897	1055.4824	1055.4744	0.0080	96 -	105	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	150 -	158	0	NLPQQCGLR
1091.5646	1090.5573	1090.5519	0.0054	139 -	146	1	QQEQQFKR
1537.8214	1536.8141	1536.7943	0.0198	150 -	162	1	NLPQQCGLRAPQR
1624.8292	1623.8219	1623.7973	0.0246	55 -	67	0	ANLRPCEQHLMQK
1640.8214	1639.8141	1639.7922	0.0219	55 -	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7123	1725.7050	1725.6835	0.0216	106 -	118	0	CCNELNEFENNQR
2483.0537	2482.0464	2482.0821	-0.0357	119 -	138	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 987.5001, 1046.6039, 1066.0782, 1074.5392, 1080.5353, 1113.5532, 1145.5479, 1194.5699, 1315.6709, 1368.6439, 1454.3724, 1471.7714, 1487.7676, 1493.7489, 1525.6989, 1555.7037, 1578.8427, 1709.6881, 1725.6913, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2531.2986, 3138.2715, 3153.2842, 3228.3186

10. gi|83776779 **Mass:** 16159 **Score:** 17 **Expect:** 19 **Queries matched:** 3

dessication protectant protein LEA 14 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1471.7714	1470.7641	1470.7500	0.0141	65 -	78	1	EIATGRMPDPGSLK
1487.7676	1486.7603	1486.7449	0.0154	65 -	78	1	EIATGRMPDPGSLK + Oxidation (M)
2531.2986	2530.2913	2530.2703	0.0211	5 -	27	1	NFAAEKISDVAKPEAHVTDVDFK

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 920.4131, 987.5001, 1046.6039, 1056.4897, 1066.0782, 1074.5392, 1080.5353, 1085.5568, 1091.5646, 1113.5532, 1145.5479, 1194.5699, 1315.6709, 1368.6439, 1454.3724, 1493.7489, 1525.6989, 1537.8214, 1555.7037, 1578.8427, 1624.8292, 1640.8214, 1709.6881, 1725.6913, 1726.7123, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2483.0537, 3138.2715, 3153.2842, 3228.3186

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 49

Protein View

Match to: **gi|15418705** Score: **98** Expect: **1.4e-007**
allergen II [Arachis hypogaea]

Nominal mass (M_r): **18612**; Calculated pI value: **5.67**
NCBI BLAST search of gi|15418705 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **49**
Number of mass values matched: **10**
Sequence Coverage: **60%**

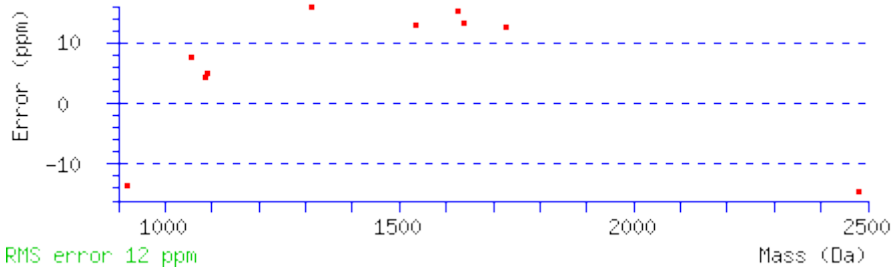
Matched peptides shown in **Bold Red**

```
     1 MAKLTILVAL ALFLLAAHAS ARQQWELQGD RRCQSQLERA NLRPCEQHLM
    51 QKIQRDEDSY ERDPYSPSQD PYSPSPYDRR GAGSSQHQER CCNELNEFEN
   101 NQRCMCEALQ QIMENQSDRL QGRQQEQQFK RELRNLPQQC GLRAPQRCDL
   151 DVESGG
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
23 - 32	1315.6709	1314.6636	1314.6429	0.0208	1	QQWELQGDRR	
33 - 39	920.4131	919.4058	919.4181	-0.0123	0	CQSQLER	
40 - 52	1624.8292	1623.8219	1623.7973	0.0246	0	ANLRPCEQHLMQK	
40 - 52	1640.8214	1639.8141	1639.7922	0.0219	0	ANLRPCEQHLMQK	Oxidation (M)
81 - 90	1056.4897	1055.4824	1055.4744	0.0080	0	GAGSSQHQER	
91 - 103	1726.7123	1725.7050	1725.6835	0.0216	0	CCNELNEFENNQR	
104 - 123	2483.0537	2482.0464	2482.0821	-0.0357	1	CMCEALQQIMENQSDRLQGR	Oxidation (M)
124 - 131	1091.5646	1090.5573	1090.5519	0.0054	1	QQEQQFKR	
135 - 143	1085.5568	1084.5495	1084.5447	0.0048	0	NLPQQCGLR	
135 - 147	1537.8214	1536.8141	1536.7943	0.0198	1	NLPQQCGLRAPQR	

No match to: 805.3918, 855.0317, 861.0488, 877.0254, 903.3884, 906.4779, 987.5001, 1046.6039, 1066.0782, 1074.5392, 1080.5353, 1113.5532, 1145.5479, 1194.5699, 1368.6439, 1454.3724, 1471.7714, 1487.7676, 1493.7489, 1525.6989, 1555.7037, 1578.8427, 1709.6881, 1725.6913, 1748.6987, 1774.8700, 2007.9446, 2185.0295, 2200.9968, 2273.1484, 2311.1270, 2327.0967, 2344.0808, 2466.0442, 2482.0234, 2531.2986, 3138.2715, 3153.2842, 3228.3186



Spot 80

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 20 Mar 2007 at 13:16:00 GMT
Top Score : 79 for gi|15418705, allergen II [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|15418705	18612	79	allergen II [Arachis hypogaea]
2.	gi|28912768	19765	79	seed storage protein [Arachis hypogaea]
3.	gi|31322017	20212	78	allergen Ara h 2 isoform [Arachis hypogaea]
4.	gi|46560480	22229	76	seed storage protein SSP1 [Arachis hypogaea]
5.	gi|26245447	20558	75	allergen Ara h 2.02 [Arachis hypogaea]
6.	gi|52001227	21293	75	2S protein 1 [Arachis hypogaea]
7.	gi|118776566	19009	71	conglutin 7 [Arachis hypogaea]
8.	gi|14347293	24390	70	unnamed protein product [Arachis hypogaea]
9.	gi|46560482	20907	67	seed storage protein SSP2 [Arachis hypogaea]
10.	gi|288479	5059	13	chitinase [Arachis hypogaea]

Results List

1. gi|15418705 **Mass:** 18612 **Score:** 79 **Expect:** 1e-005 **Queries matched:** 9
allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4224	919.4151	919.4181	-0.0030	33	39	0	CQSQLER
935.4443	934.4370	934.4508	-0.0138	124	130	0	QQEQQFK
1056.4803	1055.4730	1055.4744	-0.0014	81	90	0	GAGSSQHQER
1085.5485	1084.5412	1084.5447	-0.0035	135	143	0	NLPQQCGLR
1091.5557	1090.5484	1090.5519	-0.0035	124	131	1	QQEQQFKR
1315.6429	1314.6356	1314.6429	-0.0072	23	32	1	QQWELQGDRR
1624.8007	1623.7934	1623.7973	-0.0039	40	52	0	ANLRPCEQHLMQK
1640.8029	1639.7956	1639.7922	0.0034	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6886	1725.6813	1725.6835	-0.0021	91	103	0	CCNELNEFENNQR

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908,

870.5455, 877.0538, 893.0246, 932.4760, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1066.0886, 1068.4918, 1072.1028, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1709.6637, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2233.1152, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826

2. gi|28912768 **Mass:** 19765 **Score:** 79 **Expect:** 1.2e-005 **Queries matched:** 9

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4224	919.4151	919.4181	-0.0030	31	37	0	CQSQLER
935.4443	934.4370	934.4508	-0.0138	134	140	0	QQEQQFK
1056.4803	1055.4730	1055.4744	-0.0014	91	100	0	GAGSSQHQER
1085.5485	1084.5412	1084.5447	-0.0035	145	153	0	NLPQQCGLR
1091.5557	1090.5484	1090.5519	-0.0035	134	141	1	QQEQQFKR
1315.6429	1314.6356	1314.6429	-0.0072	21	30	1	QQWELQGDRR
1624.8007	1623.7934	1623.7973	-0.0039	38	50	0	ANLRPCEQHLMQK
1640.8029	1639.7956	1639.7922	0.0034	38	50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6886	1725.6813	1725.6835	-0.0021	101	113	0	CCNELNEFENNQR

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908, 870.5455, 877.0538, 893.0246, 932.4760, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1066.0886, 1068.4918, 1072.1028, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1709.6637, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2233.1152, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826

3. gi|31322017 **Mass:** 20212 **Score:** 78 **Expect:** 1.5e-005 **Queries matched:** 9

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4224	919.4151	919.4181	-0.0030	30	36	0	CQSQLER
935.4443	934.4370	934.4508	-0.0138	133	139	0	QQEQQFK
1056.4803	1055.4730	1055.4744	-0.0014	90	99	0	GAGSSQHQER
1085.5485	1084.5412	1084.5447	-0.0035	144	152	0	NLPQQCGLR
1091.5557	1090.5484	1090.5519	-0.0035	133	140	1	QQEQQFKR
1315.6429	1314.6356	1314.6429	-0.0072	20	29	1	QQWELQGDRR
1624.8007	1623.7934	1623.7973	-0.0039	37	49	0	ANLRPCEQHLMQK
1640.8029	1639.7956	1639.7922	0.0034	37	49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6886	1725.6813	1725.6835	-0.0021	100	112	0	CCNELNEFENNQR

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908, 870.5455, 877.0538, 893.0246, 932.4760, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1066.0886, 1068.4918, 1072.1028, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1709.6637, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2233.1152, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826

4. gi|46560480 **Mass:** 22229 **Score:** 76 **Expect:** 2.4e-005 **Queries matched:** 9

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4224	919.4151	919.4181	-0.0030	48	54	0	CQSQLER

935.4443	934.4370	934.4508	-0.0138	151 - 157	0	QQEQQFK
1056.4803	1055.4730	1055.4744	-0.0014	108 - 117	0	GAGSSQHQER
1085.5485	1084.5412	1084.5447	-0.0035	162 - 170	0	NLPQQCGLR
1091.5557	1090.5484	1090.5519	-0.0035	151 - 158	1	QQEQQFKR
1315.6429	1314.6356	1314.6429	-0.0072	38 - 47	1	QQWELQGDRR
1624.8007	1623.7934	1623.7973	-0.0039	55 - 67	0	ANLRPCEQHLMQK
1640.8029	1639.7956	1639.7922	0.0034	55 - 67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6886	1725.6813	1725.6835	-0.0021	118 - 130	0	CCNELNEFENNQR

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908, 870.5455, 877.0538, 893.0246, 932.4760, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1066.0886, 1068.4918, 1072.1028, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1709.6637, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2233.1152, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826

5. gi|26245447 **Mass:** 20558 **Score:** 75 **Expect:** 2.6e-005 **Queries matched:** 9

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4224	919.4151	919.4181	-0.0030	33 -	39	0	CQSQLER
935.4443	934.4370	934.4508	-0.0138	136 -	142	0	QQEQQFK
1056.4803	1055.4730	1055.4744	-0.0014	93 -	102	0	GAGSSQHQER
1085.5485	1084.5412	1084.5447	-0.0035	147 -	155	0	NLPQQCGLR
1091.5557	1090.5484	1090.5519	-0.0035	136 -	143	1	QQEQQFKR
1315.6429	1314.6356	1314.6429	-0.0072	23 -	32	1	QQWELQGDRR
1624.8007	1623.7934	1623.7973	-0.0039	40 -	52	0	ANLRPCEQHLMQK
1640.8029	1639.7956	1639.7922	0.0034	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6886	1725.6813	1725.6835	-0.0021	103 -	115	0	CCNELNEFENNQR

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908, 870.5455, 877.0538, 893.0246, 932.4760, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1066.0886, 1068.4918, 1072.1028, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1709.6637, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2233.1152, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826

6. gi|52001227 **Mass:** 21293 **Score:** 75 **Expect:** 2.9e-005 **Queries matched:** 9

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4224	919.4151	919.4181	-0.0030	52 -	58	0	CQSQLER
935.4443	934.4370	934.4508	-0.0138	143 -	149	0	QQEQQFK
1056.4803	1055.4730	1055.4744	-0.0014	100 -	109	0	GAGSSQHQER
1085.5485	1084.5412	1084.5447	-0.0035	154 -	162	0	NLPQQCGLR
1091.5557	1090.5484	1090.5519	-0.0035	143 -	150	1	QQEQQFKR
1315.6429	1314.6356	1314.6429	-0.0072	42 -	51	1	QQWELQGDRR
1624.8007	1623.7934	1623.7973	-0.0039	59 -	71	0	ANLRPCEQHLMQK
1640.8029	1639.7956	1639.7922	0.0034	59 -	71	0	ANLRPCEQHLMQK + Oxidation (M)

1726.6886	1725.6813	1725.6835	-0.0021	110 - 122	0	CCNELNEFENNQR

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908, 870.5455, 877.0538, 893.0246, 932.4760, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1066.0886, 1068.4918, 1072.1028, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1709.6637, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2233.1152, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826

7. gi|118776566 **Mass:** 19009 **Score:** 71 **Expect:** 7.1e-005 **Queries matched:** 9

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4224	919.4151	919.4181	-0.0030	33 -	39	0	CQSQLER
935.4443	934.4370	934.4508	-0.0138	122 -	128	0	QQEQQFK
1056.4803	1055.4730	1055.4744	-0.0014	79 -	88	0	GAGSSQHQER
1085.5485	1084.5412	1084.5447	-0.0035	133 -	141	0	NLPQQCGLR
1091.5557	1090.5484	1090.5519	-0.0035	122 -	129	1	QQEQQFKR
1315.6429	1314.6356	1314.6429	-0.0072	23 -	32	1	QQWELQGDRR
1624.8007	1623.7934	1623.7973	-0.0039	40 -	52	0	ANLRPCEQHLMQK
1640.8029	1639.7956	1639.7922	0.0034	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6886	1725.6813	1725.6835	-0.0021	89 -	101	0	CCNELNEFENNQR

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908, 870.5455, 877.0538, 893.0246, 932.4760, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1066.0886, 1068.4918, 1072.1028, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1709.6637, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2233.1152, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826

8. gi|14347293 **Mass:** 24390 **Score:** 70 **Expect:** 9.8e-005 **Queries matched:** 9

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4224	919.4151	919.4181	-0.0030	33 -	39	0	CQSQLER
935.4443	934.4370	934.4508	-0.0138	124 -	130	0	QQEQQFK
1056.4803	1055.4730	1055.4744	-0.0014	81 -	90	0	GAGSSQHQER
1085.5485	1084.5412	1084.5447	-0.0035	135 -	143	0	NLPQQCGLR
1091.5557	1090.5484	1090.5519	-0.0035	124 -	131	1	QQEQQFKR
1315.6429	1314.6356	1314.6429	-0.0072	23 -	32	1	QQWELQGDRR
1624.8007	1623.7934	1623.7973	-0.0039	40 -	52	0	ANLRPCEQHLMQK
1640.8029	1639.7956	1639.7922	0.0034	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6886	1725.6813	1725.6835	-0.0021	91 -	103	0	CCNELNEFENNQR

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908, 870.5455, 877.0538, 893.0246, 932.4760, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1066.0886, 1068.4918, 1072.1028, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1709.6637, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2233.1152, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826

9. gi|46560482 **Mass:** 20907 **Score:** 67 **Expect:** 0.00019 **Queries matched:** 8

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4224	919.4151	919.4181	-0.0030	48	54	0	CQSQLER
935.4443	934.4370	934.4508	-0.0138	139	145	0	QQEQQFK
1056.4803	1055.4730	1055.4744	-0.0014	96	105	0	GAGSSQHQER
1085.5485	1084.5412	1084.5447	-0.0035	150	158	0	NLPQQCGLR
1091.5557	1090.5484	1090.5519	-0.0035	139	146	1	QQEQQFKR
1624.8007	1623.7934	1623.7973	-0.0039	55	67	0	ANLRPCEQHLMQK
1640.8029	1639.7956	1639.7922	0.0034	55	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6886	1725.6813	1725.6835	-0.0021	106	118	0	CCNELNEFENNQR

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908, 870.5455, 877.0538, 893.0246, 932.4760, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1066.0886, 1068.4918, 1072.1028, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1315.6429, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1709.6637, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2233.1152, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826

10. gi|288479 **Mass:** 5059 **Score:** 13 **Expect:** 44 **Queries matched:** 1

chitinase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
2233.1152	2232.1079	2232.1320	-0.0241	26	47	1	AANRTLGFGLVTNIINGGLDCG

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908, 870.5455, 877.0538, 893.0246, 920.4224, 932.4760, 935.4443, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1056.4803, 1066.0886, 1068.4918, 1072.1028, 1085.5485, 1091.5557, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1315.6429, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1624.8007, 1640.8029, 1709.6637, 1726.6886, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|15418705** Score: **79** Expect: **1e-005**
allergen II [Arachis hypogaea]

Nominal mass (M_r): **18612**; Calculated pI value: **5.67**
NCBI BLAST search of gi|15418705 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **9**
Sequence Coverage: **44%**

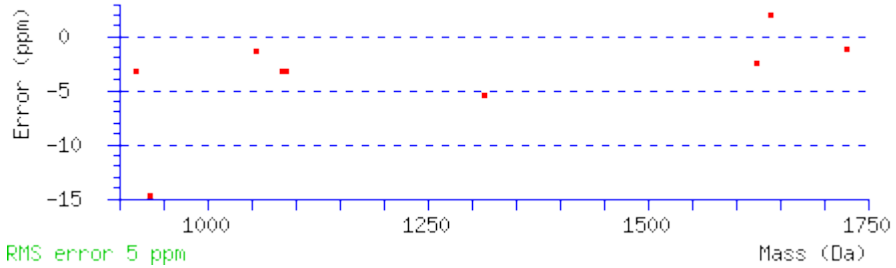
Matched peptides shown in **Bold Red**

```
     1 MAKLTILVAL ALFLLAAHAS ARQQWELQGD RRCQSQLERA NLRPCEQHLM
    51 QKIQRDEDSY ERDPYSPSQD PYSPSPYDRR GAGSSQHQER CCNELNEFEN
   101 NQRCMCEALQ QIMENQSDRL QGRQQEQQFK RELRNLPQQC GLRAPQRCDL
   151 DVESGG
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
23 - 32	1315.6429	1314.6356	1314.6429	-0.0072	1	QQWELQGDRR	
33 - 39	920.4224	919.4151	919.4181	-0.0030	0	CQSQLER	
40 - 52	1624.8007	1623.7934	1623.7973	-0.0039	0	ANLRPCEQHLMQK	
40 - 52	1640.8029	1639.7956	1639.7922	0.0034	0	ANLRPCEQHLMQK	Oxidation (M)
81 - 90	1056.4803	1055.4730	1055.4744	-0.0014	0	GAGSSQHQER	
91 - 103	1726.6886	1725.6813	1725.6835	-0.0021	0	CCNELNEFENNQR	
124 - 130	935.4443	934.4370	934.4508	-0.0138	0	QQEQQFK	
124 - 131	1091.5557	1090.5484	1090.5519	-0.0035	1	QQEQQFKR	
135 - 143	1085.5485	1084.5412	1084.5447	-0.0035	0	NLPQQCGLR	

No match to: 825.1301, 839.1033, 842.5090, 845.1050, 855.0675, 856.5217, 858.5093, 861.0844, 864.5016, 867.0908, 870.5455, 877.0538, 893.0246, 932.4760, 987.5306, 992.5796, 1003.5778, 1045.5640, 1050.1104, 1066.0886, 1068.4918, 1072.1028, 1106.5396, 1194.5485, 1212.5347, 1281.6168, 1368.6132, 1455.7186, 1471.7466, 1566.7296, 1709.6637, 1753.9141, 1940.9344, 2211.1045, 2225.1206, 2233.1152, 2299.1702, 2633.1667, 2807.3115, 3337.7581, 3347.6826


Error (ppm)
0
-5
-10
-15
1000
1250
1500
1750
Mass (Da)
RMS error 5 ppm

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
3 - 22	2227.1470	2226.1397	2226.1215	0.0182	1	GKHHTLFNTHSITTTTTMAK
42 - 51	1315.6484	1314.6411	1314.6429	-0.0017	1	QQWELQGDRR
52 - 58	920.4376	919.4303	919.4181	0.0122	0	CQSQLER
59 - 71	1624.8003	1623.7930	1623.7973	-0.0043	0	ANLRPCEQHLMQK
59 - 71	1640.7925	1639.7852	1639.7922	-0.0070	0	ANLRPCEQHLMQK Oxidation (M)
99 - 109	1212.5620	1211.5547	1211.5755	-0.0208	1	RGAGSSQHQER
100 - 109	1056.4918	1055.4845	1055.4744	0.0101	0	GAGSSQHQER
110 - 122	1726.6787	1725.6714	1725.6835	-0.0120	0	CCNELNEFENNQR
123 - 142	2483.1008	2482.0935	2482.0821	0.0114	1	CMCEALQQIMENQSDRLQGR Oxidation (M)
143 - 150	1091.5657	1090.5584	1090.5519	0.0065	1	QQEQQFKR
154 - 162	1085.5618	1084.5545	1084.5447	0.0098	0	NLPQQCGLR
154 - 166	1537.7941	1536.7868	1536.7943	-0.0075	1	NLPQQCGLRAPQR

No match to: 805.4646, 825.1322, 845.1055, 855.0643, 861.0831, 877.0501, 903.4120, 918.4190, 919.4232, 1046.6017, 1074.5435, 1080.5256, 1090.5458, 1145.0708, 1145.5737, 1175.5419, 1219.5038, 1236.5472, 1277.7076, 1307.6488, 1323.6638, 1330.6636, 1368.6204, 1384.5973, 1454.3325, 1471.7443, 1475.7449, 1487.7389, 1578.7919, 1638.8394, 1688.7561, 1707.7417, 1709.6604, 1723.6670, 1725.6555, 1741.6763, 1745.6672, 1748.7354, 1774.8420, 1851.9121, 1993.9862, 2011.8627, 2145.0396, 2146.5845, 2162.0403, 2185.0393, 2216.9875, 2225.0107, 2273.1619, 2295.1458, 2305.1423, 2311.1467, 2327.1052, 2333.1335, 2343.1108, 2351.0889, 2450.0586, 2466.0950, 2468.1030, 2501.1794, 2514.3408, 2530.3474, 2613.1914, 2705.1780, 2755.3318, 2765.1943, 3136.4939, 3166.6365, 3211.5471, 3300.7600, 3316.7588

Spot 81

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:13:50 GMT
Top Score : 44 for gi|52001227, 2S protein 1 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|52001227	21293	44	2S protein 1 [Arachis hypogaea]
2.	gi|46560482	20907	35	seed storage protein SSP2 [Arachis hypogaea]
3.	gi|15418705	18612	34	allergen II [Arachis hypogaea]
4.	gi|28912768	19765	34	seed storage protein [Arachis hypogaea]
5.	gi|31322017	20212	33	allergen Ara h 2 isoform [Arachis hypogaea]
6.	gi|26245447	20558	32	allergen Ara h 2.02 [Arachis hypogaea]
7.	gi|46560480	22229	31	seed storage protein SSP1 [Arachis hypogaea]
8.	gi|118776566	19009	30	conglutin 7 [Arachis hypogaea]
9.	gi|14347293	24390	28	unnamed protein product [Arachis hypogaea]
10.	gi|230338	23975	19	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|52001227 **Mass:** 21293 **Score:** 44 **Expect:** 0.037 **Queries matched:** 7
2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5504	1084.5431	1084.5447	-0.0016	154	162	0	NLPQQCGLR
1091.5587	1090.5514	1090.5519	-0.0005	143	150	1	QQEQQFKR
1537.8015	1536.7942	1536.7943	-0.0001	154	166	1	NLPQQCGLRAPQR
1624.7969	1623.7896	1623.7973	-0.0077	59	71	0	ANLRPCEQHLMQK
1640.7822	1639.7749	1639.7922	-0.0173	59	71	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6849	1725.6776	1725.6835	-0.0058	110	122	0	CCNELNEFENNQR
2227.1243	2226.1170	2226.1215	-0.0045	3	22	1	GKHHTLFNTHSITTTTTMAK

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1046.6002, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166,

1471.7401, 1529.6873, 1551.6853, 1606.7468, 1618.7802, 1652.7566, 1675.7762, 1709.6637, 1756.8273, 1774.8267, 1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2273.1616, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2514.3389, 2530.3533, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837

2. gi|46560482 **Mass:** 20907 **Score:** 35 **Expect:** 0.27 **Queries matched:** 6

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5504	1084.5431	1084.5447	-0.0016	150	158	0	NLPQQCGLR
1091.5587	1090.5514	1090.5519	-0.0005	139	146	1	QQEQQFKR
1537.8015	1536.7942	1536.7943	-0.0001	150	162	1	NLPQQCGLRAPQR
1624.7969	1623.7896	1623.7973	-0.0077	55	67	0	ANLRPCEQHLMQK
1640.7822	1639.7749	1639.7922	-0.0173	55	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6849	1725.6776	1725.6835	-0.0058	106	118	0	CCNELNEFENNQR

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1046.6002, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166, 1471.7401, 1529.6873, 1551.6853, 1606.7468, 1618.7802, 1652.7566, 1675.7762, 1709.6637, 1756.8273, 1774.8267, 1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2227.1243, 2273.1616, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2514.3389, 2530.3533, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837

3. gi|15418705 **Mass:** 18612 **Score:** 34 **Expect:** 0.33 **Queries matched:** 6

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5504	1084.5431	1084.5447	-0.0016	135	143	0	NLPQQCGLR
1091.5587	1090.5514	1090.5519	-0.0005	124	131	1	QQEQQFKR
1537.8015	1536.7942	1536.7943	-0.0001	135	147	1	NLPQQCGLRAPQR
1624.7969	1623.7896	1623.7973	-0.0077	40	52	0	ANLRPCEQHLMQK
1640.7822	1639.7749	1639.7922	-0.0173	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6849	1725.6776	1725.6835	-0.0058	91	103	0	CCNELNEFENNQR

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1046.6002, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166, 1471.7401, 1529.6873, 1551.6853, 1606.7468, 1618.7802, 1652.7566, 1675.7762, 1709.6637, 1756.8273, 1774.8267, 1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2227.1243, 2273.1616, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2514.3389, 2530.3533, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837

4. gi|28912768 **Mass:** 19765 **Score:** 34 **Expect:** 0.36 **Queries matched:** 6

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5504	1084.5431	1084.5447	-0.0016	145	153	0	NLPQQCGLR

1091.5587	1090.5514	1090.5519	-0.0005	134 - 141	1	QQEQQFKR
1537.8015	1536.7942	1536.7943	-0.0001	145 - 157	1	NLPQQCGLRAPQR
1624.7969	1623.7896	1623.7973	-0.0077	38 - 50	0	ANLRPCEQHLMQK
1640.7822	1639.7749	1639.7922	-0.0173	38 - 50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6849	1725.6776	1725.6835	-0.0058	101 - 113	0	CCNELNEFENNQR

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1046.6002, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166, 1471.7401, 1529.6873, 1551.6853, 1606.7468, 1618.7802, 1652.7566, 1675.7762, 1709.6637, 1756.8273, 1774.8267, 1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2227.1243, 2273.1616, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2514.3389, 2530.3533, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837

5. gi|31322017 **Mass:** 20212 **Score:** 33 **Expect:** 0.43 **Queries matched:** 6

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
1085.5504	1084.5431	1084.5447	-0.0016	144 - 152	0	NLPQQCGLR
1091.5587	1090.5514	1090.5519	-0.0005	133 - 140	1	QQEQQFKR
1537.8015	1536.7942	1536.7943	-0.0001	144 - 156	1	NLPQQCGLRAPQR
1624.7969	1623.7896	1623.7973	-0.0077	37 - 49	0	ANLRPCEQHLMQK
1640.7822	1639.7749	1639.7922	-0.0173	37 - 49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6849	1725.6776	1725.6835	-0.0058	100 - 112	0	CCNELNEFENNQR

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1046.6002, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166, 1471.7401, 1529.6873, 1551.6853, 1606.7468, 1618.7802, 1652.7566, 1675.7762, 1709.6637, 1756.8273, 1774.8267, 1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2227.1243, 2273.1616, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2514.3389, 2530.3533, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837

6. gi|26245447 **Mass:** 20558 **Score:** 32 **Expect:** 0.62 **Queries matched:** 6

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
1085.5504	1084.5431	1084.5447	-0.0016	147 - 155	0	NLPQQCGLR
1091.5587	1090.5514	1090.5519	-0.0005	136 - 143	1	QQEQQFKR
1537.8015	1536.7942	1536.7943	-0.0001	147 - 159	1	NLPQQCGLRAPQR
1624.7969	1623.7896	1623.7973	-0.0077	40 - 52	0	ANLRPCEQHLMQK
1640.7822	1639.7749	1639.7922	-0.0173	40 - 52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6849	1725.6776	1725.6835	-0.0058	103 - 115	0	CCNELNEFENNQR

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1046.6002, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166, 1471.7401, 1529.6873, 1551.6853, 1606.7468, 1618.7802, 1652.7566, 1675.7762, 1709.6637, 1756.8273, 1774.8267,

1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2227.1243, 2273.1616, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2514.3389, 2530.3533, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837

7. gi|46560480 **Mass:** 22229 **Score:** 31 **Expect:** 0.66 **Queries matched:** 6

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5504	1084.5431	1084.5447	-0.0016	162	170	0	NLPQQCGLR
1091.5587	1090.5514	1090.5519	-0.0005	151	158	1	QQEQQFKR
1537.8015	1536.7942	1536.7943	-0.0001	162	174	1	NLPQQCGLRAPQR
1624.7969	1623.7896	1623.7973	-0.0077	55	67	0	ANLRPCEQHLMQK
1640.7822	1639.7749	1639.7922	-0.0173	55	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6849	1725.6776	1725.6835	-0.0058	118	130	0	CCNELNEFENNQR

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1046.6002, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166, 1471.7401, 1529.6873, 1551.6853, 1606.7468, 1618.7802, 1652.7566, 1675.7762, 1709.6637, 1756.8273, 1774.8267, 1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2227.1243, 2273.1616, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2514.3389, 2530.3533, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837

8. gi|118776566 **Mass:** 19009 **Score:** 30 **Expect:** 0.87 **Queries matched:** 6

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5504	1084.5431	1084.5447	-0.0016	133	141	0	NLPQQCGLR
1091.5587	1090.5514	1090.5519	-0.0005	122	129	1	QQEQQFKR
1537.8015	1536.7942	1536.7943	-0.0001	133	145	1	NLPQQCGLRAPQR
1624.7969	1623.7896	1623.7973	-0.0077	40	52	0	ANLRPCEQHLMQK
1640.7822	1639.7749	1639.7922	-0.0173	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6849	1725.6776	1725.6835	-0.0058	89	101	0	CCNELNEFENNQR

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1046.6002, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166, 1471.7401, 1529.6873, 1551.6853, 1606.7468, 1618.7802, 1652.7566, 1675.7762, 1709.6637, 1756.8273, 1774.8267, 1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2227.1243, 2273.1616, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2514.3389, 2530.3533, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837

9. gi|14347293 **Mass:** 24390 **Score:** 28 **Expect:** 1.3 **Queries matched:** 6

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5504	1084.5431	1084.5447	-0.0016	135	143	0	NLPQQCGLR
1091.5587	1090.5514	1090.5519	-0.0005	124	131	1	QQEQQFKR

1537.8015	1536.7942	1536.7943	-0.0001	135 - 147	1	NLPQQCGLRAPQR
1624.7969	1623.7896	1623.7973	-0.0077	40 - 52	0	ANLRPCEQHLMQK
1640.7822	1639.7749	1639.7922	-0.0173	40 - 52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6849	1725.6776	1725.6835	-0.0058	91 - 103	0	CCNELNEFENNQR

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1046.6002, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166, 1471.7401, 1529.6873, 1551.6853, 1606.7468, 1618.7802, 1652.7566, 1675.7762, 1709.6637, 1756.8273, 1774.8267, 1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2227.1243, 2273.1616, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2514.3389, 2530.3533, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837

10. gi|230338 **Mass:** 23975 **Score:** 19 **Expect:** 12 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.6002	1045.5929	1045.5880	0.0050	90 -	99	1	LKSAASLNSR
2273.1616	2272.1543	2272.1521	0.0022	70 -	89	0	SIVHPSYNSNTLNNDIMLIK
2514.3389	2513.3316	2513.3311	0.0005	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK
2530.3533	2529.3460	2529.3260	0.0200	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1085.5504, 1091.5587, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166, 1471.7401, 1529.6873, 1537.8015, 1551.6853, 1606.7468, 1618.7802, 1624.7969, 1640.7822, 1652.7566, 1675.7762, 1709.6637, 1726.6849, 1756.8273, 1774.8267, 1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2227.1243, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 73

Protein View

Match to: **gi|52001227** Score: **44** Expect: **0.037**
2S protein 1 [Arachis hypogaea]

Nominal mass (M_r): **21293**; Calculated pI value: **7.14**
NCBI BLAST search of gi|52001227 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **73**
Number of mass values matched: **7**
Sequence Coverage: **37%**

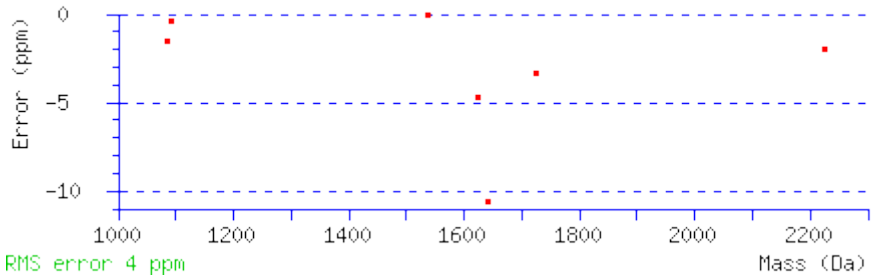
Matched peptides shown in **Bold Red**

```
     1 GR[GKHHTLFN THSITTTTTM AK]LTILVALA LFLLAAHASA RQQWELQGDR
    51 RCQSQLER[AN LRPCEQHLMQ K]IQRDEDSYE RDPYSPSQDP YSPSPYDRRG
   101 AGSSQHQER[C CNELNEFENN QR]CMCEALQQ IMENQSDRLQ GR[QQEQQFKR
   151 ELR[NLPQQCG LRAPQR]CDLD VESGGRDRY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
3 - 22	2227.1243	2226.1170	2226.1215	-0.0045	1	GKHHTLFNTHSITTTTTMAK	
59 - 71	1624.7969	1623.7896	1623.7973	-0.0077	0	ANLRPCEQHLMQK	
59 - 71	1640.7822	1639.7749	1639.7922	-0.0173	0	ANLRPCEQHLMQK	Oxidation (M)
110 - 122	1726.6849	1725.6776	1725.6835	-0.0058	0	CCNELNEFENNQR	
143 - 150	1091.5587	1090.5514	1090.5519	-0.0005	1	QQEQQFKR	
154 - 162	1085.5504	1084.5431	1084.5447	-0.0016	0	NLPQQCGLR	
154 - 166	1537.8015	1536.7942	1536.7943	-0.0001	1	NLPQQCGLRAPQR	

No match to: 805.4598, 827.4130, 839.1026, 845.1277, 848.4460, 854.0636, 855.0664, 861.0805, 867.3599, 877.0461, 1023.5054, 1046.6002, 1066.0782, 1074.5414, 1080.5356, 1082.5247, 1111.5498, 1137.0889, 1137.5789, 1145.0764, 1145.5760, 1175.5603, 1208.5333, 1215.4991, 1217.5388, 1277.1033, 1308.6685, 1319.4391, 1406.6914, 1444.7166, 1471.7401, 1529.6873, 1551.6853, 1606.7468, 1618.7802, 1652.7566, 1675.7762, 1709.6637, 1756.8273, 1774.8267, 1786.8364, 1850.8970, 1918.8501, 1933.8737, 2145.0486, 2146.5928, 2185.0322, 2201.0088, 2207.0344, 2225.0010, 2273.1616, 2295.1475, 2305.1567, 2311.1394, 2333.1455, 2335.1052, 2351.0906, 2354.0981, 2514.3389, 2530.3533, 2612.1948, 3136.4709, 3166.5239, 3211.5334, 3300.7698, 3316.7837


0
-5
-10
Error (ppm)
1000
1200
1400
1600
1800
2000
2200
Mass (Da)
RMS error 4 ppm

Spot 82

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:45:25 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **146 for gi|52001225, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|52001225	76343	146	conarachin [Arachis hypogaea]
2.	gi|544005	4754	15	Endochitinase 1A (CHIT 1A)
3.	gi|544009	4726	15	Endochitinase 1B (CHIT 1B)
4.	gi|288485	4783	15	chitinase [Arachis hypogaea]
5.	gi|288481	4811	15	chitinase [Arachis hypogaea]
6.	gi|55736075	9680	12	auxin-induced putative aldo/keto reductase family protein [Arachis hypogaea]
7.	gi|62361235	16047	11	resistance protein PLTR [Arachis hypogaea]
8.	gi|62361283	19749	11	resistance protein PLTR [Arachis hypogaea]
9.	gi|62361213	19843	11	resistance protein PLTR [Arachis hypogaea]
10.	gi|52001227	21293	10	2S protein 1 [Arachis hypogaea]

Results List

1. gi|52001225 **Mass:** 76343 **Score:** 146 **Expect:** 2.2e-012 **Queries matched:** 6
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1081.4893	1080.4820	1080.4988	-0.0168	470	479	0	---	ADFYNPAAGR
1081.4893	1080.4820	1080.4988	-0.0168	470	479	0	40	ADFYNPAAGR
1418.7817	1417.7744	1417.7929	-0.0184	480	492	0	28	ISSANSLTFPILR
1418.7817	1417.7744	1417.7929	-0.0184	480	492	0	---	ISSANSLTFPILR
1814.9607	1813.9534	1813.9798	-0.0263	530	546	0	---	IQVVNSQGNAVFNGVLR
1814.9607	1813.9534	1813.9798	-0.0263	530	546	0	57	IQVVNSQGNAVFNGVLR

No match to: 982.5593, 1151.7026, 1434.8820, 1455.8099, 1455.8099, 1665.8510, 1796.9578, 2229.0889, 2229.0889, 2242.0342, 2243.0134, 2909.3962

2. gi|544005 **Mass:** 4754 **Score:** 15 **Expect:** 26 **Queries matched:** 2

Endochitinase 1A (CHIT 1A)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1814.9607	1813.9534	1813.8740	0.0794	1 -	17	0	---	MTAQGNKPSSHDVITGR + Oxidation (M)
1814.9607	1813.9534	1813.8740	0.0794	1 -	17	0	---	MTAQGNKPSSHDVITGR + Oxidation (M)

No match to: 982.5593, 1081.4893, 1081.4893, 1151.7026, 1418.7817, 1418.7817, 1434.8820, 1455.8099, 1455.8099, 1665.8510, 1796.9578, 2229.0889, 2229.0889, 2242.0342, 2243.0134, 2909.3962

3. gi|544009 **Mass:** 4726 **Score:** 15 **Expect:** 26 **Queries matched:** 2

Endochitinase 1B (CHIT 1B)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1814.9607	1813.9534	1813.8740	0.0794	1 -	17	0	---	MTAQGNKPSSHDVITGR + Oxidation (M)
1814.9607	1813.9534	1813.8740	0.0794	1 -	17	0	---	MTAQGNKPSSHDVITGR + Oxidation (M)

No match to: 982.5593, 1081.4893, 1081.4893, 1151.7026, 1418.7817, 1418.7817, 1434.8820, 1455.8099, 1455.8099, 1665.8510, 1796.9578, 2229.0889, 2229.0889, 2242.0342, 2243.0134, 2909.3962

4. gi|288485 **Mass:** 4783 **Score:** 15 **Expect:** 26 **Queries matched:** 2

chitinase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1814.9607	1813.9534	1813.8740	0.0794	1 -	17	0	---	MTAQGNKPSSHDVITGR + Oxidation (M)
1814.9607	1813.9534	1813.8740	0.0794	1 -	17	0	---	MTAQGNKPSSHDVITGR + Oxidation (M)

No match to: 982.5593, 1081.4893, 1081.4893, 1151.7026, 1418.7817, 1418.7817, 1434.8820, 1455.8099, 1455.8099, 1665.8510, 1796.9578, 2229.0889, 2229.0889, 2242.0342, 2243.0134, 2909.3962

5. gi|288481 **Mass:** 4811 **Score:** 15 **Expect:** 26 **Queries matched:** 2

chitinase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1814.9607	1813.9534	1813.8740	0.0794	1 -	17	0	---	MTAQGNKPSSHDVITGR + Oxidation (M)
1814.9607	1813.9534	1813.8740	0.0794	1 -	17	0	---	MTAQGNKPSSHDVITGR + Oxidation (M)

No match to: 982.5593, 1081.4893, 1081.4893, 1151.7026, 1418.7817, 1418.7817, 1434.8820, 1455.8099, 1455.8099, 1665.8510, 1796.9578, 2229.0889, 2229.0889, 2242.0342, 2243.0134, 2909.3962

6. gi|55736075 **Mass:** 9680 **Score:** 12 **Expect:** 61 **Queries matched:** 2

auxin-induced putative aldo/keto reductase family protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8099	1454.8026	1454.7054	0.0972	64 -	75	1	---	HFNETHGKATWK
1455.8099	1454.8026	1454.7054	0.0972	64 -	75	1	---	HFNETHGKATWK

No match to: 982.5593, 1081.4893, 1081.4893, 1151.7026, 1418.7817, 1418.7817, 1434.8820, 1665.8510, 1796.9578, 1814.9607, 1814.9607, 2229.0889, 2229.0889, 2242.0342, 2243.0134, 2909.3962

7. gi|62361235 **Mass:** 16047 **Score:** 11 **Expect:** 65 **Queries matched:** 2

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2229.0889	2228.0816	2228.1411	-0.0595	95	114	1	---	MIAGGLDWFGYGSRVIITTR + Oxidation (M)
2229.0889	2228.0816	2228.1411	-0.0595	95	114	1	---	MIAGGLDWFGYGSRVIITTR + Oxidation (M)

No match to: 982.5593, 1081.4893, 1081.4893, 1151.7026, 1418.7817, 1418.7817, 1434.8820, 1455.8099, 1455.8099, 1665.8510, 1796.9578, 1814.9607, 1814.9607, 2242.0342, 2243.0134, 2909.3962

8. gi|62361283 **Mass:** 19749 **Score:** 11 **Expect:** 78 **Queries matched:** 2

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2229.0889	2228.0816	2228.1411	-0.0595	93	112	1	---	MIAGGLDWFGYGSRVIITTR + Oxidation (M)
2229.0889	2228.0816	2228.1411	-0.0595	93	112	1	---	MIAGGLDWFGYGSRVIITTR + Oxidation (M)

No match to: 982.5593, 1081.4893, 1081.4893, 1151.7026, 1418.7817, 1418.7817, 1434.8820, 1455.8099, 1455.8099, 1665.8510, 1796.9578, 1814.9607, 1814.9607, 2242.0342, 2243.0134, 2909.3962

9. gi|62361213 **Mass:** 19843 **Score:** 11 **Expect:** 78 **Queries matched:** 2

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2229.0889	2228.0816	2228.1411	-0.0595	93	112	1	---	MIAGGLDWFGYGSRVIITTR + Oxidation (M)
2229.0889	2228.0816	2228.1411	-0.0595	93	112	1	---	MIAGGLDWFGYGSRVIITTR + Oxidation (M)

No match to: 982.5593, 1081.4893, 1081.4893, 1151.7026, 1418.7817, 1418.7817, 1434.8820, 1455.8099, 1455.8099, 1665.8510, 1796.9578, 1814.9607, 1814.9607, 2242.0342, 2243.0134, 2909.3962

10. gi|52001227 **Mass:** 21293 **Score:** 10 **Expect:** 84 **Queries matched:** 1

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2243.0134	2242.0061	2242.1164	-0.1103	3	22	1	---	GKHHTLFNTHSITTTTTMAK + Oxidation (M)

No match to: 982.5593, 1081.4893, 1081.4893, 1151.7026, 1418.7817, 1418.7817, 1434.8820, 1455.8099, 1455.8099, 1665.8510, 1796.9578, 1814.9607, 1814.9607, 2229.0889, 2229.0889, 2242.0342, 2909.3962

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Number of Queries: 18

Protein View

Match to: **gi|52001225** Score: **146** Expect: **2.2e-012**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **76343**; Calculated pI value: **5.23**
NCBI BLAST search of gi|52001225 against nr
Unformatted sequence string for pasting into other applications

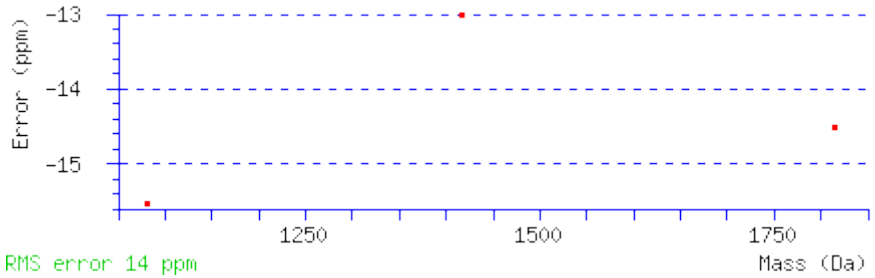
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **6%**

Matched peptides shown in **Bold Red**

```
    1 MVIGPFRLSL CVCLVFLTSA CFGTRLEESF NECQLDRLNA LTPDNRIESQ
   51 GGITETWNSN HPELRCAGVT LLKRTIFPNG FHLPSYANYP QLIFIAQGNG
  101 VFGVSLPGCP VTYEEAESQS REDRRQRIVI KRESEQEQEQ QGDSHHKIYH
  151 FRQGHLLAIP AGVPYWSFNY GNEPIVAITL LDTSNLDNQL DPSPRRFYLA
  201 GNPEEEHPET QQQQPQTRRR HGQHQQDEYG SQGEEEGNNV LSGFSTQLLA
  251 HAFGVDEEIA RILQNPPEQT KDQIVRVEGG FRDVISPRWG EGKQYEDELE
  301 ERQRQPPRRD EQGKGYDYDD DRRPRHRQDP YREGDEDDRR PRGSRQGQGR
  351 GYDDDDRRPG QYEEGEEDDR RPRRSSRPKR QGRRHDDDDR RADEDDRRGY
  401 DDDERRPDED DRRGYDDDER RPDDDDRQGY DDDDRRPRWS SRPKGQGRNG
  451 VEETLCSPTL VEDIARPSRA DFYNPAAGRI SSANSLTFPI LRWFQLSAEH
  501 VLLYRNGIYS PHWNNNANSI IYGLRGEGRI QVVNSQGNAV FNGVLREGQI
  551 LLVPQNFAVG KQAGNEGFEY VAFKTADRAS PATSSKCLGE SPLMFSSMLL
  601 AFEIIKSVLS NTMETRPLWS LLMIPSMGLN VVINLNHNNN AQVDSKNNDG
  651 SRLWWPSSII IK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
470 - 479	1081.4893	1080.4820	1080.4988	-0.0168	0	**ADFYNPAAGR**	(No match)
470 - 479	1081.4893	1080.4820	1080.4988	-0.0168	0	**ADFYNPAAGR**	(Ions score 40)
480 - 492	1418.7817	1417.7744	1417.7929	-0.0184	0	**ISSANSLTFPILR**	(Ions score 28)
480 - 492	1418.7817	1417.7744	1417.7929	-0.0184	0	**ISSANSLTFPILR**	(No match)
530 - 546	1814.9607	1813.9534	1813.9798	-0.0263	0	**IQVVNSQGNAVFNGVLR**	(No match)
530 - 546	1814.9607	1813.9534	1813.9798	-0.0263	0	**IQVVNSQGNAVFNGVLR**	(Ions score 57)


-13
-14
-15
Error (ppm)
1250
1500
1750
Mass (Da)
RMS error 14 ppm

Spot 83

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:45:12 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **315 for gi|52001225, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|52001225	76343	315	conarachin [Arachis hypogaea]
2.	gi|62361199	19790	21	resistance protein PLTR [Arachis hypogaea]
3.	gi|71040673	14892	20	ubiquitin fusion protein [Arachis hypogaea]
4.	gi|6093763	353436	19	Genome polyprotein [Contains: P1 proteinase (N-terminal protein); Helper component proteinase (
5.	gi|62361291	19935	19	resistance protein PLTR [Arachis hypogaea]
6.	gi|57639276	27048	18	putative root-knot resistance protein [Arachis hypogaea]
7.	gi|11095605	22519	17	coat protein [Groundnut rosette assistor virus]
8.	gi|11095601	22487	17	coat protein [Groundnut rosette assistor virus]
9.	gi|11095597	22512	17	coat protein [Groundnut rosette assistor virus]
10.	gi|11095593	22457	17	coat protein [Groundnut rosette assistor virus]

Results List

1. gi|52001225 **Mass:** 76343 **Score:** 315 **Expect:** 2.8e-029 **Queries matched:** 9
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1081.4954	1080.4881	1080.4988	-0.0107	470	479	0	---	ADFYNPAAGR
1081.4954	1080.4881	1080.4988	-0.0107	470	479	0	75	ADFYNPAAGR
1418.7866	1417.7793	1417.7929	-0.0135	480	492	0	---	ISSANSLTFPILR
1418.7866	1417.7793	1417.7929	-0.0135	480	492	0	81	ISSANSLTFPILR
1459.6683	1458.6610	1458.6778	-0.0168	562	574	0	---	QAGNEGFEYVAFK
1612.8901	1611.8828	1611.8983	-0.0155	547	561	0	---	EGQILLVPQNFAVGK
1661.8689	1660.8616	1660.8725	-0.0109	493	505	0	---	WFQLSAEHVLLYR
1814.9736	1813.9663	1813.9798	-0.0134	530	546	0	---	IQVVNSQGNAVFNGVLR

1814.9736	1813.9663	1813.9798	-0.0134	530 - 546	0	111	IQVVNSQGNAVFNGVLR

No match to: 1151.7109, 1442.6455, 1455.8188, 1455.8188, 1665.8604, 1677.8613, 1796.9624, 1888.9202, 2229.1028, 2242.0361, 2242.0361, 2308.1055, 2398.1450, 3409.8501

2. gi|62361199 **Mass:** 19790 **Score:** 21 **Expect:** 7.3 **Queries matched:** 2

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1888.9202	1887.9129	1887.9114	0.0015	89 -	105	0	---	LLENLAGEQDWFGPGSR
2308.1055	2307.0982	2307.1633	-0.0651	143 -	163	1	---	AFKQAAEPTEGFLDLSEEVVK

No match to: 1081.4954, 1081.4954, 1151.7109, 1418.7866, 1418.7866, 1442.6455, 1455.8188, 1455.8188, 1459.6683, 1612.8901, 1661.8689, 1665.8604, 1677.8613, 1796.9624, 1814.9736, 1814.9736, 2229.1028, 2242.0361, 2242.0361, 2398.1450, 3409.8501

3. gi|71040673 **Mass:** 14892 **Score:** 20 **Expect:** 8.4 **Queries matched:** 3

ubiquitin fusion protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8188	1454.8115	1454.8278	-0.0163	75 -	88	1	---	GGIIEPSLMALARK
1455.8188	1454.8115	1454.8278	-0.0163	75 -	88	1	---	GGIIEPSLMALARK
1612.8901	1611.8828	1611.9130	-0.0301	73 -	87	1	---	LRGGIIEPSLMALAR + Oxidation (M)

No match to: 1081.4954, 1081.4954, 1151.7109, 1418.7866, 1418.7866, 1442.6455, 1459.6683, 1661.8689, 1665.8604, 1677.8613, 1796.9624, 1814.9736, 1814.9736, 1888.9202, 2229.1028, 2242.0361, 2242.0361, 2308.1055, 2398.1450, 3409.8501

4. gi|6093763 **Mass:** 353436 **Score:** 19 **Expect:** 10 **Queries matched:** 6

Genome polyprotein [Contains: P1 proteinase (N-terminal protein); Helper component proteinase (HC-p

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1661.8689	1660.8616	1660.9148	-0.0531	2489 -	2504	1	---	TRTFTAAPIDTLLGGK
1796.9624	1795.9551	1795.9541	0.0010	1140 -	1155	0	---	VVAYLALIAMIFDGER + Oxidation (M)
1814.9736	1813.9663	1813.9832	-0.0169	443 -	457	1	---	LLQNLNQTQARQLMK + Oxidation (M)
1814.9736	1813.9663	1813.9832	-0.0169	443 -	457	1	7	LLQNLNQTQARQLMK + Oxidation (M)
1888.9202	1887.9129	1887.8528	0.0601	196 -	211	1	---	ICSADCKQVEFISMGK + Oxidation (M)
3409.8501	3408.8428	3408.6758	0.1670	1942 -	1971	1	---	FVDPLTGYAIDENITCDISLVQDEVAEVRK

No match to: 1081.4954, 1081.4954, 1151.7109, 1418.7866, 1418.7866, 1442.6455, 1455.8188, 1455.8188, 1459.6683, 1612.8901, 1665.8604, 1677.8613, 2229.1028, 2242.0361, 2242.0361, 2308.1055, 2398.1450

5. gi|62361291 **Mass:** 19935 **Score:** 19 **Expect:** 10 **Queries matched:** 2

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1459.6683	1458.6610	1458.7606	-0.0995	146 -	158	0	---	LPEPTEGFLDLTK
1796.9624	1795.9551	1795.9507	0.0044	159 -	175	1	---	EVVNYSGGFPFALKVLG

No match to: 1081.4954, 1081.4954, 1151.7109, 1418.7866, 1418.7866, 1442.6455, 1455.8188, 1455.8188, 1612.8901, 1661.8689, 1665.8604, 1677.8613, 1814.9736, 1814.9736, 1888.9202, 2229.1028, 2242.0361, 2242.0361, 2308.1055, 2398.1450, 3409.8501

6. gi|57639276 **Mass:** 27048 **Score:** 18 **Expect:** 15 **Queries matched:** 2

putative root-knot resistance protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1677.8613	1676.8540	1676.8872	-0.0332	2 -	16	0	---	IPELEETPPTEPVVK
2229.1028	2228.0955	2227.9967	0.0988	106 -	124	0	---	EETTQEEPAEPEQEQEVVK

No match to: 1081.4954, 1081.4954, 1151.7109, 1418.7866, 1418.7866, 1442.6455, 1455.8188, 1455.8188, 1459.6683, 1612.8901, 1661.8689, 1665.8604, 1796.9624, 1814.9736, 1814.9736, 1888.9202, 2242.0361, 2242.0361, 2308.1055, 2398.1450, 3409.8501

7. gi|11095605 **Mass:** 22519 **Score:** 17 **Expect:** 18 **Queries matched:** 3

coat protein [Groundnut rosette assistor virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8188	1454.8115	1454.7888	0.0228	1 -	13	1	---	MNTVVVRRPGNGR
1455.8188	1454.8115	1454.7888	0.0228	1 -	13	1	---	MNTVVVRRPGNGR
1612.8901	1611.8828	1611.8368	0.0460	177 -	192	1	---	GNGSSAIAGSFRFTIK

No match to: 1081.4954, 1081.4954, 1151.7109, 1418.7866, 1418.7866, 1442.6455, 1459.6683, 1661.8689, 1665.8604, 1677.8613, 1796.9624, 1814.9736, 1814.9736, 1888.9202, 2229.1028, 2242.0361, 2242.0361, 2308.1055, 2398.1450, 3409.8501

8. gi|11095601 **Mass:** 22487 **Score:** 17 **Expect:** 18 **Queries matched:** 3

coat protein [Groundnut rosette assistor virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8188	1454.8115	1454.7888	0.0228	1 -	13	1	---	MNTVVVRRPGNGR
1455.8188	1454.8115	1454.7888	0.0228	1 -	13	1	---	MNTVVVRRPGNGR
1612.8901	1611.8828	1611.8368	0.0460	177 -	192	1	---	GNGSSAIAGSFRFTIK

No match to: 1081.4954, 1081.4954, 1151.7109, 1418.7866, 1418.7866, 1442.6455, 1459.6683, 1661.8689, 1665.8604, 1677.8613, 1796.9624, 1814.9736, 1814.9736, 1888.9202, 2229.1028, 2242.0361, 2242.0361, 2308.1055, 2398.1450, 3409.8501

9. gi|11095597 **Mass:** 22512 **Score:** 17 **Expect:** 18 **Queries matched:** 3

coat protein [Groundnut rosette assistor virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8188	1454.8115	1454.7888	0.0228	1 -	13	1	---	MNTVVVRRPGNGR
1455.8188	1454.8115	1454.7888	0.0228	1 -	13	1	---	MNTVVVRRPGNGR
1612.8901	1611.8828	1611.8368	0.0460	177 -	192	1	---	GNGSSAIAGSFRFTIK

No match to: 1081.4954, 1081.4954, 1151.7109, 1418.7866, 1418.7866, 1442.6455, 1459.6683, 1661.8689, 1665.8604, 1677.8613, 1796.9624, 1814.9736, 1814.9736, 1888.9202, 2229.1028, 2242.0361, 2242.0361, 2308.1055, 2398.1450, 3409.8501

10. gi|11095593 **Mass:** 22457 **Score:** 17 **Expect:** 18 **Queries matched:** 3

coat protein [Groundnut rosette assistor virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8188	1454.8115	1454.7888	0.0228	1 -	13	1	---	MNTVVVRRPGNGR
1455.8188	1454.8115	1454.7888	0.0228	1 -	13	1	---	MNTVVVRRPGNGR

1612.8901 1611.8828 1611.8368 0.0460 177 - 192 1 --- GNGSSAIAGSFRFTIK

No match to: 1081.4954, 1081.4954, 1151.7109, 1418.7866, 1418.7866, 1442.6455, 1459.6683, 1661.8689, 1665.8604, 1677.8613, 1796.9624, 1814.9736, 1814.9736, 1888.9202, 2229.1028, 2242.0361, 2242.0361, 2308.1055, 2398.1450, 3409.8501

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1

Protein View

Match to: **gi|52001225** Score: **315** Expect: **2.8e-029**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **76343**; Calculated pI value: **5.23**
NCBI BLAST search of gi|52001225 against nr
Unformatted sequence string for pasting into other applications

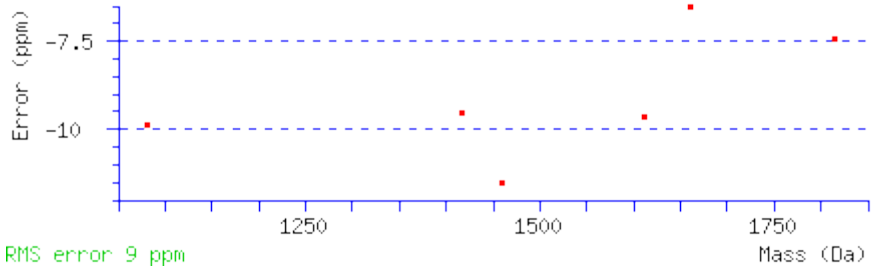
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

```
   1 MVIGPFRLSL CVCLVFLTSA CFGTRLEESF NECQLDRLNA LTPDNRIESQ
  51 GGITETWNSN HPELRCAGVT LLKRTIFPNG FHLPSYANYP QLIFIAQGNG
 101 VFGVSLPGCP VTYEEAESQS REDRRQRIVI KRESEQEQEQ QGDSHHKIYH
 151 FRQGHLLAIP AGVPYWSFNY GNEPIVAITL LDTSNLDNQL DPSPRRFYLA
 201 GNPEEEHPET QQQQPQTRRR HGQHQQDEYG SQGEEEGNNV LSGFSTQLLA
 251 HAFGVDEEIA RILQNPPEQT KDQIVRVEGG FRDVISPRWG EGKQYEDELE
 301 ERQRQPPRRD EQGKGYDYDD DRRPRHRQDP YREGDEDDRR PRGSRQGQGR
 351 GYDDDDRRPG QYEEGEEDDR RPRRSSRPKR QGRRHDDDDR RADEDDRRGY
 401 DDDERRPDED DRRGYDDDER RPDDDDRQGY DDDDRRPRWS SRPKGQGRNG
 451 VEETLCSPTL VEDIARPSRA DFYNPAAGRI SSANSLTFPI LRWFQLSAEH
 501 VLLYRNGIYS PHWNNNANSI IYGLRGEGRI QVVNSQGNAV FNGVLREGQI
 551 LLVPQNFAVG KQAGNEGFEY VAFKTADRAS PATSSKCLGE SPLMFSSMLL
 601 AFEIIKSVLS NTMETRPLWS LLMIPSMGLN VVINLNHNNN AQVDSKNNDG
 651 SRLWWPSSII IK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
470 - 479	1081.4954	1080.4881	1080.4988	-0.0107	0	ADFYNPAAGR	(No match)
470 - 479	1081.4954	1080.4881	1080.4988	-0.0107	0	ADFYNPAAGR	(Ions score 75)
480 - 492	1418.7866	1417.7793	1417.7929	-0.0135	0	ISSANSLTFPILR	(No match)
480 - 492	1418.7866	1417.7793	1417.7929	-0.0135	0	ISSANSLTFPILR	(Ions score 81)
493 - 505	1661.8689	1660.8616	1660.8725	-0.0109	0	WFQLSAEHVLLYR	(No match)
530 - 546	1814.9736	1813.9663	1813.9798	-0.0134	0	IQVVNSQGNAVFNGVLR	(No match)
530 - 546	1814.9736	1813.9663	1813.9798	-0.0134	0	IQVVNSQGNAVFNGVLR	(Ions score 111)
547 - 561	1612.8901	1611.8828	1611.8983	-0.0155	0	EGQILLVPQNFAVGK	(No match)
562 - 574	1459.6683	1458.6610	1458.6778	-0.0168	0	QAGNEGFEYVAFK	(No match)



Spot 84

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:44:59 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **303 for gi|52001225, conarachin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|52001225	76343	303	conarachin [Arachis hypogaea]
2.	gi|6093763	353436	23	Genome polyprotein [Contains: P1 proteinase (N-terminal protein); Helper component proteinase (
3.	gi|62361199	19790	20	resistance protein PLTR [Arachis hypogaea]
4.	gi|71040673	14892	19	ubiquitin fusion protein [Arachis hypogaea]
5.	gi|62361291	19935	18	resistance protein PLTR [Arachis hypogaea]
6.	gi|57639276	27048	16	putative root-knot resistance protein [Arachis hypogaea]
7.	gi|11095605	22519	16	coat protein [Groundnut rosette assistor virus]
8.	gi|11095601	22487	16	coat protein [Groundnut rosette assistor virus]
9.	gi|11095597	22512	16	coat protein [Groundnut rosette assistor virus]
10.	gi|11095593	22457	16	coat protein [Groundnut rosette assistor virus]

Results List

1. gi|52001225 **Mass:** 76343 **Score:** 303 **Expect:** 4.4e-028 **Queries matched:** 9
conarachin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1081.4969	1080.4896	1080.4988	-0.0092	470	479	0	---	ADFYNPAAGR
1081.4969	1080.4896	1080.4988	-0.0092	470	479	0	73	ADFYNPAAGR
1418.7865	1417.7792	1417.7929	-0.0136	480	492	0	---	ISSANSLTFPILR
1418.7865	1417.7792	1417.7929	-0.0136	480	492	0	62	ISSANSLTFPILR
1459.6681	1458.6608	1458.6778	-0.0170	562	574	0	---	QAGNEGFEYVAFK
1612.8899	1611.8826	1611.8983	-0.0157	547	561	0	---	EGQILLVPQNFAVGK
1661.8640	1660.8567	1660.8725	-0.0158	493	505	0	---	WFQLSAEHVLLYR

1814.9678	1813.9605	1813.9798	-0.0192	530 - 546	0	---	IQVVNSQGNAVFNGVLR
1814.9678	1813.9605	1813.9798	-0.0192	530 - 546	0	125	IQVVNSQGNAVFNGVLR

No match to: 886.9793, 1151.7120, 1442.6407, 1455.8171, 1455.8171, 1665.8569, 1677.8583, 1693.8557, 1796.9583, 1888.9125, 2229.0977, 2242.0259, 2242.0259, 2304.1011, 2307.0977, 2308.0981, 2398.1318, 3409.8184

2. gi|6093763 **Mass:** 353436 **Score:** 23 **Expect:** 4.3 **Queries matched:** 6

Genome polyprotein [Contains: P1 proteinase (N-terminal protein); Helper component proteinase (HC-p

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1661.8640	1660.8567	1660.9148	-0.0580	2489 -	2504	1	---	TRTFTAAPIDTLLGGK
1796.9583	1795.9510	1795.9541	-0.0031	1140 -	1155	0	---	VVAYLALIAMIFDGER + Oxidation (M)
1814.9678	1813.9605	1813.9832	-0.0227	443 -	457	1	---	LLQNLNQTQARQLMK + Oxidation (M)
1814.9678	1813.9605	1813.9832	-0.0227	443 -	457	1	12	LLQNLNQTQARQLMK + Oxidation (M)
1888.9125	1887.9052	1887.8528	0.0524	196 -	211	1	---	ICSADCKQVEFISMGK + Oxidation (M)
3409.8184	3408.8111	3408.6758	0.1353	1942 -	1971	1	---	FVDPLTGYAIDENITCDISLVQDEVAEVRK

No match to: 886.9793, 1081.4969, 1081.4969, 1151.7120, 1418.7865, 1418.7865, 1442.6407, 1455.8171, 1455.8171, 1459.6681, 1612.8899, 1665.8569, 1677.8583, 1693.8557, 2229.0977, 2242.0259, 2242.0259, 2304.1011, 2307.0977, 2308.0981, 2398.1318

3. gi|62361199 **Mass:** 19790 **Score:** 20 **Expect:** 9.8 **Queries matched:** 2

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1888.9125	1887.9052	1887.9114	-0.0062	89 -	105	0	---	LLENLAGEQDWFGPGSR
2308.0981	2307.0908	2307.1633	-0.0725	143 -	163	1	---	AFKQAAEPTEGFLDLSEEVVK

No match to: 886.9793, 1081.4969, 1081.4969, 1151.7120, 1418.7865, 1418.7865, 1442.6407, 1455.8171, 1455.8171, 1459.6681, 1612.8899, 1661.8640, 1665.8569, 1677.8583, 1693.8557, 1796.9583, 1814.9678, 1814.9678, 2229.0977, 2242.0259, 2242.0259, 2304.1011, 2307.0977, 2398.1318, 3409.8184

4. gi|71040673 **Mass:** 14892 **Score:** 19 **Expect:** 12 **Queries matched:** 3

ubiquitin fusion protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8171	1454.8098	1454.8278	-0.0180	75 -	88	1	---	GGIIEPSLMALARK
1455.8171	1454.8098	1454.8278	-0.0180	75 -	88	1	---	GGIIEPSLMALARK
1612.8899	1611.8826	1611.9130	-0.0303	73 -	87	1	---	LRGGIIEPSLMALAR + Oxidation (M)

No match to: 886.9793, 1081.4969, 1081.4969, 1151.7120, 1418.7865, 1418.7865, 1442.6407, 1459.6681, 1661.8640,

1665.8569, 1677.8583, 1693.8557, 1796.9583, 1814.9678, 1814.9678, 1888.9125, 2229.0977, 2242.0259, 2242.0259, 2304.1011, 2307.0977, 2308.0981, 2398.1318, 3409.8184

5. gi|62361291 **Mass:** 19935 **Score:** 18 **Expect:** 14 **Queries matched:** 2

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1459.6681	1458.6608	1458.7606	-0.0997	146	158	0	---	LPEPTEGFLDLTK
1796.9583	1795.9510	1795.9507	0.0003	159	175	1	---	EVVNYSGGFPFALKVLG

No match to: 886.9793, 1081.4969, 1081.4969, 1151.7120, 1418.7865, 1418.7865, 1442.6407, 1455.8171, 1455.8171, 1612.8899, 1661.8640, 1665.8569, 1677.8583, 1693.8557, 1814.9678, 1814.9678, 1888.9125, 2229.0977, 2242.0259, 2242.0259, 2304.1011, 2307.0977, 2308.0981, 2398.1318, 3409.8184

6. gi|57639276 **Mass:** 27048 **Score:** 16 **Expect:** 20 **Queries matched:** 2

putative root-knot resistance protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1677.8583	1676.8510	1676.8872	-0.0362	2	16	0	---	IPELEETPPTEPVVK
2229.0977	2228.0904	2227.9967	0.0937	106	124	0	---	EETTQEEPAEPEQEQEVVK

No match to: 886.9793, 1081.4969, 1081.4969, 1151.7120, 1418.7865, 1418.7865, 1442.6407, 1455.8171, 1455.8171, 1459.6681, 1612.8899, 1661.8640, 1665.8569, 1693.8557, 1796.9583, 1814.9678, 1814.9678, 1888.9125, 2242.0259, 2242.0259, 2304.1011, 2307.0977, 2308.0981, 2398.1318, 3409.8184

7. gi|11095605 **Mass:** 22519 **Score:** 16 **Expect:** 24 **Queries matched:** 3

coat protein [Groundnut rosette assistor virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8171	1454.8098	1454.7888	0.0211	1	13	1	---	MNTVVVRRPGNGR
1455.8171	1454.8098	1454.7888	0.0211	1	13	1	---	MNTVVVRRPGNGR
1612.8899	1611.8826	1611.8368	0.0458	177	192	1	---	GNGSSAIAGSFRFTIK

No match to: 886.9793, 1081.4969, 1081.4969, 1151.7120, 1418.7865, 1418.7865, 1442.6407, 1459.6681, 1661.8640, 1665.8569, 1677.8583, 1693.8557, 1796.9583, 1814.9678, 1814.9678, 1888.9125, 2229.0977, 2242.0259, 2242.0259, 2304.1011, 2307.0977, 2308.0981, 2398.1318, 3409.8184

8. gi|11095601 **Mass:** 22487 **Score:** 16 **Expect:** 24 **Queries matched:** 3

coat protein [Groundnut rosette assistor virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8171	1454.8098	1454.7888	0.0211	1	13	1	---	MNTVVVRRPGNGR

1455.8171	1454.8098	1454.7888	0.0211	1 - 13	1	---	MNTVVVRRPGNGR
1612.8899	1611.8826	1611.8368	0.0458	177 - 192	1	---	GNGSSAIAGSFRFTIK

No match to: 886.9793, 1081.4969, 1081.4969, 1151.7120, 1418.7865, 1418.7865, 1442.6407, 1459.6681, 1661.8640, 1665.8569, 1677.8583, 1693.8557, 1796.9583, 1814.9678, 1814.9678, 1888.9125, 2229.0977, 2242.0259, 2242.0259, 2304.1011, 2307.0977, 2308.0981, 2398.1318, 3409.8184

9. gi|11095597 **Mass:** 22512 **Score:** 16 **Expect:** 24 **Queries matched:** 3

coat protein [Groundnut rosette assistor virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8171	1454.8098	1454.7888	0.0211	1 -	13	1	---	MNTVVVRRPGNGR
1455.8171	1454.8098	1454.7888	0.0211	1 -	13	1	---	MNTVVVRRPGNGR
1612.8899	1611.8826	1611.8368	0.0458	177 -	192	1	---	GNGSSAIAGSFRFTIK

No match to: 886.9793, 1081.4969, 1081.4969, 1151.7120, 1418.7865, 1418.7865, 1442.6407, 1459.6681, 1661.8640, 1665.8569, 1677.8583, 1693.8557, 1796.9583, 1814.9678, 1814.9678, 1888.9125, 2229.0977, 2242.0259, 2242.0259, 2304.1011, 2307.0977, 2308.0981, 2398.1318, 3409.8184

10. gi|11095593 **Mass:** 22457 **Score:** 16 **Expect:** 24 **Queries matched:** 3

coat protein [Groundnut rosette assistor virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1455.8171	1454.8098	1454.7888	0.0211	1 -	13	1	---	MNTVVVRRPGNGR
1455.8171	1454.8098	1454.7888	0.0211	1 -	13	1	---	MNTVVVRRPGNGR
1612.8899	1611.8826	1611.8368	0.0458	177 -	192	1	---	GNGSSAIAGSFRFTIK

No match to: 886.9793, 1081.4969, 1081.4969, 1151.7120, 1418.7865, 1418.7865, 1442.6407, 1459.6681, 1661.8640, 1665.8569, 1677.8583, 1693.8557, 1796.9583, 1814.9678, 1814.9678, 1888.9125, 2229.0977, 2242.0259, 2242.0259, 2304.1011, 2307.0977, 2308.0981, 2398.1318, 3409.8184

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Number of Queries: 26

Protein View

Match to: **gi|52001225** Score: **303** Expect: **2.8e-029**
conarachin [Arachis hypogaea]

Nominal mass (M_r): **76343**; Calculated pI value: **5.23**
NCBI BLAST search of gi|52001225 against nr
Unformatted sequence string for pasting into other applications

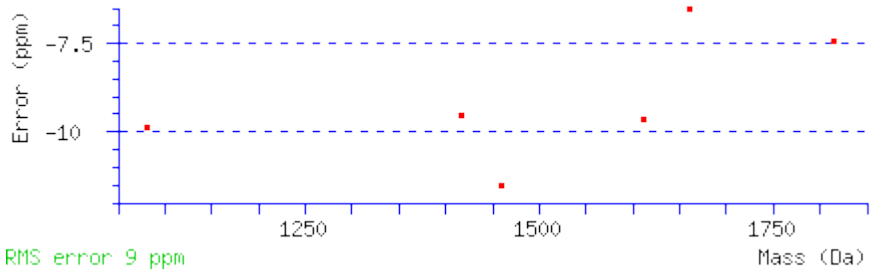
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

```
    1 MVIGPFRLSL CVCLVFLTSA CFGTRLEESF NECQLDRLNA LTPDNRIESQ
   51 GGITETWNSN HPELRCAGVT LLKRTIFPNG FHLPSYANYP QLIFIAQGNG
  101 VFGVSLPGCP VTYEEAESQS REDRRQRIVI KRESEQEQEQ QGDSHHKIYH
  151 FRQGHLLAIP AGVPYWSFNY GNEPIVAITL LDTSNLDNQL DPSPRRFYLA
  201 GNPEEEHPET QQQQPQTRRR HGQHQQDEYG SQGEEEGNNV LSGFSTQLLA
  251 HAFGVDEEIA RILQNPPEQT KDQIVRVEGG FRDVISPRWG EGKQYEDELE
  301 ERQRQPPRRD EQGKGYDYDD DRRPRHRQDP YREGDEDDRR PRGSRQGQGR
  351 GYDDDDRRPG QYEEGEEDDR RPRRSSRPKR QGRRHDDDDR RADEDDRRGY
  401 DDDERRPDED DRRGYDDDER RPDDDDRQGY DDDDRRPRWS SRPKGQGRNG
  451 VEETLCSPTL VEDIARPSRA DFYNPAAGRI SSANSLTFPI LRWFQLSAEH
  501 VLLYRNGIYS PHWNNNANSI IYGLRGEGRI QVVNSQGNAV FNGVLREGQI
  551 LLVPQNFAVG KQAGNEGFEY VAFKTADRAS PATSSKCLGE SPLMFSSMLL
  601 AFEIIKSVLS NTMETRPLWS LLMIPSMGLN VVINLNHNNN AQVDSKNNDG
  651 SRLWWPSSII IK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
470 - 479	1081.4954	1080.4881	1080.4988	-0.0107	0	ADFYNPAAGR	(No match)
470 - 479	1081.4954	1080.4881	1080.4988	-0.0107	0	ADFYNPAAGR	(Ions score 75)
480 - 492	1418.7866	1417.7793	1417.7929	-0.0135	0	ISSANSLTFPILR	(No match)
480 - 492	1418.7866	1417.7793	1417.7929	-0.0135	0	ISSANSLTFPILR	(Ions score 81)
493 - 505	1661.8689	1660.8616	1660.8725	-0.0109	0	WFQLSAEHVLLYR	(No match)
530 - 546	1814.9736	1813.9663	1813.9798	-0.0134	0	IQVVNSQGNAVFNGVLR	(No match)
530 - 546	1814.9736	1813.9663	1813.9798	-0.0134	0	IQVVNSQGNAVFNGVLR	(Ions score 111)
547 - 561	1612.8901	1611.8828	1611.8983	-0.0155	0	EGQILLVPQNFAVGK	(No match)
562 - 574	1459.6683	1458.6610	1458.6778	-0.0168	0	QAGNEGFEYVAFK	(No match)



RMS error 9 ppm

Spot 85

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 20 Mar 2007 at 13:16:22 GMT
Top Score : 111 for gi|15418705, allergen II [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|15418705	18612	111	allergen II [Arachis hypogaea]
2.	gi|52001227	21293	105	2S protein 1 [Arachis hypogaea]
3.	gi|14347293	24390	99	unnamed protein product [Arachis hypogaea]
4.	gi|46560482	20907	97	seed storage protein SSP2 [Arachis hypogaea]
5.	gi|28912768	19765	96	seed storage protein [Arachis hypogaea]
6.	gi|31322017	20212	95	allergen Ara h 2 isoform [Arachis hypogaea]
7.	gi|46560480	22229	92	seed storage protein SSP1 [Arachis hypogaea]
8.	gi|26245447	20558	92	allergen Ara h 2.02 [Arachis hypogaea]
9.	gi|118776566	19009	88	conglutin 7 [Arachis hypogaea]
10.	gi|73697921	35066	23	NodC [Bradyrhizobium sp. SEMIA 6144]

Results List

1. gi|15418705 **Mass:** 18612 **Score:** 111 **Expect:** 7e-009 **Queries matched:** 13
allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
913.3579	912.3506	912.3461	0.0046	56	62	0	DEDSYER
920.4269	919.4196	919.4181	0.0015	33	39	0	CQSQLER
935.4523	934.4450	934.4508	-0.0058	124	130	0	QQEQQFK
1056.4867	1055.4794	1055.4744	0.0050	81	90	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	135	143	0	NLPQQCGLR
1091.5623	1090.5550	1090.5519	0.0031	124	131	1	QQEQQFKR
1315.6486	1314.6413	1314.6429	-0.0015	23	32	1	QQWELQGDRR
1624.8081	1623.8008	1623.7973	0.0035	40	52	0	ANLRPCEQHLMQK
1640.8041	1639.7968	1639.7922	0.0046	40	52	0	ANLRPCEQHLMQK + Oxidation (M)

1726.6954	1725.6881	1725.6835	0.0047	91 - 103	0	CCNELNEFENNQR
2012.8202	2011.8129	2011.8220	-0.0091	104 - 119	0	CMCEALQQIMENQSDR
2028.8213	2027.8140	2027.8169	-0.0029	104 - 119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8213	2043.8140	2043.8118	0.0022	104 - 119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 864.4877, 867.0810, 870.5410, 877.0464, 903.4022, 918.4312, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1066.0864, 1072.0902, 1074.5354, 1101.5441, 1107.5150, 1277.1097, 1470.7159, 1471.7496, 1669.6792, 1709.6672, 1725.6655, 1742.6825, 1748.6785, 2002.8303, 2011.8193, 2018.8293, 2027.8086, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

2. gi|52001227 **Mass:** 21293 **Score:** 105 **Expect:** 2.8e-008 **Queries matched:** 13

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
913.3579	912.3506	912.3461	0.0046	75 -	81	0	DEDSYER
920.4269	919.4196	919.4181	0.0015	52 -	58	0	CQSQLER
935.4523	934.4450	934.4508	-0.0058	143 -	149	0	QQEQQFK
1056.4867	1055.4794	1055.4744	0.0050	100 -	109	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	154 -	162	0	NLPQQCGLR
1091.5623	1090.5550	1090.5519	0.0031	143 -	150	1	QQEQQFKR
1315.6486	1314.6413	1314.6429	-0.0015	42 -	51	1	QQWELQGDRR
1624.8081	1623.8008	1623.7973	0.0035	59 -	71	0	ANLRPCEQHLMQK
1640.8041	1639.7968	1639.7922	0.0046	59 -	71	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6954	1725.6881	1725.6835	0.0047	110 -	122	0	CCNELNEFENNQR
2012.8202	2011.8129	2011.8220	-0.0091	123 -	138	0	CMCEALQQIMENQSDR
2028.8213	2027.8140	2027.8169	-0.0029	123 -	138	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8213	2043.8140	2043.8118	0.0022	123 -	138	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 864.4877, 867.0810, 870.5410, 877.0464, 903.4022, 918.4312, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1066.0864, 1072.0902, 1074.5354, 1101.5441, 1107.5150, 1277.1097, 1470.7159, 1471.7496, 1669.6792, 1709.6672, 1725.6655, 1742.6825, 1748.6785, 2002.8303, 2011.8193, 2018.8293, 2027.8086, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

3. gi|14347293 **Mass:** 24390 **Score:** 99 **Expect:** 1.1e-007 **Queries matched:** 13

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
913.3579	912.3506	912.3461	0.0046	56 -	62	0	DEDSYER
920.4269	919.4196	919.4181	0.0015	33 -	39	0	CQSQLER
935.4523	934.4450	934.4508	-0.0058	124 -	130	0	QQEQQFK
1056.4867	1055.4794	1055.4744	0.0050	81 -	90	0	GAGSSQHQER

1085.5568	1084.5495	1084.5447	0.0048	135 - 143	0	NLPQQCGLR
1091.5623	1090.5550	1090.5519	0.0031	124 - 131	1	QQEQQFKR
1315.6486	1314.6413	1314.6429	-0.0015	23 - 32	1	QQWELQGDRR
1624.8081	1623.8008	1623.7973	0.0035	40 - 52	0	ANLRPCEQHLMQK
1640.8041	1639.7968	1639.7922	0.0046	40 - 52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6954	1725.6881	1725.6835	0.0047	91 - 103	0	CCNELNEFENNQR
2012.8202	2011.8129	2011.8220	-0.0091	104 - 119	0	CMCEALQQIMENQSDR
2028.8213	2027.8140	2027.8169	-0.0029	104 - 119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8213	2043.8140	2043.8118	0.0022	104 - 119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 864.4877, 867.0810, 870.5410, 877.0464, 903.4022, 918.4312, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1066.0864, 1072.0902, 1074.5354, 1101.5441, 1107.5150, 1277.1097, 1470.7159, 1471.7496, 1669.6792, 1709.6672, 1725.6655, 1742.6825, 1748.6785, 2002.8303, 2011.8193, 2018.8293, 2027.8086, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

4. gi|46560482 **Mass:** 20907 **Score:** 97 **Expect:** 1.9e-007 **Queries matched:** 12

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
913.3579	912.3506	912.3461	0.0046	71 -	77	0	DEDSYER
920.4269	919.4196	919.4181	0.0015	48 -	54	0	CQSQLER
935.4523	934.4450	934.4508	-0.0058	139 -	145	0	QQEQQFK
1056.4867	1055.4794	1055.4744	0.0050	96 -	105	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	150 -	158	0	NLPQQCGLR
1091.5623	1090.5550	1090.5519	0.0031	139 -	146	1	QQEQQFKR
1624.8081	1623.8008	1623.7973	0.0035	55 -	67	0	ANLRPCEQHLMQK
1640.8041	1639.7968	1639.7922	0.0046	55 -	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6954	1725.6881	1725.6835	0.0047	106 -	118	0	CCNELNEFENNQR
2012.8202	2011.8129	2011.8220	-0.0091	119 -	134	0	CMCEALQQIMENQSDR
2028.8213	2027.8140	2027.8169	-0.0029	119 -	134	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8213	2043.8140	2043.8118	0.0022	119 -	134	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 864.4877, 867.0810, 870.5410, 877.0464, 903.4022, 918.4312, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1066.0864, 1072.0902, 1074.5354, 1101.5441, 1107.5150, 1277.1097, 1315.6486, 1470.7159, 1471.7496, 1669.6792, 1709.6672, 1725.6655, 1742.6825, 1748.6785, 2002.8303, 2011.8193, 2018.8293, 2027.8086, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

5. gi|28912768 **Mass:** 19765 **Score:** 96 **Expect:** 2.4e-007 **Queries matched:** 12

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

920.4269	919.4196	919.4181	0.0015	31 - 37	0	CQSQLER
935.4523	934.4450	934.4508	-0.0058	134 - 140	0	QQEQQFK
1056.4867	1055.4794	1055.4744	0.0050	91 - 100	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	145 - 153	0	NLPQQCGLR
1091.5623	1090.5550	1090.5519	0.0031	134 - 141	1	QQEQQFKR
1315.6486	1314.6413	1314.6429	-0.0015	21 - 30	1	QQWELQGDRR
1624.8081	1623.8008	1623.7973	0.0035	38 - 50	0	ANLRPCEQHLMQK
1640.8041	1639.7968	1639.7922	0.0046	38 - 50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6954	1725.6881	1725.6835	0.0047	101 - 113	0	CCNELNEFENNQR
2012.8202	2011.8129	2011.8220	-0.0091	114 - 129	0	CMCEALQQIMENQSDR
2028.8213	2027.8140	2027.8169	-0.0029	114 - 129	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8213	2043.8140	2043.8118	0.0022	114 - 129	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 864.4877, 867.0810, 870.5410, 877.0464, 903.4022, 913.3579, 918.4312, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1066.0864, 1072.0902, 1074.5354, 1101.5441, 1107.5150, 1277.1097, 1470.7159, 1471.7496, 1669.6792, 1709.6672, 1725.6655, 1742.6825, 1748.6785, 2002.8303, 2011.8193, 2018.8293, 2027.8086, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

6. gi|31322017 **Mass:** 20212 **Score:** 95 **Expect:** 3.1e-007 **Queries matched:** 12

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start End	Miss	Peptide
920.4269	919.4196	919.4181	0.0015	30 - 36	0	CQSQLER
935.4523	934.4450	934.4508	-0.0058	133 - 139	0	QQEQQFK
1056.4867	1055.4794	1055.4744	0.0050	90 - 99	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	144 - 152	0	NLPQQCGLR
1091.5623	1090.5550	1090.5519	0.0031	133 - 140	1	QQEQQFKR
1315.6486	1314.6413	1314.6429	-0.0015	20 - 29	1	QQWELQGDRR
1624.8081	1623.8008	1623.7973	0.0035	37 - 49	0	ANLRPCEQHLMQK
1640.8041	1639.7968	1639.7922	0.0046	37 - 49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6954	1725.6881	1725.6835	0.0047	100 - 112	0	CCNELNEFENNQR
2012.8202	2011.8129	2011.8220	-0.0091	113 - 128	0	CMCEALQQIMENQSDR
2028.8213	2027.8140	2027.8169	-0.0029	113 - 128	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8213	2043.8140	2043.8118	0.0022	113 - 128	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 864.4877, 867.0810, 870.5410, 877.0464, 903.4022, 913.3579, 918.4312, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1066.0864, 1072.0902, 1074.5354, 1101.5441, 1107.5150, 1277.1097, 1470.7159, 1471.7496, 1669.6792, 1709.6672, 1725.6655, 1742.6825, 1748.6785, 2002.8303, 2011.8193, 2018.8293, 2027.8086, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

7. gi|46560480 **Mass:** 22229 **Score:** 92 **Expect:** 5.4e-007 **Queries matched:** 12

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4269	919.4196	919.4181	0.0015	48 -	54	0	CQSQLER
935.4523	934.4450	934.4508	-0.0058	151 -	157	0	QQEQQFK
1056.4867	1055.4794	1055.4744	0.0050	108 -	117	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	162 -	170	0	NLPQQCGLR
1091.5623	1090.5550	1090.5519	0.0031	151 -	158	1	QQEQQFKR
1315.6486	1314.6413	1314.6429	-0.0015	38 -	47	1	QQWELQGDRR
1624.8081	1623.8008	1623.7973	0.0035	55 -	67	0	ANLRPCEQHLMQK
1640.8041	1639.7968	1639.7922	0.0046	55 -	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6954	1725.6881	1725.6835	0.0047	118 -	130	0	CCNELNEFENNQR
2012.8202	2011.8129	2011.8220	-0.0091	131 -	146	0	CMCEALQQIMENQSDR
2028.8213	2027.8140	2027.8169	-0.0029	131 -	146	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8213	2043.8140	2043.8118	0.0022	131 -	146	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 864.4877, 867.0810, 870.5410, 877.0464, 903.4022, 913.3579, 918.4312, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1066.0864, 1072.0902, 1074.5354, 1101.5441, 1107.5150, 1277.1097, 1470.7159, 1471.7496, 1669.6792, 1709.6672, 1725.6655, 1742.6825, 1748.6785, 2002.8303, 2011.8193, 2018.8293, 2027.8086, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

8. gi|26245447 **Mass:** 20558 **Score:** 92 **Expect:** 6.1e-007 **Queries matched:** 12

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4269	919.4196	919.4181	0.0015	33 -	39	0	CQSQLER
935.4523	934.4450	934.4508	-0.0058	136 -	142	0	QQEQQFK
1056.4867	1055.4794	1055.4744	0.0050	93 -	102	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	147 -	155	0	NLPQQCGLR
1091.5623	1090.5550	1090.5519	0.0031	136 -	143	1	QQEQQFKR
1315.6486	1314.6413	1314.6429	-0.0015	23 -	32	1	QQWELQGDRR
1624.8081	1623.8008	1623.7973	0.0035	40 -	52	0	ANLRPCEQHLMQK
1640.8041	1639.7968	1639.7922	0.0046	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6954	1725.6881	1725.6835	0.0047	103 -	115	0	CCNELNEFENNQR
2012.8202	2011.8129	2011.8220	-0.0091	116 -	131	0	CMCEALQQIMENQSDR
2028.8213	2027.8140	2027.8169	-0.0029	116 -	131	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8213	2043.8140	2043.8118	0.0022	116 -	131	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 864.4877, 867.0810, 870.5410, 877.0464, 903.4022, 913.3579, 918.4312, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1066.0864, 1072.0902, 1074.5354, 1101.5441, 1107.5150, 1277.1097, 1470.7159, 1471.7496, 1669.6792, 1709.6672, 1725.6655, 1742.6825, 1748.6785, 2002.8303, 2011.8193,

2018.8293, 2027.8086, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

9. gi|118776566 **Mass:** 19009 **Score:** 88 **Expect:** 1.6e-006 **Queries matched:** 12

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4269	919.4196	919.4181	0.0015	33	39	0	CQSQLER
935.4523	934.4450	934.4508	-0.0058	122	128	0	QQEQQFK
1056.4867	1055.4794	1055.4744	0.0050	79	88	0	GAGSSQHQER
1085.5568	1084.5495	1084.5447	0.0048	133	141	0	NLPQQCGLR
1091.5623	1090.5550	1090.5519	0.0031	122	129	1	QQEQQFKR
1315.6486	1314.6413	1314.6429	-0.0015	23	32	1	QQWELQGDRR
1624.8081	1623.8008	1623.7973	0.0035	40	52	0	ANLRPCEQHLMQK
1640.8041	1639.7968	1639.7922	0.0046	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6954	1725.6881	1725.6835	0.0047	89	101	0	CCNELNEFENNQR
2012.8202	2011.8129	2011.8220	-0.0091	102	117	0	CMCEALQQIMENQSDR
2028.8213	2027.8140	2027.8169	-0.0029	102	117	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8213	2043.8140	2043.8118	0.0022	102	117	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 864.4877, 867.0810, 870.5410, 877.0464, 903.4022, 913.3579, 918.4312, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1066.0864, 1072.0902, 1074.5354, 1101.5441, 1107.5150, 1277.1097, 1470.7159, 1471.7496, 1669.6792, 1709.6672, 1725.6655, 1742.6825, 1748.6785, 2002.8303, 2011.8193, 2018.8293, 2027.8086, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

10. gi|73697921 **Mass:** 35066 **Score:** 23 **Expect:** 4.6 **Queries matched:** 5

NodC [Bradyrhizobium sp. SEMIA 6144]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
864.4877	863.4804	863.4864	-0.0060	12	19	0	DVVAPVHK
870.5410	869.5337	869.5446	-0.0109	40	47	1	KAQIAAIR
1107.5150	1106.5077	1106.4992	0.0085	151	160	0	GKPSDFGEDR
2011.8193	2010.8120	2010.7813	0.0307	119	134	1	FGAVMCCCGPCAMYRR + Oxidation (M)
2027.8086	2026.8013	2026.7762	0.0251	119	134	1	FGAVMCCCGPCAMYRR + 2 Oxidation (M)

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 867.0810, 877.0464, 903.4022, 913.3579, 918.4312, 920.4269, 935.4523, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1056.4867, 1066.0864, 1072.0902, 1074.5354, 1085.5568, 1091.5623, 1101.5441, 1277.1097, 1315.6486, 1470.7159, 1471.7496, 1624.8081, 1640.8041, 1669.6792, 1709.6672, 1725.6655, 1726.6954, 1742.6825, 1748.6785, 2002.8303, 2012.8202, 2018.8293, 2028.8213, 2044.8213, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|15418705** Score: **111** Expect: **7e-009**
allergen II [Arachis hypogaea]

Nominal mass (M_r): **18612**; Calculated pI value: **5.67**
NCBI BLAST search of gi|15418705 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **13**
Sequence Coverage: **59%**

Matched peptides shown in **Bold Red**

```
     1 MAKLTILVAL ALFLLAAHAS ARQQWELQGD RRCQSQLERA NLRPCEQHLM
    51 QKIQRDEDSY ERDPYSPSQD PYSPSPYDRR GAGSSQHQER CCNELNEFEN
   101 NQRCMCEALQ QIMENQSDRL QGRQQEQQFK RELRNLPQQC GLRAPQRCDL
   151 DVESGG
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
23 - 32	1315.6486	1314.6413	1314.6429	-0.0015	1	QQWELQGDRR	
33 - 39	920.4269	919.4196	919.4181	0.0015	0	CQSQLER	
40 - 52	1624.8081	1623.8008	1623.7973	0.0035	0	ANLRPCEQHLMQK	
40 - 52	1640.8041	1639.7968	1639.7922	0.0046	0	ANLRPCEQHLMQK	Oxidation (M)

56 - 62	913.3579	912.3506	912.3461	0.0046	0	DEDSYER
81 - 90	1056.4867	1055.4794	1055.4744	0.0050	0	GAGSSQHQER
91 - 103	1726.6954	1725.6881	1725.6835	0.0047	0	CCNELNEFENNQR
104 - 119	2012.8202	2011.8129	2011.8220	-0.0091	0	CMCEALQQIMENQSDR
104 - 119	2028.8213	2027.8140	2027.8169	-0.0029	0	CMCEALQQIMENQSDR Oxidation (M)
104 - 119	2044.8213	2043.8140	2043.8118	0.0022	0	CMCEALQQIMENQSDR 2 Oxidation (M)
124 - 130	935.4523	934.4450	934.4508	-0.0058	0	QQEQQFK
124 - 131	1091.5623	1090.5550	1090.5519	0.0031	1	QQEQQFKR
135 - 143	1085.5568	1084.5495	1084.5447	0.0048	0	NLPQQCGLR

No match to: 839.0878, 842.5090, 845.0970, 855.0583, 861.0776, 864.4877, 867.0810, 870.5410, 877.0464, 903.4022, 918.4312, 987.5076, 1028.5298, 1045.5640, 1050.1115, 1066.0864, 1072.0902, 1074.5354, 1101.5441, 1107.5150, 1277.1097, 1470.7159, 1471.7496, 1669.6792, 1709.6672, 1725.6655, 1742.6825, 1748.6785, 2002.8303, 2011.8193, 2018.8293, 2027.8086, 2158.9192, 2211.1057, 2225.1167, 2283.1675, 2299.1814

Spot 86

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 10:01:15 GMT**
Top Score : **116 for gi|15418705, allergen II [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|15418705	18612	116	allergen II [Arachis hypogaea]
2.	gi|28912768	19765	116	seed storage protein [Arachis hypogaea]
3.	gi|31322017	20212	115	allergen Ara h 2 isoform [Arachis hypogaea]
4.	gi|46560480	22229	112	seed storage protein SSP1 [Arachis hypogaea]
5.	gi|26245447	20558	111	allergen Ara h 2.02 [Arachis hypogaea]
6.	gi|52001227	21293	111	2S protein 1 [Arachis hypogaea]
7.	gi|118776566	19009	107	conglutin 7 [Arachis hypogaea]
8.	gi|14347293	24390	104	unnamed protein product [Arachis hypogaea]
9.	gi|46560482	20907	101	seed storage protein SSP2 [Arachis hypogaea]
10.	gi|230338	23975	21	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|15418705 **Mass:** 18612 **Score:** 116 **Expect:** 2.2e-009 **Queries matched:** 11
allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4243	919.4170	919.4181	-0.0011	33	39	0	CQSQLER
1056.4875	1055.4802	1055.4744	0.0058	81	90	0	GAGSSQHQER
1085.5598	1084.5525	1084.5447	0.0078	135	143	0	NLPQQCGLR
1091.5673	1090.5600	1090.5519	0.0081	124	131	1	QQEQQFKR
1212.5953	1211.5880	1211.5755	0.0125	80	90	1	RGAGSSQHQER
1315.6584	1314.6511	1314.6429	0.0083	23	32	1	QQWELQGDRR
1537.8134	1536.8061	1536.7943	0.0118	135	147	1	NLPQQCGLRAPQR
1624.8204	1623.8131	1623.7973	0.0158	40	52	0	ANLRPCEQHLMQK
1640.8116	1639.8043	1639.7922	0.0121	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7009	1725.6936	1725.6835	0.0102	91	103	0	CCNELNEFENNQR

2483.0691	2482.0618	2482.0821	-0.0203	104 - 123	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 861.0660, 877.0463, 903.3985, 906.4898, 919.3918, 987.5021, 1046.5972, 1074.5421, 1089.5638, 1111.5657, 1205.4834, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1541.6791, 1578.8368, 1669.6873, 1709.6761, 1725.6792, 1993.9344, 2185.0286, 2273.1521, 2450.0488, 2466.0579, 2482.0662, 2741.2517, 2765.1235, 3137.3550, 3153.3909, 3212.3782, 3229.4580, 3451.4514

2. gi|28912768 **Mass:** 19765 **Score:** 116 **Expect:** 2.2e-009 **Queries matched:** 11

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4243	919.4170	919.4181	-0.0011	31 -	37	0	CQSQLER
1056.4875	1055.4802	1055.4744	0.0058	91 -	100	0	GAGSSQHQER
1085.5598	1084.5525	1084.5447	0.0078	145 -	153	0	NLPQQCGLR
1091.5673	1090.5600	1090.5519	0.0081	134 -	141	1	QQEQQFKR
1212.5953	1211.5880	1211.5755	0.0125	90 -	100	1	RGAGSSQHQER
1315.6584	1314.6511	1314.6429	0.0083	21 -	30	1	QQWELQGDRR
1537.8134	1536.8061	1536.7943	0.0118	145 -	157	1	NLPQQCGLRAPQR
1624.8204	1623.8131	1623.7973	0.0158	38 -	50	0	ANLRPCEQHLMQK
1640.8116	1639.8043	1639.7922	0.0121	38 -	50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7009	1725.6936	1725.6835	0.0102	101 -	113	0	CCNELNEFENNQR
2483.0691	2482.0618	2482.0821	-0.0203	114 -	133	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 861.0660, 877.0463, 903.3985, 906.4898, 919.3918, 987.5021, 1046.5972, 1074.5421, 1089.5638, 1111.5657, 1205.4834, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1541.6791, 1578.8368, 1669.6873, 1709.6761, 1725.6792, 1993.9344, 2185.0286, 2273.1521, 2450.0488, 2466.0579, 2482.0662, 2741.2517, 2765.1235, 3137.3550, 3153.3909, 3212.3782, 3229.4580, 3451.4514

3. gi|31322017 **Mass:** 20212 **Score:** 115 **Expect:** 2.8e-009 **Queries matched:** 11

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4243	919.4170	919.4181	-0.0011	30 -	36	0	CQSQLER
1056.4875	1055.4802	1055.4744	0.0058	90 -	99	0	GAGSSQHQER
1085.5598	1084.5525	1084.5447	0.0078	144 -	152	0	NLPQQCGLR
1091.5673	1090.5600	1090.5519	0.0081	133 -	140	1	QQEQQFKR
1212.5953	1211.5880	1211.5755	0.0125	89 -	99	1	RGAGSSQHQER
1315.6584	1314.6511	1314.6429	0.0083	20 -	29	1	QQWELQGDRR
1537.8134	1536.8061	1536.7943	0.0118	144 -	156	1	NLPQQCGLRAPQR
1624.8204	1623.8131	1623.7973	0.0158	37 -	49	0	ANLRPCEQHLMQK
1640.8116	1639.8043	1639.7922	0.0121	37 -	49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7009	1725.6936	1725.6835	0.0102	100 -	112	0	CCNELNEFENNQR
2483.0691	2482.0618	2482.0821	-0.0203	113 -	132	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 861.0660, 877.0463, 903.3985, 906.4898, 919.3918, 987.5021, 1046.5972, 1074.5421, 1089.5638, 1111.5657, 1205.4834, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1541.6791, 1578.8368, 1669.6873, 1709.6761, 1725.6792, 1993.9344, 2185.0286, 2273.1521, 2450.0488, 2466.0579, 2482.0662, 2741.2517, 2765.1235, 3137.3550, 3153.3909,

3212.3782, 3229.4580, 3451.4514

4. gi|46560480 **Mass:** 22229 **Score:** 112 **Expect:** 5.5e-009 **Queries matched:** 11

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4243	919.4170	919.4181	-0.0011	48	54	0	CQSQLER
1056.4875	1055.4802	1055.4744	0.0058	108	117	0	GAGSSQHQER
1085.5598	1084.5525	1084.5447	0.0078	162	170	0	NLPQQCGLR
1091.5673	1090.5600	1090.5519	0.0081	151	158	1	QQEQQFKR
1212.5953	1211.5880	1211.5755	0.0125	107	117	1	RGAGSSQHQER
1315.6584	1314.6511	1314.6429	0.0083	38	47	1	QQWELQGDRR
1537.8134	1536.8061	1536.7943	0.0118	162	174	1	NLPQQCGLRAPQR
1624.8204	1623.8131	1623.7973	0.0158	55	67	0	ANLRPCEQHLMQK
1640.8116	1639.8043	1639.7922	0.0121	55	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7009	1725.6936	1725.6835	0.0102	118	130	0	CCNELNEFENNQR
2483.0691	2482.0618	2482.0821	-0.0203	131	150	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 861.0660, 877.0463, 903.3985, 906.4898, 919.3918, 987.5021, 1046.5972, 1074.5421, 1089.5638, 1111.5657, 1205.4834, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1541.6791, 1578.8368, 1669.6873, 1709.6761, 1725.6792, 1993.9344, 2185.0286, 2273.1521, 2450.0488, 2466.0579, 2482.0662, 2741.2517, 2765.1235, 3137.3550, 3153.3909, 3212.3782, 3229.4580, 3451.4514

5. gi|26245447 **Mass:** 20558 **Score:** 111 **Expect:** 7e-009 **Queries matched:** 11

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4243	919.4170	919.4181	-0.0011	33	39	0	CQSQLER
1056.4875	1055.4802	1055.4744	0.0058	93	102	0	GAGSSQHQER
1085.5598	1084.5525	1084.5447	0.0078	147	155	0	NLPQQCGLR
1091.5673	1090.5600	1090.5519	0.0081	136	143	1	QQEQQFKR
1212.5953	1211.5880	1211.5755	0.0125	92	102	1	RGAGSSQHQER
1315.6584	1314.6511	1314.6429	0.0083	23	32	1	QQWELQGDRR
1537.8134	1536.8061	1536.7943	0.0118	147	159	1	NLPQQCGLRAPQR
1624.8204	1623.8131	1623.7973	0.0158	40	52	0	ANLRPCEQHLMQK
1640.8116	1639.8043	1639.7922	0.0121	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7009	1725.6936	1725.6835	0.0102	103	115	0	CCNELNEFENNQR
2483.0691	2482.0618	2482.0821	-0.0203	116	135	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 861.0660, 877.0463, 903.3985, 906.4898, 919.3918, 987.5021, 1046.5972, 1074.5421, 1089.5638, 1111.5657, 1205.4834, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1541.6791, 1578.8368, 1669.6873, 1709.6761, 1725.6792, 1993.9344, 2185.0286, 2273.1521, 2450.0488, 2466.0579, 2482.0662, 2741.2517, 2765.1235, 3137.3550, 3153.3909, 3212.3782, 3229.4580, 3451.4514

6. gi|52001227 **Mass:** 21293 **Score:** 111 **Expect:** 7e-009 **Queries matched:** 11

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4243	919.4170	919.4181	-0.0011	52	-	58	0	CQSQLER
1056.4875	1055.4802	1055.4744	0.0058	100	-	109	0	GAGSSQHQER
1085.5598	1084.5525	1084.5447	0.0078	154	-	162	0	NLPQQCGLR
1091.5673	1090.5600	1090.5519	0.0081	143	-	150	1	QQEQQFKR
1212.5953	1211.5880	1211.5755	0.0125	99	-	109	1	RGAGSSQHQER
1315.6584	1314.6511	1314.6429	0.0083	42	-	51	1	QQWELQGDRR
1537.8134	1536.8061	1536.7943	0.0118	154	-	166	1	NLPQQCGLRAPQR
1624.8204	1623.8131	1623.7973	0.0158	59	-	71	0	ANLRPCEQHLMQK
1640.8116	1639.8043	1639.7922	0.0121	59	-	71	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7009	1725.6936	1725.6835	0.0102	110	-	122	0	CCNELNEFENNQR
2483.0691	2482.0618	2482.0821	-0.0203	123	-	142	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 861.0660, 877.0463, 903.3985, 906.4898, 919.3918, 987.5021, 1046.5972, 1074.5421, 1089.5638, 1111.5657, 1205.4834, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1541.6791, 1578.8368, 1669.6873, 1709.6761, 1725.6792, 1993.9344, 2185.0286, 2273.1521, 2450.0488, 2466.0579, 2482.0662, 2741.2517, 2765.1235, 3137.3550, 3153.3909, 3212.3782, 3229.4580, 3451.4514

7. gi|118776566 **Mass:** 19009 **Score:** 107 **Expect:** 1.7e-008 **Queries matched:** 11

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4243	919.4170	919.4181	-0.0011	33	-	39	0	CQSQLER
1056.4875	1055.4802	1055.4744	0.0058	79	-	88	0	GAGSSQHQER
1085.5598	1084.5525	1084.5447	0.0078	133	-	141	0	NLPQQCGLR
1091.5673	1090.5600	1090.5519	0.0081	122	-	129	1	QQEQQFKR
1212.5953	1211.5880	1211.5755	0.0125	78	-	88	1	RGAGSSQHQER
1315.6584	1314.6511	1314.6429	0.0083	23	-	32	1	QQWELQGDRR
1537.8134	1536.8061	1536.7943	0.0118	133	-	145	1	NLPQQCGLRAPQR
1624.8204	1623.8131	1623.7973	0.0158	40	-	52	0	ANLRPCEQHLMQK
1640.8116	1639.8043	1639.7922	0.0121	40	-	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7009	1725.6936	1725.6835	0.0102	89	-	101	0	CCNELNEFENNQR
2483.0691	2482.0618	2482.0821	-0.0203	102	-	121	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 861.0660, 877.0463, 903.3985, 906.4898, 919.3918, 987.5021, 1046.5972, 1074.5421, 1089.5638, 1111.5657, 1205.4834, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1541.6791, 1578.8368, 1669.6873, 1709.6761, 1725.6792, 1993.9344, 2185.0286, 2273.1521, 2450.0488, 2466.0579, 2482.0662, 2741.2517, 2765.1235, 3137.3550, 3153.3909, 3212.3782, 3229.4580, 3451.4514

8. gi|14347293 **Mass:** 24390 **Score:** 104 **Expect:** 3.5e-008 **Queries matched:** 11

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4243	919.4170	919.4181	-0.0011	33	-	39	0	CQSQLER

1056.4875	1055.4802	1055.4744	0.0058	81 - 90	0	GAGSSQHQER
1085.5598	1084.5525	1084.5447	0.0078	135 - 143	0	NLPQQCGLR
1091.5673	1090.5600	1090.5519	0.0081	124 - 131	1	QQEQQFKR
1212.5953	1211.5880	1211.5755	0.0125	80 - 90	1	RGAGSSQHQER
1315.6584	1314.6511	1314.6429	0.0083	23 - 32	1	QQWELQGDRR
1537.8134	1536.8061	1536.7943	0.0118	135 - 147	1	NLPQQCGLRAPQR
1624.8204	1623.8131	1623.7973	0.0158	40 - 52	0	ANLRPCEQHLMQK
1640.8116	1639.8043	1639.7922	0.0121	40 - 52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7009	1725.6936	1725.6835	0.0102	91 - 103	0	CCNELNEFENNQR
2483.0691	2482.0618	2482.0821	-0.0203	104 - 123	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 861.0660, 877.0463, 903.3985, 906.4898, 919.3918, 987.5021, 1046.5972, 1074.5421, 1089.5638, 1111.5657, 1205.4834, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1541.6791, 1578.8368, 1669.6873, 1709.6761, 1725.6792, 1993.9344, 2185.0286, 2273.1521, 2450.0488, 2466.0579, 2482.0662, 2741.2517, 2765.1235, 3137.3550, 3153.3909, 3212.3782, 3229.4580, 3451.4514

9. gi|46560482 **Mass:** 20907 **Score:** 101 **Expect:** 7e-008 **Queries matched:** 10

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4243	919.4170	919.4181	-0.0011	48 -	54	0	CQSQLER
1056.4875	1055.4802	1055.4744	0.0058	96 -	105	0	GAGSSQHQER
1085.5598	1084.5525	1084.5447	0.0078	150 -	158	0	NLPQQCGLR
1091.5673	1090.5600	1090.5519	0.0081	139 -	146	1	QQEQQFKR
1212.5953	1211.5880	1211.5755	0.0125	95 -	105	1	RGAGSSQHQER
1537.8134	1536.8061	1536.7943	0.0118	150 -	162	1	NLPQQCGLRAPQR
1624.8204	1623.8131	1623.7973	0.0158	55 -	67	0	ANLRPCEQHLMQK
1640.8116	1639.8043	1639.7922	0.0121	55 -	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7009	1725.6936	1725.6835	0.0102	106 -	118	0	CCNELNEFENNQR
2483.0691	2482.0618	2482.0821	-0.0203	119 -	138	1	CMCEALQQIMENQSDRLQGR + Oxidation (M)

No match to: 861.0660, 877.0463, 903.3985, 906.4898, 919.3918, 987.5021, 1046.5972, 1074.5421, 1089.5638, 1111.5657, 1205.4834, 1315.6584, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1541.6791, 1578.8368, 1669.6873, 1709.6761, 1725.6792, 1993.9344, 2185.0286, 2273.1521, 2450.0488, 2466.0579, 2482.0662, 2741.2517, 2765.1235, 3137.3550, 3153.3909, 3212.3782, 3229.4580, 3451.4514

10. gi|230338 **Mass:** 23975 **Score:** 21 **Expect:** 7.4 **Queries matched:** 3

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
906.4898	905.4825	905.4970	-0.0145	201 -	208	0	NKPGVYTK
1046.5972	1045.5899	1045.5880	0.0020	90 -	99	1	LKSAASLNSR
2273.1521	2272.1448	2272.1521	-0.0073	70 -	89	0	SIVHPSYNSNTLNNDIMLIK

No match to: 861.0660, 877.0463, 903.3985, 919.3918, 920.4243, 987.5021, 1056.4875, 1074.5421, 1085.5598, 1089.5638, 1091.5673, 1111.5657, 1205.4834, 1212.5953, 1315.6584, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1537.8134, 1541.6791, 1578.8368, 1624.8204, 1640.8116, 1669.6873, 1709.6761, 1725.6792, 1726.7009, 1993.9344, 2185.0286,

2450.0488, 2466.0579, 2482.0662, 2483.0691, 2741.2517, 2765.1235, 3137.3550, 3153.3909, 3212.3782, 3229.4580, 3451.4514

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 46

Protein View

Match to: **gi|15418705** Score: **116** Expect: **2.2e-009**
allergen II [Arachis hypogaea]

Nominal mass (M_r): **18612**; Calculated pI value: **5.67**
NCBI BLAST search of gi|15418705 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **46**
Number of mass values matched: **11**
Sequence Coverage: **60%**

Matched peptides shown in **Bold Red**

```
     1 MAKLTILVAL ALFLLAAHAS ARQQWELQGD RRCQSQLERA NLRPCEQHLM
    51 QKIQRDEDSY ERDPYSPSQD PYSPSPYDRR GAGSSQHQER CCNELNEFEN
   101 NQRCMCEALQ QIMENQSDRL QGRQQEQQFK RELRNLPQQC GLRAPQRCDL
   151 DVESGG
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
23 - 32	1315.6584	1314.6511	1314.6429	0.0083	1	QQWELQGDRR	
33 - 39	920.4243	919.4170	919.4181	-0.0011	0	CQSQLER	
40 - 52	1624.8204	1623.8131	1623.7973	0.0158	0	ANLRPCEQHLMQK	
40 - 52	1640.8116	1639.8043	1639.7922	0.0121	0	ANLRPCEQHLMQK	Oxidation (M)
80 - 90	1212.5953	1211.5880	1211.5755	0.0125	1	RGAGSSQHQER	
81 - 90	1056.4875	1055.4802	1055.4744	0.0058	0	GAGSSQHQER	
91 - 103	1726.7009	1725.6936	1725.6835	0.0102	0	CCNELNEFENNQR	
104 - 123	2483.0691	2482.0618	2482.0821	-0.0203	1	CMCEALQQIMENQSDRLQGR	Oxidation (M)
124 - 131	1091.5673	1090.5600	1090.5519	0.0081	1	QQEQQFKR	
135 - 143	1085.5598	1084.5525	1084.5447	0.0078	0	NLPQQCGLR	
135 - 147	1537.8134	1536.8061	1536.7943	0.0118	1	NLPQQCGLRAPQR	

No match to: 861.0660, 877.0463, 903.3985, 906.4898, 919.3918, 987.5021, 1046.5972, 1074.5421, 1089.5638, 1111.5657, 1205.4834, 1454.3446, 1455.3326, 1471.7614, 1487.7581, 1503.7520, 1525.6710, 1541.6791, 1578.8368, 1669.6873, 1709.6761, 1725.6792, 1993.9344, 2185.0286, 2273.1521, 2450.0488, 2466.0579, 2482.0662, 2741.2517, 2765.1235, 3137.3550, 3153.3909, 3212.3782, 3229.4580, 3451.4514

Spot 87

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **4 May 2007 at 10:01:10 GMT**
Top Score : **98 for gi|15418705, allergen II [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|15418705	18612	98	allergen II [Arachis hypogaea]
2.	gi|28912768	19765	98	seed storage protein [Arachis hypogaea]
3.	gi|31322017	20212	97	allergen Ara h 2 isoform [Arachis hypogaea]
4.	gi|46560480	22229	94	seed storage protein SSP1 [Arachis hypogaea]
5.	gi|26245447	20558	94	allergen Ara h 2.02 [Arachis hypogaea]
6.	gi|52001227	21293	93	2S protein 1 [Arachis hypogaea]
7.	gi|118776566	19009	90	conglutin 7 [Arachis hypogaea]
8.	gi|14347293	24390	87	unnamed protein product [Arachis hypogaea]
9.	gi|46560482	20907	84	seed storage protein SSP2 [Arachis hypogaea]
10.	gi|230338	23975	13	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|15418705 **Mass:** 18612 **Score:** 98 **Expect:** 1.4e-007 **Queries matched:** 10
allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4205	919.4132	919.4181	-0.0049	33	39	0	CQSQLER
1056.4852	1055.4779	1055.4744	0.0035	81	90	0	GAGSSQHQER
1085.5575	1084.5502	1084.5447	0.0055	135	143	0	NLPQQCGLR
1091.5649	1090.5576	1090.5519	0.0057	124	131	1	QQEQQFKR
1315.6560	1314.6487	1314.6429	0.0059	23	32	1	QQWELQGDRR
1537.8165	1536.8092	1536.7943	0.0149	135	147	1	NLPQQCGLRAPQR
1624.8195	1623.8122	1623.7973	0.0149	40	52	0	ANLRPCEQHLMQK
1640.8142	1639.8069	1639.7922	0.0147	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7080	1725.7007	1725.6835	0.0173	91	103	0	CCNELNEFENNQR
2499.0820	2498.0747	2498.0770	-0.0023	104	123	1	CMCEALQQIMENQSDRLQGR + 2 Oxidation (M)

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 987.5007, 1019.4987, 1046.5962, 1074.5381, 1107.4971, 1113.5380, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1541.6816, 1576.8187, 1578.8457, 1709.6815, 1725.6838, 1993.9237, 2185.0339, 2273.1563, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628

2. gi|28912768 **Mass:** 19765 **Score:** 98 **Expect:** 1.5e-007 **Queries matched:** 10

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4205	919.4132	919.4181	-0.0049	31	37	0	CQSQLER
1056.4852	1055.4779	1055.4744	0.0035	91	100	0	GAGSSQHQER
1085.5575	1084.5502	1084.5447	0.0055	145	153	0	NLPQQCGLR
1091.5649	1090.5576	1090.5519	0.0057	134	141	1	QQEQQFKR
1315.6560	1314.6487	1314.6429	0.0059	21	30	1	QQWELQGDRR
1537.8165	1536.8092	1536.7943	0.0149	145	157	1	NLPQQCGLRAPQR
1624.8195	1623.8122	1623.7973	0.0149	38	50	0	ANLRPCEQHLMQK
1640.8142	1639.8069	1639.7922	0.0147	38	50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7080	1725.7007	1725.6835	0.0173	101	113	0	CCNELNEFENNQR
2499.0820	2498.0747	2498.0770	-0.0023	114	133	1	CMCEALQQIMENQSDRLQGR + 2 Oxidation (M)

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 987.5007, 1019.4987, 1046.5962, 1074.5381, 1107.4971, 1113.5380, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1541.6816, 1576.8187, 1578.8457, 1709.6815, 1725.6838, 1993.9237, 2185.0339, 2273.1563, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628

3. gi|31322017 **Mass:** 20212 **Score:** 97 **Expect:** 1.9e-007 **Queries matched:** 10

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4205	919.4132	919.4181	-0.0049	30	36	0	CQSQLER
1056.4852	1055.4779	1055.4744	0.0035	90	99	0	GAGSSQHQER
1085.5575	1084.5502	1084.5447	0.0055	144	152	0	NLPQQCGLR
1091.5649	1090.5576	1090.5519	0.0057	133	140	1	QQEQQFKR
1315.6560	1314.6487	1314.6429	0.0059	20	29	1	QQWELQGDRR
1537.8165	1536.8092	1536.7943	0.0149	144	156	1	NLPQQCGLRAPQR
1624.8195	1623.8122	1623.7973	0.0149	37	49	0	ANLRPCEQHLMQK
1640.8142	1639.8069	1639.7922	0.0147	37	49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7080	1725.7007	1725.6835	0.0173	100	112	0	CCNELNEFENNQR
2499.0820	2498.0747	2498.0770	-0.0023	113	132	1	CMCEALQQIMENQSDRLQGR + 2 Oxidation (M)

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 987.5007, 1019.4987, 1046.5962, 1074.5381, 1107.4971, 1113.5380, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1541.6816, 1576.8187, 1578.8457, 1709.6815, 1725.6838, 1993.9237, 2185.0339, 2273.1563, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628

4. gi|46560480 **Mass:** 22229 **Score:** 94 **Expect:** 3.6e-007 **Queries matched:** 10

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4205	919.4132	919.4181	-0.0049	48	-	54	0	CQSQLER
1056.4852	1055.4779	1055.4744	0.0035	108	-	117	0	GAGSSQHQER
1085.5575	1084.5502	1084.5447	0.0055	162	-	170	0	NLPQQCGLR
1091.5649	1090.5576	1090.5519	0.0057	151	-	158	1	QQEQQFKR
1315.6560	1314.6487	1314.6429	0.0059	38	-	47	1	QQWELQGDRR
1537.8165	1536.8092	1536.7943	0.0149	162	-	174	1	NLPQQCGLRAPQR
1624.8195	1623.8122	1623.7973	0.0149	55	-	67	0	ANLRPCEQHLMQK
1640.8142	1639.8069	1639.7922	0.0147	55	-	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7080	1725.7007	1725.6835	0.0173	118	-	130	0	CCNELNEFENNQR
2499.0820	2498.0747	2498.0770	-0.0023	131	-	150	1	CMCEALQQIMENQSDRLQGR + 2 Oxidation (M)

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 987.5007, 1019.4987, 1046.5962, 1074.5381, 1107.4971, 1113.5380, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1541.6816, 1576.8187, 1578.8457, 1709.6815, 1725.6838, 1993.9237, 2185.0339, 2273.1563, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628

5. gi|26245447 **Mass:** 20558 **Score:** 94 **Expect:** 3.7e-007 **Queries matched:** 10

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4205	919.4132	919.4181	-0.0049	33	-	39	0	CQSQLER
1056.4852	1055.4779	1055.4744	0.0035	93	-	102	0	GAGSSQHQER
1085.5575	1084.5502	1084.5447	0.0055	147	-	155	0	NLPQQCGLR
1091.5649	1090.5576	1090.5519	0.0057	136	-	143	1	QQEQQFKR
1315.6560	1314.6487	1314.6429	0.0059	23	-	32	1	QQWELQGDRR
1537.8165	1536.8092	1536.7943	0.0149	147	-	159	1	NLPQQCGLRAPQR
1624.8195	1623.8122	1623.7973	0.0149	40	-	52	0	ANLRPCEQHLMQK
1640.8142	1639.8069	1639.7922	0.0147	40	-	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7080	1725.7007	1725.6835	0.0173	103	-	115	0	CCNELNEFENNQR
2499.0820	2498.0747	2498.0770	-0.0023	116	-	135	1	CMCEALQQIMENQSDRLQGR + 2 Oxidation (M)

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 987.5007, 1019.4987, 1046.5962, 1074.5381, 1107.4971, 1113.5380, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1541.6816, 1576.8187, 1578.8457, 1709.6815, 1725.6838, 1993.9237, 2185.0339, 2273.1563, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628

6. gi|52001227 **Mass:** 21293 **Score:** 93 **Expect:** 4.3e-007 **Queries matched:** 10

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4205	919.4132	919.4181	-0.0049	52	-	58	0	CQSQLER
1056.4852	1055.4779	1055.4744	0.0035	100	-	109	0	GAGSSQHQER
1085.5575	1084.5502	1084.5447	0.0055	154	-	162	0	NLPQQCGLR

1091.5649	1090.5576	1090.5519	0.0057	143 - 150	1	QQEQQFKR
1315.6560	1314.6487	1314.6429	0.0059	42 - 51	1	QQWELQGDRR
1537.8165	1536.8092	1536.7943	0.0149	154 - 166	1	NLPQQCGLRAPQR
1624.8195	1623.8122	1623.7973	0.0149	59 - 71	0	ANLRPCEQHLMQK
1640.8142	1639.8069	1639.7922	0.0147	59 - 71	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7080	1725.7007	1725.6835	0.0173	110 - 122	0	CCNELNEFENNQR
2499.0820	2498.0747	2498.0770	-0.0023	123 - 142	1	CMCEALQQIMENQSDRLQGR + 2 Oxidation (M)

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 987.5007, 1019.4987, 1046.5962, 1074.5381, 1107.4971, 1113.5380, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1541.6816, 1576.8187, 1578.8457, 1709.6815, 1725.6838, 1993.9237, 2185.0339, 2273.1563, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628

7. gi|118776566 **Mass:** 19009 **Score:** 90 **Expect:** 9.2e-007 **Queries matched:** 10

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4205	919.4132	919.4181	-0.0049	33	39	0	CQSQLER
1056.4852	1055.4779	1055.4744	0.0035	79	88	0	GAGSSQHQER
1085.5575	1084.5502	1084.5447	0.0055	133	141	0	NLPQQCGLR
1091.5649	1090.5576	1090.5519	0.0057	122	129	1	QQEQQFKR
1315.6560	1314.6487	1314.6429	0.0059	23	32	1	QQWELQGDRR
1537.8165	1536.8092	1536.7943	0.0149	133	145	1	NLPQQCGLRAPQR
1624.8195	1623.8122	1623.7973	0.0149	40	52	0	ANLRPCEQHLMQK
1640.8142	1639.8069	1639.7922	0.0147	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7080	1725.7007	1725.6835	0.0173	89	101	0	CCNELNEFENNQR
2499.0820	2498.0747	2498.0770	-0.0023	102	121	1	CMCEALQQIMENQSDRLQGR + 2 Oxidation (M)

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 987.5007, 1019.4987, 1046.5962, 1074.5381, 1107.4971, 1113.5380, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1541.6816, 1576.8187, 1578.8457, 1709.6815, 1725.6838, 1993.9237, 2185.0339, 2273.1563, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628

8. gi|14347293 **Mass:** 24390 **Score:** 87 **Expect:** 1.7e-006 **Queries matched:** 10

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4205	919.4132	919.4181	-0.0049	33	39	0	CQSQLER
1056.4852	1055.4779	1055.4744	0.0035	81	90	0	GAGSSQHQER
1085.5575	1084.5502	1084.5447	0.0055	135	143	0	NLPQQCGLR
1091.5649	1090.5576	1090.5519	0.0057	124	131	1	QQEQQFKR
1315.6560	1314.6487	1314.6429	0.0059	23	32	1	QQWELQGDRR
1537.8165	1536.8092	1536.7943	0.0149	135	147	1	NLPQQCGLRAPQR
1624.8195	1623.8122	1623.7973	0.0149	40	52	0	ANLRPCEQHLMQK
1640.8142	1639.8069	1639.7922	0.0147	40	52	0	ANLRPCEQHLMQK + Oxidation (M)

1726.7080	1725.7007	1725.6835	0.0173	91 - 103	0	CCNELNEFENNQR
2499.0820	2498.0747	2498.0770	-0.0023	104 - 123	1	CMCEALQQIMENQSDRLQGR + 2 Oxidation (M)

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 987.5007, 1019.4987, 1046.5962, 1074.5381, 1107.4971, 1113.5380, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1541.6816, 1576.8187, 1578.8457, 1709.6815, 1725.6838, 1993.9237, 2185.0339, 2273.1563, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628

9. gi|46560482 **Mass:** 20907 **Score:** 84 **Expect:** 3.6e-006 **Queries matched:** 9

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4205	919.4132	919.4181	-0.0049	48 -	54	0	CQSQLER
1056.4852	1055.4779	1055.4744	0.0035	96 -	105	0	GAGSSQHQER
1085.5575	1084.5502	1084.5447	0.0055	150 -	158	0	NLPQQCGLR
1091.5649	1090.5576	1090.5519	0.0057	139 -	146	1	QQEQQFKR
1537.8165	1536.8092	1536.7943	0.0149	150 -	162	1	NLPQQCGLRAPQR
1624.8195	1623.8122	1623.7973	0.0149	55 -	67	0	ANLRPCEQHLMQK
1640.8142	1639.8069	1639.7922	0.0147	55 -	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.7080	1725.7007	1725.6835	0.0173	106 -	118	0	CCNELNEFENNQR
2499.0820	2498.0747	2498.0770	-0.0023	119 -	138	1	CMCEALQQIMENQSDRLQGR + 2 Oxidation (M)

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 987.5007, 1019.4987, 1046.5962, 1074.5381, 1107.4971, 1113.5380, 1315.6560, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1541.6816, 1576.8187, 1578.8457, 1709.6815, 1725.6838, 1993.9237, 2185.0339, 2273.1563, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628

10. gi|230338 **Mass:** 23975 **Score:** 13 **Expect:** 48 **Queries matched:** 2

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.5962	1045.5889	1045.5880	0.0010	90 -	99	1	LKSAASLNSR
2273.1563	2272.1490	2272.1521	-0.0031	70 -	89	0	SIVHPSYNSNTLNNDIMLIK

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 920.4205, 987.5007, 1019.4987, 1056.4852, 1074.5381, 1085.5575, 1091.5649, 1107.4971, 1113.5380, 1315.6560, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1537.8165, 1541.6816, 1576.8187, 1578.8457, 1624.8195, 1640.8142, 1709.6815, 1725.6838, 1726.7080, 1993.9237, 2185.0339, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2499.0820, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 49

Match to: **gi|15418705** Score: **98** Expect: **1.4e-007**
allergen II [Arachis hypogaea]

Nominal mass (M_r): **18612**; Calculated pI value: **5.67**
NCBI BLAST search of gi|15418705 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **49**
Number of mass values matched: **10**
Sequence Coverage: **60%**

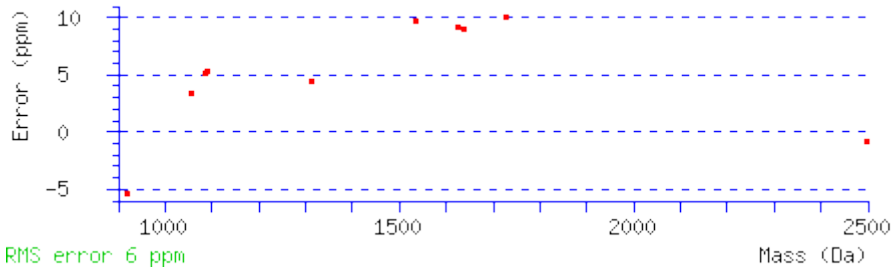
Matched peptides shown in **Bold Red**

```
     1 MAKLTILVAL ALFLLAAHAS ARQQWELQGD RRCQSQLERA NLRPCEQHLM
    51 QKIQRDEDSY ERDPYSPSQD PYSPSPYDRR GAGSSQHQER CCNELNEFEN
   101 NQRCMCEALQ QIMENQSDRL QGRQQEQQFK RELRNLPQQC GLRAPQRCDL
   151 DVESGG
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
23 - 32	1315.6560	1314.6487	1314.6429	0.0059	1	QQWELQGDRR	
33 - 39	920.4205	919.4132	919.4181	-0.0049	0	CQSQLER	
40 - 52	1624.8195	1623.8122	1623.7973	0.0149	0	ANLRPCEQHLMQK	
40 - 52	1640.8142	1639.8069	1639.7922	0.0147	0	ANLRPCEQHLMQK	Oxidation (M)
81 - 90	1056.4852	1055.4779	1055.4744	0.0035	0	GAGSSQHQER	
91 - 103	1726.7080	1725.7007	1725.6835	0.0173	0	CCNELNEFENNQR	
104 - 123	2499.0820	2498.0747	2498.0770	-0.0023	1	CMCEALQQIMENQSDRLQGR	2 Oxidation (M)
124 - 131	1091.5649	1090.5576	1090.5519	0.0057	1	QQEQQFKR	
135 - 143	1085.5575	1084.5502	1084.5447	0.0055	0	NLPQQCGLR	
135 - 147	1537.8165	1536.8092	1536.7943	0.0149	1	NLPQQCGLRAPQR	

No match to: 855.0538, 861.0576, 877.0426, 903.3916, 906.4805, 919.3932, 987.5007, 1019.4987, 1046.5962, 1074.5381, 1107.4971, 1113.5380, 1319.6588, 1347.6461, 1454.3556, 1455.3284, 1471.7637, 1475.7611, 1487.7582, 1503.7550, 1524.6548, 1541.6816, 1576.8187, 1578.8457, 1709.6815, 1725.6838, 1993.9237, 2185.0339, 2273.1563, 2312.1321, 2422.1064, 2450.0435, 2466.0413, 2482.0559, 2765.1108, 3061.3521, 3154.3459, 3228.3784, 3450.3628



Spot 88

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 20 Mar 2007 at 13:16:33 GMT
Top Score : 67 for gi|46560482, seed storage protein SSP2 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560482	20907	67	seed storage protein SSP2 [Arachis hypogaea]
2.	gi|15418705	18612	66	allergen II [Arachis hypogaea]
3.	gi|28912768	19765	66	seed storage protein [Arachis hypogaea]
4.	gi|31322017	20212	65	allergen Ara h 2 isoform [Arachis hypogaea]
5.	gi|46560480	22229	63	seed storage protein SSP1 [Arachis hypogaea]
6.	gi|26245447	20558	63	allergen Ara h 2.02 [Arachis hypogaea]
7.	gi|52001227	21293	63	2S protein 1 [Arachis hypogaea]
8.	gi|118776566	19009	60	conglutin 7 [Arachis hypogaea]
9.	gi|14347293	24390	58	unnamed protein product [Arachis hypogaea]
10.	gi|230338	23975	23	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|46560482 **Mass:** 20907 **Score:** 67 **Expect:** 0.00018 **Queries matched:** 7
seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4321	919.4248	919.4181	0.0067	48	-	54	0	CQSQLER
1056.4907	1055.4834	1055.4744	0.0090	96	-	105	0	GAGSSQHQER
1085.5615	1084.5542	1084.5447	0.0095	150	-	158	0	NLPQQCGLR
1091.5682	1090.5609	1090.5519	0.0090	139	-	146	1	QQEQQFKR
1537.7998	1536.7925	1536.7943	-0.0018	150	-	162	1	NLPQQCGLRAPQR
1640.7955	1639.7882	1639.7922	-0.0040	55	-	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6855	1725.6782	1725.6835	-0.0052	106	-	118	0	CCNELNEFENNQR

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 1046.6035, 1051.7054, 1074.5397, 1090.5618, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384, 1524.6359, 1541.6609, 1578.8318, 1638.8328, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2273.1616, 2305.1499, 2311.1287, 2514.3538, 2530.3630,

3300.7717, 3316.7839

2. gi|15418705 **Mass:** 18612 **Score:** 66 **Expect:** 0.00021 **Queries matched:** 7

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4321	919.4248	919.4181	0.0067	33 -	39	0	CQSQLER
1056.4907	1055.4834	1055.4744	0.0090	81 -	90	0	GAGSSQHQER
1085.5615	1084.5542	1084.5447	0.0095	135 -	143	0	NLPQQCGLR
1091.5682	1090.5609	1090.5519	0.0090	124 -	131	1	QQEQQFKR
1537.7998	1536.7925	1536.7943	-0.0018	135 -	147	1	NLPQQCGLRAPQR
1640.7955	1639.7882	1639.7922	-0.0040	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6855	1725.6782	1725.6835	-0.0052	91 -	103	0	CCNELNEFENNQR

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 1046.6035, 1051.7054, 1074.5397, 1090.5618, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384, 1524.6359, 1541.6609, 1578.8318, 1638.8328, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2273.1616, 2305.1499, 2311.1287, 2514.3538, 2530.3630, 3300.7717, 3316.7839

3. gi|28912768 **Mass:** 19765 **Score:** 66 **Expect:** 0.00022 **Queries matched:** 7

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4321	919.4248	919.4181	0.0067	31 -	37	0	CQSQLER
1056.4907	1055.4834	1055.4744	0.0090	91 -	100	0	GAGSSQHQER
1085.5615	1084.5542	1084.5447	0.0095	145 -	153	0	NLPQQCGLR
1091.5682	1090.5609	1090.5519	0.0090	134 -	141	1	QQEQQFKR
1537.7998	1536.7925	1536.7943	-0.0018	145 -	157	1	NLPQQCGLRAPQR
1640.7955	1639.7882	1639.7922	-0.0040	38 -	50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6855	1725.6782	1725.6835	-0.0052	101 -	113	0	CCNELNEFENNQR

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 1046.6035, 1051.7054, 1074.5397, 1090.5618, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384, 1524.6359, 1541.6609, 1578.8318, 1638.8328, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2273.1616, 2305.1499, 2311.1287, 2514.3538, 2530.3630, 3300.7717, 3316.7839

4. gi|31322017 **Mass:** 20212 **Score:** 65 **Expect:** 0.00028 **Queries matched:** 7

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4321	919.4248	919.4181	0.0067	30 -	36	0	CQSQLER
1056.4907	1055.4834	1055.4744	0.0090	90 -	99	0	GAGSSQHQER
1085.5615	1084.5542	1084.5447	0.0095	144 -	152	0	NLPQQCGLR
1091.5682	1090.5609	1090.5519	0.0090	133 -	140	1	QQEQQFKR
1537.7998	1536.7925	1536.7943	-0.0018	144 -	156	1	NLPQQCGLRAPQR

1640.7955	1639.7882	1639.7922	-0.0040	37 - 49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6855	1725.6782	1725.6835	-0.0052	100 - 112	0	CCNELNEFENNQR

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 1046.6035, 1051.7054, 1074.5397, 1090.5618, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384, 1524.6359, 1541.6609, 1578.8318, 1638.8328, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2273.1616, 2305.1499, 2311.1287, 2514.3538, 2530.3630, 3300.7717, 3316.7839

5. gi|46560480 **Mass:** 22229 **Score:** 63 **Expect:** 0.00044 **Queries matched:** 7

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4321	919.4248	919.4181	0.0067	48 -	54	0	CQSQLER
1056.4907	1055.4834	1055.4744	0.0090	108 -	117	0	GAGSSQHQER
1085.5615	1084.5542	1084.5447	0.0095	162 -	170	0	NLPQQCGLR
1091.5682	1090.5609	1090.5519	0.0090	151 -	158	1	QQEQQFKR
1537.7998	1536.7925	1536.7943	-0.0018	162 -	174	1	NLPQQCGLRAPQR
1640.7955	1639.7882	1639.7922	-0.0040	55 -	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6855	1725.6782	1725.6835	-0.0052	118 -	130	0	CCNELNEFENNQR

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 1046.6035, 1051.7054, 1074.5397, 1090.5618, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384, 1524.6359, 1541.6609, 1578.8318, 1638.8328, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2273.1616, 2305.1499, 2311.1287, 2514.3538, 2530.3630, 3300.7717, 3316.7839

6. gi|26245447 **Mass:** 20558 **Score:** 63 **Expect:** 0.00046 **Queries matched:** 7

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4321	919.4248	919.4181	0.0067	33 -	39	0	CQSQLER
1056.4907	1055.4834	1055.4744	0.0090	93 -	102	0	GAGSSQHQER
1085.5615	1084.5542	1084.5447	0.0095	147 -	155	0	NLPQQCGLR
1091.5682	1090.5609	1090.5519	0.0090	136 -	143	1	QQEQQFKR
1537.7998	1536.7925	1536.7943	-0.0018	147 -	159	1	NLPQQCGLRAPQR
1640.7955	1639.7882	1639.7922	-0.0040	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6855	1725.6782	1725.6835	-0.0052	103 -	115	0	CCNELNEFENNQR

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 1046.6035, 1051.7054, 1074.5397, 1090.5618, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384, 1524.6359, 1541.6609, 1578.8318, 1638.8328, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2273.1616, 2305.1499, 2311.1287, 2514.3538, 2530.3630, 3300.7717, 3316.7839

7. gi|52001227 **Mass:** 21293 **Score:** 63 **Expect:** 0.00049 **Queries matched:** 7

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4321	919.4248	919.4181	0.0067	52	-	58	0	CQSQLER
1056.4907	1055.4834	1055.4744	0.0090	100	-	109	0	GAGSSQHQER
1085.5615	1084.5542	1084.5447	0.0095	154	-	162	0	NLPQQCGLR
1091.5682	1090.5609	1090.5519	0.0090	143	-	150	1	QQEQQFKR
1537.7998	1536.7925	1536.7943	-0.0018	154	-	166	1	NLPQQCGLRAPQR
1640.7955	1639.7882	1639.7922	-0.0040	59	-	71	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6855	1725.6782	1725.6835	-0.0052	110	-	122	0	CCNELNEFENNQR

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 1046.6035, 1051.7054, 1074.5397, 1090.5618, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384, 1524.6359, 1541.6609, 1578.8318, 1638.8328, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2273.1616, 2305.1499, 2311.1287, 2514.3538, 2530.3630, 3300.7717, 3316.7839

8. gi|118776566 **Mass:** 19009 **Score:** 60 **Expect:** 0.00098 **Queries matched:** 7

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4321	919.4248	919.4181	0.0067	33	-	39	0	CQSQLER
1056.4907	1055.4834	1055.4744	0.0090	79	-	88	0	GAGSSQHQER
1085.5615	1084.5542	1084.5447	0.0095	133	-	141	0	NLPQQCGLR
1091.5682	1090.5609	1090.5519	0.0090	122	-	129	1	QQEQQFKR
1537.7998	1536.7925	1536.7943	-0.0018	133	-	145	1	NLPQQCGLRAPQR
1640.7955	1639.7882	1639.7922	-0.0040	40	-	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6855	1725.6782	1725.6835	-0.0052	89	-	101	0	CCNELNEFENNQR

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 1046.6035, 1051.7054, 1074.5397, 1090.5618, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384, 1524.6359, 1541.6609, 1578.8318, 1638.8328, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2273.1616, 2305.1499, 2311.1287, 2514.3538, 2530.3630, 3300.7717, 3316.7839

9. gi|14347293 **Mass:** 24390 **Score:** 58 **Expect:** 0.0015 **Queries matched:** 7

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
920.4321	919.4248	919.4181	0.0067	33	-	39	0	CQSQLER
1056.4907	1055.4834	1055.4744	0.0090	81	-	90	0	GAGSSQHQER
1085.5615	1084.5542	1084.5447	0.0095	135	-	143	0	NLPQQCGLR
1091.5682	1090.5609	1090.5519	0.0090	124	-	131	1	QQEQQFKR
1537.7998	1536.7925	1536.7943	-0.0018	135	-	147	1	NLPQQCGLRAPQR
1640.7955	1639.7882	1639.7922	-0.0040	40	-	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6855	1725.6782	1725.6835	-0.0052	91	-	103	0	CCNELNEFENNQR

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 1046.6035, 1051.7054, 1074.5397, 1090.5618, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384,

1524.6359, 1541.6609, 1578.8318, 1638.8328, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2273.1616, 2305.1499, 2311.1287, 2514.3538, 2530.3630, 3300.7717, 3316.7839

10. gi|230338 **Mass:** 23975 **Score:** 23 **Expect:** 4.1 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.6035	1045.5962	1045.5880	0.0083	90 -	99	1	LKSAASLNSR
2273.1616	2272.1543	2272.1521	0.0022	70 -	89	0	SIVHPSYNSNTLNNDIMLIK
2514.3538	2513.3465	2513.3311	0.0154	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK
2530.3630	2529.3557	2529.3260	0.0297	70 -	91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 920.4321, 1051.7054, 1056.4907, 1074.5397, 1085.5615, 1090.5618, 1091.5682, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384, 1524.6359, 1537.7998, 1541.6609, 1578.8318, 1638.8328, 1640.7955, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1726.6855, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2305.1499, 2311.1287, 3300.7717, 3316.7839

Search Parameters

Type of search	**: Peptide Mass Fingerprint**
Enzyme	**: Trypsin**
Fixed modifications	**: Carbamidomethyl (C)**
Variable modifications	**: Oxidation (M)**
Mass values	**: MONOISOTOPIC**
Protein Mass	**: Unrestricted**
Peptide Mass Tolerance	**: ± 20 ppm**
Peptide Charge State	**: 1+**
Max Missed Cleavages	**: 1**
Number of queries	**: 50**

Protein View

Match to: **gi|46560482** Score: **67** Expect: **0.00018**
seed storage protein SSP2 [Arachis hypogaea]

Nominal mass (M_r): **20907**; Calculated pI value: **5.98**
NCBI BLAST search of gi|46560482 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **7**
Sequence Coverage: **36%**

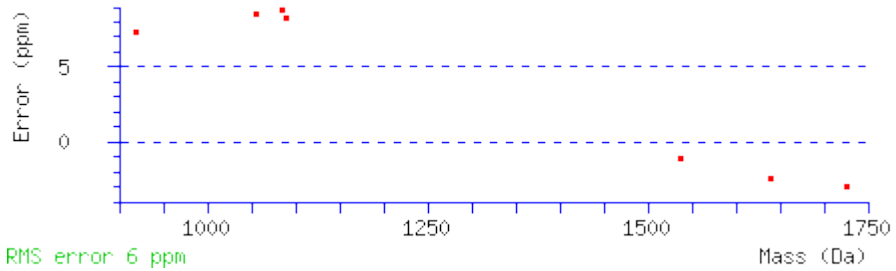
Matched peptides shown in **Bold Red**

```
     1 DHTLFNTHSI TTTTTMAKLT ILVALALFLL AAHASARQQW EFQGDRRCQS
    51 QLERANLRPC EQHLMQKIQR DEDSYERDPY SPSQDPYSPS PYDRRGAGSS
   101 QHQERCCNEL NEFENNQRCM CEALQQIMEN QSDRLQGRQQ EQQFKRELRN
   151 LPQQCGLRAP QRCDLDVESG GRDRY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
48 - 54	920.4321	919.4248	919.4181	0.0067	0	CQSQLER	
55 - 67	1640.7955	1639.7882	1639.7922	-0.0040	0	ANLRPCEQHLMQK	Oxidation (M)
96 - 105	1056.4907	1055.4834	1055.4744	0.0090	0	GAGSSQHQER	
106 - 118	1726.6855	1725.6782	1725.6835	-0.0052	0	CCNELNEFENNQR	
139 - 146	1091.5682	1090.5609	1090.5519	0.0090	1	QQEQQFKR	
150 - 158	1085.5615	1084.5542	1084.5447	0.0095	0	NLPQQCGLR	
150 - 162	1537.7998	1536.7925	1536.7943	-0.0018	1	NLPQQCGLRAPQR	

No match to: 805.4747, 824.5701, 827.5129, 829.5123, 838.5515, 861.0901, 868.5645, 881.2874, 882.5763, 903.4312, 919.4115, 1046.6035, 1051.7054, 1074.5397, 1090.5618, 1101.5524, 1145.0824, 1145.5699, 1471.7476, 1487.7399, 1503.7384, 1524.6359, 1541.6609, 1578.8318, 1638.8328, 1656.7783, 1669.6986, 1709.6633, 1725.6666, 1742.6705, 1745.6619, 1774.8079, 1993.9135, 2145.6345, 2161.0461, 2185.0374, 2273.1616, 2305.1499, 2311.1287, 2514.3538, 2530.3630, 3300.7717, 3316.7839



Spot 89

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 20 Mar 2007 at 13:17:01 GMT
Top Score : 101 for gi|46560482, seed storage protein SSP2 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560482	20907	101	seed storage protein SSP2 [Arachis hypogaea]
2.	gi|15418705	18612	100	allergen II [Arachis hypogaea]
3.	gi|28912768	19765	99	seed storage protein [Arachis hypogaea]
4.	gi|31322017	20212	98	allergen Ara h 2 isoform [Arachis hypogaea]
5.	gi|46560480	22229	96	seed storage protein SSP1 [Arachis hypogaea]
6.	gi|26245447	20558	95	allergen Ara h 2.02 [Arachis hypogaea]
7.	gi|52001227	21293	95	2S protein 1 [Arachis hypogaea]
8.	gi|118776566	19009	91	conglutin 7 [Arachis hypogaea]
9.	gi|14347293	24390	89	unnamed protein product [Arachis hypogaea]
10.	gi|114309696	27933	21	MADS-box transcription factor [Arachis hypogaea]

Results List

1. gi|46560482 **Mass:** 20907 **Score:** 101 **Expect:** 7e-008 **Queries matched:** 12
seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4199	919.4126	919.4181	-0.0055	48	54	0	CQSQLER
935.4493	934.4420	934.4508	-0.0088	139	145	0	QQEQQFK
1056.4810	1055.4737	1055.4744	-0.0007	96	105	0	GAGSSQHQER
1085.5446	1084.5373	1084.5447	-0.0074	150	158	0	NLPQQCGLR
1091.5541	1090.5468	1090.5519	-0.0051	139	146	1	QQEQQFKR
1212.5635	1211.5562	1211.5755	-0.0193	95	105	1	RGAGSSQHQER
1624.7988	1623.7915	1623.7973	-0.0058	55	67	0	ANLRPCEQHLMQK
1640.7905	1639.7832	1639.7922	-0.0090	55	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6835	1725.6762	1725.6835	-0.0072	106	118	0	CCNELNEFENNQR

2012.8240	2011.8167	2011.8220	-0.0053	119 - 134	0	CMCEALQQIMENQSDR
2028.8229	2027.8156	2027.8169	-0.0013	119 - 134	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8170	2043.8097	2043.8118	-0.0021	119 - 134	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 1045.5647, 1050.1147, 1066.0924, 1072.1003, 1106.5363, 1107.5088, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1709.6591, 1940.9307, 2002.8278, 2211.1055, 2225.1204, 2230.1873, 2233.1331, 2247.1860, 2283.1641, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

2. gi|15418705 **Mass:** 18612 **Score:** 100 **Expect:** 8.7e-008 **Queries matched:** 12

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4199	919.4126	919.4181	-0.0055	33 -	39	0	CQSQLER
935.4493	934.4420	934.4508	-0.0088	124 -	130	0	QQEQQFK
1056.4810	1055.4737	1055.4744	-0.0007	81 -	90	0	GAGSSQHQER
1085.5446	1084.5373	1084.5447	-0.0074	135 -	143	0	NLPQQCGLR
1091.5541	1090.5468	1090.5519	-0.0051	124 -	131	1	QQEQQFKR
1212.5635	1211.5562	1211.5755	-0.0193	80 -	90	1	RGAGSSQHQER
1624.7988	1623.7915	1623.7973	-0.0058	40 -	52	0	ANLRPCEQHLMQK
1640.7905	1639.7832	1639.7922	-0.0090	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6835	1725.6762	1725.6835	-0.0072	91 -	103	0	CCNELNEFENNQR
2012.8240	2011.8167	2011.8220	-0.0053	104 -	119	0	CMCEALQQIMENQSDR
2028.8229	2027.8156	2027.8169	-0.0013	104 -	119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8170	2043.8097	2043.8118	-0.0021	104 -	119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 1045.5647, 1050.1147, 1066.0924, 1072.1003, 1106.5363, 1107.5088, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1709.6591, 1940.9307, 2002.8278, 2211.1055, 2225.1204, 2230.1873, 2233.1331, 2247.1860, 2283.1641, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

3. gi|28912768 **Mass:** 19765 **Score:** 99 **Expect:** 1e-007 **Queries matched:** 12

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4199	919.4126	919.4181	-0.0055	31 -	37	0	CQSQLER
935.4493	934.4420	934.4508	-0.0088	134 -	140	0	QQEQQFK
1056.4810	1055.4737	1055.4744	-0.0007	91 -	100	0	GAGSSQHQER
1085.5446	1084.5373	1084.5447	-0.0074	145 -	153	0	NLPQQCGLR
1091.5541	1090.5468	1090.5519	-0.0051	134 -	141	1	QQEQQFKR
1212.5635	1211.5562	1211.5755	-0.0193	90 -	100	1	RGAGSSQHQER
1624.7988	1623.7915	1623.7973	-0.0058	38 -	50	0	ANLRPCEQHLMQK
1640.7905	1639.7832	1639.7922	-0.0090	38 -	50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6835	1725.6762	1725.6835	-0.0072	101 -	113	0	CCNELNEFENNQR
2012.8240	2011.8167	2011.8220	-0.0053	114 -	129	0	CMCEALQQIMENQSDR

2028.8229	2027.8156	2027.8169	-0.0013	114 - 129	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8170	2043.8097	2043.8118	-0.0021	114 - 129	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 1045.5647, 1050.1147, 1066.0924, 1072.1003, 1106.5363, 1107.5088, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1709.6591, 1940.9307, 2002.8278, 2211.1055, 2225.1204, 2230.1873, 2233.1331, 2247.1860, 2283.1641, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

4. gi|31322017 **Mass:** 20212 **Score:** 98 **Expect:** 1.3e-007 **Queries matched:** 12

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4199	919.4126	919.4181	-0.0055	30 -	36	0	CQSQLER
935.4493	934.4420	934.4508	-0.0088	133 -	139	0	QQEQQFK
1056.4810	1055.4737	1055.4744	-0.0007	90 -	99	0	GAGSSQHQER
1085.5446	1084.5373	1084.5447	-0.0074	144 -	152	0	NLPQQCGLR
1091.5541	1090.5468	1090.5519	-0.0051	133 -	140	1	QQEQQFKR
1212.5635	1211.5562	1211.5755	-0.0193	89 -	99	1	RGAGSSQHQER
1624.7988	1623.7915	1623.7973	-0.0058	37 -	49	0	ANLRPCEQHLMQK
1640.7905	1639.7832	1639.7922	-0.0090	37 -	49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6835	1725.6762	1725.6835	-0.0072	100 -	112	0	CCNELNEFENNQR
2012.8240	2011.8167	2011.8220	-0.0053	113 -	128	0	CMCEALQQIMENQSDR
2028.8229	2027.8156	2027.8169	-0.0013	113 -	128	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8170	2043.8097	2043.8118	-0.0021	113 -	128	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 1045.5647, 1050.1147, 1066.0924, 1072.1003, 1106.5363, 1107.5088, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1709.6591, 1940.9307, 2002.8278, 2211.1055, 2225.1204, 2230.1873, 2233.1331, 2247.1860, 2283.1641, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

5. gi|46560480 **Mass:** 22229 **Score:** 96 **Expect:** 2.4e-007 **Queries matched:** 12

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4199	919.4126	919.4181	-0.0055	48 -	54	0	CQSQLER
935.4493	934.4420	934.4508	-0.0088	151 -	157	0	QQEQQFK
1056.4810	1055.4737	1055.4744	-0.0007	108 -	117	0	GAGSSQHQER
1085.5446	1084.5373	1084.5447	-0.0074	162 -	170	0	NLPQQCGLR
1091.5541	1090.5468	1090.5519	-0.0051	151 -	158	1	QQEQQFKR
1212.5635	1211.5562	1211.5755	-0.0193	107 -	117	1	RGAGSSQHQER
1624.7988	1623.7915	1623.7973	-0.0058	55 -	67	0	ANLRPCEQHLMQK
1640.7905	1639.7832	1639.7922	-0.0090	55 -	67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6835	1725.6762	1725.6835	-0.0072	118 -	130	0	CCNELNEFENNQR
2012.8240	2011.8167	2011.8220	-0.0053	131 -	146	0	CMCEALQQIMENQSDR
2028.8229	2027.8156	2027.8169	-0.0013	131 -	146	0	CMCEALQQIMENQSDR + Oxidation (M)

2044.8170	2043.8097	2043.8118	-0.0021	131 - 146	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 1045.5647, 1050.1147, 1066.0924, 1072.1003, 1106.5363, 1107.5088, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1709.6591, 1940.9307, 2002.8278, 2211.1055, 2225.1204, 2230.1873, 2233.1331, 2247.1860, 2283.1641, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

6. gi|26245447 **Mass:** 20558 **Score:** 95 **Expect:** 2.6e-007 **Queries matched:** 12

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4199	919.4126	919.4181	-0.0055	33 -	39	0	CQSQLER
935.4493	934.4420	934.4508	-0.0088	136 -	142	0	QQEQQFK
1056.4810	1055.4737	1055.4744	-0.0007	93 -	102	0	GAGSSQHQER
1085.5446	1084.5373	1084.5447	-0.0074	147 -	155	0	NLPQQCGLR
1091.5541	1090.5468	1090.5519	-0.0051	136 -	143	1	QQEQQFKR
1212.5635	1211.5562	1211.5755	-0.0193	92 -	102	1	RGAGSSQHQER
1624.7988	1623.7915	1623.7973	-0.0058	40 -	52	0	ANLRPCEQHLMQK
1640.7905	1639.7832	1639.7922	-0.0090	40 -	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6835	1725.6762	1725.6835	-0.0072	103 -	115	0	CCNELNEFENNQR
2012.8240	2011.8167	2011.8220	-0.0053	116 -	131	0	CMCEALQQIMENQSDR
2028.8229	2027.8156	2027.8169	-0.0013	116 -	131	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8170	2043.8097	2043.8118	-0.0021	116 -	131	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 1045.5647, 1050.1147, 1066.0924, 1072.1003, 1106.5363, 1107.5088, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1709.6591, 1940.9307, 2002.8278, 2211.1055, 2225.1204, 2230.1873, 2233.1331, 2247.1860, 2283.1641, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

7. gi|52001227 **Mass:** 21293 **Score:** 95 **Expect:** 2.8e-007 **Queries matched:** 12

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4199	919.4126	919.4181	-0.0055	52 -	58	0	CQSQLER
935.4493	934.4420	934.4508	-0.0088	143 -	149	0	QQEQQFK
1056.4810	1055.4737	1055.4744	-0.0007	100 -	109	0	GAGSSQHQER
1085.5446	1084.5373	1084.5447	-0.0074	154 -	162	0	NLPQQCGLR
1091.5541	1090.5468	1090.5519	-0.0051	143 -	150	1	QQEQQFKR
1212.5635	1211.5562	1211.5755	-0.0193	99 -	109	1	RGAGSSQHQER
1624.7988	1623.7915	1623.7973	-0.0058	59 -	71	0	ANLRPCEQHLMQK
1640.7905	1639.7832	1639.7922	-0.0090	59 -	71	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6835	1725.6762	1725.6835	-0.0072	110 -	122	0	CCNELNEFENNQR
2012.8240	2011.8167	2011.8220	-0.0053	123 -	138	0	CMCEALQQIMENQSDR
2028.8229	2027.8156	2027.8169	-0.0013	123 -	138	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8170	2043.8097	2043.8118	-0.0021	123 -	138	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 1045.5647, 1050.1147, 1066.0924, 1072.1003, 1106.5363, 1107.5088, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1709.6591, 1940.9307, 2002.8278, 2211.1055, 2225.1204, 2230.1873, 2233.1331, 2247.1860, 2283.1641, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

8. gi|118776566 **Mass:** 19009 **Score:** 91 **Expect:** 6.5e-007 **Queries matched:** 12

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4199	919.4126	919.4181	-0.0055	33	39	0	CQSQLER
935.4493	934.4420	934.4508	-0.0088	122	128	0	QQEQQFK
1056.4810	1055.4737	1055.4744	-0.0007	79	88	0	GAGSSQHQER
1085.5446	1084.5373	1084.5447	-0.0074	133	141	0	NLPQQCGLR
1091.5541	1090.5468	1090.5519	-0.0051	122	129	1	QQEQQFKR
1212.5635	1211.5562	1211.5755	-0.0193	78	88	1	RGAGSSQHQER
1624.7988	1623.7915	1623.7973	-0.0058	40	52	0	ANLRPCEQHLMQK
1640.7905	1639.7832	1639.7922	-0.0090	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6835	1725.6762	1725.6835	-0.0072	89	101	0	CCNELNEFENNQR
2012.8240	2011.8167	2011.8220	-0.0053	102	117	0	CMCEALQQIMENQSDR
2028.8229	2027.8156	2027.8169	-0.0013	102	117	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8170	2043.8097	2043.8118	-0.0021	102	117	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 1045.5647, 1050.1147, 1066.0924, 1072.1003, 1106.5363, 1107.5088, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1709.6591, 1940.9307, 2002.8278, 2211.1055, 2225.1204, 2230.1873, 2233.1331, 2247.1860, 2283.1641, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

9. gi|14347293 **Mass:** 24390 **Score:** 89 **Expect:** 1.1e-006 **Queries matched:** 12

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
920.4199	919.4126	919.4181	-0.0055	33	39	0	CQSQLER
935.4493	934.4420	934.4508	-0.0088	124	130	0	QQEQQFK
1056.4810	1055.4737	1055.4744	-0.0007	81	90	0	GAGSSQHQER
1085.5446	1084.5373	1084.5447	-0.0074	135	143	0	NLPQQCGLR
1091.5541	1090.5468	1090.5519	-0.0051	124	131	1	QQEQQFKR
1212.5635	1211.5562	1211.5755	-0.0193	80	90	1	RGAGSSQHQER
1624.7988	1623.7915	1623.7973	-0.0058	40	52	0	ANLRPCEQHLMQK
1640.7905	1639.7832	1639.7922	-0.0090	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6835	1725.6762	1725.6835	-0.0072	91	103	0	CCNELNEFENNQR
2012.8240	2011.8167	2011.8220	-0.0053	104	119	0	CMCEALQQIMENQSDR
2028.8229	2027.8156	2027.8169	-0.0013	104	119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8170	2043.8097	2043.8118	-0.0021	104	119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 1045.5647, 1050.1147,

1066.0924, 1072.1003, 1106.5363, 1107.5088, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1709.6591, 1940.9307, 2002.8278, 2211.1055, 2225.1204, 2230.1873, 2233.1331, 2247.1860, 2283.1641, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

10. gi|114309696 **Mass:** 27933 **Score:** 21 **Expect:** 6.3 **Queries matched:** 3

MADS-box transcription factor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1624.7988	1623.7915	1623.7926	-0.0011	145	157	0	TQFMLDQLSELQR + Oxidation (M)
2233.1331	2232.1258	2232.0943	0.0315	112	131	1	NLMGEDLGPLSSKELESLER + Oxidation (M)
2283.1641	2282.1568	2282.1616	-0.0048	32	51	0	AYELSVLCDAEVALIIFSNR

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 920.4199, 935.4493, 1045.5647, 1050.1147, 1056.4810, 1066.0924, 1072.1003, 1085.5446, 1091.5541, 1106.5363, 1107.5088, 1212.5635, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1640.7905, 1709.6591, 1726.6835, 1940.9307, 2002.8278, 2012.8240, 2028.8229, 2044.8170, 2211.1055, 2225.1204, 2230.1873, 2247.1860, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 46

Protein View

Match to: **gi|46560482** Score: **101** Expect: **7e-008**
seed storage protein SSP2 [Arachis hypogaea]

Nominal mass (M_r): **20907**; Calculated pI value: **5.98**
NCBI BLAST search of gi|46560482 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: **46**
Number of mass values matched: **12**
Sequence Coverage: **44%**

Matched peptides shown in **Bold Red**

```
     1 DHTLFNTHSI TTTTTMAKLT ILVALALFLL AAHASARQQW EFQGDRRCQS
    51 QLERANLRPC EQHLMQKIQR DEDSYERDPY SPSQDPYSPS PYDRRGAGSS
   101 QHQERCCNEL NEFENNQRCM CEALQQIMEN QSDRLQGRQQ EQQFKRELRN
   151 LPQQCGLRAP QRCDLDVESG GRDRY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
48 - 54	920.4199	919.4126	919.4181	-0.0055	0	CQSQLER	
55 - 67	1624.7988	1623.7915	1623.7973	-0.0058	0	ANLRPCEQHLMQK	
55 - 67	1640.7905	1639.7832	1639.7922	-0.0090	0	ANLRPCEQHLMQK	Oxidation (M)
95 - 105	1212.5635	1211.5562	1211.5755	-0.0193	1	RGAGSSQHQER	
96 - 105	1056.4810	1055.4737	1055.4744	-0.0007	0	GAGSSQHQER	
106 - 118	1726.6835	1725.6762	1725.6835	-0.0072	0	CCNELNEFENNQR	
119 - 134	2012.8240	2011.8167	2011.8220	-0.0053	0	CMCEALQQIMENQSDR	
119 - 134	2028.8229	2027.8156	2027.8169	-0.0013	0	CMCEALQQIMENQSDR	Oxidation (M)
119 - 134	2044.8170	2043.8097	2043.8118	-0.0021	0	CMCEALQQIMENQSDR	2 Oxidation (M)
139 - 145	935.4493	934.4420	934.4508	-0.0088	0	QQEQQFK	
139 - 146	1091.5541	1090.5468	1090.5519	-0.0051	1	QQEQQFKR	
150 - 158	1085.5446	1084.5373	1084.5447	-0.0074	0	NLPQQCGLR	

No match to: 839.0961, 842.5089, 845.1082, 855.0710, 861.0854, 864.4980, 867.0914, 877.0543, 1045.5647, 1050.1147, 1066.0924, 1072.1003, 1106.5363, 1107.5088, 1277.1110, 1283.1243, 1455.7172, 1549.7167, 1565.7202, 1709.6591, 1940.9307, 2002.8278, 2211.1055, 2225.1204, 2230.1873, 2233.1331, 2247.1860, 2283.1641, 2299.1799, 2780.9580, 2787.9695, 2788.4985, 3338.7759, 3347.7192

Spot 90

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:45:19 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **412 for gi|118776570, arachin 6 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	412	arachin 6 [Arachis hypogaea]
2.	gi|52001233	9496	16	trypsin inhibitor [Arachis hypogaea]
3.	gi|33090235	9496	16	Bowman-Birk trypsin inhibitor [Arachis hypogaea]
4.	gi|84028521	16251	11	actin depolymerizing factor-like protein [Arachis hypogaea]
5.	gi|37221961	18605	11	resistance protein [Arachis simpsonii]
6.	gi|37221947	18735	11	resistance protein [Arachis hypogaea]
7.	gi|6093763	353436	10	Genome polyprotein [Contains: P1 proteinase (N-terminal protein); Helper component proteinase (H
8.	gi|71040671	18291	9	calcium-binding pollen allergen [Arachis hypogaea]
9.	gi|37221983	18301	9	resistance protein [Arachis cardenasii]
10.	gi|62177371	18155	9	resistance protein Cre [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 412 **Expect:** 5.5e-039 **Queries matched:** 8
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
870.5197	869.5124	869.5083	0.0042	279	285	0	---	QIVQNLR
2262.8184	2261.8111	2261.8243	-0.0132	312	329	0	---	SPDEEEEYDEDEYAEEER
2262.8184	2261.8111	2261.8243	-0.0132	312	329	0	150	SPDEEEEYDEDEYAEEER
2390.9128	2389.9055	2389.9193	-0.0138	311	329	1	---	KSPDEEEEYDEDEYAEEER
2441.2480	2440.2407	2440.2557	-0.0149	279	300	1	---	QIVQNLRGENESEEQGAIVTVK
2441.2480	2440.2407	2440.2557	-0.0149	279	300	1	52	QIVQNLRGENESEEQGAIVTVK
3291.4583	3290.4510	3290.4751	-0.0241	249	278	0	159	AGQEQENEGGNIFSGFTSEFLAQAFQVDDR
3291.4583	3290.4510	3290.4751	-0.0241	249	278	0	---	AGQEQENEGGNIFSGFTSEFLAQAFQVDDR

No match to: 853.4767, 982.5637, 1017.6588, 1033.6849, 1151.7114, 1314.6147, 1314.6147, 1434.8931, 1618.0563, 1732.0919,

2424.2161, 2424.2161

2. gi|52001233 **Mass:** 9496 **Score:** 16 **Expect:** 23 **Queries matched:** 2

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
3291.4583	3290.4510	3290.3366	0.1144	1 -	29	0	---	MLSQVINNIGEASSSSDDNVCCNGCLCDR + Oxidation (M)
3291.4583	3290.4510	3290.3366	0.1144	1 -	29	0	---	MLSQVINNIGEASSSSDDNVCCNGCLCDR + Oxidation (M)

No match to: 853.4767, 870.5197, 982.5637, 1017.6588, 1033.6849, 1151.7114, 1314.6147, 1314.6147, 1434.8931, 1618.0563, 1732.0919, 2262.8184, 2262.8184, 2390.9128, 2424.2161, 2424.2161, 2441.2480, 2441.2480

3. gi|33090235 **Mass:** 9496 **Score:** 16 **Expect:** 23 **Queries matched:** 2

Bowman-Birk trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
3291.4583	3290.4510	3290.3366	0.1144	1 -	29	0	---	MLSQVINNIGEASSSSDDNVCCNGCLCDR + Oxidation (M)
3291.4583	3290.4510	3290.3366	0.1144	1 -	29	0	---	MLSQVINNIGEASSSSDDNVCCNGCLCDR + Oxidation (M)

No match to: 853.4767, 870.5197, 982.5637, 1017.6588, 1033.6849, 1151.7114, 1314.6147, 1314.6147, 1434.8931, 1618.0563, 1732.0919, 2262.8184, 2262.8184, 2390.9128, 2424.2161, 2424.2161, 2441.2480, 2441.2480

4. gi|84028521 **Mass:** 16251 **Score:** 11 **Expect:** 66 **Queries matched:** 2

actin depolymerizing factor-like protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2424.2161	2423.2088	2423.0521	0.1567	46 -	66	0	---	LGEPAQGYEDFTACLPPNECR
2424.2161	2423.2088	2423.0521	0.1567	46 -	66	0	---	LGEPAQGYEDFTACLPPNECR

No match to: 853.4767, 870.5197, 982.5637, 1017.6588, 1033.6849, 1151.7114, 1314.6147, 1314.6147, 1434.8931, 1618.0563, 1732.0919, 2262.8184, 2262.8184, 2390.9128, 2441.2480, 2441.2480, 3291.4583, 3291.4583

5. gi|37221961 **Mass:** 18605 **Score:** 11 **Expect:** 78 **Queries matched:** 2

resistance protein [Arachis simpsonii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2424.2161	2423.2088	2423.1175	0.0913	139 -	158	1	---	MTRPKENYEDLSNQAIHYAQ + Oxidation (M)
2424.2161	2423.2088	2423.1175	0.0913	139 -	158	1	---	MTRPKENYEDLSNQAIHYAQ + Oxidation (M)

No match to: 853.4767, 870.5197, 982.5637, 1017.6588, 1033.6849, 1151.7114, 1314.6147, 1314.6147, 1434.8931, 1618.0563, 1732.0919, 2262.8184, 2262.8184, 2390.9128, 2441.2480, 2441.2480, 3291.4583, 3291.4583

6. gi|37221947 **Mass:** 18735 **Score:** 11 **Expect:** 78 **Queries matched:** 2

resistance protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2424.2161	2423.2088	2423.1175	0.0913	139 -	158	1	---	MTRPKENYEDLSNQAIHYAQ + Oxidation (M)
2424.2161	2423.2088	2423.1175	0.0913	139 -	158	1	---	MTRPKENYEDLSNQAIHYAQ + Oxidation (M)

No match to: 853.4767, 870.5197, 982.5637, 1017.6588, 1033.6849, 1151.7114, 1314.6147, 1314.6147, 1434.8931, 1618.0563, 1732.0919, 2262.8184, 2262.8184, 2390.9128, 2441.2480, 2441.2480, 3291.4583, 3291.4583

7. gi|6093763 **Mass:** 353436 **Score:** 10 **Expect:** 86 **Queries matched:** 7

Genome polyprotein [Contains: P1 proteinase (N-terminal protein); Helper component proteinase (HC-p

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
870.5197	869.5124	869.4719	0.0406	1910 -	1917	1	---	SKGNHTVK
1314.6147	1313.6074	1313.5822	0.0252	1613 -	1623	0	---	YNGSMHPEVHK + Oxidation (M)
1314.6147	1313.6074	1313.5822	0.0252	1613 -	1623	0	---	YNGSMHPEVHK + Oxidation (M)
2424.2161	2423.2088	2423.2036	0.0053	897 -	918	1	---	NELVSALTMMLARSDVDSTLNK + Oxidation (M)
2424.2161	2423.2088	2423.2036	0.0053	897 -	918	1	---	NELVSALTMMLARSDVDSTLNK + Oxidation (M)
3291.4583	3290.4510	3290.6216	-0.1705	1315 -	1344	1	---	MRGLTTFGSSNIVIMTSGFALHYYANNPTK
3291.4583	3290.4510	3290.6216	-0.1705	1315 -	1344	1	---	MRGLTTFGSSNIVIMTSGFALHYYANNPTK

No match to: 853.4767, 982.5637, 1017.6588, 1033.6849, 1151.7114, 1434.8931, 1618.0563, 1732.0919, 2262.8184, 2262.8184, 2390.9128, 2441.2480, 2441.2480

8. gi|71040671 **Mass:** 18291 **Score:** 9 **Expect:** 1e+002 **Queries matched:** 2

calcium-binding pollen allergen [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
2424.2161	2423.2088	2423.1637	0.0451	20 -	43	1	---	FDVNGDGKIDASELGAVMGSLGQK + Oxidation (M)
2424.2161	2423.2088	2423.1637	0.0451	20 -	43	1	---	FDVNGDGKIDASELGAVMGSLGQK + Oxidation (M)

No match to: 853.4767, 870.5197, 982.5637, 1017.6588, 1033.6849, 1151.7114, 1314.6147, 1314.6147, 1434.8931, 1618.0563, 1732.0919, 2262.8184, 2262.8184, 2390.9128, 2441.2480, 2441.2480, 3291.4583, 3291.4583

9. gi|37221983 **Mass:** 18301 **Score:** 9 **Expect:** 1.1e+002 **Queries matched:** 1

resistance protein [Arachis cardenasii]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1732.0919	1731.0846	1730.9753	0.1094	31 -	44	1	---	ELLLSLIRCLSTWK

No match to: 853.4767, 870.5197, 982.5637, 1017.6588, 1033.6849, 1151.7114, 1314.6147, 1314.6147, 1434.8931, 1618.0563, 2262.8184, 2262.8184, 2390.9128, 2424.2161, 2424.2161, 2441.2480, 2441.2480, 3291.4583, 3291.4583

10. gi|62177371 **Mass:** 18155 **Score:** 9 **Expect:** 1.1e+002 **Queries matched:** 2

resistance protein Cre [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1314.6147	1313.6074	1313.6364	-0.0289	6 -	16	1	---	NDQVAYFSRSK
1314.6147	1313.6074	1313.6364	-0.0289	6 -	16	1	---	NDQVAYFSRSK

No match to: 853.4767, 870.5197, 982.5637, 1017.6588, 1033.6849, 1151.7114, 1434.8931, 1618.0563, 1732.0919, 2262.8184, 2262.8184, 2390.9128, 2424.2161, 2424.2161, 2441.2480, 2441.2480, 3291.4583, 3291.4583

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Number of Queries: 20

Protein View

Match to: **gi|118776570** Score: **412** Expect: **5.5e-039**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

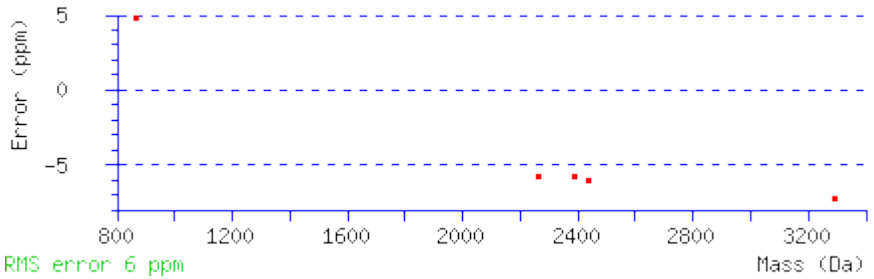
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **13%**

Matched peptides shown in **Bold Red**

```
     1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
    51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
   101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
   151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
   201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
   251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
   301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
   351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
   401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
   451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
   501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
249 - 278	3291.4583	3290.4510	3290.4751	-0.0241	0	AGQEQENEGGNIFSGFTSEFLAQAFQVDDR	(Ions score 159)
249 - 278	3291.4583	3290.4510	3290.4751	-0.0241	0	AGQEQENEGGNIFSGFTSEFLAQAFQVDDR	(No match)
279 - 285	870.5197	869.5124	869.5083	0.0042	0	QIVQNLR	(No match)
279 - 300	2441.2480	2440.2407	2440.2557	-0.0149	1	QIVQNLRGENESEEQGAIVTVK	(No match)
279 - 300	2441.2480	2440.2407	2440.2557	-0.0149	1	QIVQNLRGENESEEQGAIVTVK	(Ions score 52)
311 - 329	2390.9128	2389.9055	2389.9193	-0.0138	1	KSPDEEEEYDEDEYAEEER	(No match)
312 - 329	2262.8184	2261.8111	2261.8243	-0.0132	0	SPDEEEEYDEDEYAEEER	(No match)
312 - 329	2262.8184	2261.8111	2261.8243	-0.0132	0	SPDEEEEYDEDEYAEEER	(Ions score 150)



Spot 91

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **20 Mar 2007 at 13:18:09 GMT**
Top Score : **43 for gi|46560482, seed storage protein SSP2 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560482	20907	43	seed storage protein SSP2 [Arachis hypogaea]
2.	gi|15418705	18612	43	allergen II [Arachis hypogaea]
3.	gi|28912768	19765	42	seed storage protein [Arachis hypogaea]
4.	gi|31322017	20212	42	allergen Ara h 2 isoform [Arachis hypogaea]
5.	gi|17225991	17349	41	conglutin [Arachis hypogaea]
6.	gi|26245447	20558	40	allergen Ara h 2.02 [Arachis hypogaea]
7.	gi|52001227	21293	40	2S protein 1 [Arachis hypogaea]
8.	gi|57014074	17479	40	conglutin [Arachis hypogaea]
9.	gi|52001229	17479	40	conglutin [Arachis hypogaea]
10.	gi|75114094	17479	40	Conglutin precursor (Allergen Ara h 6)

Results List

1. gi|46560482 **Mass:** 20907 **Score:** **43** **Expect:** 0.041 **Queries matched:** 6
seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5566	1084.5493	1084.5447	0.0046	150	158	0	NLPQQCGLR
1091.5634	1090.5561	1090.5519	0.0042	139	146	1	QQEQQFKR
1212.5625	1211.5552	1211.5755	-0.0203	95	105	1	RGAGSSQHQER
1726.6969	1725.6896	1725.6835	0.0062	106	118	0	CCNELNEFENNQR
2028.8248	2027.8175	2027.8169	0.0006	119	134	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8240	2043.8167	2043.8118	0.0049	119	134	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1126.5684, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1549.7334, 1565.7234, 1652.8397,

1668.8364, 1698.6534, 1709.6760, 1715.6563, 1746.7678, 1753.9237, 1762.7656, 1940.9369, 2101.8279, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639

2. gi|15418705 **Mass:** 18612 **Score:** 43 **Expect:** 0.045 **Queries matched:** 6

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5566	1084.5493	1084.5447	0.0046	135	143	0	NLPQQCGLR
1091.5634	1090.5561	1090.5519	0.0042	124	131	1	QQEQQFKR
1212.5625	1211.5552	1211.5755	-0.0203	80	90	1	RGAGSSQHQER
1726.6969	1725.6896	1725.6835	0.0062	91	103	0	CCNELNEFENNQR
2028.8248	2027.8175	2027.8169	0.0006	104	119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8240	2043.8167	2043.8118	0.0049	104	119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1126.5684, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1549.7334, 1565.7234, 1652.8397, 1668.8364, 1698.6534, 1709.6760, 1715.6563, 1746.7678, 1753.9237, 1762.7656, 1940.9369, 2101.8279, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639

3. gi|28912768 **Mass:** 19765 **Score:** 42 **Expect:** 0.053 **Queries matched:** 6

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5566	1084.5493	1084.5447	0.0046	145	153	0	NLPQQCGLR
1091.5634	1090.5561	1090.5519	0.0042	134	141	1	QQEQQFKR
1212.5625	1211.5552	1211.5755	-0.0203	90	100	1	RGAGSSQHQER
1726.6969	1725.6896	1725.6835	0.0062	101	113	0	CCNELNEFENNQR
2028.8248	2027.8175	2027.8169	0.0006	114	129	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8240	2043.8167	2043.8118	0.0049	114	129	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1126.5684, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1549.7334, 1565.7234, 1652.8397, 1668.8364, 1698.6534, 1709.6760, 1715.6563, 1746.7678, 1753.9237, 1762.7656, 1940.9369, 2101.8279, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639

4. gi|31322017 **Mass:** 20212 **Score:** 42 **Expect:** 0.061 **Queries matched:** 6

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1085.5566	1084.5493	1084.5447	0.0046	144 - 152	0	NLPQQCGLR
1091.5634	1090.5561	1090.5519	0.0042	133 - 140	1	QQEQQFKR
1212.5625	1211.5552	1211.5755	-0.0203	89 - 99	1	RGAGSSQHQER
1726.6969	1725.6896	1725.6835	0.0062	100 - 112	0	CCNELNEFENNQR
2028.8248	2027.8175	2027.8169	0.0006	113 - 128	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8240	2043.8167	2043.8118	0.0049	113 - 128	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1126.5684, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1549.7334, 1565.7234, 1652.8397, 1668.8364, 1698.6534, 1709.6760, 1715.6563, 1746.7678, 1753.9237, 1762.7656, 1940.9369, 2101.8279, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639

5. gi|17225991 **Mass:** 17349 **Score:** 41 **Expect:** 0.073 **Queries matched:** 8

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1549.7334	1548.7261	1548.7177	0.0084	119 - 130		0	ELMNLPQQCNFR
1565.7234	1564.7161	1564.7126	0.0035	119 - 130		0	ELMNLPQQCNFR + Oxidation (M)
1652.8397	1651.8324	1651.8286	0.0038	41 - 53		0	VNLKPCEQHIMQR
1668.8364	1667.8291	1667.8235	0.0056	41 - 53		0	VNLKPCEQHIMQR + Oxidation (M)
1715.6563	1714.6490	1714.6233	0.0258	78 - 90		0	CCDELDQMENTER + Oxidation (M)
1746.7678	1745.7605	1745.7566	0.0039	54 - 67		0	IMGEQEQYDSYDIR
1762.7656	1761.7583	1761.7515	0.0068	54 - 67		0	IMGEQEQYDSYDIR + Oxidation (M)
2101.8279	2100.8206	2100.8155	0.0051	91 - 106		0	CMCEALQQIMENQCDR + Oxidation (M)

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1085.5566, 1091.5634, 1126.5684, 1212.5625, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1698.6534, 1709.6760, 1726.6969, 1753.9237, 1940.9369, 2028.8248, 2044.8240, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639

6. gi|26245447 **Mass:** 20558 **Score:** 40 **Expect:** 0.09 **Queries matched:** 6

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5566	1084.5493	1084.5447	0.0046	147 - 155		0	NLPQQCGLR
1091.5634	1090.5561	1090.5519	0.0042	136 - 143		1	QQEQQFKR
1212.5625	1211.5552	1211.5755	-0.0203	92 - 102		1	RGAGSSQHQER
1726.6969	1725.6896	1725.6835	0.0062	103 - 115		0	CCNELNEFENNQR
2028.8248	2027.8175	2027.8169	0.0006	116 - 131		0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8240	2043.8167	2043.8118	0.0049	116 - 131		0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1126.5684, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1549.7334, 1565.7234, 1652.8397, 1668.8364, 1698.6534, 1709.6760, 1715.6563, 1746.7678, 1753.9237, 1762.7656, 1940.9369, 2101.8279, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639

7. gi|52001227 **Mass:** 21293 **Score:** 40 **Expect:** 0.092 **Queries matched:** 6

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5566	1084.5493	1084.5447	0.0046	154	162	0	NLPQQCGLR
1091.5634	1090.5561	1090.5519	0.0042	143	150	1	QQEQQFKR
1212.5625	1211.5552	1211.5755	-0.0203	99	109	1	RGAGSSQHQER
1726.6969	1725.6896	1725.6835	0.0062	110	122	0	CCNELNEFENNQR
2028.8248	2027.8175	2027.8169	0.0006	123	138	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8240	2043.8167	2043.8118	0.0049	123	138	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1126.5684, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1549.7334, 1565.7234, 1652.8397, 1668.8364, 1698.6534, 1709.6760, 1715.6563, 1746.7678, 1753.9237, 1762.7656, 1940.9369, 2101.8279, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639

8. gi|57014074 **Mass:** 17479 **Score:** 40 **Expect:** 0.094 **Queries matched:** 8

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1549.7334	1548.7261	1548.7177	0.0084	120	131	0	ELMNLPQQCNFR
1565.7234	1564.7161	1564.7126	0.0035	120	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8397	1651.8324	1651.8286	0.0038	42	54	0	VNLKPCEQHIMQR
1668.8364	1667.8291	1667.8235	0.0056	42	54	0	VNLKPCEQHIMQR + Oxidation (M)
1698.6534	1697.6461	1697.6443	0.0018	79	91	0	CCDELNEMENTQR
1746.7678	1745.7605	1745.7566	0.0039	55	68	0	IMGEQEQYDSYDIR
1762.7656	1761.7583	1761.7515	0.0068	55	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2101.8279	2100.8206	2100.8155	0.0051	92	107	0	CMCEALQQIMENQCDR + Oxidation (M)

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1085.5566, 1091.5634, 1126.5684, 1212.5625, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1709.6760, 1715.6563, 1726.6969, 1753.9237, 1940.9369, 2028.8248, 2044.8240, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639

9. gi|52001229 **Mass:** 17479 **Score:** 40 **Expect:** 0.094 **Queries matched:** 8

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1549.7334	1548.7261	1548.7177	0.0084	120 -	131	0	ELMNLPQQCNFR
1565.7234	1564.7161	1564.7126	0.0035	120 -	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8397	1651.8324	1651.8286	0.0038	42 -	54	0	VNLKPCEQHIMQR
1668.8364	1667.8291	1667.8235	0.0056	42 -	54	0	VNLKPCEQHIMQR + Oxidation (M)
1698.6534	1697.6461	1697.6443	0.0018	79 -	91	0	CCDELNEMENTQR
1746.7678	1745.7605	1745.7566	0.0039	55 -	68	0	IMGEQEQYDSYDIR
1762.7656	1761.7583	1761.7515	0.0068	55 -	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2101.8279	2100.8206	2100.8155	0.0051	92 -	107	0	CMCEALQQIMENQCDR + Oxidation (M)

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1085.5566, 1091.5634, 1126.5684, 1212.5625, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1709.6760, 1715.6563, 1726.6969, 1753.9237, 1940.9369, 2028.8248, 2044.8240, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639

10. gi|75114094 **Mass:** 17479 **Score:** 40 **Expect:** 0.094 **Queries matched:** 8

Conglutin precursor (Allergen Ara h 6)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1549.7334	1548.7261	1548.7177	0.0084	120 -	131	0	ELMNLPQQCNFR
1565.7234	1564.7161	1564.7126	0.0035	120 -	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8397	1651.8324	1651.8286	0.0038	42 -	54	0	VNLKPCEQHIMQR
1668.8364	1667.8291	1667.8235	0.0056	42 -	54	0	VNLKPCEQHIMQR + Oxidation (M)
1698.6534	1697.6461	1697.6443	0.0018	79 -	91	0	CCDELNEMENTQR
1746.7678	1745.7605	1745.7566	0.0039	55 -	68	0	IMGEQEQYDSYDIR
1762.7656	1761.7583	1761.7515	0.0068	55 -	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2101.8279	2100.8206	2100.8155	0.0051	92 -	107	0	CMCEALQQIMENQCDR + Oxidation (M)

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1085.5566, 1091.5634, 1126.5684, 1212.5625, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1709.6760, 1715.6563, 1726.6969, 1753.9237, 1940.9369, 2028.8248, 2044.8240, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639

Search Parameters

Type of search : **Peptide Mass Fingerprint**
Enzyme : **Trypsin**
Fixed modifications : **Carbamidomethyl (C)**
Variable modifications : **Oxidation (M)**
Mass values : **MONOISOTOPIC**
Protein Mass : **Unrestricted**
Peptide Mass Tolerance : **± 20 ppm**
Peptide Charge State : **1+**
Max Missed Cleavages : **1**
Number of queries : **50**

Protein View

Match to: **gi|46560482** Score: **43** Expect: **0.041**
seed storage protein SSP2 [Arachis hypogaea]

Nominal mass (M_r): **20907**; Calculated pI value: **5.98**
NCBI BLAST search of gi|46560482 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **6**
Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

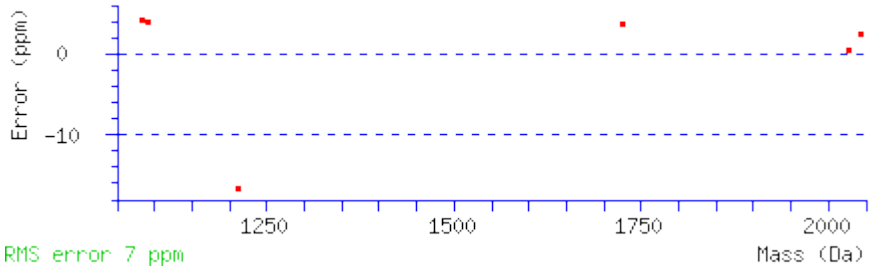
```
     1 DHTLFNTHSI TTTTTMAKLT ILVALALFLL AAHASARQQW EFQGDRRCQS
    51 QLERANLRPC EQHLMQKIQR DEDSYERDPY SPSQDPYSPS PYDRRGAGSS
   101 QHQERCCNEL NEFENNQRCM CEALQQIMEN QSDRLQGRQQ EQQFKRELRN
   151 LPQQCGLRAP QRCDLDVESG GRDRY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
95 - 105	1212.5625	1211.5552	1211.5755	-0.0203	1	RGAGSSQHQER	
106 - 118	1726.6969	1725.6896	1725.6835	0.0062	0	CCNELNEFENNQR	
119 - 134	2028.8248	2027.8175	2027.8169	0.0006	0	CMCEALQQIMENQSDR	Oxidation (M)
119 - 134	2044.8240	2043.8167	2043.8118	0.0049	0	CMCEALQQIMENQSDR	2 Oxidation (M)
139 - 146	1091.5634	1090.5561	1090.5519	0.0042	1	QQEQQFKR	

150 - 158	**1085.5566**	**1084.5493**	**1084.5447**	**0.0046**	**0**	**NLPQQCGLR**

No match to: 842.5088, 845.0960, 855.0533, 861.0737, 864.4929, 870.5406, 877.0449, 1003.5773, 1045.5657, 1050.1058, 1066.0789, 1072.0906, 1126.5684, 1277.1041, 1368.6229, 1455.7268, 1477.7260, 1549.7334, 1565.7234, 1652.8397, 1668.8364, 1698.6534, 1709.6760, 1715.6563, 1746.7678, 1753.9237, 1762.7656, 1940.9369, 2101.8279, 2211.1040, 2225.1189, 2233.1077, 2247.1663, 2299.1741, 2692.3184, 2749.3267, 2780.4502, 2788.4587, 2807.3218, 3337.7595, 3346.6694, 3351.6426, 3354.7483, 3355.7639



Spot 92

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **20 Mar 2007 at 13:18:32 GMT**
Top Score : **54 for gi|46560482, seed storage protein SSP2 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560482	20907	54	seed storage protein SSP2 [Arachis hypogaea]
2.	gi|15418705	18612	54	allergen II [Arachis hypogaea]
3.	gi|28912768	19765	53	seed storage protein [Arachis hypogaea]
4.	gi|31322017	20212	52	allergen Ara h 2 isoform [Arachis hypogaea]
5.	gi|26245447	20558	50	allergen Ara h 2.02 [Arachis hypogaea]
6.	gi|46560480	22229	50	seed storage protein SSP1 [Arachis hypogaea]
7.	gi|52001227	21293	50	2S protein 1 [Arachis hypogaea]
8.	gi|118776566	19009	48	conglutin 7 [Arachis hypogaea]
9.	gi|14347293	24390	46	unnamed protein product [Arachis hypogaea]
10.	gi|230338	23975	23	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|46560482 **Mass:** 20907 **Score:** 54 **Expect:** 0.0033 **Queries matched:** 6
seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4858	1055.4785	1055.4744	0.0041	96	105	0	GAGSSQHQER
1085.5553	1084.5480	1084.5447	0.0033	150	158	0	NLPQQCGLR
1091.5630	1090.5557	1090.5519	0.0038	139	146	1	QQEQQFKR
1212.5894	1211.5821	1211.5755	0.0066	95	105	1	RGAGSSQHQER
1537.7946	1536.7873	1536.7943	-0.0070	150	162	1	NLPQQCGLRAPQR
1726.6802	1725.6729	1725.6835	-0.0105	106	118	0	CCNELNEFENNQR

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1046.6060, 1051.7135, 1074.5442, 1080.5435, 1137.5796, 1145.0693, 1145.5720, 1339.6561, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2273.1599, 2305.1487, 2311.1431, 2514.3672, 2530.3379, 2694.1978, 3211.5366, 3300.8171, 3316.8137

2. gi|15418705 **Mass:** 18612 **Score:** 54 **Expect:** 0.0038 **Queries matched:** 6

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4858	1055.4785	1055.4744	0.0041	81	90	0	GAGSSQHQER
1085.5553	1084.5480	1084.5447	0.0033	135	143	0	NLPQQCGLR
1091.5630	1090.5557	1090.5519	0.0038	124	131	1	QQEQQFKR
1212.5894	1211.5821	1211.5755	0.0066	80	90	1	RGAGSSQHQER
1537.7946	1536.7873	1536.7943	-0.0070	135	147	1	NLPQQCGLRAPQR
1726.6802	1725.6729	1725.6835	-0.0105	91	103	0	CCNELNEFENNQR

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1046.6060, 1051.7135, 1074.5442, 1080.5435, 1137.5796, 1145.0693, 1145.5720, 1339.6561, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2273.1599, 2305.1487, 2311.1431, 2514.3672, 2530.3379, 2694.1978, 3211.5366, 3300.8171, 3316.8137

3. gi|28912768 **Mass:** 19765 **Score:** 53 **Expect:** 0.0043 **Queries matched:** 6

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4858	1055.4785	1055.4744	0.0041	91	100	0	GAGSSQHQER
1085.5553	1084.5480	1084.5447	0.0033	145	153	0	NLPQQCGLR
1091.5630	1090.5557	1090.5519	0.0038	134	141	1	QQEQQFKR
1212.5894	1211.5821	1211.5755	0.0066	90	100	1	RGAGSSQHQER
1537.7946	1536.7873	1536.7943	-0.0070	145	157	1	NLPQQCGLRAPQR
1726.6802	1725.6729	1725.6835	-0.0105	101	113	0	CCNELNEFENNQR

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1046.6060, 1051.7135, 1074.5442, 1080.5435, 1137.5796, 1145.0693, 1145.5720, 1339.6561, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2273.1599, 2305.1487, 2311.1431, 2514.3672, 2530.3379, 2694.1978, 3211.5366, 3300.8171, 3316.8137

4. gi|31322017 **Mass:** 20212 **Score:** 52 **Expect:** 0.005 **Queries matched:** 6

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4858	1055.4785	1055.4744	0.0041	90	99	0	GAGSSQHQER
1085.5553	1084.5480	1084.5447	0.0033	144	152	0	NLPQQCGLR
1091.5630	1090.5557	1090.5519	0.0038	133	140	1	QQEQQFKR
1212.5894	1211.5821	1211.5755	0.0066	89	99	1	RGAGSSQHQER
1537.7946	1536.7873	1536.7943	-0.0070	144	156	1	NLPQQCGLRAPQR
1726.6802	1725.6729	1725.6835	-0.0105	100	112	0	CCNELNEFENNQR

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1046.6060, 1051.7135, 1074.5442, 1080.5435, 1137.5796, 1145.0693,

1145.5720, 1339.6561, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2273.1599, 2305.1487, 2311.1431, 2514.3672, 2530.3379, 2694.1978, 3211.5366, 3300.8171, 3316.8137

5. gi|26245447 **Mass:** 20558 **Score:** 50 **Expect:** 0.008 **Queries matched:** 6

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4858	1055.4785	1055.4744	0.0041	93	102	0	GAGSSQHQER
1085.5553	1084.5480	1084.5447	0.0033	147	155	0	NLPQQCGLR
1091.5630	1090.5557	1090.5519	0.0038	136	143	1	QQEQQFKR
1212.5894	1211.5821	1211.5755	0.0066	92	102	1	RGAGSSQHQER
1537.7946	1536.7873	1536.7943	-0.0070	147	159	1	NLPQQCGLRAPQR
1726.6802	1725.6729	1725.6835	-0.0105	103	115	0	CCNELNEFENNQR

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1046.6060, 1051.7135, 1074.5442, 1080.5435, 1137.5796, 1145.0693, 1145.5720, 1339.6561, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2273.1599, 2305.1487, 2311.1431, 2514.3672, 2530.3379, 2694.1978, 3211.5366, 3300.8171, 3316.8137

6. gi|46560480 **Mass:** 22229 **Score:** 50 **Expect:** 0.008 **Queries matched:** 6

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4858	1055.4785	1055.4744	0.0041	108	117	0	GAGSSQHQER
1085.5553	1084.5480	1084.5447	0.0033	162	170	0	NLPQQCGLR
1091.5630	1090.5557	1090.5519	0.0038	151	158	1	QQEQQFKR
1212.5894	1211.5821	1211.5755	0.0066	107	117	1	RGAGSSQHQER
1537.7946	1536.7873	1536.7943	-0.0070	162	174	1	NLPQQCGLRAPQR
1726.6802	1725.6729	1725.6835	-0.0105	118	130	0	CCNELNEFENNQR

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1046.6060, 1051.7135, 1074.5442, 1080.5435, 1137.5796, 1145.0693, 1145.5720, 1339.6561, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2273.1599, 2305.1487, 2311.1431, 2514.3672, 2530.3379, 2694.1978, 3211.5366, 3300.8171, 3316.8137

7. gi|52001227 **Mass:** 21293 **Score:** 50 **Expect:** 0.0084 **Queries matched:** 6

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4858	1055.4785	1055.4744	0.0041	100	109	0	GAGSSQHQER
1085.5553	1084.5480	1084.5447	0.0033	154	162	0	NLPQQCGLR
1091.5630	1090.5557	1090.5519	0.0038	143	150	1	QQEQQFKR
1212.5894	1211.5821	1211.5755	0.0066	99	109	1	RGAGSSQHQER
1537.7946	1536.7873	1536.7943	-0.0070	154	166	1	NLPQQCGLRAPQR

1726.6802	1725.6729	1725.6835	-0.0105	110 - 122	0	CCNELNEFENNQR

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1046.6060, 1051.7135, 1074.5442, 1080.5435, 1137.5796, 1145.0693, 1145.5720, 1339.6561, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2273.1599, 2305.1487, 2311.1431, 2514.3672, 2530.3379, 2694.1978, 3211.5366, 3300.8171, 3316.8137

8. gi|118776566 **Mass:** 19009 **Score:** 48 **Expect:** 0.014 **Queries matched:** 6

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4858	1055.4785	1055.4744	0.0041	79 -	88	0	GAGSSQHQER
1085.5553	1084.5480	1084.5447	0.0033	133 -	141	0	NLPQQCGLR
1091.5630	1090.5557	1090.5519	0.0038	122 -	129	1	QQEQQFKR
1212.5894	1211.5821	1211.5755	0.0066	78 -	88	1	RGAGSSQHQER
1537.7946	1536.7873	1536.7943	-0.0070	133 -	145	1	NLPQQCGLRAPQR
1726.6802	1725.6729	1725.6835	-0.0105	89 -	101	0	CCNELNEFENNQR

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1046.6060, 1051.7135, 1074.5442, 1080.5435, 1137.5796, 1145.0693, 1145.5720, 1339.6561, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2273.1599, 2305.1487, 2311.1431, 2514.3672, 2530.3379, 2694.1978, 3211.5366, 3300.8171, 3316.8137

9. gi|14347293 **Mass:** 24390 **Score:** 46 **Expect:** 0.021 **Queries matched:** 6

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4858	1055.4785	1055.4744	0.0041	81 -	90	0	GAGSSQHQER
1085.5553	1084.5480	1084.5447	0.0033	135 -	143	0	NLPQQCGLR
1091.5630	1090.5557	1090.5519	0.0038	124 -	131	1	QQEQQFKR
1212.5894	1211.5821	1211.5755	0.0066	80 -	90	1	RGAGSSQHQER
1537.7946	1536.7873	1536.7943	-0.0070	135 -	147	1	NLPQQCGLRAPQR
1726.6802	1725.6729	1725.6835	-0.0105	91 -	103	0	CCNELNEFENNQR

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1046.6060, 1051.7135, 1074.5442, 1080.5435, 1137.5796, 1145.0693, 1145.5720, 1339.6561, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2273.1599, 2305.1487, 2311.1431, 2514.3672, 2530.3379, 2694.1978, 3211.5366, 3300.8171, 3316.8137

10. gi|230338 **Mass:** 23975 **Score:** 23 **Expect:** 4.1 **Queries matched:** 4

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1046.6060	1045.5987	1045.5880	0.0108	90 -	99	1	LKSAASLNSR
2273.1599	2272.1526	2272.1521	0.0005	70 -	89	0	SIVHPSYNSNTLNNDIMLIK

2514.3672	2513.3599	2513.3311	0.0288	70 - 91	1	SIVHPSYNSNTLNNDIMLIKLK
2530.3379	2529.3306	2529.3260	0.0046	70 - 91	1	SIVHPSYNSNTLNNDIMLIKLK + Oxidation (M)

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1051.7135, 1056.4858, 1074.5442, 1080.5435, 1085.5553, 1091.5630, 1137.5796, 1145.0693, 1145.5720, 1212.5894, 1339.6561, 1537.7946, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1726.6802, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2305.1487, 2311.1431, 2694.1978, 3211.5366, 3300.8171, 3316.8137

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|46560482** Score: **54** Expect: **0.0033**
seed storage protein SSP2 [Arachis hypogaea]

Nominal mass (M_r): **20907**; Calculated pI value: **5.98**
NCBI BLAST search of gi|46560482 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **6**
Sequence Coverage: **25%**

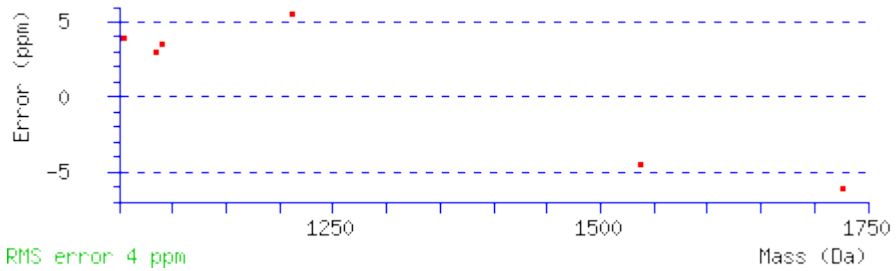
Matched peptides shown in **Bold Red**

```
     1 DHTLFNTHSI TTTTTMAKLT ILVALALFLL AAHASARQQW EFQGDRRCQS
    51 QLERANLRPC EQHLMQKIQR DEDSYERDPY SPSQDPYSPS PYDRRGAGSS
   101 QHQERCCNEL NEFENNQRCM CEALQQIMEN QSDRLQGRQQ EQQFKRELRN
   151 LPQQCGLRAP QRCDLDVESG GRDRY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
95 - 105	1212.5894	1211.5821	1211.5755	0.0066	1	RGAGSSQHQER
96 - 105	1056.4858	1055.4785	1055.4744	0.0041	0	GAGSSQHQER
106 - 118	1726.6802	1725.6729	1725.6835	-0.0105	0	CCNELNEFENNQR
139 - 146	1091.5630	1090.5557	1090.5519	0.0038	1	QQEQQFKR
150 - 158	1085.5553	1084.5480	1084.5447	0.0033	0	NLPQQCGLR
150 - 162	1537.7946	1536.7873	1536.7943	-0.0070	1	NLPQQCGLRAPQR

No match to: 805.4796, 814.5278, 823.5698, 828.4952, 834.5198, 838.5601, 847.5002, 851.5267, 861.0978, 867.5244, 868.5721, 881.2903, 882.5872, 935.5615, 997.5737, 1046.6060, 1051.7135, 1074.5442, 1080.5435, 1137.5796, 1145.0693, 1145.5720, 1339.6561, 1541.6656, 1565.7056, 1638.8203, 1669.6989, 1709.6521, 1725.6523, 1756.8329, 1762.7469, 1774.8529, 2145.0447, 2146.5999, 2185.0376, 2273.1599, 2305.1487, 2311.1431, 2514.3672, 2530.3379, 2694.1978, 3211.5366, 3300.8171, 3316.8137



Spot 93A

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 26 Feb 2007 at 15:16:28 GMT
Top Score : 58 for gi|46560482, seed storage protein SSP2 [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560482	20907	58	seed storage protein SSP2 [Arachis hypogaea]
2.	gi|15418705	18612	57	allergen II [Arachis hypogaea]
3.	gi|28912768	19765	57	seed storage protein [Arachis hypogaea]
4.	gi|31322017	20212	56	allergen Ara h 2 isoform [Arachis hypogaea]
5.	gi|26245447	20558	54	allergen Ara h 2.02 [Arachis hypogaea]
6.	gi|52001227	21293	54	2S protein 1 [Arachis hypogaea]
7.	gi|46560480	22229	54	seed storage protein SSP1 [Arachis hypogaea]
8.	gi|118776566	19009	52	conglutin 7 [Arachis hypogaea]
9.	gi|14347293	24390	50	unnamed protein product [Arachis hypogaea]
10.	gi|71040687	13451	25	auxin-repressed protein [Arachis hypogaea]

Results List

1. gi|46560482 **Mass:** 20907 **Score:** 58 **Expect:** 0.0015 **Queries matched:** 6
seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4923	1055.4850	1055.4744	0.0106	96	105	0	GAGSSQHQER
1085.5525	1084.5452	1084.5447	0.0005	150	158	0	NLPQQCGLR
1091.5559	1090.5486	1090.5519	-0.0033	139	146	1	QQEQQFKR
1537.7909	1536.7836	1536.7943	-0.0107	150	162	1	NLPQQCGLRAPQR
1726.6821	1725.6748	1725.6835	-0.0086	106	118	0	CCNELNEFENNQR
2467.1284	2466.1211	2466.0872	0.0339	119	138	1	CMCEALQQIMENQSDRLQGR

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1066.0797, 1072.0846, 1074.5354, 1080.5281, 1082.0470, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1674.7540, 1709.6582,

1725.6567, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3137.4683, 3211.6416, 3213.5132

2. gi|15418705 **Mass:** 18612 **Score:** 57 **Expect:** 0.0017 **Queries matched:** 6

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4923	1055.4850	1055.4744	0.0106	81	90	0	GAGSSQHQER
1085.5525	1084.5452	1084.5447	0.0005	135	143	0	NLPQQCGLR
1091.5559	1090.5486	1090.5519	-0.0033	124	131	1	QQEQQFKR
1537.7909	1536.7836	1536.7943	-0.0107	135	147	1	NLPQQCGLRAPQR
1726.6821	1725.6748	1725.6835	-0.0086	91	103	0	CCNELNEFENNQR
2467.1284	2466.1211	2466.0872	0.0339	104	123	1	CMCEALQQIMENQSDRLQGR

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1066.0797, 1072.0846, 1074.5354, 1080.5281, 1082.0470, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1674.7540, 1709.6582, 1725.6567, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3137.4683, 3211.6416, 3213.5132

3. gi|28912768 **Mass:** 19765 **Score:** 57 **Expect:** 0.0018 **Queries matched:** 6

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4923	1055.4850	1055.4744	0.0106	91	100	0	GAGSSQHQER
1085.5525	1084.5452	1084.5447	0.0005	145	153	0	NLPQQCGLR
1091.5559	1090.5486	1090.5519	-0.0033	134	141	1	QQEQQFKR
1537.7909	1536.7836	1536.7943	-0.0107	145	157	1	NLPQQCGLRAPQR
1726.6821	1725.6748	1725.6835	-0.0086	101	113	0	CCNELNEFENNQR
2467.1284	2466.1211	2466.0872	0.0339	114	133	1	CMCEALQQIMENQSDRLQGR

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1066.0797, 1072.0846, 1074.5354, 1080.5281, 1082.0470, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1674.7540, 1709.6582, 1725.6567, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3137.4683, 3211.6416, 3213.5132

4. gi|31322017 **Mass:** 20212 **Score:** 56 **Expect:** 0.0022 **Queries matched:** 6

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1056.4923	1055.4850	1055.4744	0.0106	90 - 99	0	GAGSSQHQER
1085.5525	1084.5452	1084.5447	0.0005	144 - 152	0	NLPQQCGLR
1091.5559	1090.5486	1090.5519	-0.0033	133 - 140	1	QQEQQFKR
1537.7909	1536.7836	1536.7943	-0.0107	144 - 156	1	NLPQQCGLRAPQR
1726.6821	1725.6748	1725.6835	-0.0086	100 - 112	0	CCNELNEFENNQR
2467.1284	2466.1211	2466.0872	0.0339	113 - 132	1	CMCEALQQIMENQSDRLQGR

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1066.0797, 1072.0846, 1074.5354, 1080.5281, 1082.0470, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1674.7540, 1709.6582, 1725.6567, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3137.4683, 3211.6416, 3213.5132

5. gi|26245447 **Mass:** 20558 **Score:** 54 **Expect:** 0.0036 **Queries matched:** 6

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4923	1055.4850	1055.4744	0.0106	93 - 102		0	GAGSSQHQER
1085.5525	1084.5452	1084.5447	0.0005	147 - 155		0	NLPQQCGLR
1091.5559	1090.5486	1090.5519	-0.0033	136 - 143		1	QQEQQFKR
1537.7909	1536.7836	1536.7943	-0.0107	147 - 159		1	NLPQQCGLRAPQR
1726.6821	1725.6748	1725.6835	-0.0086	103 - 115		0	CCNELNEFENNQR
2467.1284	2466.1211	2466.0872	0.0339	116 - 135		1	CMCEALQQIMENQSDRLQGR

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1066.0797, 1072.0846, 1074.5354, 1080.5281, 1082.0470, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1674.7540, 1709.6582, 1725.6567, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3137.4683, 3211.6416, 3213.5132

6. gi|52001227 **Mass:** 21293 **Score:** 54 **Expect:** 0.0037 **Queries matched:** 6

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4923	1055.4850	1055.4744	0.0106	100 - 109		0	GAGSSQHQER
1085.5525	1084.5452	1084.5447	0.0005	154 - 162		0	NLPQQCGLR
1091.5559	1090.5486	1090.5519	-0.0033	143 - 150		1	QQEQQFKR
1537.7909	1536.7836	1536.7943	-0.0107	154 - 166		1	NLPQQCGLRAPQR
1726.6821	1725.6748	1725.6835	-0.0086	110 - 122		0	CCNELNEFENNQR
2467.1284	2466.1211	2466.0872	0.0339	123 - 142		1	CMCEALQQIMENQSDRLQGR

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1066.0797, 1072.0846,

1074.5354, 1080.5281, 1082.0470, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1674.7540, 1709.6582, 1725.6567, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3137.4683, 3211.6416, 3213.5132

7. gi|46560480 **Mass:** 22229 **Score:** 54 **Expect:** 0.0039 **Queries matched:** 6

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4923	1055.4850	1055.4744	0.0106	108	117	0	GAGSSQHQER
1085.5525	1084.5452	1084.5447	0.0005	162	170	0	NLPQQCGLR
1091.5559	1090.5486	1090.5519	-0.0033	151	158	1	QQEQQFKR
1537.7909	1536.7836	1536.7943	-0.0107	162	174	1	NLPQQCGLRAPQR
1726.6821	1725.6748	1725.6835	-0.0086	118	130	0	CCNELNEFENNQR
2467.1284	2466.1211	2466.0872	0.0339	131	150	1	CMCEALQQIMENQSDRLQGR

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1066.0797, 1072.0846, 1074.5354, 1080.5281, 1082.0470, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1674.7540, 1709.6582, 1725.6567, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3137.4683, 3211.6416, 3213.5132

8. gi|118776566 **Mass:** 19009 **Score:** 52 **Expect:** 0.005 **Queries matched:** 6

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4923	1055.4850	1055.4744	0.0106	79	88	0	GAGSSQHQER
1085.5525	1084.5452	1084.5447	0.0005	133	141	0	NLPQQCGLR
1091.5559	1090.5486	1090.5519	-0.0033	122	129	1	QQEQQFKR
1537.7909	1536.7836	1536.7943	-0.0107	133	145	1	NLPQQCGLRAPQR
1726.6821	1725.6748	1725.6835	-0.0086	89	101	0	CCNELNEFENNQR
2467.1284	2466.1211	2466.0872	0.0339	102	121	1	CMCEALQQIMENQSDRLQGR

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1066.0797, 1072.0846, 1074.5354, 1080.5281, 1082.0470, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1674.7540, 1709.6582, 1725.6567, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3137.4683, 3211.6416, 3213.5132

9. gi|14347293 **Mass:** 24390 **Score:** 50 **Expect:** 0.0094 **Queries matched:** 6

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1056.4923	1055.4850	1055.4744	0.0106	81 -	90	0	GAGSSQHQER
1085.5525	1084.5452	1084.5447	0.0005	135 -	143	0	NLPQQCGLR
1091.5559	1090.5486	1090.5519	-0.0033	124 -	131	1	QQEQQFKR
1537.7909	1536.7836	1536.7943	-0.0107	135 -	147	1	NLPQQCGLRAPQR
1726.6821	1725.6748	1725.6835	-0.0086	91 -	103	0	CCNELNEFENNQR
2467.1284	2466.1211	2466.0872	0.0339	104 -	123	1	CMCEALQQIMENQSDRLQGR

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1066.0797, 1072.0846, 1074.5354, 1080.5281, 1082.0470, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1674.7540, 1709.6582, 1725.6567, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3137.4683, 3211.6416, 3213.5132

10. gi|71040687 **Mass:** 13451 **Score:** 25 **Expect:** 2.8 **Queries matched:** 2

auxin-repressed protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
3137.4683	3136.4610	3136.5029	-0.0418	91 -	117	0	TIGSDYFDKPLLNSPTVYDWLYSGETR
3211.6416	3210.6343	3210.5802	0.0542	49 -	78	1	SMSMPATPTTPGTPTTPLSATPRKPDNVWR + Oxidation (M)

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1056.4923, 1066.0797, 1072.0846, 1074.5354, 1080.5281, 1082.0470, 1085.5525, 1091.5559, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1537.7909, 1674.7540, 1709.6582, 1725.6567, 1726.6821, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2467.1284, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3213.5132

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 47

Protein View

Match to: **gi|46560482** Score: **58** Expect: **0.0015**
seed storage protein SSP2 [Arachis hypogaea]

Nominal mass (M_r): **20907**; Calculated pI value: **5.98**
NCBI BLAST search of gi|46560482 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **47**
Number of mass values matched: **6**
Sequence Coverage: **36%**

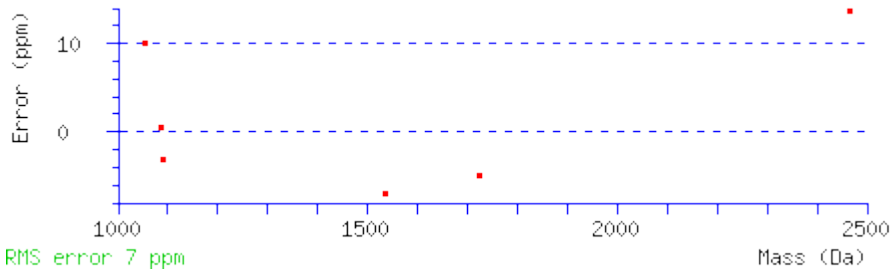
Matched peptides shown in **Bold Red**

```
     1 DHTLFNTHSI TTTTTMAKLT ILVALALFLL AAHASARQQW EFQGDRRCQS
    51 QLERANLRPC EQHLMQKIQR DEDSYERDPY SPSQDPYSPS PYDRRGAGSS
   101 QHQERCCNEL NEFENNQRCM CEALQQIMEN QSDRLQGRQQ EQQFKRELRN
   151 LPQQCGLRAP QRCDLDVESG GRDRY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
96 - 105	1056.4923	1055.4850	1055.4744	0.0106	0	GAGSSQHQER
106 - 118	1726.6821	1725.6748	1725.6835	-0.0086	0	CCNELNEFENNQR
119 - 138	2467.1284	2466.1211	2466.0872	0.0339	1	CMCEALQQIMENQSDRLQGR
139 - 146	1091.5559	1090.5486	1090.5519	-0.0033	1	QQEQQFKR
150 - 158	1085.5525	1084.5452	1084.5447	0.0005	0	NLPQQCGLR
150 - 162	1537.7909	1536.7836	1536.7943	-0.0107	1	NLPQQCGLRAPQR

No match to: 805.4623, 845.0994, 855.0666, 861.0807, 877.0466, 881.2742, 968.4404, 1046.5953, 1066.0797, 1072.0846, 1074.5354, 1080.5281, 1082.0470, 1145.0706, 1145.5709, 1175.5483, 1277.0894, 1339.6533, 1674.7540, 1709.6582, 1725.6567, 1727.6787, 1729.6604, 1745.6577, 1774.8170, 1799.8724, 2146.6094, 2162.0161, 2185.0417, 2224.9919, 2273.1563, 2311.1282, 2351.0815, 2353.0842, 2476.2649, 2528.3127, 2694.2310, 2710.1877, 3137.4683, 3211.6416, 3213.5132


Error (ppm)
10
0
1000
1500
2000
2500
Mass (Da)
RMS error 7 ppm

Spot 93B

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **20 Mar 2007 at 13:17:37 GMT**
Top Score : **131 for Mixture 1, gi|52001229 + gi|46560482**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	Mixture 1		131	gi|52001229 + gi|46560482
2.	Mixture 2		131	gi|57669906 + gi|46560482
3.	gi|17225991	17349	91	conglutin [Arachis hypogaea]
4.	gi|52001229	17479	89	conglutin [Arachis hypogaea]
5.	gi|75114094	17479	89	Conglutin precursor (Allergen Ara h 6)
6.	gi|57014074	17479	89	conglutin [Arachis hypogaea]
7.	gi|57669906	17480	89	conglutin [Arachis hypogaea]
8.	gi|83753503	15575	51	Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)
9.	gi|57118278	15280	51	Ara h 6 allergen [Arachis hypogaea]
10.	gi|118776568	17335	48	conglutin 8 [Arachis hypogaea]

Results List

1. **Mixture 1** **Total score: 131** **Expect:** 7e-011 **Queries matched:** 17

Components: 1. gi|52001229 conglutin [Arachis hypogaea]
2. gi|46560482 seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Comp	Peptide
1025.4077	1024.4004	1024.3880	0.0125	29	37	0	1	QGDSSSCER
1056.4974	1055.4901	1055.4744	0.0157	96	105	0	2	GAGSSQHQER
1064.5566	1063.5493	1063.5596	-0.0103	112	119	1	1	QMVQQFKR
1080.5652	1079.5579	1079.5546	0.0034	112	119	1	1	QMVQQFKR + Oxidation (M)
1085.5588	1084.5515	1084.5447	0.0068	150	158	0	2	NLPQQCGLR
1091.5671	1090.5598	1090.5519	0.0079	139	146	1	2	QQEQQFKR
1238.5190	1237.5117	1237.5105	0.0012	27	37	1	1	GRQGDSSSCER
1537.7900	1536.7827	1536.7943	-0.0116	150	162	1	2	NLPQQCGLRAPQR

1549.7142	1548.7069	1548.7177	-0.0108	120 - 131	0	1	ELMNLPQQCNFR
1565.7089	1564.7016	1564.7126	-0.0110	120 - 131	0	1	ELMNLPQQCNFR + Oxidation (M)
1668.8181	1667.8108	1667.8235	-0.0127	42 - 54	0	1	VNLKPCEQHIMQR + Oxidation (M)
1714.6318	1713.6245	1713.6392	-0.0147	79 - 91	0	1	CCDELNEMENTQR + Oxidation (M)
1726.6772	1725.6699	1725.6835	-0.0135	106 - 118	0	2	CCNELNEFENNQR
1746.7491	1745.7418	1745.7566	-0.0148	55 - 68	0	1	IMGEQEQYDSYDIR
1762.7466	1761.7393	1761.7515	-0.0122	55 - 68	0	1	IMGEQEQYDSYDIR + Oxidation (M)
2017.9589	2016.9516	2016.9621	-0.0105	120 - 135	1	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2106.9495	2105.9422	2105.9323	0.0099	55 - 71	1	1	IMGEQEQYDSYDIRSTR + Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1063.5392, 1074.5464, 1079.5321, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1715.6230, 1778.7520, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

2. Mixture 2 **Total score: 131** **Expect:** 7e-011 **Queries matched:** 17

Components: 1. gi|57669906 conglutin [Arachis hypogaea]
2. gi|46560482 seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Comp	Peptide
1025.4077	1024.4004	1024.3880	0.0125	29 -	37	0	1	QGDSSSCER
1056.4974	1055.4901	1055.4744	0.0157	96 -	105	0	2	GAGSSQHQER
1064.5566	1063.5493	1063.5596	-0.0103	112 -	119	1	1	QMVQQFKR
1080.5652	1079.5579	1079.5546	0.0034	112 -	119	1	1	QMVQQFKR + Oxidation (M)
1085.5588	1084.5515	1084.5447	0.0068	150 -	158	0	2	NLPQQCGLR
1091.5671	1090.5598	1090.5519	0.0079	139 -	146	1	2	QQEQQFKR
1238.5190	1237.5117	1237.5105	0.0012	27 -	37	1	1	GRQGDSSSCER
1537.7900	1536.7827	1536.7943	-0.0116	150 -	162	1	2	NLPQQCGLRAPQR
1549.7142	1548.7069	1548.7177	-0.0108	120 -	131	0	1	ELMNLPQQCNFR
1565.7089	1564.7016	1564.7126	-0.0110	120 -	131	0	1	ELMNLPQQCNFR + Oxidation (M)
1668.8181	1667.8108	1667.8235	-0.0127	42 -	54	0	1	VNLKPCEQHIMQR + Oxidation (M)
1715.6230	1714.6157	1714.6233	-0.0075	79 -	91	0	1	CCDELDQMENTER + Oxidation (M)
1726.6772	1725.6699	1725.6835	-0.0135	106 -	118	0	2	CCNELNEFENNQR
1746.7491	1745.7418	1745.7566	-0.0148	55 -	68	0	1	IMGEQEQYDSYDIR
1762.7466	1761.7393	1761.7515	-0.0122	55 -	68	0	1	IMGEQEQYDSYDIR + Oxidation (M)
2017.9589	2016.9516	2016.9621	-0.0105	120 -	135	1	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2106.9495	2105.9422	2105.9323	0.0099	55 -	71	1	1	IMGEQEQYDSYDIRSTR + Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1063.5392, 1074.5464, 1079.5321, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1714.6318, 1778.7520, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

3. gi|17225991 **Mass:** 17349 **Score: 91** **Expect:** 7.4e-007 **Queries matched:** 12

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1025.4077	1024.4004	1024.3880	0.0125	28	36	0	QGDSSSCER
1064.5566	1063.5493	1063.5596	-0.0103	111	118	1	QMVQQFKR
1080.5652	1079.5579	1079.5546	0.0034	111	118	1	QMVQQFKR + Oxidation (M)
1238.5190	1237.5117	1237.5105	0.0012	26	36	1	GRQGDSSSCER
1549.7142	1548.7069	1548.7177	-0.0108	119	130	0	ELMNLPQQCNFR
1565.7089	1564.7016	1564.7126	-0.0110	119	130	0	ELMNLPQQCNFR + Oxidation (M)
1668.8181	1667.8108	1667.8235	-0.0127	41	53	0	VNLKPCEQHIMQR + Oxidation (M)
1715.6230	1714.6157	1714.6233	-0.0075	78	90	0	CCDELDQMENTER + Oxidation (M)
1746.7491	1745.7418	1745.7566	-0.0148	54	67	0	IMGEQEQYDSYDIR
1762.7466	1761.7393	1761.7515	-0.0122	54	67	0	IMGEQEQYDSYDIR + Oxidation (M)
2017.9589	2016.9516	2016.9621	-0.0105	119	134	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2106.9495	2105.9422	2105.9323	0.0099	54	70	1	IMGEQEQYDSYDIRSTR + Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1056.4974, 1063.5392, 1074.5464, 1079.5321, 1085.5588, 1091.5671, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1537.7900, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1714.6318, 1726.6772, 1778.7520, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

4. gi|52001229 **Mass:** 17479 **Score:** 89 **Expect:** 1.2e-006 **Queries matched:** 12

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1025.4077	1024.4004	1024.3880	0.0125	29	37	0	QGDSSSCER
1064.5566	1063.5493	1063.5596	-0.0103	112	119	1	QMVQQFKR
1080.5652	1079.5579	1079.5546	0.0034	112	119	1	QMVQQFKR + Oxidation (M)
1238.5190	1237.5117	1237.5105	0.0012	27	37	1	GRQGDSSSCER
1549.7142	1548.7069	1548.7177	-0.0108	120	131	0	ELMNLPQQCNFR
1565.7089	1564.7016	1564.7126	-0.0110	120	131	0	ELMNLPQQCNFR + Oxidation (M)
1668.8181	1667.8108	1667.8235	-0.0127	42	54	0	VNLKPCEQHIMQR + Oxidation (M)
1714.6318	1713.6245	1713.6392	-0.0147	79	91	0	CCDELNEMENTQR + Oxidation (M)
1746.7491	1745.7418	1745.7566	-0.0148	55	68	0	IMGEQEQYDSYDIR
1762.7466	1761.7393	1761.7515	-0.0122	55	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2017.9589	2016.9516	2016.9621	-0.0105	120	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2106.9495	2105.9422	2105.9323	0.0099	55	71	1	IMGEQEQYDSYDIRSTR + Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1056.4974, 1063.5392, 1074.5464, 1079.5321, 1085.5588, 1091.5671, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1537.7900, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1715.6230, 1726.6772, 1778.7520, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

5. gi|75114094 **Mass:** 17479 **Score:** 89 **Expect:** 1.2e-006 **Queries matched:** 12

Conglutin precursor (Allergen Ara h 6)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1025.4077	1024.4004	1024.3880	0.0125	29	-	37	0	QGDSSSCER
1064.5566	1063.5493	1063.5596	-0.0103	112	-	119	1	QMVQQFKR
1080.5652	1079.5579	1079.5546	0.0034	112	-	119	1	QMVQQFKR + Oxidation (M)
1238.5190	1237.5117	1237.5105	0.0012	27	-	37	1	GRQGDSSSCER
1549.7142	1548.7069	1548.7177	-0.0108	120	-	131	0	ELMNLPQQCNFR
1565.7089	1564.7016	1564.7126	-0.0110	120	-	131	0	ELMNLPQQCNFR + Oxidation (M)
1668.8181	1667.8108	1667.8235	-0.0127	42	-	54	0	VNLKPCEQHIMQR + Oxidation (M)
1714.6318	1713.6245	1713.6392	-0.0147	79	-	91	0	CCDELNEMENTQR + Oxidation (M)
1746.7491	1745.7418	1745.7566	-0.0148	55	-	68	0	IMGEQEQYDSYDIR
1762.7466	1761.7393	1761.7515	-0.0122	55	-	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2017.9589	2016.9516	2016.9621	-0.0105	120	-	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2106.9495	2105.9422	2105.9323	0.0099	55	-	71	1	IMGEQEQYDSYDIRSTR + Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1056.4974, 1063.5392, 1074.5464, 1079.5321, 1085.5588, 1091.5671, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1537.7900, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1715.6230, 1726.6772, 1778.7520, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

6. gi|57014074 **Mass:** 17479 **Score:** 89 **Expect:** 1.2e-006 **Queries matched:** 12

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1025.4077	1024.4004	1024.3880	0.0125	29	-	37	0	QGDSSSCER
1064.5566	1063.5493	1063.5596	-0.0103	112	-	119	1	QMVQQFKR
1080.5652	1079.5579	1079.5546	0.0034	112	-	119	1	QMVQQFKR + Oxidation (M)
1238.5190	1237.5117	1237.5105	0.0012	27	-	37	1	GRQGDSSSCER
1549.7142	1548.7069	1548.7177	-0.0108	120	-	131	0	ELMNLPQQCNFR
1565.7089	1564.7016	1564.7126	-0.0110	120	-	131	0	ELMNLPQQCNFR + Oxidation (M)
1668.8181	1667.8108	1667.8235	-0.0127	42	-	54	0	VNLKPCEQHIMQR + Oxidation (M)
1714.6318	1713.6245	1713.6392	-0.0147	79	-	91	0	CCDELNEMENTQR + Oxidation (M)
1746.7491	1745.7418	1745.7566	-0.0148	55	-	68	0	IMGEQEQYDSYDIR
1762.7466	1761.7393	1761.7515	-0.0122	55	-	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2017.9589	2016.9516	2016.9621	-0.0105	120	-	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2106.9495	2105.9422	2105.9323	0.0099	55	-	71	1	IMGEQEQYDSYDIRSTR + Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1056.4974, 1063.5392, 1074.5464, 1079.5321, 1085.5588, 1091.5671, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1537.7900, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1715.6230, 1726.6772, 1778.7520, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

7. gi|57669906 **Mass:** 17480 **Score:** 89 **Expect:** 1.2e-006 **Queries matched:** 12

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide

1025.4077	1024.4004	1024.3880	0.0125	29 -	37	0	QGDSSSCER
1064.5566	1063.5493	1063.5596	-0.0103	112 -	119	1	QMVQQFKR
1080.5652	1079.5579	1079.5546	0.0034	112 -	119	1	QMVQQFKR + Oxidation (M)
1238.5190	1237.5117	1237.5105	0.0012	27 -	37	1	GRQGDSSSCER
1549.7142	1548.7069	1548.7177	-0.0108	120 -	131	0	ELMNLPQQCNFR
1565.7089	1564.7016	1564.7126	-0.0110	120 -	131	0	ELMNLPQQCNFR + Oxidation (M)
1668.8181	1667.8108	1667.8235	-0.0127	42 -	54	0	VNLKPCEQHIMQR + Oxidation (M)
1715.6230	1714.6157	1714.6233	-0.0075	79 -	91	0	CCDELDQMENTER + Oxidation (M)
1746.7491	1745.7418	1745.7566	-0.0148	55 -	68	0	IMGEQEQYDSYDIR
1762.7466	1761.7393	1761.7515	-0.0122	55 -	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2017.9589	2016.9516	2016.9621	-0.0105	120 -	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2106.9495	2105.9422	2105.9323	0.0099	55 -	71	1	IMGEQEQYDSYDIRSTR + Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1056.4974, 1063.5392, 1074.5464, 1079.5321, 1085.5588, 1091.5671, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1537.7900, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1714.6318, 1726.6772, 1778.7520, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

8. gi|83753503 **Mass:** 15575 **Score:** 51 **Expect:** 0.0073 **Queries matched:** 8

Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1025.4077	1024.4004	1024.3880	0.0125	10 -	18	0	QGDSSSCER
1064.5566	1063.5493	1063.5596	-0.0103	93 -	100	1	QMVQQFKR
1080.5652	1079.5579	1079.5546	0.0034	93 -	100	1	QMVQQFKR + Oxidation (M)
1238.5190	1237.5117	1237.5105	0.0012	8 -	18	1	GRQGDSSSCER
1668.8181	1667.8108	1667.8235	-0.0127	23 -	35	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7491	1745.7418	1745.7566	-0.0148	36 -	49	0	IMGEQEQYDSYDIR
1762.7466	1761.7393	1761.7515	-0.0122	36 -	49	0	IMGEQEQYDSYDIR + Oxidation (M)
2106.9495	2105.9422	2105.9323	0.0099	36 -	52	1	IMGEQEQYDSYDIRSTR + Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1056.4974, 1063.5392, 1074.5464, 1079.5321, 1085.5588, 1091.5671, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1537.7900, 1549.7142, 1565.7089, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1714.6318, 1715.6230, 1726.6772, 1778.7520, 2017.9589, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

9. gi|57118278 **Mass:** 15280 **Score:** 51 **Expect:** 0.0076 **Queries matched:** 8

Ara h 6 allergen [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1025.4077	1024.4004	1024.3880	0.0125	8 -	16	0	QGDSSSCER
1064.5566	1063.5493	1063.5596	-0.0103	91 -	98	1	QMVQQFKR
1080.5652	1079.5579	1079.5546	0.0034	91 -	98	1	QMVQQFKR + Oxidation (M)
1238.5190	1237.5117	1237.5105	0.0012	6 -	16	1	GRQGDSSSCER

1668.8181	1667.8108	1667.8235	-0.0127	21 -	33	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7491	1745.7418	1745.7566	-0.0148	34 -	47	0	IMGEQEQYDSYDIR
1762.7466	1761.7393	1761.7515	-0.0122	34 -	47	0	IMGEQEQYDSYDIR + Oxidation (M)
2106.9495	2105.9422	2105.9323	0.0099	34 -	50	1	IMGEQEQYDSYDIRSTR + Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1056.4974, 1063.5392, 1074.5464, 1079.5321, 1085.5588, 1091.5671, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1537.7900, 1549.7142, 1565.7089, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1714.6318, 1715.6230, 1726.6772, 1778.7520, 2017.9589, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

10. gi|118776568 **Mass:** 17335 **Score:** 48 **Expect:** 0.016 **Queries matched:** 7

conglutin 8 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1025.4077	1024.4004	1024.3880	0.0125	29 -	37	0	QGDSSSCER
1238.5190	1237.5117	1237.5105	0.0012	27 -	37	1	GRQGDSSSCER
1668.8181	1667.8108	1667.8235	-0.0127	42 -	54	0	VNLKPCEQHIMQR + Oxidation (M)
1714.6318	1713.6245	1713.6392	-0.0147	79 -	91	0	CCDELNEMENTQR + Oxidation (M)
1746.7491	1745.7418	1745.7566	-0.0148	55 -	68	0	IMGEQEQYDSYDIR
1762.7466	1761.7393	1761.7515	-0.0122	55 -	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2106.9495	2105.9422	2105.9323	0.0099	55 -	71	1	IMGEQEQYDSYDIRSTR + Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1056.4974, 1063.5392, 1064.5566, 1074.5464, 1079.5321, 1080.5652, 1085.5588, 1091.5671, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1537.7900, 1549.7142, 1565.7089, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1715.6230, 1726.6772, 1778.7520, 2017.9589, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Mixture: 1. Protein

gi|52001229 Score: **89** Expect: **1.2e-006**
conglutin [Arachis hypogaea]

Nominal mass (M_r): **17479**; Calculated pI value: **6.13**
NCBI BLAST search of gi|52001229 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **12**
Sequence Coverage: **53%**

Matched peptides shown in **Bold Red**

```
     1 MAKSTILVAL LALVLVAHAS AMRRERGRQG DSSSCERQVD RVNLKPCEQH
    51 IMQRIMGEQE QYDSYDIRST RSSDQQQRCC DELNEMENTQ RCMCEALQQI
   101 MENQCDRLQD RQMVQQFKRE LMNLPQQCNF RAPQRCDLDV SGGRC
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
27 - 37	1238.5190	1237.5117	1237.5105	0.0012	1	GRQGDSSSCER
29 - 37	1025.4077	1024.4004	1024.3880	0.0125	0	QGDSSSCER
42 - 54	1668.8181	1667.8108	1667.8235	-0.0127	0	VNLKPCEQHIMQR Oxidation (M)
55 - 68	1746.7491	1745.7418	1745.7566	-0.0148	0	IMGEQEQYDSYDIR
55 - 68	1762.7466	1761.7393	1761.7515	-0.0122	0	IMGEQEQYDSYDIR Oxidation (M)
55 - 71	2106.9495	2105.9422	2105.9323	0.0099	1	IMGEQEQYDSYDIRSTR Oxidation (M)
79 - 91	1714.6318	1713.6245	1713.6392	-0.0147	0	CCDELNEMENTQR Oxidation (M)
112 - 119	1064.5566	1063.5493	1063.5596	-0.0103	1	QMVQQFKR
112 - 119	1080.5652	1079.5579	1079.5546	0.0034	1	QMVQQFKR Oxidation (M)
120 - 131	1549.7142	1548.7069	1548.7177	-0.0108	0	ELMNLPQQCNFR
120 - 131	1565.7089	1564.7016	1564.7126	-0.0110	0	ELMNLPQQCNFR Oxidation (M)
120 - 135	2017.9589	2016.9516	2016.9621	-0.0105	1	ELMNLPQQCNFRAPQR Oxidation (M)

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1046.6036, 1056.4974, 1063.5392, 1074.5464, 1079.5321, 1085.5588, 1091.5671, 1096.5612, 1138.4894, 1145.5706, 1477.8240, 1502.7263, 1503.7260, 1537.7900, 1581.7041, 1590.7096, 1652.7759, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1715.6230, 1726.6772, 1778.7520, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440

Mixture: 2. Protein

gi|46560482 Score: **42** Expect: **0.053**
seed storage protein SSP2 [Arachis hypogaea]

Nominal mass (M_r): **20907**; Calculated pI value: **5.98**
NCBI BLAST search of gi|46560482 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **5**
Sequence Coverage: **25%**

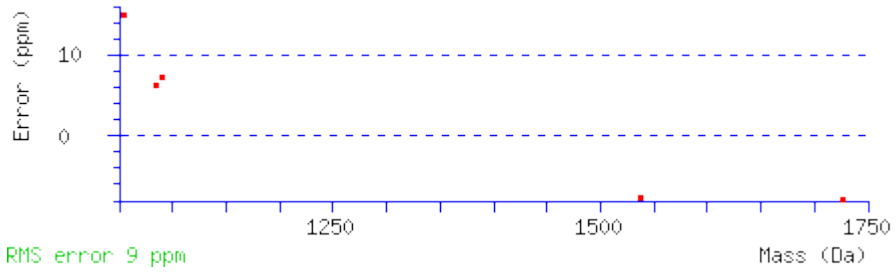
Matched peptides shown in **Bold Red**

```
     1 DHTLFNTHSI TTTTTMAKLT ILVALALFLL AAHASARQQW EFQGDRRCQS
    51 QLERANLRPC EQHLMQKIQR DEDSYERDPY SPSQDPYSPS PYDRRGAGSS
   101 QHQERCCNEL NEFENNQRCM CEALQQIMEN QSDRLQGRQQ EQQFKRELRN
   151 LPQQCGLRAP QRCDLDVESG GRDRY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
96 - 105	1056.4974	1055.4901	1055.4744	0.0157	0	GAGSSQHQER
106 - 118	1726.6772	1725.6699	1725.6835	-0.0135	0	CCNELNEFENNQR
139 - 146	1091.5671	1090.5598	1090.5519	0.0079	1	QQEQQFKR
150 - 158	1085.5588	1084.5515	1084.5447	0.0068	0	NLPQQCGLR
150 - 162	1537.7900	1536.7827	1536.7943	-0.0116	1	NLPQQCGLRAPQR

No match to: 805.4766, 848.4062, 861.0878, 868.5667, 882.5710, 1001.4827, 1016.5755, 1018.5107, 1025.4077, 1046.6036, 1063.5392, 1064.5566, 1074.5464, 1079.5321, 1080.5652, 1096.5612, 1138.4894, 1145.5706, 1238.5190, 1477.8240, 1502.7263, 1503.7260, 1549.7142, 1565.7089, 1581.7041, 1590.7096, 1652.7759, 1668.8181, 1682.6182, 1698.6135, 1700.7042, 1709.6605, 1714.6318, 1715.6230, 1746.7491, 1762.7466, 1778.7520, 2017.9589, 2106.9495, 2150.0605, 2168.0823, 2185.0425, 2273.1611, 2305.1550, 2311.1440



Spot 94

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **20 Mar 2007 at 13:16:49 GMT**
Top Score : **45 for gi|17225991, conglutin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|17225991	17349	45	conglutin [Arachis hypogaea]
2.	gi|57669906	17480	44	conglutin [Arachis hypogaea]
3.	gi|52001229	17479	33	conglutin [Arachis hypogaea]
4.	gi|75114094	17479	33	Conglutin precursor (Allergen Ara h 6)
5.	gi|57014074	17479	33	conglutin [Arachis hypogaea]
6.	gi|46560482	20907	25	seed storage protein SSP2 [Arachis hypogaea]
7.	gi|15418705	18612	25	allergen II [Arachis hypogaea]
8.	gi|28912768	19765	24	seed storage protein [Arachis hypogaea]
9.	gi|31322017	20212	24	allergen Ara h 2 isoform [Arachis hypogaea]
10.	gi|26245447	20558	23	allergen Ara h 2.02 [Arachis hypogaea]

Results List

1. gi|17225991 **Mass:** 17349 **Score:** 45 **Expect:** 0.026 **Queries matched:** 8
conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1549.7281	1548.7208	1548.7177	0.0031	119	130	0	ELMNLPQQCNFR
1565.7133	1564.7060	1564.7126	-0.0066	119	130	0	ELMNLPQQCNFR + Oxidation (M)
1668.8253	1667.8180	1667.8235	-0.0055	41	53	0	VNLKPCEQHIMQR + Oxidation (M)
1699.6425	1698.6352	1698.6284	0.0069	78	90	0	CCDELDQMENTER
1746.7609	1745.7536	1745.7566	-0.0030	54	67	0	IMGEQEQYDSYDIR
1762.7590	1761.7517	1761.7515	0.0002	54	67	0	IMGEQEQYDSYDIR + Oxidation (M)
2085.8328	2084.8255	2084.8206	0.0049	91	106	0	CMCEALQQIMENQCDR
2101.8267	2100.8194	2100.8155	0.0039	91	106	0	CMCEALQQIMENQCDR + Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1085.5536, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1709.6664, 1726.6842, 1940.9381, 2002.8342, 2012.8419, 2028.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181

2. gi|57669906 **Mass:** 17480 **Score:** 44 **Expect:** 0.035 **Queries matched:** 8

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1549.7281	1548.7208	1548.7177	0.0031	120	131	0	ELMNLPQQCNFR
1565.7133	1564.7060	1564.7126	-0.0066	120	131	0	ELMNLPQQCNFR + Oxidation (M)
1668.8253	1667.8180	1667.8235	-0.0055	42	54	0	VNLKPCEQHIMQR + Oxidation (M)
1699.6425	1698.6352	1698.6284	0.0069	79	91	0	CCDELDQMENTER
1746.7609	1745.7536	1745.7566	-0.0030	55	68	0	IMGEQEQYDSYDIR
1762.7590	1761.7517	1761.7515	0.0002	55	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2085.8328	2084.8255	2084.8206	0.0049	92	107	0	CMCEALQQIMENQCDR
2101.8267	2100.8194	2100.8155	0.0039	92	107	0	CMCEALQQIMENQCDR + Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1085.5536, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1709.6664, 1726.6842, 1940.9381, 2002.8342, 2012.8419, 2028.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181

3. gi|52001229 **Mass:** 17479 **Score:** 33 **Expect:** 0.49 **Queries matched:** 7

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1549.7281	1548.7208	1548.7177	0.0031	120	131	0	ELMNLPQQCNFR
1565.7133	1564.7060	1564.7126	-0.0066	120	131	0	ELMNLPQQCNFR + Oxidation (M)
1668.8253	1667.8180	1667.8235	-0.0055	42	54	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7609	1745.7536	1745.7566	-0.0030	55	68	0	IMGEQEQYDSYDIR
1762.7590	1761.7517	1761.7515	0.0002	55	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2085.8328	2084.8255	2084.8206	0.0049	92	107	0	CMCEALQQIMENQCDR
2101.8267	2100.8194	2100.8155	0.0039	92	107	0	CMCEALQQIMENQCDR + Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1085.5536, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1699.6425, 1709.6664, 1726.6842, 1940.9381, 2002.8342, 2012.8419, 2028.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181

4. gi|75114094 **Mass:** 17479 **Score:** 33 **Expect:** 0.49 **Queries matched:** 7

Conglutin precursor (Allergen Ara h 6)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1549.7281	1548.7208	1548.7177	0.0031	120	131	0	ELMNLPQQCNFR
1565.7133	1564.7060	1564.7126	-0.0066	120	131	0	ELMNLPQQCNFR + Oxidation (M)
1668.8253	1667.8180	1667.8235	-0.0055	42	54	0	VNLKPCEQHIMQR + Oxidation (M)

1746.7609	1745.7536	1745.7566	-0.0030	55 - 68	0	IMGEQEQYDSYDIR
1762.7590	1761.7517	1761.7515	0.0002	55 - 68	0	IMGEQEQYDSYDIR + Oxidation (M)
2085.8328	2084.8255	2084.8206	0.0049	92 - 107	0	CMCEALQQIMENQCDR
2101.8267	2100.8194	2100.8155	0.0039	92 - 107	0	CMCEALQQIMENQCDR + Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1085.5536, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1699.6425, 1709.6664, 1726.6842, 1940.9381, 2002.8342, 2012.8419, 2028.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181

5. gi|57014074 **Mass:** 17479 **Score:** 33 **Expect:** 0.49 **Queries matched:** 7

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1549.7281	1548.7208	1548.7177	0.0031	120 - 131		0	ELMNLPQQCNFR
1565.7133	1564.7060	1564.7126	-0.0066	120 - 131		0	ELMNLPQQCNFR + Oxidation (M)
1668.8253	1667.8180	1667.8235	-0.0055	42 - 54		0	VNLKPCEQHIMQR + Oxidation (M)
1746.7609	1745.7536	1745.7566	-0.0030	55 - 68		0	IMGEQEQYDSYDIR
1762.7590	1761.7517	1761.7515	0.0002	55 - 68		0	IMGEQEQYDSYDIR + Oxidation (M)
2085.8328	2084.8255	2084.8206	0.0049	92 - 107		0	CMCEALQQIMENQCDR
2101.8267	2100.8194	2100.8155	0.0039	92 - 107		0	CMCEALQQIMENQCDR + Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1085.5536, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1699.6425, 1709.6664, 1726.6842, 1940.9381, 2002.8342, 2012.8419, 2028.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181

6. gi|46560482 **Mass:** 20907 **Score:** 25 **Expect:** 3 **Queries matched:** 4

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5536	1084.5463	1084.5447	0.0016	150 - 158		0	NLPQQCGLR
1726.6842	1725.6769	1725.6835	-0.0065	106 - 118		0	CCNELNEFENNQR
2012.8419	2011.8346	2011.8220	0.0126	119 - 134		0	CMCEALQQIMENQSDR
2028.8267	2027.8194	2027.8169	0.0025	119 - 134		0	CMCEALQQIMENQSDR + Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1549.7281, 1565.7133, 1668.8253, 1699.6425, 1709.6664, 1746.7609, 1762.7590, 1940.9381, 2002.8342, 2085.8328, 2101.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181

7. gi|15418705 **Mass:** 18612 **Score:** 25 **Expect:** 3 **Queries matched:** 4

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5536	1084.5463	1084.5447	0.0016	135 - 143		0	NLPQQCGLR
1726.6842	1725.6769	1725.6835	-0.0065	91 - 103		0	CCNELNEFENNQR
2012.8419	2011.8346	2011.8220	0.0126	104 - 119		0	CMCEALQQIMENQSDR

2028.8267	2027.8194	2027.8169	0.0025	104 - 119	0	CMCEALQQIMENQSDR + Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1549.7281, 1565.7133, 1668.8253, 1699.6425, 1709.6664, 1746.7609, 1762.7590, 1940.9381, 2002.8342, 2085.8328, 2101.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181

8. gi|28912768 **Mass:** 19765 **Score:** 24 **Expect:** 3.3 **Queries matched:** 4

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5536	1084.5463	1084.5447	0.0016	145 -	153	0	NLPQQCGLR
1726.6842	1725.6769	1725.6835	-0.0065	101 -	113	0	CCNELNEFENNQR
2012.8419	2011.8346	2011.8220	0.0126	114 -	129	0	CMCEALQQIMENQSDR
2028.8267	2027.8194	2027.8169	0.0025	114 -	129	0	CMCEALQQIMENQSDR + Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1549.7281, 1565.7133, 1668.8253, 1699.6425, 1709.6664, 1746.7609, 1762.7590, 1940.9381, 2002.8342, 2085.8328, 2101.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181

9. gi|31322017 **Mass:** 20212 **Score:** 24 **Expect:** 3.6 **Queries matched:** 4

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5536	1084.5463	1084.5447	0.0016	144 -	152	0	NLPQQCGLR
1726.6842	1725.6769	1725.6835	-0.0065	100 -	112	0	CCNELNEFENNQR
2012.8419	2011.8346	2011.8220	0.0126	113 -	128	0	CMCEALQQIMENQSDR
2028.8267	2027.8194	2027.8169	0.0025	113 -	128	0	CMCEALQQIMENQSDR + Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1549.7281, 1565.7133, 1668.8253, 1699.6425, 1709.6664, 1746.7609, 1762.7590, 1940.9381, 2002.8342, 2085.8328, 2101.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181

10. gi|26245447 **Mass:** 20558 **Score:** 23 **Expect:** 4.6 **Queries matched:** 4

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5536	1084.5463	1084.5447	0.0016	147 -	155	0	NLPQQCGLR
1726.6842	1725.6769	1725.6835	-0.0065	103 -	115	0	CCNELNEFENNQR
2012.8419	2011.8346	2011.8220	0.0126	116 -	131	0	CMCEALQQIMENQSDR
2028.8267	2027.8194	2027.8169	0.0025	116 -	131	0	CMCEALQQIMENQSDR + Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1549.7281, 1565.7133, 1668.8253, 1699.6425, 1709.6664, 1746.7609, 1762.7590, 1940.9381, 2002.8342, 2085.8328, 2101.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 41

Protein View

Match to: **gi|17225991** Score: **45** Expect: **0.026**
conglutin [Arachis hypogaea]

Nominal mass (M_r): **17349**; Calculated pI value: **5.74**
NCBI BLAST search of gi|17225991 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **41**
Number of mass values matched: **8**
Sequence Coverage: **47%**

Matched peptides shown in **Bold Red**

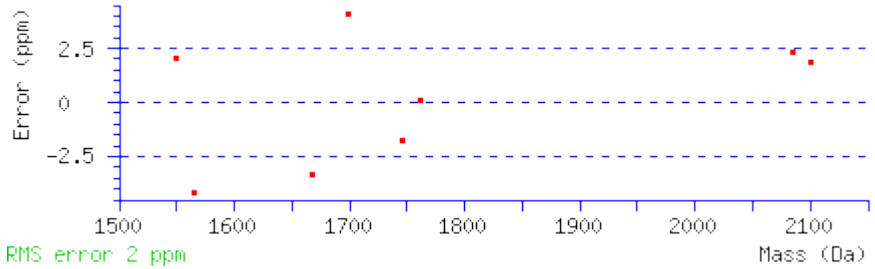
```
     1 AKSTILVALL ALVLVAHASA MRRERGRQGD SSSCERQVDR VNLKPCEQHI
    51 MQRIMGEQEQ YDSYDIRSTR SSDQQQRCCD ELDQMENTER CMCEALQQIM
   101 ENQCDRLQDR QMVQQFKREL MNLPQQCNFR APQRCDLDVS GGRC
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
41 - 53	1668.8253	1667.8180	1667.8235	-0.0055	0	VNLKPCEQHIMQR Oxidation (M)
54 - 67	1746.7609	1745.7536	1745.7566	-0.0030	0	IMGEQEQYDSYDIR
54 - 67	1762.7590	1761.7517	1761.7515	0.0002	0	IMGEQEQYDSYDIR Oxidation (M)
78 - 90	1699.6425	1698.6352	1698.6284	0.0069	0	CCDELDQMENTER
91 - 106	2085.8328	2084.8255	2084.8206	0.0049	0	CMCEALQQIMENQCDR

91 - 106	2101.8267	2100.8194	2100.8155	0.0039	0	**CMCEALQQIMENQCDR** Oxidation (M)
119 - 130	1549.7281	1548.7208	1548.7177	0.0031	0	**ELMNLPQQCNFR**
119 - 130	1565.7133	1564.7060	1564.7126	-0.0066	0	**ELMNLPQQCNFR** Oxidation (M)

No match to: 842.5091, 861.0624, 877.0481, 881.2670, 1045.5623, 1085.5536, 1091.5326, 1106.0494, 1106.5543, 1455.7224, 1475.7354, 1709.6664, 1726.6842, 1940.9381, 2002.8342, 2012.8419, 2028.8267, 2211.1025, 2225.1221, 2239.1345, 2283.1755, 2299.1780, 2313.1953, 2678.3567, 2787.9856, 2788.4849, 2807.3103, 2915.4900, 3036.6252, 3338.7666, 3348.7080, 3353.7534, 3354.8181



Spot 95

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **20 Mar 2007 at 13:17:55 GMT**
Top Score : **96 for gi|17225991, conglutin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|17225991	17349	96	conglutin [Arachis hypogaea]
2.	gi|52001229	17479	94	conglutin [Arachis hypogaea]
3.	gi|75114094	17479	94	Conglutin precursor (Allergen Ara h 6)
4.	gi|57014074	17479	94	conglutin [Arachis hypogaea]
5.	gi|57669906	17480	94	conglutin [Arachis hypogaea]
6.	gi|83753503	15575	55	Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)
7.	gi|57118278	15280	55	Ara h 6 allergen [Arachis hypogaea]
8.	gi|118776568	17335	52	conglutin 8 [Arachis hypogaea]
9.	gi|230338	23975	13	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)
10.	gi|62361163	18560	13	resistance protein PLTR [Arachis hypogaea]

Results List

1. gi|17225991 **Mass:** 17349 **Score:** 96 **Expect:** 2.1e-007 **Queries matched:** 16
conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1064.5623	1063.5550	1063.5596	-0.0046	111	118	1	QMVQQFKR
1080.5674	1079.5601	1079.5546	0.0056	111	118	1	QMVQQFKR + Oxidation (M)
1238.5237	1237.5164	1237.5105	0.0059	26	36	1	GRQGDSSSCER
1549.7207	1548.7134	1548.7177	-0.0043	119	130	0	ELMNLPQQCNFR
1565.7130	1564.7057	1564.7126	-0.0069	119	130	0	ELMNLPQQCNFR + Oxidation (M)
1652.8248	1651.8175	1651.8286	-0.0111	41	53	0	VNLKPCEQHIMQR
1668.8224	1667.8151	1667.8235	-0.0084	41	53	0	VNLKPCEQHIMQR + Oxidation (M)
1715.6191	1714.6118	1714.6233	-0.0114	78	90	0	CCDELDQMENTER + Oxidation (M)
1746.7563	1745.7490	1745.7566	-0.0076	54	67	0	IMGEQEQYDSYDIR
1762.7528	1761.7455	1761.7515	-0.0060	54	67	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9677	2000.9604	2000.9672	-0.0068	119	134	1	ELMNLPQQCNFRAPQR

2017.9678	2016.9605	2016.9621	-0.0016	119 - 134	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2090.9297	2089.9224	2089.9374	-0.0150	54 - 70	1	IMGEQEQYDSYDIRSTR
2106.9431	2105.9358	2105.9323	0.0035	54 - 70	1	IMGEQEQYDSYDIRSTR + Oxidation (M)
2151.0774	2150.0701	2150.0837	-0.0135	37 - 53	1	QVDRVNLKPCEQHIMQR
2167.0820	2166.0747	2166.0786	-0.0038	37 - 53	1	QVDRVNLKPCEQHIMQR + Oxidation (M)

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1046.6112, 1047.5836, 1051.7053, 1063.5441, 1084.5653, 1138.5004, 1477.8378, 1503.7498, 1581.7122, 1606.8407, 1636.6715, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1714.6166, 1726.6906, 2045.0101, 2105.1106, 2150.0662, 2185.0569, 2273.1636

2. gi|52001229 **Mass:** 17479 **Score:** 94 **Expect:** 3.3e-007 **Queries matched:** 16

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1064.5623	1063.5550	1063.5596	-0.0046	112 - 119		1	QMVQQFKR
1080.5674	1079.5601	1079.5546	0.0056	112 - 119		1	QMVQQFKR + Oxidation (M)
1238.5237	1237.5164	1237.5105	0.0059	27 - 37		1	GRQGDSSSCER
1549.7207	1548.7134	1548.7177	-0.0043	120 - 131		0	ELMNLPQQCNFR
1565.7130	1564.7057	1564.7126	-0.0069	120 - 131		0	ELMNLPQQCNFR + Oxidation (M)
1652.8248	1651.8175	1651.8286	-0.0111	42 - 54		0	VNLKPCEQHIMQR
1668.8224	1667.8151	1667.8235	-0.0084	42 - 54		0	VNLKPCEQHIMQR + Oxidation (M)
1714.6166	1713.6093	1713.6392	-0.0299	79 - 91		0	CCDELNEMENTQR + Oxidation (M)
1746.7563	1745.7490	1745.7566	-0.0076	55 - 68		0	IMGEQEQYDSYDIR
1762.7528	1761.7455	1761.7515	-0.0060	55 - 68		0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9677	2000.9604	2000.9672	-0.0068	120 - 135		1	ELMNLPQQCNFRAPQR
2017.9678	2016.9605	2016.9621	-0.0016	120 - 135		1	ELMNLPQQCNFRAPQR + Oxidation (M)
2090.9297	2089.9224	2089.9374	-0.0150	55 - 71		1	IMGEQEQYDSYDIRSTR
2106.9431	2105.9358	2105.9323	0.0035	55 - 71		1	IMGEQEQYDSYDIRSTR + Oxidation (M)
2151.0774	2150.0701	2150.0837	-0.0135	38 - 54		1	QVDRVNLKPCEQHIMQR
2167.0820	2166.0747	2166.0786	-0.0038	38 - 54		1	QVDRVNLKPCEQHIMQR + Oxidation (M)

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1046.6112, 1047.5836, 1051.7053, 1063.5441, 1084.5653, 1138.5004, 1477.8378, 1503.7498, 1581.7122, 1606.8407, 1636.6715, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1715.6191, 1726.6906, 2045.0101, 2105.1106, 2150.0662, 2185.0569, 2273.1636

3. gi|75114094 **Mass:** 17479 **Score:** 94 **Expect:** 3.3e-007 **Queries matched:** 16

Conglutin precursor (Allergen Ara h 6)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1064.5623	1063.5550	1063.5596	-0.0046	112 - 119		1	QMVQQFKR
1080.5674	1079.5601	1079.5546	0.0056	112 - 119		1	QMVQQFKR + Oxidation (M)
1238.5237	1237.5164	1237.5105	0.0059	27 - 37		1	GRQGDSSSCER
1549.7207	1548.7134	1548.7177	-0.0043	120 - 131		0	ELMNLPQQCNFR

1565.7130	1564.7057	1564.7126	-0.0069	120 - 131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8248	1651.8175	1651.8286	-0.0111	42 - 54	0	VNLKPCEQHIMQR
1668.8224	1667.8151	1667.8235	-0.0084	42 - 54	0	VNLKPCEQHIMQR + Oxidation (M)
1714.6166	1713.6093	1713.6392	-0.0299	79 - 91	0	CCDELNEMENTQR + Oxidation (M)
1746.7563	1745.7490	1745.7566	-0.0076	55 - 68	0	IMGEQEQYDSYDIR
1762.7528	1761.7455	1761.7515	-0.0060	55 - 68	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9677	2000.9604	2000.9672	-0.0068	120 - 135	1	ELMNLPQQCNFRAPQR
2017.9678	2016.9605	2016.9621	-0.0016	120 - 135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2090.9297	2089.9224	2089.9374	-0.0150	55 - 71	1	IMGEQEQYDSYDIRSTR
2106.9431	2105.9358	2105.9323	0.0035	55 - 71	1	IMGEQEQYDSYDIRSTR + Oxidation (M)
2151.0774	2150.0701	2150.0837	-0.0135	38 - 54	1	QVDRVNLKPCEQHIMQR
2167.0820	2166.0747	2166.0786	-0.0038	38 - 54	1	QVDRVNLKPCEQHIMQR + Oxidation (M)

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1046.6112, 1047.5836, 1051.7053, 1063.5441, 1084.5653, 1138.5004, 1477.8378, 1503.7498, 1581.7122, 1606.8407, 1636.6715, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1715.6191, 1726.6906, 2045.0101, 2105.1106, 2150.0662, 2185.0569, 2273.1636

4. gi|57014074 **Mass:** 17479 **Score:** 94 **Expect:** 3.3e-007 **Queries matched:** 16

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1064.5623	1063.5550	1063.5596	-0.0046	112 - 119		1	QMVQQFKR
1080.5674	1079.5601	1079.5546	0.0056	112 - 119		1	QMVQQFKR + Oxidation (M)
1238.5237	1237.5164	1237.5105	0.0059	27 - 37		1	GRQGDSSSCER
1549.7207	1548.7134	1548.7177	-0.0043	120 - 131		0	ELMNLPQQCNFR
1565.7130	1564.7057	1564.7126	-0.0069	120 - 131		0	ELMNLPQQCNFR + Oxidation (M)
1652.8248	1651.8175	1651.8286	-0.0111	42 - 54		0	VNLKPCEQHIMQR
1668.8224	1667.8151	1667.8235	-0.0084	42 - 54		0	VNLKPCEQHIMQR + Oxidation (M)
1714.6166	1713.6093	1713.6392	-0.0299	79 - 91		0	CCDELNEMENTQR + Oxidation (M)
1746.7563	1745.7490	1745.7566	-0.0076	55 - 68		0	IMGEQEQYDSYDIR
1762.7528	1761.7455	1761.7515	-0.0060	55 - 68		0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9677	2000.9604	2000.9672	-0.0068	120 - 135		1	ELMNLPQQCNFRAPQR
2017.9678	2016.9605	2016.9621	-0.0016	120 - 135		1	ELMNLPQQCNFRAPQR + Oxidation (M)
2090.9297	2089.9224	2089.9374	-0.0150	55 - 71		1	IMGEQEQYDSYDIRSTR
2106.9431	2105.9358	2105.9323	0.0035	55 - 71		1	IMGEQEQYDSYDIRSTR + Oxidation (M)
2151.0774	2150.0701	2150.0837	-0.0135	38 - 54		1	QVDRVNLKPCEQHIMQR
2167.0820	2166.0747	2166.0786	-0.0038	38 - 54		1	QVDRVNLKPCEQHIMQR + Oxidation (M)

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1046.6112, 1047.5836, 1051.7053, 1063.5441, 1084.5653, 1138.5004, 1477.8378, 1503.7498, 1581.7122, 1606.8407, 1636.6715, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1715.6191, 1726.6906, 2045.0101, 2105.1106, 2150.0662, 2185.0569, 2273.1636

5. gi|57669906 **Mass:** 17480 **Score:** 94 **Expect:** 3.3e-007 **Queries matched:** 16

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1064.5623	1063.5550	1063.5596	-0.0046	112	119	1	QMVQQFKR
1080.5674	1079.5601	1079.5546	0.0056	112	119	1	QMVQQFKR + Oxidation (M)
1238.5237	1237.5164	1237.5105	0.0059	27	37	1	GRQGDSSSCER
1549.7207	1548.7134	1548.7177	-0.0043	120	131	0	ELMNLPQQCNFR
1565.7130	1564.7057	1564.7126	-0.0069	120	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8248	1651.8175	1651.8286	-0.0111	42	54	0	VNLKPCEQHIMQR
1668.8224	1667.8151	1667.8235	-0.0084	42	54	0	VNLKPCEQHIMQR + Oxidation (M)
1715.6191	1714.6118	1714.6233	-0.0114	79	91	0	CCDELDQMENTER + Oxidation (M)
1746.7563	1745.7490	1745.7566	-0.0076	55	68	0	IMGEQEQYDSYDIR
1762.7528	1761.7455	1761.7515	-0.0060	55	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9677	2000.9604	2000.9672	-0.0068	120	135	1	ELMNLPQQCNFRAPQR
2017.9678	2016.9605	2016.9621	-0.0016	120	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2090.9297	2089.9224	2089.9374	-0.0150	55	71	1	IMGEQEQYDSYDIRSTR
2106.9431	2105.9358	2105.9323	0.0035	55	71	1	IMGEQEQYDSYDIRSTR + Oxidation (M)
2151.0774	2150.0701	2150.0837	-0.0135	38	54	1	QVDRVNLKPCEQHIMQR
2167.0820	2166.0747	2166.0786	-0.0038	38	54	1	QVDRVNLKPCEQHIMQR + Oxidation (M)

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1046.6112, 1047.5836, 1051.7053, 1063.5441, 1084.5653, 1138.5004, 1477.8378, 1503.7498, 1581.7122, 1606.8407, 1636.6715, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1714.6166, 1726.6906, 2045.0101, 2105.1106, 2150.0662, 2185.0569, 2273.1636

6. gi|83753503 **Mass:** 15575 **Score:** 55 **Expect:** 0.003 **Queries matched:** 11

Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1064.5623	1063.5550	1063.5596	-0.0046	93	100	1	QMVQQFKR
1080.5674	1079.5601	1079.5546	0.0056	93	100	1	QMVQQFKR + Oxidation (M)
1238.5237	1237.5164	1237.5105	0.0059	8	18	1	GRQGDSSSCER
1652.8248	1651.8175	1651.8286	-0.0111	23	35	0	VNLKPCEQHIMQR
1668.8224	1667.8151	1667.8235	-0.0084	23	35	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7563	1745.7490	1745.7566	-0.0076	36	49	0	IMGEQEQYDSYDIR
1762.7528	1761.7455	1761.7515	-0.0060	36	49	0	IMGEQEQYDSYDIR + Oxidation (M)
2090.9297	2089.9224	2089.9374	-0.0150	36	52	1	IMGEQEQYDSYDIRSTR
2106.9431	2105.9358	2105.9323	0.0035	36	52	1	IMGEQEQYDSYDIRSTR + Oxidation (M)
2151.0774	2150.0701	2150.0837	-0.0135	19	35	1	QVDRVNLKPCEQHIMQR
2167.0820	2166.0747	2166.0786	-0.0038	19	35	1	QVDRVNLKPCEQHIMQR + Oxidation (M)

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1046.6112, 1047.5836, 1051.7053, 1063.5441, 1084.5653, 1138.5004, 1477.8378, 1503.7498, 1549.7207, 1565.7130, 1581.7122, 1606.8407, 1636.6715, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1714.6166,

1715.6191, 1726.6906, 2001.9677, 2017.9678, 2045.0101, 2105.1106, 2150.0662, 2185.0569, 2273.1636

7. gi|57118278 **Mass:** 15280 **Score:** 55 **Expect:** 0.0031 **Queries matched:** 11

Ara h 6 allergen [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1064.5623	1063.5550	1063.5596	-0.0046	91	-	98	1	QMVQQFKR
1080.5674	1079.5601	1079.5546	0.0056	91	-	98	1	QMVQQFKR + Oxidation (M)
1238.5237	1237.5164	1237.5105	0.0059	6	-	16	1	GRQGDSSSCER
1652.8248	1651.8175	1651.8286	-0.0111	21	-	33	0	VNLKPCEQHIMQR
1668.8224	1667.8151	1667.8235	-0.0084	21	-	33	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7563	1745.7490	1745.7566	-0.0076	34	-	47	0	IMGEQEQYDSYDIR
1762.7528	1761.7455	1761.7515	-0.0060	34	-	47	0	IMGEQEQYDSYDIR + Oxidation (M)
2090.9297	2089.9224	2089.9374	-0.0150	34	-	50	1	IMGEQEQYDSYDIRSTR
2106.9431	2105.9358	2105.9323	0.0035	34	-	50	1	IMGEQEQYDSYDIRSTR + Oxidation (M)
2151.0774	2150.0701	2150.0837	-0.0135	17	-	33	1	QVDRVNLKPCEQHIMQR
2167.0820	2166.0747	2166.0786	-0.0038	17	-	33	1	QVDRVNLKPCEQHIMQR + Oxidation (M)

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1046.6112, 1047.5836, 1051.7053, 1063.5441, 1084.5653, 1138.5004, 1477.8378, 1503.7498, 1549.7207, 1565.7130, 1581.7122, 1606.8407, 1636.6715, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1714.6166, 1715.6191, 1726.6906, 2001.9677, 2017.9678, 2045.0101, 2105.1106, 2150.0662, 2185.0569, 2273.1636

8. gi|118776568 **Mass:** 17335 **Score:** 52 **Expect:** 0.0062 **Queries matched:** 10

conglutin 8 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1238.5237	1237.5164	1237.5105	0.0059	27	-	37	1	GRQGDSSSCER
1652.8248	1651.8175	1651.8286	-0.0111	42	-	54	0	VNLKPCEQHIMQR
1668.8224	1667.8151	1667.8235	-0.0084	42	-	54	0	VNLKPCEQHIMQR + Oxidation (M)
1714.6166	1713.6093	1713.6392	-0.0299	79	-	91	0	CCDELNEMENTQR + Oxidation (M)
1746.7563	1745.7490	1745.7566	-0.0076	55	-	68	0	IMGEQEQYDSYDIR
1762.7528	1761.7455	1761.7515	-0.0060	55	-	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2090.9297	2089.9224	2089.9374	-0.0150	55	-	71	1	IMGEQEQYDSYDIRSTR
2106.9431	2105.9358	2105.9323	0.0035	55	-	71	1	IMGEQEQYDSYDIRSTR + Oxidation (M)
2151.0774	2150.0701	2150.0837	-0.0135	38	-	54	1	QVDRVNLKPCEQHIMQR
2167.0820	2166.0747	2166.0786	-0.0038	38	-	54	1	QVDRVNLKPCEQHIMQR + Oxidation (M)

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1046.6112, 1047.5836, 1051.7053, 1063.5441, 1064.5623, 1080.5674, 1084.5653, 1138.5004, 1477.8378, 1503.7498, 1549.7207, 1565.7130, 1581.7122, 1606.8407, 1636.6715, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1715.6191, 1726.6906, 2001.9677, 2017.9678, 2045.0101, 2105.1106, 2150.0662, 2185.0569, 2273.1636

9. gi|230338 **Mass:** 23975 **Score:** 13 **Expect:** 47 **Queries matched:** 2

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1046.6112	1045.6039	1045.5880	0.0160	90	-	99	1	LKSAASLNSR
2273.1636	2272.1563	2272.1521	0.0042	70	-	89	0	SIVHPSYNSNTLNNDIMLIK

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1047.5836, 1051.7053, 1063.5441, 1064.5623, 1080.5674, 1084.5653, 1138.5004, 1238.5237, 1477.8378, 1503.7498, 1549.7207, 1565.7130, 1581.7122, 1606.8407, 1636.6715, 1652.8248, 1668.8224, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1714.6166, 1715.6191, 1726.6906, 1746.7563, 1762.7528, 2001.9677, 2017.9678, 2045.0101, 2090.9297, 2105.1106, 2106.9431, 2150.0662, 2151.0774, 2167.0820, 2185.0569

10. gi|62361163 **Mass:** 18560 **Score:** 13 **Expect:** 49 **Queries matched:** 2

resistance protein PLTR [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1477.8378	1476.8305	1476.8412	-0.0107	76	-	88	1	RVLLVLDDVNHGK
1503.7498	1502.7425	1502.7225	0.0200	53	-	65	1	INSNSVHNKYDGR

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1046.6112, 1047.5836, 1051.7053, 1063.5441, 1064.5623, 1080.5674, 1084.5653, 1138.5004, 1238.5237, 1549.7207, 1565.7130, 1581.7122, 1606.8407, 1636.6715, 1652.8248, 1668.8224, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1714.6166, 1715.6191, 1726.6906, 1746.7563, 1762.7528, 2001.9677, 2017.9678, 2045.0101, 2090.9297, 2105.1106, 2106.9431, 2150.0662, 2151.0774, 2167.0820, 2185.0569, 2273.1636

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|17225991** Score: **96** Expect: **2.1e-007**
conglutin [Arachis hypogaea]

Nominal mass (M_r): **17349**; Calculated pI value: **5.74**
NCBI BLAST search of gi|17225991 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **16**
Sequence Coverage: **56%**

Matched peptides shown in **Bold Red**

```
     1 AKSTILVALL ALVLVAHASA MRRERGRQGD SSSCERQVDR VNLKPCEQHI
    51 MQRIMGEQEQ YDSYDIRSTR SSDQQQRCCD ELDQMENTER CMCEALQQIM
   101 ENQCDRLQDR QMVQQFKREL MNLPQQCNFR APQRCDLDVS GGRC
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
26 - 36	1238.5237	1237.5164	1237.5105	0.0059	1	GRQGDSSSCER
37 - 53	2151.0774	2150.0701	2150.0837	-0.0135	1	QVDRVNLKPCEQHIMQR
37 - 53	2167.0820	2166.0747	2166.0786	-0.0038	1	QVDRVNLKPCEQHIMQR Oxidation (M)
41 - 53	1652.8248	1651.8175	1651.8286	-0.0111	0	VNLKPCEQHIMQR
41 - 53	1668.8224	1667.8151	1667.8235	-0.0084	0	VNLKPCEQHIMQR Oxidation (M)
54 - 67	1746.7563	1745.7490	1745.7566	-0.0076	0	IMGEQEQYDSYDIR
54 - 67	1762.7528	1761.7455	1761.7515	-0.0060	0	IMGEQEQYDSYDIR Oxidation (M)
54 - 70	2090.9297	2089.9224	2089.9374	-0.0150	1	IMGEQEQYDSYDIRSTR
54 - 70	2106.9431	2105.9358	2105.9323	0.0035	1	IMGEQEQYDSYDIRSTR Oxidation (M)
78 - 90	1715.6191	1714.6118	1714.6233	-0.0114	0	CCDELDQMENTER Oxidation (M)
111 - 118	1064.5623	1063.5550	1063.5596	-0.0046	1	QMVQQFKR
111 - 118	1080.5674	1079.5601	1079.5546	0.0056	1	QMVQQFKR Oxidation (M)
119 - 130	1549.7207	1548.7134	1548.7177	-0.0043	0	ELMNLPQQCNFR
119 - 130	1565.7130	1564.7057	1564.7126	-0.0069	0	ELMNLPQQCNFR Oxidation (M)
119 - 134	2001.9677	2000.9604	2000.9672	-0.0068	1	ELMNLPQQCNFRAPQR
119 - 134	2017.9678	2016.9605	2016.9621	-0.0016	1	ELMNLPQQCNFRAPQR Oxidation (M)

No match to: 805.4742, 813.5660, 823.5883, 827.5668, 848.4142, 867.5887, 881.2953, 882.5884, 906.5376, 1001.5146, 1018.5231, 1025.4193, 1046.6112, 1047.5836, 1051.7053, 1063.5441, 1084.5653, 1138.5004, 1477.8378, 1503.7498, 1581.7122, 1606.8407, 1636.6715, 1682.6096, 1697.6067, 1698.6061, 1700.7161, 1714.6166, 1726.6906, 2045.0101, 2105.1106, 2150.0662, 2185.0569, 2273.1636

Spot 96

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:15:46 GMT**
Top Score : **81 for gi|17225991, conglutin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|17225991	17349	81	conglutin [Arachis hypogaea]
2.	gi|57669906	17480	79	conglutin [Arachis hypogaea]
3.	gi|57014074	17479	79	conglutin [Arachis hypogaea]
4.	gi|52001229	17479	79	conglutin [Arachis hypogaea]
5.	gi|75114094	17479	79	Conglutin precursor (Allergen Ara h 6)
6.	gi|83753503	15575	32	Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)
7.	gi|57118278	15280	32	Ara h 6 allergen [Arachis hypogaea]
8.	gi|118776568	17335	30	conglutin 8 [Arachis hypogaea]
9.	gi|71040687	13451	23	auxin-repressed protein [Arachis hypogaea]
10.	gi|5923742	15489	17	allergen Arah6 [Arachis hypogaea]

Results List

1. gi|17225991 **Mass:** 17349 **Score:** 81 **Expect:** 6.6e-006 **Queries matched:** 14
conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.4045	847.3972	847.3784	0.0188	71	77	0	SSDQQQR
1064.5574	1063.5501	1063.5596	-0.0095	111	118	1	QMVQQFKR
1080.5605	1079.5532	1079.5546	-0.0013	111	118	1	QMVQQFKR + Oxidation (M)
1238.5302	1237.5229	1237.5105	0.0124	26	36	1	GRQGDSSSCER
1549.7228	1548.7155	1548.7177	-0.0022	119	130	0	ELMNLPQQCNFR
1565.7095	1564.7022	1564.7126	-0.0104	119	130	0	ELMNLPQQCNFR + Oxidation (M)
1652.8368	1651.8295	1651.8286	0.0009	41	53	0	VNLKPCEQHIMQR
1668.8137	1667.8064	1667.8235	-0.0171	41	53	0	VNLKPCEQHIMQR + Oxidation (M)
1699.6333	1698.6260	1698.6284	-0.0023	78	90	0	CCDELDQMENTER

1746.7582	1745.7509	1745.7566	-0.0057	54 - 67	0	IMGEQEQYDSYDIR
1762.7537	1761.7464	1761.7515	-0.0051	54 - 67	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9391	2000.9318	2000.9672	-0.0354	119 - 134	1	ELMNLPQQCNFRAPQR
2017.9536	2016.9463	2016.9621	-0.0158	119 - 134	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2614.1394	2613.1321	2613.0862	0.0459	91 - 110	1	CMCEALQQIMENQCDRLQDR + Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1066.0767, 1079.5308, 1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1581.7048, 1682.6033, 1698.6040, 1700.6709, 1714.6514, 1716.6215, 1774.8241, 1784.7208, 1934.8929, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 3137.4731, 3211.5571

2. gi|57669906 **Mass:** 17480 **Score:** 79 **Expect:** 1e-005 **Queries matched:** 14

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.4045	847.3972	847.3784	0.0188	72 -	78	0	SSDQQQR
1064.5574	1063.5501	1063.5596	-0.0095	112 -	119	1	QMVQQFKR
1080.5605	1079.5532	1079.5546	-0.0013	112 -	119	1	QMVQQFKR + Oxidation (M)
1238.5302	1237.5229	1237.5105	0.0124	27 -	37	1	GRQGDSSSCER
1549.7228	1548.7155	1548.7177	-0.0022	120 -	131	0	ELMNLPQQCNFR
1565.7095	1564.7022	1564.7126	-0.0104	120 -	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8368	1651.8295	1651.8286	0.0009	42 -	54	0	VNLKPCEQHIMQR
1668.8137	1667.8064	1667.8235	-0.0171	42 -	54	0	VNLKPCEQHIMQR + Oxidation (M)
1699.6333	1698.6260	1698.6284	-0.0023	79 -	91	0	CCDELDQMENTER
1746.7582	1745.7509	1745.7566	-0.0057	55 -	68	0	IMGEQEQYDSYDIR
1762.7537	1761.7464	1761.7515	-0.0051	55 -	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9391	2000.9318	2000.9672	-0.0354	120 -	135	1	ELMNLPQQCNFRAPQR
2017.9536	2016.9463	2016.9621	-0.0158	120 -	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2614.1394	2613.1321	2613.0862	0.0459	92 -	111	1	CMCEALQQIMENQCDRLQDR + Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1066.0767, 1079.5308, 1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1581.7048, 1682.6033, 1698.6040, 1700.6709, 1714.6514, 1716.6215, 1774.8241, 1784.7208, 1934.8929, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 3137.4731, 3211.5571

3. gi|57014074 **Mass:** 17479 **Score:** 79 **Expect:** 1e-005 **Queries matched:** 14

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.4045	847.3972	847.3784	0.0188	72 -	78	0	SSDQQQR
1064.5574	1063.5501	1063.5596	-0.0095	112 -	119	1	QMVQQFKR
1080.5605	1079.5532	1079.5546	-0.0013	112 -	119	1	QMVQQFKR + Oxidation (M)

1238.5302	1237.5229	1237.5105	0.0124	27 -	37	1	GRQGDSSSCER
1549.7228	1548.7155	1548.7177	-0.0022	120 -	131	0	ELMNLPQQCNFR
1565.7095	1564.7022	1564.7126	-0.0104	120 -	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8368	1651.8295	1651.8286	0.0009	42 -	54	0	VNLKPCEQHIMQR
1668.8137	1667.8064	1667.8235	-0.0171	42 -	54	0	VNLKPCEQHIMQR + Oxidation (M)
1714.6514	1713.6441	1713.6392	0.0049	79 -	91	0	CCDELNEMENTQR + Oxidation (M)
1746.7582	1745.7509	1745.7566	-0.0057	55 -	68	0	IMGEQEQYDSYDIR
1762.7537	1761.7464	1761.7515	-0.0051	55 -	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9391	2000.9318	2000.9672	-0.0354	120 -	135	1	ELMNLPQQCNFRAPQR
2017.9536	2016.9463	2016.9621	-0.0158	120 -	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2614.1394	2613.1321	2613.0862	0.0459	92 -	111	1	CMCEALQQIMENQCDRLQDR + Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1066.0767, 1079.5308, 1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1581.7048, 1682.6033, 1698.6040, 1699.6333, 1700.6709, 1716.6215, 1774.8241, 1784.7208, 1934.8929, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 3137.4731, 3211.5571

4. gi|52001229 **Mass:** 17479 **Score:** 79 **Expect:** 1e-005 **Queries matched:** 14

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.4045	847.3972	847.3784	0.0188	72 -	78	0	SSDQQQR
1064.5574	1063.5501	1063.5596	-0.0095	112 -	119	1	QMVQQFKR
1080.5605	1079.5532	1079.5546	-0.0013	112 -	119	1	QMVQQFKR + Oxidation (M)
1238.5302	1237.5229	1237.5105	0.0124	27 -	37	1	GRQGDSSSCER
1549.7228	1548.7155	1548.7177	-0.0022	120 -	131	0	ELMNLPQQCNFR
1565.7095	1564.7022	1564.7126	-0.0104	120 -	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8368	1651.8295	1651.8286	0.0009	42 -	54	0	VNLKPCEQHIMQR
1668.8137	1667.8064	1667.8235	-0.0171	42 -	54	0	VNLKPCEQHIMQR + Oxidation (M)
1714.6514	1713.6441	1713.6392	0.0049	79 -	91	0	CCDELNEMENTQR + Oxidation (M)
1746.7582	1745.7509	1745.7566	-0.0057	55 -	68	0	IMGEQEQYDSYDIR
1762.7537	1761.7464	1761.7515	-0.0051	55 -	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9391	2000.9318	2000.9672	-0.0354	120 -	135	1	ELMNLPQQCNFRAPQR
2017.9536	2016.9463	2016.9621	-0.0158	120 -	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2614.1394	2613.1321	2613.0862	0.0459	92 -	111	1	CMCEALQQIMENQCDRLQDR + Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1066.0767, 1079.5308, 1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1581.7048, 1682.6033, 1698.6040, 1699.6333, 1700.6709, 1716.6215, 1774.8241, 1784.7208, 1934.8929, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 3137.4731, 3211.5571

5. gi|75114094 **Mass:** 17479 **Score:** 79 **Expect:** 1e-005 **Queries matched:** 14

Conglutin precursor (Allergen Ara h 6)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.4045	847.3972	847.3784	0.0188	72	78	0	SSDQQQR
1064.5574	1063.5501	1063.5596	-0.0095	112	119	1	QMVQQFKR
1080.5605	1079.5532	1079.5546	-0.0013	112	119	1	QMVQQFKR + Oxidation (M)
1238.5302	1237.5229	1237.5105	0.0124	27	37	1	GRQGDSSSCER
1549.7228	1548.7155	1548.7177	-0.0022	120	131	0	ELMNLPQQCNFR
1565.7095	1564.7022	1564.7126	-0.0104	120	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8368	1651.8295	1651.8286	0.0009	42	54	0	VNLKPCEQHIMQR
1668.8137	1667.8064	1667.8235	-0.0171	42	54	0	VNLKPCEQHIMQR + Oxidation (M)
1714.6514	1713.6441	1713.6392	0.0049	79	91	0	CCDELNEMENTQR + Oxidation (M)
1746.7582	1745.7509	1745.7566	-0.0057	55	68	0	IMGEQEQYDSYDIR
1762.7537	1761.7464	1761.7515	-0.0051	55	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9391	2000.9318	2000.9672	-0.0354	120	135	1	ELMNLPQQCNFRAPQR
2017.9536	2016.9463	2016.9621	-0.0158	120	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2614.1394	2613.1321	2613.0862	0.0459	92	111	1	CMCEALQQIMENQCDRLQDR + Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1066.0767, 1079.5308, 1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1581.7048, 1682.6033, 1698.6040, 1699.6333, 1700.6709, 1716.6215, 1774.8241, 1784.7208, 1934.8929, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 3137.4731, 3211.5571

6. gi|83753503 **Mass:** 15575 **Score:** 32 **Expect:** 0.52 **Queries matched:** 8

Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.4045	847.3972	847.3784	0.0188	53	59	0	SSDQQQR
1064.5574	1063.5501	1063.5596	-0.0095	93	100	1	QMVQQFKR
1080.5605	1079.5532	1079.5546	-0.0013	93	100	1	QMVQQFKR + Oxidation (M)
1238.5302	1237.5229	1237.5105	0.0124	8	18	1	GRQGDSSSCER
1652.8368	1651.8295	1651.8286	0.0009	23	35	0	VNLKPCEQHIMQR
1668.8137	1667.8064	1667.8235	-0.0171	23	35	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7582	1745.7509	1745.7566	-0.0057	36	49	0	IMGEQEQYDSYDIR
1762.7537	1761.7464	1761.7515	-0.0051	36	49	0	IMGEQEQYDSYDIR + Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1066.0767, 1079.5308, 1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1549.7228, 1565.7095, 1581.7048, 1682.6033, 1698.6040, 1699.6333, 1700.6709, 1714.6514, 1716.6215, 1774.8241, 1784.7208, 1934.8929, 2001.9391, 2017.9536, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 2614.1394, 3137.4731, 3211.5571

7. gi|57118278 **Mass:** 15280 **Score:** 32 **Expect:** 0.54 **Queries matched:** 8

Ara h 6 allergen [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
848.4045	847.3972	847.3784	0.0188	51	-	57	0	SSDQQQR
1064.5574	1063.5501	1063.5596	-0.0095	91	-	98	1	QMVQQFKR
1080.5605	1079.5532	1079.5546	-0.0013	91	-	98	1	QMVQQFKR + Oxidation (M)
1238.5302	1237.5229	1237.5105	0.0124	6	-	16	1	GRQGDSSSCER
1652.8368	1651.8295	1651.8286	0.0009	21	-	33	0	VNLKPCEQHIMQR
1668.8137	1667.8064	1667.8235	-0.0171	21	-	33	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7582	1745.7509	1745.7566	-0.0057	34	-	47	0	IMGEQEQYDSYDIR
1762.7537	1761.7464	1761.7515	-0.0051	34	-	47	0	IMGEQEQYDSYDIR + Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1066.0767, 1079.5308, 1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1549.7228, 1565.7095, 1581.7048, 1682.6033, 1698.6040, 1699.6333, 1700.6709, 1714.6514, 1716.6215, 1774.8241, 1784.7208, 1934.8929, 2001.9391, 2017.9536, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 2614.1394, 3137.4731, 3211.5571

8. gi|118776568 **Mass:** 17335 **Score:** 30 **Expect:** 0.92 **Queries matched:** 7

conglutin 8 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
848.4045	847.3972	847.3784	0.0188	72	-	78	0	SSDQQQR
1238.5302	1237.5229	1237.5105	0.0124	27	-	37	1	GRQGDSSSCER
1652.8368	1651.8295	1651.8286	0.0009	42	-	54	0	VNLKPCEQHIMQR
1668.8137	1667.8064	1667.8235	-0.0171	42	-	54	0	VNLKPCEQHIMQR + Oxidation (M)
1714.6514	1713.6441	1713.6392	0.0049	79	-	91	0	CCDELNEMENTQR + Oxidation (M)
1746.7582	1745.7509	1745.7566	-0.0057	55	-	68	0	IMGEQEQYDSYDIR
1762.7537	1761.7464	1761.7515	-0.0051	55	-	68	0	IMGEQEQYDSYDIR + Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1064.5574, 1066.0767, 1079.5308, 1080.5605, 1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1549.7228, 1565.7095, 1581.7048, 1682.6033, 1698.6040, 1699.6333, 1700.6709, 1716.6215, 1774.8241, 1784.7208, 1934.8929, 2001.9391, 2017.9536, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 2614.1394, 3137.4731, 3211.5571

9. gi|71040687 **Mass:** 13451 **Score:** 23 **Expect:** 4.9 **Queries matched:** 2

auxin-repressed protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
3137.4731	3136.4658	3136.5029	-0.0370	91	-	117	0	TIGSDYFDKPLLNSPTVYDWLYSGETR
3211.5571	3210.5498	3210.5802	-0.0303	49	-	78	1	SMSMPATPTTPGTPTTPLSATPRKPDNVWR + Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 848.4045, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1064.5574, 1066.0767, 1079.5308, 1080.5605,

1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1238.5302, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1549.7228, 1565.7095, 1581.7048, 1652.8368, 1668.8137, 1682.6033, 1698.6040, 1699.6333, 1700.6709, 1714.6514, 1716.6215, 1746.7582, 1762.7537, 1774.8241, 1784.7208, 1934.8929, 2001.9391, 2017.9536, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 2614.1394

10. gi|5923742 **Mass:** 15489 **Score:** 17 **Expect:** 16 **Queries matched:** 3

allergen Arah6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.4045	847.3972	847.3784	0.0188	56 -	62	0	SSDQQQR
1238.5302	1237.5229	1237.5105	0.0124	11 -	21	1	GRQGDSSSCER
1714.6514	1713.6441	1713.6392	0.0049	63 -	75	0	CCDELNEMENTQR + Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1064.5574, 1066.0767, 1079.5308, 1080.5605, 1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1549.7228, 1565.7095, 1581.7048, 1652.8368, 1668.8137, 1682.6033, 1698.6040, 1699.6333, 1700.6709, 1716.6215, 1746.7582, 1762.7537, 1774.8241, 1784.7208, 1934.8929, 2001.9391, 2017.9536, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 2614.1394, 3137.4731, 3211.5571

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 65

Protein View

Match to: **gi|17225991** Score: **81** Expect: **6.6e-006**
conglutin [Arachis hypogaea]

Nominal mass (M_r): **17349**; Calculated pI value: **5.74**
NCBI BLAST search of gi|17225991 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **65**
Number of mass values matched: **14**
Sequence Coverage: **70%**

Matched peptides shown in **Bold Red**

```
     1 AKSTILVALL ALVLVAHASA MRRERGRQGD SSSCERQVDR VNLKPCEQHI
    51 MQRIMGEQEQ YDSYDIRSTR SSDQQQRCCD ELDQMENTER CMCEALQQIM
   101 ENQCDRLQDR QMVQQFKREL MNLPQQCNFR APQRCDLDVS GGRC
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
26 - 36	1238.5302	1237.5229	1237.5105	0.0124	1	GRQGDSSSCER
41 - 53	1652.8368	1651.8295	1651.8286	0.0009	0	VNLKPCEQHIMQR
41 - 53	1668.8137	1667.8064	1667.8235	-0.0171	0	VNLKPCEQHIMQR Oxidation (M)
54 - 67	1746.7582	1745.7509	1745.7566	-0.0057	0	IMGEQEQYDSYDIR
54 - 67	1762.7537	1761.7464	1761.7515	-0.0051	0	IMGEQEQYDSYDIR Oxidation (M)
71 - 77	848.4045	847.3972	847.3784	0.0188	0	SSDQQQR
78 - 90	1699.6333	1698.6260	1698.6284	-0.0023	0	CCDELDQMENTER
91 - 110	2614.1394	2613.1321	2613.0862	0.0459	1	CMCEALQQIMENQCDRLQDR Oxidation (M)
111 - 118	1064.5574	1063.5501	1063.5596	-0.0095	1	QMVQQFKR
111 - 118	1080.5605	1079.5532	1079.5546	-0.0013	1	QMVQQFKR Oxidation (M)
119 - 130	1549.7228	1548.7155	1548.7177	-0.0022	0	ELMNLPQQCNFR
119 - 130	1565.7095	1564.7022	1564.7126	-0.0104	0	ELMNLPQQCNFR Oxidation (M)
119 - 134	2001.9391	2000.9318	2000.9672	-0.0354	1	ELMNLPQQCNFRAPQR
119 - 134	2017.9536	2016.9463	2016.9621	-0.0158	1	ELMNLPQQCNFRAPQR Oxidation (M)

No match to: 805.4589, 827.4121, 845.1245, 854.0514, 855.0638, 861.0792, 877.0549, 881.3515, 917.3467, 1001.4800, 1015.5385, 1018.4933, 1046.6041, 1047.5563, 1063.5374, 1066.0767, 1079.5308, 1083.5574, 1145.0725, 1145.5803, 1175.5681, 1215.5029, 1296.6071, 1477.7357, 1502.7131, 1503.7411, 1504.7689, 1581.7048, 1682.6033, 1698.6040, 1700.6709, 1714.6514, 1716.6215, 1774.8241, 1784.7208, 1934.8929, 2134.0483, 2150.0452, 2169.0735, 2185.0337, 2224.9802, 2227.0532, 2273.1560, 2311.1450, 2333.1299, 2351.0750, 2354.0767, 2597.1338, 2612.2468, 3137.4731, 3211.5571

Spot 97

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **26 Feb 2007 at 15:15:56 GMT**
Top Score : **88 for gi|57014074, conglutin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|57014074	17479	88	conglutin [Arachis hypogaea]
2.	gi|52001229	17479	88	conglutin [Arachis hypogaea]
3.	gi|75114094	17479	88	Conglutin precursor (Allergen Ara h 6)
4.	gi|17225991	17349	78	conglutin [Arachis hypogaea]
5.	gi|57669906	17480	76	conglutin [Arachis hypogaea]
6.	gi|83753503	15575	41	Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)
7.	gi|57118278	15280	41	Ara h 6 allergen [Arachis hypogaea]
8.	gi|118776568	17335	38	conglutin 8 [Arachis hypogaea]
9.	gi|40738308	112559	20	1a protein [Cucumber mosaic virus]
10.	gi|40738310	112681	19	1a protein [Cucumber mosaic virus]

Results List

1. gi|57014074 **Mass:** 17479 **Score:** 88 **Expect:** 1.4e-006 **Queries matched:** 15
conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
848.3984	847.3911	847.3784	0.0127	72	-	78	0	SSDQQQR
1064.5616	1063.5543	1063.5596	-0.0053	112	-	119	1	QMVQQFKR
1080.5568	1079.5495	1079.5546	-0.0050	112	-	119	1	QMVQQFKR + Oxidation (M)
1238.5435	1237.5362	1237.5105	0.0257	27	-	37	1	GRQGDSSSCER
1549.7155	1548.7082	1548.7177	-0.0095	120	-	131	0	ELMNLPQQCNFR
1565.7186	1564.7113	1564.7126	-0.0013	120	-	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8313	1651.8240	1651.8286	-0.0046	42	-	54	0	VNLKPCEQHIMQR
1668.8217	1667.8144	1667.8235	-0.0091	42	-	54	0	VNLKPCEQHIMQR + Oxidation (M)
1698.6506	1697.6433	1697.6443	-0.0010	79	-	91	0	CCDELNEMENTQR
1746.7607	1745.7534	1745.7566	-0.0032	55	-	68	0	IMGEQEQYDSYDIR

1762.7509	1761.7436	1761.7515	-0.0079	55 - 68	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9791	2000.9718	2000.9672	0.0046	120 - 135	1	ELMNLPQQCNFRAPQR
2017.9646	2016.9573	2016.9621	-0.0048	120 - 135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2151.0808	2150.0735	2150.0837	-0.0101	38 - 54	1	QVDRVNLKPCEQHIMQR
2598.1196	2597.1123	2597.0913	0.0210	92 - 111	1	CMCEALQQIMENQCDRLQDR

No match to: 805.4597, 827.4127, 847.4230, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1066.0736, 1137.0826, 1137.5796, 1145.0714, 1145.5778, 1175.5717, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1638.8303, 1681.6244, 1697.6066, 1700.7145, 1756.8301, 1774.8334, 1918.9457, 1934.8644, 2134.0796, 2146.6460, 2185.0388, 2273.1675, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2461.2024, 2514.3318, 2530.3491, 2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

2. gi|52001229 **Mass:** 17479 **Score:** 88 **Expect:** 1.4e-006 **Queries matched:** 15

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3984	847.3911	847.3784	0.0127	72 -	78	0	SSDQQQR
1064.5616	1063.5543	1063.5596	-0.0053	112 -	119	1	QMVQQFKR
1080.5568	1079.5495	1079.5546	-0.0050	112 -	119	1	QMVQQFKR + Oxidation (M)
1238.5435	1237.5362	1237.5105	0.0257	27 -	37	1	GRQGDSSSCER
1549.7155	1548.7082	1548.7177	-0.0095	120 -	131	0	ELMNLPQQCNFR
1565.7186	1564.7113	1564.7126	-0.0013	120 -	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8313	1651.8240	1651.8286	-0.0046	42 -	54	0	VNLKPCEQHIMQR
1668.8217	1667.8144	1667.8235	-0.0091	42 -	54	0	VNLKPCEQHIMQR + Oxidation (M)
1698.6506	1697.6433	1697.6443	-0.0010	79 -	91	0	CCDELNEMENTQR
1746.7607	1745.7534	1745.7566	-0.0032	55 -	68	0	IMGEQEQYDSYDIR
1762.7509	1761.7436	1761.7515	-0.0079	55 -	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9791	2000.9718	2000.9672	0.0046	120 -	135	1	ELMNLPQQCNFRAPQR
2017.9646	2016.9573	2016.9621	-0.0048	120 -	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2151.0808	2150.0735	2150.0837	-0.0101	38 -	54	1	QVDRVNLKPCEQHIMQR
2598.1196	2597.1123	2597.0913	0.0210	92 -	111	1	CMCEALQQIMENQCDRLQDR

No match to: 805.4597, 827.4127, 847.4230, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1066.0736, 1137.0826, 1137.5796, 1145.0714, 1145.5778, 1175.5717, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1638.8303, 1681.6244, 1697.6066, 1700.7145, 1756.8301, 1774.8334, 1918.9457, 1934.8644, 2134.0796, 2146.6460, 2185.0388, 2273.1675, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2461.2024, 2514.3318, 2530.3491, 2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

3. gi|75114094 **Mass:** 17479 **Score:** 88 **Expect:** 1.4e-006 **Queries matched:** 15

Conglutin precursor (Allergen Ara h 6)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3984	847.3911	847.3784	0.0127	72 -	78	0	SSDQQQR
1064.5616	1063.5543	1063.5596	-0.0053	112 -	119	1	QMVQQFKR

1080.5568	1079.5495	1079.5546	-0.0050	112 - 119	1	QMVQQFKR + Oxidation (M)
1238.5435	1237.5362	1237.5105	0.0257	27 - 37	1	GRQGDSSSCER
1549.7155	1548.7082	1548.7177	-0.0095	120 - 131	0	ELMNLPQQCNFR
1565.7186	1564.7113	1564.7126	-0.0013	120 - 131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8313	1651.8240	1651.8286	-0.0046	42 - 54	0	VNLKPCEQHIMQR
1668.8217	1667.8144	1667.8235	-0.0091	42 - 54	0	VNLKPCEQHIMQR + Oxidation (M)
1698.6506	1697.6433	1697.6443	-0.0010	79 - 91	0	CCDELNEMENTQR
1746.7607	1745.7534	1745.7566	-0.0032	55 - 68	0	IMGEQEQYDSYDIR
1762.7509	1761.7436	1761.7515	-0.0079	55 - 68	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9791	2000.9718	2000.9672	0.0046	120 - 135	1	ELMNLPQQCNFRAPQR
2017.9646	2016.9573	2016.9621	-0.0048	120 - 135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2151.0808	2150.0735	2150.0837	-0.0101	38 - 54	1	QVDRVNLKPCEQHIMQR
2598.1196	2597.1123	2597.0913	0.0210	92 - 111	1	CMCEALQQIMENQCDRLQDR

No match to: 805.4597, 827.4127, 847.4230, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1066.0736, 1137.0826, 1137.5796, 1145.0714, 1145.5778, 1175.5717, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1638.8303, 1681.6244, 1697.6066, 1700.7145, 1756.8301, 1774.8334, 1918.9457, 1934.8644, 2134.0796, 2146.6460, 2185.0388, 2273.1675, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2461.2024, 2514.3318, 2530.3491, 2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

4. gi|17225991 **Mass:** 17349 **Score:** 78 **Expect:** 1.5e-005 **Queries matched:** 14

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3984	847.3911	847.3784	0.0127	71 -	77	0	SSDQQQR
1064.5616	1063.5543	1063.5596	-0.0053	111 -	118	1	QMVQQFKR
1080.5568	1079.5495	1079.5546	-0.0050	111 -	118	1	QMVQQFKR + Oxidation (M)
1238.5435	1237.5362	1237.5105	0.0257	26 -	36	1	GRQGDSSSCER
1549.7155	1548.7082	1548.7177	-0.0095	119 -	130	0	ELMNLPQQCNFR
1565.7186	1564.7113	1564.7126	-0.0013	119 -	130	0	ELMNLPQQCNFR + Oxidation (M)
1652.8313	1651.8240	1651.8286	-0.0046	41 -	53	0	VNLKPCEQHIMQR
1668.8217	1667.8144	1667.8235	-0.0091	41 -	53	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7607	1745.7534	1745.7566	-0.0032	54 -	67	0	IMGEQEQYDSYDIR
1762.7509	1761.7436	1761.7515	-0.0079	54 -	67	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9791	2000.9718	2000.9672	0.0046	119 -	134	1	ELMNLPQQCNFRAPQR
2017.9646	2016.9573	2016.9621	-0.0048	119 -	134	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2151.0808	2150.0735	2150.0837	-0.0101	37 -	53	1	QVDRVNLKPCEQHIMQR
2598.1196	2597.1123	2597.0913	0.0210	91 -	110	1	CMCEALQQIMENQCDRLQDR

No match to: 805.4597, 827.4127, 847.4230, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1066.0736, 1137.0826, 1137.5796, 1145.0714, 1145.5778, 1175.5717, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1638.8303, 1681.6244, 1697.6066, 1698.6506, 1700.7145, 1756.8301, 1774.8334, 1918.9457, 1934.8644, 2134.0796, 2146.6460, 2185.0388, 2273.1675, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2461.2024, 2514.3318, 2530.3491,

2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

5. gi|57669906 **Mass:** 17480 **Score:** 76 **Expect:** 2.4e-005 **Queries matched:** 14

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
848.3984	847.3911	847.3784	0.0127	72	-	78	0	SSDQQQR
1064.5616	1063.5543	1063.5596	-0.0053	112	-	119	1	QMVQQFKR
1080.5568	1079.5495	1079.5546	-0.0050	112	-	119	1	QMVQQFKR + Oxidation (M)
1238.5435	1237.5362	1237.5105	0.0257	27	-	37	1	GRQGDSSSCER
1549.7155	1548.7082	1548.7177	-0.0095	120	-	131	0	ELMNLPQQCNFR
1565.7186	1564.7113	1564.7126	-0.0013	120	-	131	0	ELMNLPQQCNFR + Oxidation (M)
1652.8313	1651.8240	1651.8286	-0.0046	42	-	54	0	VNLKPCEQHIMQR
1668.8217	1667.8144	1667.8235	-0.0091	42	-	54	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7607	1745.7534	1745.7566	-0.0032	55	-	68	0	IMGEQEQYDSYDIR
1762.7509	1761.7436	1761.7515	-0.0079	55	-	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2001.9791	2000.9718	2000.9672	0.0046	120	-	135	1	ELMNLPQQCNFRAPQR
2017.9646	2016.9573	2016.9621	-0.0048	120	-	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2151.0808	2150.0735	2150.0837	-0.0101	38	-	54	1	QVDRVNLKPCEQHIMQR
2598.1196	2597.1123	2597.0913	0.0210	92	-	111	1	CMCEALQQIMENQCDRLQDR

No match to: 805.4597, 827.4127, 847.4230, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1066.0736, 1137.0826, 1137.5796, 1145.0714, 1145.5778, 1175.5717, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1638.8303, 1681.6244, 1697.6066, 1698.6506, 1700.7145, 1756.8301, 1774.8334, 1918.9457, 1934.8644, 2134.0796, 2146.6460, 2185.0388, 2273.1675, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2461.2024, 2514.3318, 2530.3491, 2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

6. gi|83753503 **Mass:** 15575 **Score:** 41 **Expect:** 0.07 **Queries matched:** 9

Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
848.3984	847.3911	847.3784	0.0127	53	-	59	0	SSDQQQR
1064.5616	1063.5543	1063.5596	-0.0053	93	-	100	1	QMVQQFKR
1080.5568	1079.5495	1079.5546	-0.0050	93	-	100	1	QMVQQFKR + Oxidation (M)
1238.5435	1237.5362	1237.5105	0.0257	8	-	18	1	GRQGDSSSCER
1652.8313	1651.8240	1651.8286	-0.0046	23	-	35	0	VNLKPCEQHIMQR
1668.8217	1667.8144	1667.8235	-0.0091	23	-	35	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7607	1745.7534	1745.7566	-0.0032	36	-	49	0	IMGEQEQYDSYDIR
1762.7509	1761.7436	1761.7515	-0.0079	36	-	49	0	IMGEQEQYDSYDIR + Oxidation (M)
2151.0808	2150.0735	2150.0837	-0.0101	19	-	35	1	QVDRVNLKPCEQHIMQR

No match to: 805.4597, 827.4127, 847.4230, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1066.0736, 1137.0826, 1137.5796, 1145.0714, 1145.5778, 1175.5717, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1549.7155, 1565.7186, 1638.8303, 1681.6244, 1697.6066, 1698.6506, 1700.7145, 1756.8301, 1774.8334, 1918.9457, 1934.8644, 2001.9791, 2017.9646, 2134.0796,

2146.6460, 2185.0388, 2273.1675, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2461.2024, 2514.3318, 2530.3491, 2598.1196, 2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

7. gi|57118278 **Mass:** 15280 **Score:** 41 **Expect:** 0.073 **Queries matched:** 9

Ara h 6 allergen [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
848.3984	847.3911	847.3784	0.0127	51	-	57	0	SSDQQQR
1064.5616	1063.5543	1063.5596	-0.0053	91	-	98	1	QMVQQFKR
1080.5568	1079.5495	1079.5546	-0.0050	91	-	98	1	QMVQQFKR + Oxidation (M)
1238.5435	1237.5362	1237.5105	0.0257	6	-	16	1	GRQGDSSSCER
1652.8313	1651.8240	1651.8286	-0.0046	21	-	33	0	VNLKPCEQHIMQR
1668.8217	1667.8144	1667.8235	-0.0091	21	-	33	0	VNLKPCEQHIMQR + Oxidation (M)
1746.7607	1745.7534	1745.7566	-0.0032	34	-	47	0	IMGEQEQYDSYDIR
1762.7509	1761.7436	1761.7515	-0.0079	34	-	47	0	IMGEQEQYDSYDIR + Oxidation (M)
2151.0808	2150.0735	2150.0837	-0.0101	17	-	33	1	QVDRVNLKPCEQHIMQR

No match to: 805.4597, 827.4127, 847.4230, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1066.0736, 1137.0826, 1137.5796, 1145.0714, 1145.5778, 1175.5717, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1549.7155, 1565.7186, 1638.8303, 1681.6244, 1697.6066, 1698.6506, 1700.7145, 1756.8301, 1774.8334, 1918.9457, 1934.8644, 2001.9791, 2017.9646, 2134.0796, 2146.6460, 2185.0388, 2273.1675, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2461.2024, 2514.3318, 2530.3491, 2598.1196, 2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

8. gi|118776568 **Mass:** 17335 **Score:** 38 **Expect:** 0.14 **Queries matched:** 8

conglutin 8 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
848.3984	847.3911	847.3784	0.0127	72	-	78	0	SSDQQQR
1238.5435	1237.5362	1237.5105	0.0257	27	-	37	1	GRQGDSSSCER
1652.8313	1651.8240	1651.8286	-0.0046	42	-	54	0	VNLKPCEQHIMQR
1668.8217	1667.8144	1667.8235	-0.0091	42	-	54	0	VNLKPCEQHIMQR + Oxidation (M)
1698.6506	1697.6433	1697.6443	-0.0010	79	-	91	0	CCDELNEMENTQR
1746.7607	1745.7534	1745.7566	-0.0032	55	-	68	0	IMGEQEQYDSYDIR
1762.7509	1761.7436	1761.7515	-0.0079	55	-	68	0	IMGEQEQYDSYDIR + Oxidation (M)
2151.0808	2150.0735	2150.0837	-0.0101	38	-	54	1	QVDRVNLKPCEQHIMQR

No match to: 805.4597, 827.4127, 847.4230, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1064.5616, 1066.0736, 1080.5568, 1137.0826, 1137.5796, 1145.0714, 1145.5778, 1175.5717, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1549.7155, 1565.7186, 1638.8303, 1681.6244, 1697.6066, 1700.7145, 1756.8301, 1774.8334, 1918.9457, 1934.8644, 2001.9791, 2017.9646, 2134.0796, 2146.6460, 2185.0388, 2273.1675, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2461.2024, 2514.3318, 2530.3491, 2598.1196, 2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

9. gi|40738308 **Mass:** 112559 **Score:** 20 **Expect:** 8.8 **Queries matched:** 8

1a protein [Cucumber mosaic virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1064.5616	1063.5543	1063.5410	0.0133	623	631	1	RNSFEGNLK
1137.5796	1136.5723	1136.5682	0.0042	585	594	1	MAERATAMLK + Oxidation (M)
1565.7186	1564.7113	1564.7344	-0.0231	917	928	1	EMNLPKTFWDER
1652.8313	1651.8240	1651.8127	0.0113	726	740	0	SIFEPSTDMIVTANK
1668.8217	1667.8144	1667.8076	0.0068	726	740	0	SIFEPSTDMIVTANK + Oxidation (M)
2273.1675	2272.1602	2272.1958	-0.0356	780	799	0	VLVDEVVLLHFGQLCAVMSK + Oxidation (M)
2461.2024	2460.1951	2460.2113	-0.0162	632	652	0	FVFDTYFTVDPLVNVHFSTGR
2514.3318	2513.3245	2513.3749	-0.0503	780	801	1	VLVDEVVLLHFGQLCAVMSKLK + Oxidation (M)

No match to: 805.4597, 827.4127, 847.4230, 848.3984, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1066.0736, 1080.5568, 1137.0826, 1145.0714, 1145.5778, 1175.5717, 1238.5435, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1549.7155, 1638.8303, 1681.6244, 1697.6066, 1698.6506, 1700.7145, 1746.7607, 1756.8301, 1762.7509, 1774.8334, 1918.9457, 1934.8644, 2001.9791, 2017.9646, 2134.0796, 2146.6460, 2151.0808, 2185.0388, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2530.3491, 2598.1196, 2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

10. gi|40738310 **Mass:** 112681 **Score:** 19 **Expect:** 11 **Queries matched:** 7

1a protein [Cucumber mosaic virus]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1565.7186	1564.7113	1564.7344	-0.0231	917	928	1	EMNLPKTFWDER
1652.8313	1651.8240	1651.8127	0.0113	726	740	0	SIFEPSTDMIVTANK
1668.8217	1667.8144	1667.8076	0.0068	726	740	0	SIFEPSTDMIVTANK + Oxidation (M)
2134.0796	2133.0723	2133.0894	-0.0171	414	431	0	IDINDYHYIGFATLLHTK
2273.1675	2272.1602	2272.1958	-0.0356	780	799	0	VLVDEVVLLHFGQLCAVMSK + Oxidation (M)
2461.2024	2460.1951	2460.2113	-0.0162	632	652	0	FVFDTYFTVDPLVNVHFSTGR
2514.3318	2513.3245	2513.3749	-0.0503	780	801	1	VLVDEVVLLHFGQLCAVMSKLK + Oxidation (M)

No match to: 805.4597, 827.4127, 847.4230, 848.3984, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1064.5616, 1066.0736, 1080.5568, 1137.0826, 1137.5796, 1145.0714, 1145.5778, 1175.5717, 1238.5435, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1549.7155, 1638.8303, 1681.6244, 1697.6066, 1698.6506, 1700.7145, 1746.7607, 1756.8301, 1762.7509, 1774.8334, 1918.9457, 1934.8644, 2001.9791, 2017.9646, 2146.6460, 2151.0808, 2185.0388, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2530.3491, 2598.1196, 2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 72

Protein View

Match to: **gi|52001229** Score: **88** Expect: **1.4e-006**
conglutin [Arachis hypogaea]

Nominal mass (M_r): **17479**; Calculated pI value: **6.13**
NCBI BLAST search of gi|52001229 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **72**
Number of mass values matched: **15**
Sequence Coverage: **73%**

Matched peptides shown in **Bold Red**

```
     1 MAKSTILVAL LALVLVAHAS AMRRERGRQG DSSSCERQVD RVNLKPCEQH
    51 IMQRIMGEQE QYDSYDIRST RSSDQQQRCC DELNEMENTQ RCMCEALQQI
   101 MENQCDRLQD RQMVQQFKRE LMNLPQQCNF RAPQRCDLDV SGGRC
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
27 - 37	1238.5435	1237.5362	1237.5105	0.0257	1	GRQGDSSSCER
38 - 54	2151.0808	2150.0735	2150.0837	-0.0101	1	QVDRVNLKPCEQHIMQR
42 - 54	1652.8313	1651.8240	1651.8286	-0.0046	0	VNLKPCEQHIMQR

42 - 54	1668.8217	1667.8144	1667.8235	-0.0091	0	**VNLKPCEQHIMQR** Oxidation (M)
55 - 68	1746.7607	1745.7534	1745.7566	-0.0032	0	**IMGEQEQYDSYDIR**
55 - 68	1762.7509	1761.7436	1761.7515	-0.0079	0	**IMGEQEQYDSYDIR** Oxidation (M)
72 - 78	848.3984	847.3911	847.3784	0.0127	0	**SSDQQQR**
79 - 91	1698.6506	1697.6433	1697.6443	-0.0010	0	**CCDELNEMENTQR**
92 - 111	2598.1196	2597.1123	2597.0913	0.0210	1	**CMCEALQQIMENQCDRLQDR**
112 - 119	1064.5616	1063.5543	1063.5596	-0.0053	1	**QMVQQFKR**
112 - 119	1080.5568	1079.5495	1079.5546	-0.0050	1	**QMVQQFKR** Oxidation (M)
120 - 131	1549.7155	1548.7082	1548.7177	-0.0095	0	**ELMNLPQQCNFR**
120 - 131	1565.7186	1564.7113	1564.7126	-0.0013	0	**ELMNLPQQCNFR** Oxidation (M)
120 - 135	2001.9791	2000.9718	2000.9672	0.0046	1	**ELMNLPQQCNFRAPQR**
120 - 135	2017.9646	2016.9573	2016.9621	-0.0048	1	**ELMNLPQQCNFRAPQR** Oxidation (M)

No match to: 805.4597, 827.4127, 847.4230, 855.0609, 861.0731, 877.0498, 881.2839, 928.4884, 1018.4756, 1046.5994, 1047.5629, 1063.5310, 1066.0736, 1137.0826, 1137.5796, 1145.0714, 1145.5778, 1175.5717, 1277.0756, 1277.7112, 1308.6290, 1320.5962, 1407.6890, 1435.7267, 1475.7787, 1503.7097, 1638.8303, 1681.6244, 1697.6066, 1700.7145, 1756.8301, 1774.8334, 1918.9457, 1934.8644, 2134.0796, 2146.6460, 2185.0388, 2273.1675, 2295.1392, 2305.1472, 2311.1421, 2327.1069, 2333.1218, 2336.1057, 2351.0876, 2353.1047, 2461.2024, 2514.3318, 2530.3491, 2612.2224, 2614.1807, 2706.2019, 3136.4775, 3168.5281, 3211.5288, 3233.5103, 3300.8062

Spot 98

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **20 Mar 2007 at 13:19:24 GMT**
Top Score : **82 for gi|66735602, LEA protein [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|66735602	10408	82	LEA protein [Arachis hypogaea]
2.	gi|28194651	10390	56	putative lea 1 [Arachis hypogaea]
3.	gi|15418705	18612	54	allergen II [Arachis hypogaea]
4.	gi|28912768	19765	54	seed storage protein [Arachis hypogaea]
5.	gi|31322017	20212	53	allergen Ara h 2 isoform [Arachis hypogaea]
6.	gi|26245447	20558	51	allergen Ara h 2.02 [Arachis hypogaea]
7.	gi|46560480	22229	51	seed storage protein SSP1 [Arachis hypogaea]
8.	gi|52001227	21293	51	2S protein 1 [Arachis hypogaea]
9.	gi|118776566	19009	48	conglutin 7 [Arachis hypogaea]
10.	gi|71040659	9898	47	lea protein 1 [Arachis hypogaea]

Results List

1. gi|66735602 **Mass:** 10408 **Score:** 82 **Expect:** 5.2e-006 **Queries matched:** 7
LEA protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1000.4895	999.4822	999.4695	0.0128	62	-	70	1	KGGFSTMEK + Oxidation (M)
1315.6344	1314.6271	1314.6276	-0.0005	4	-	13	1	QQNRQELDER
1339.6597	1338.6524	1338.6527	-0.0003	29	-	40	0	SLEAQEHLAEGR
1513.6500	1512.6427	1512.6514	-0.0087	49	-	61	0	EQLGTEGYQEMGR + Oxidation (M)
1641.7506	1640.7433	1640.7464	-0.0030	49	-	62	1	EQLGTEGYQEMGRK + Oxidation (M)
1669.7502	1668.7429	1668.7525	-0.0096	48	-	61	1	REQLGTEGYQEMGR + Oxidation (M)
2507.2859	2506.2786	2506.2411	0.0376	16	-	40	1	QGETVVPGGTGGKSLEAQEHLAEGR

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1020.5323, 1046.6025, 1074.5498, 1085.5603, 1091.5699, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1353.6705, 1451.6694, 1501.7577, 1529.6732, 1537.7931, 1579.7875, 1607.7700, 1640.7688, 1643.7858, 1700.8820, 1726.6819, 1774.8528, 1797.8450, 1820.7969,

1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033

2. gi|28194651 **Mass:** 10390 **Score:** 56 **Expect:** 0.0022 **Queries matched:** 5

putative lea 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1000.4895	999.4822	999.4695	0.0128	62	-	70	1	KGGFSTMEK + Oxidation (M)
1315.6344	1314.6271	1314.6276	-0.0005	5	-	14	1	QQNRQELDER
1339.6597	1338.6524	1338.6527	-0.0003	30	-	41	0	SLEAQEHLAEGR
1820.7969	1819.7896	1819.8071	-0.0174	71	-	87	1	SGGERAEEEGVEIDESK
2507.2859	2506.2786	2506.2411	0.0376	17	-	41	1	QGETVVPGGTGGKSLEAQEHLAEGR

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1020.5323, 1046.6025, 1074.5498, 1085.5603, 1091.5699, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1353.6705, 1451.6694, 1501.7577, 1513.6500, 1529.6732, 1537.7931, 1579.7875, 1607.7700, 1640.7688, 1641.7506, 1643.7858, 1669.7502, 1700.8820, 1726.6819, 1774.8528, 1797.8450, 1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033

3. gi|15418705 **Mass:** 18612 **Score:** 54 **Expect:** 0.0036 **Queries matched:** 6

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1085.5603	1084.5530	1084.5447	0.0083	135	-	143	0	NLPQQCGLR
1091.5699	1090.5626	1090.5519	0.0107	124	-	131	1	QQEQQFKR
1315.6344	1314.6271	1314.6429	-0.0157	23	-	32	1	QQWELQGDRR
1537.7931	1536.7858	1536.7943	-0.0085	135	-	147	1	NLPQQCGLRAPQR
1640.7688	1639.7615	1639.7922	-0.0307	40	-	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6819	1725.6746	1725.6835	-0.0088	91	-	103	0	CCNELNEFENNQR

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1000.4895, 1020.5323, 1046.6025, 1074.5498, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1339.6597, 1353.6705, 1451.6694, 1501.7577, 1513.6500, 1529.6732, 1579.7875, 1607.7700, 1641.7506, 1643.7858, 1669.7502, 1700.8820, 1774.8528, 1797.8450, 1820.7969, 1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2507.2859, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033

4. gi|28912768 **Mass:** 19765 **Score:** 54 **Expect:** 0.0039 **Queries matched:** 6

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1085.5603	1084.5530	1084.5447	0.0083	145	-	153	0	NLPQQCGLR
1091.5699	1090.5626	1090.5519	0.0107	134	-	141	1	QQEQQFKR
1315.6344	1314.6271	1314.6429	-0.0157	21	-	30	1	QQWELQGDRR
1537.7931	1536.7858	1536.7943	-0.0085	145	-	157	1	NLPQQCGLRAPQR
1640.7688	1639.7615	1639.7922	-0.0307	38	-	50	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6819	1725.6746	1725.6835	-0.0088	101	-	113	0	CCNELNEFENNQR

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1000.4895, 1020.5323, 1046.6025,

1074.5498, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1339.6597, 1353.6705, 1451.6694, 1501.7577, 1513.6500, 1529.6732, 1579.7875, 1607.7700, 1641.7506, 1643.7858, 1669.7502, 1700.8820, 1774.8528, 1797.8450, 1820.7969, 1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2507.2859, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033

5. gi|31322017 **Mass:** 20212 **Score:** 53 **Expect:** 0.0047 **Queries matched:** 6

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5603	1084.5530	1084.5447	0.0083	144	152	0	NLPQQCGLR
1091.5699	1090.5626	1090.5519	0.0107	133	140	1	QQEQQFKR
1315.6344	1314.6271	1314.6429	-0.0157	20	29	1	QQWELQGDRR
1537.7931	1536.7858	1536.7943	-0.0085	144	156	1	NLPQQCGLRAPQR
1640.7688	1639.7615	1639.7922	-0.0307	37	49	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6819	1725.6746	1725.6835	-0.0088	100	112	0	CCNELNEFENNQR

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1000.4895, 1020.5323, 1046.6025, 1074.5498, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1339.6597, 1353.6705, 1451.6694, 1501.7577, 1513.6500, 1529.6732, 1579.7875, 1607.7700, 1641.7506, 1643.7858, 1669.7502, 1700.8820, 1774.8528, 1797.8450, 1820.7969, 1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2507.2859, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033

6. gi|26245447 **Mass:** 20558 **Score:** 51 **Expect:** 0.0074 **Queries matched:** 6

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5603	1084.5530	1084.5447	0.0083	147	155	0	NLPQQCGLR
1091.5699	1090.5626	1090.5519	0.0107	136	143	1	QQEQQFKR
1315.6344	1314.6271	1314.6429	-0.0157	23	32	1	QQWELQGDRR
1537.7931	1536.7858	1536.7943	-0.0085	147	159	1	NLPQQCGLRAPQR
1640.7688	1639.7615	1639.7922	-0.0307	40	52	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6819	1725.6746	1725.6835	-0.0088	103	115	0	CCNELNEFENNQR

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1000.4895, 1020.5323, 1046.6025, 1074.5498, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1339.6597, 1353.6705, 1451.6694, 1501.7577, 1513.6500, 1529.6732, 1579.7875, 1607.7700, 1641.7506, 1643.7858, 1669.7502, 1700.8820, 1774.8528, 1797.8450, 1820.7969, 1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2507.2859, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033

7. gi|46560480 **Mass:** 22229 **Score:** 51 **Expect:** 0.0076 **Queries matched:** 6

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5603	1084.5530	1084.5447	0.0083	162	170	0	NLPQQCGLR
1091.5699	1090.5626	1090.5519	0.0107	151	158	1	QQEQQFKR
1315.6344	1314.6271	1314.6429	-0.0157	38	47	1	QQWELQGDRR
1537.7931	1536.7858	1536.7943	-0.0085	162	174	1	NLPQQCGLRAPQR

1640.7688	1639.7615	1639.7922	-0.0307	55 - 67	0	ANLRPCEQHLMQK + Oxidation (M)
1726.6819	1725.6746	1725.6835	-0.0088	118 - 130	0	CCNELNEFENNQR

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1000.4895, 1020.5323, 1046.6025, 1074.5498, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1339.6597, 1353.6705, 1451.6694, 1501.7577, 1513.6500, 1529.6732, 1579.7875, 1607.7700, 1641.7506, 1643.7858, 1669.7502, 1700.8820, 1774.8528, 1797.8450, 1820.7969, 1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2507.2859, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033

8. gi|52001227 **Mass:** 21293 **Score:** 51 **Expect:** 0.0078 **Queries matched:** 6

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5603	1084.5530	1084.5447	0.0083	154 - 162		0	NLPQQCGLR
1091.5699	1090.5626	1090.5519	0.0107	143 - 150		1	QQEQQFKR
1315.6344	1314.6271	1314.6429	-0.0157	42 - 51		1	QQWELQGDRR
1537.7931	1536.7858	1536.7943	-0.0085	154 - 166		1	NLPQQCGLRAPQR
1640.7688	1639.7615	1639.7922	-0.0307	59 - 71		0	ANLRPCEQHLMQK + Oxidation (M)
1726.6819	1725.6746	1725.6835	-0.0088	110 - 122		0	CCNELNEFENNQR

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1000.4895, 1020.5323, 1046.6025, 1074.5498, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1339.6597, 1353.6705, 1451.6694, 1501.7577, 1513.6500, 1529.6732, 1579.7875, 1607.7700, 1641.7506, 1643.7858, 1669.7502, 1700.8820, 1774.8528, 1797.8450, 1820.7969, 1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2507.2859, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033

9. gi|118776566 **Mass:** 19009 **Score:** 48 **Expect:** 0.013 **Queries matched:** 6

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1085.5603	1084.5530	1084.5447	0.0083	133 - 141		0	NLPQQCGLR
1091.5699	1090.5626	1090.5519	0.0107	122 - 129		1	QQEQQFKR
1315.6344	1314.6271	1314.6429	-0.0157	23 - 32		1	QQWELQGDRR
1537.7931	1536.7858	1536.7943	-0.0085	133 - 145		1	NLPQQCGLRAPQR
1640.7688	1639.7615	1639.7922	-0.0307	40 - 52		0	ANLRPCEQHLMQK + Oxidation (M)
1726.6819	1725.6746	1725.6835	-0.0088	89 - 101		0	CCNELNEFENNQR

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1000.4895, 1020.5323, 1046.6025, 1074.5498, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1339.6597, 1353.6705, 1451.6694, 1501.7577, 1513.6500, 1529.6732, 1579.7875, 1607.7700, 1641.7506, 1643.7858, 1669.7502, 1700.8820, 1774.8528, 1797.8450, 1820.7969, 1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2507.2859, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033

10. gi|71040659 **Mass:** 9898 **Score:** 47 **Expect:** 0.02 **Queries matched:** 5

lea protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1000.4895	999.4822	999.4695	0.0128	63 - 71		1	KGGFSTMEK + Oxidation (M)

1315.6344	1314.6271	1314.6276	-0.0005	5 -	14	1	QQNRQELDER
1513.6500	1512.6427	1512.6514	-0.0087	50 -	62	0	EQLGTEGYQEMGR + Oxidation (M)
1641.7506	1640.7433	1640.7464	-0.0030	50 -	63	1	EQLGTEGYQEMGRK + Oxidation (M)
1669.7502	1668.7429	1668.7525	-0.0096	49 -	62	1	REQLGTEGYQEMGR + Oxidation (M)

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1020.5323, 1046.6025, 1074.5498, 1085.5603, 1091.5699, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1339.6597, 1353.6705, 1451.6694, 1501.7577, 1529.6732, 1537.7931, 1579.7875, 1607.7700, 1640.7688, 1643.7858, 1700.8820, 1726.6819, 1774.8528, 1797.8450, 1820.7969, 1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2507.2859, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|66735602** Score: **82** Expect: **5.2e-006**
LEA protein [Arachis hypogaea]

Nominal mass (M_r): **10408**; Calculated pI value: **5.31**
NCBI BLAST search of gi|66735602 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **7**
Sequence Coverage: **61%**

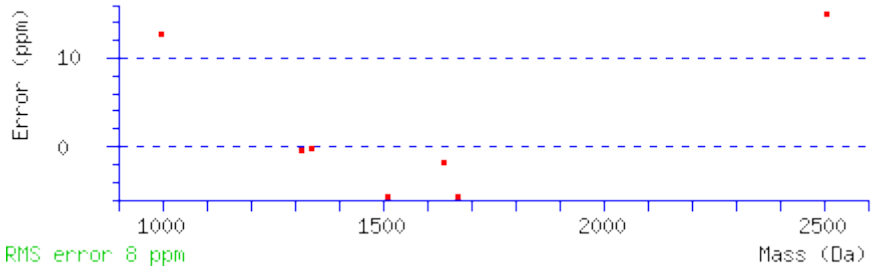
Matched peptides shown in **Bold Red**

```
   1 ASKQQNRQEL DERAKQGETV VPGGTGGKSL EAQEHLAEGR SKGGQTRREQ
  51 LGTEGYQEMG RKGGFSTMEK SGEERAEEEG VEIDESKFAT KNQNK
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
4 - 13	1315.6344	1314.6271	1314.6276	-0.0005	1	QQNRQELDER
16 - 40	2507.2859	2506.2786	2506.2411	0.0376	1	QGETVVPGGTGGKSLEAQEHLAEGR
29 - 40	1339.6597	1338.6524	1338.6527	-0.0003	0	SLEAQEHLAEGR
48 - 61	1669.7502	1668.7429	1668.7525	-0.0096	1	REQLGTEGYQEMGR Oxidation (M)
49 - 61	1513.6500	1512.6427	1512.6514	-0.0087	0	EQLGTEGYQEMGR Oxidation (M)
49 - 62	1641.7506	1640.7433	1640.7464	-0.0030	1	EQLGTEGYQEMGRK Oxidation (M)
62 - 70	1000.4895	999.4822	999.4695	0.0128	1	KGGFSTMEK Oxidation (M)

No match to: 805.4722, 835.4509, 861.0908, 868.5660, 873.4845, 882.5790, 889.5234, 1020.5323, 1046.6025, 1074.5498, 1085.5603, 1091.5699, 1145.0730, 1145.5768, 1173.5900, 1253.5924, 1353.6705, 1451.6694, 1501.7577, 1529.6732, 1537.7931, 1579.7875, 1607.7700, 1640.7688, 1643.7858, 1700.8820, 1726.6819, 1774.8528, 1797.8450, 1820.7969, 1842.9338, 2185.0388, 2268.0713, 2273.1653, 2296.1089, 2299.1008, 2305.1460, 2311.1470, 2706.4246, 2752.3438, 2782.3601, 2868.5293, 3010.6033



Spot 99

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **20 Mar 2007 at 13:18:44 GMT**
Top Score : **55 for gi|46560482, seed storage protein SSP2 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|46560482	20907	55	seed storage protein SSP2 [Arachis hypogaea]
2.	gi|15418705	18612	54	allergen II [Arachis hypogaea]
3.	gi|28912768	19765	53	seed storage protein [Arachis hypogaea]
4.	gi|31322017	20212	52	allergen Ara h 2 isoform [Arachis hypogaea]
5.	gi|52001227	21293	50	2S protein 1 [Arachis hypogaea]
6.	gi|26245447	20558	50	allergen Ara h 2.02 [Arachis hypogaea]
7.	gi|46560480	22229	50	seed storage protein SSP1 [Arachis hypogaea]
8.	gi|118776566	19009	49	conglutin 7 [Arachis hypogaea]
9.	gi|14347293	24390	47	unnamed protein product [Arachis hypogaea]
10.	gi|288479	5059	13	chitinase [Arachis hypogaea]

Results List

1. gi|46560482 **Mass:** 20907 **Score:** 55 **Expect:** 0.0027 **Queries matched:** 8
seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4590	934.4517	934.4508	0.0009	139	145	0	QQEQQFK
1056.4843	1055.4770	1055.4744	0.0026	96	105	0	GAGSSQHQER
1085.5533	1084.5460	1084.5447	0.0013	150	158	0	NLPQQCGLR
1091.5597	1090.5524	1090.5519	0.0005	139	146	1	QQEQQFKR
1726.6926	1725.6853	1725.6835	0.0019	106	118	0	CCNELNEFENNQR
2012.8281	2011.8208	2011.8220	-0.0012	119	134	0	CMCEALQQIMENQSDR
2028.8220	2027.8147	2027.8169	-0.0022	119	134	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8180	2043.8107	2043.8118	-0.0011	119	134	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1062.7854, 1074.5315, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1753.9185, 1940.9397, 2211.1025, 2225.1230, 2233.1162, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413

2. gi|15418705 **Mass:** 18612 **Score:** 54 **Expect:** 0.0033 **Queries matched:** 8

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4590	934.4517	934.4508	0.0009	124	130	0	QQEQQFK
1056.4843	1055.4770	1055.4744	0.0026	81	90	0	GAGSSQHQER
1085.5533	1084.5460	1084.5447	0.0013	135	143	0	NLPQQCGLR
1091.5597	1090.5524	1090.5519	0.0005	124	131	1	QQEQQFKR
1726.6926	1725.6853	1725.6835	0.0019	91	103	0	CCNELNEFENNQR
2012.8281	2011.8208	2011.8220	-0.0012	104	119	0	CMCEALQQIMENQSDR
2028.8220	2027.8147	2027.8169	-0.0022	104	119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8180	2043.8107	2043.8118	-0.0011	104	119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1062.7854, 1074.5315, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1753.9185, 1940.9397, 2211.1025, 2225.1230, 2233.1162, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413

3. gi|28912768 **Mass:** 19765 **Score:** 53 **Expect:** 0.0041 **Queries matched:** 8

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4590	934.4517	934.4508	0.0009	134	140	0	QQEQQFK
1056.4843	1055.4770	1055.4744	0.0026	91	100	0	GAGSSQHQER
1085.5533	1084.5460	1084.5447	0.0013	145	153	0	NLPQQCGLR
1091.5597	1090.5524	1090.5519	0.0005	134	141	1	QQEQQFKR
1726.6926	1725.6853	1725.6835	0.0019	101	113	0	CCNELNEFENNQR
2012.8281	2011.8208	2011.8220	-0.0012	114	129	0	CMCEALQQIMENQSDR
2028.8220	2027.8147	2027.8169	-0.0022	114	129	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8180	2043.8107	2043.8118	-0.0011	114	129	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1062.7854, 1074.5315, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1753.9185, 1940.9397, 2211.1025, 2225.1230, 2233.1162, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413

4. gi|31322017 **Mass:** 20212 **Score:** 52 **Expect:** 0.005 **Queries matched:** 8

allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4590	934.4517	934.4508	0.0009	133 -	139	0	QQEQQFK
1056.4843	1055.4770	1055.4744	0.0026	90 -	99	0	GAGSSQHQER
1085.5533	1084.5460	1084.5447	0.0013	144 -	152	0	NLPQQCGLR
1091.5597	1090.5524	1090.5519	0.0005	133 -	140	1	QQEQQFKR
1726.6926	1725.6853	1725.6835	0.0019	100 -	112	0	CCNELNEFENNQR
2012.8281	2011.8208	2011.8220	-0.0012	113 -	128	0	CMCEALQQIMENQSDR
2028.8220	2027.8147	2027.8169	-0.0022	113 -	128	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8180	2043.8107	2043.8118	-0.0011	113 -	128	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1062.7854, 1074.5315, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1753.9185, 1940.9397, 2211.1025, 2225.1230, 2233.1162, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413

5. gi|52001227 **Mass:** 21293 **Score:** 50 **Expect:** 0.0082 **Queries matched:** 8

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4590	934.4517	934.4508	0.0009	143 -	149	0	QQEQQFK
1056.4843	1055.4770	1055.4744	0.0026	100 -	109	0	GAGSSQHQER
1085.5533	1084.5460	1084.5447	0.0013	154 -	162	0	NLPQQCGLR
1091.5597	1090.5524	1090.5519	0.0005	143 -	150	1	QQEQQFKR
1726.6926	1725.6853	1725.6835	0.0019	110 -	122	0	CCNELNEFENNQR
2012.8281	2011.8208	2011.8220	-0.0012	123 -	138	0	CMCEALQQIMENQSDR
2028.8220	2027.8147	2027.8169	-0.0022	123 -	138	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8180	2043.8107	2043.8118	-0.0011	123 -	138	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1062.7854, 1074.5315, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1753.9185, 1940.9397, 2211.1025, 2225.1230, 2233.1162, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413

6. gi|26245447 **Mass:** 20558 **Score:** 50 **Expect:** 0.0082 **Queries matched:** 8

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4590	934.4517	934.4508	0.0009	136 -	142	0	QQEQQFK
1056.4843	1055.4770	1055.4744	0.0026	93 -	102	0	GAGSSQHQER
1085.5533	1084.5460	1084.5447	0.0013	147 -	155	0	NLPQQCGLR
1091.5597	1090.5524	1090.5519	0.0005	136 -	143	1	QQEQQFKR
1726.6926	1725.6853	1725.6835	0.0019	103 -	115	0	CCNELNEFENNQR
2012.8281	2011.8208	2011.8220	-0.0012	116 -	131	0	CMCEALQQIMENQSDR
2028.8220	2027.8147	2027.8169	-0.0022	116 -	131	0	CMCEALQQIMENQSDR + Oxidation (M)

2044.8180	2043.8107	2043.8118	-0.0011	116 - 131	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1062.7854, 1074.5315, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1753.9185, 1940.9397, 2211.1025, 2225.1230, 2233.1162, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413

7. gi|46560480 **Mass:** 22229 **Score:** 50 **Expect:** 0.0082 **Queries matched:** 8

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4590	934.4517	934.4508	0.0009	151 -	157	0	QQEQQFK
1056.4843	1055.4770	1055.4744	0.0026	108 -	117	0	GAGSSQHQER
1085.5533	1084.5460	1084.5447	0.0013	162 -	170	0	NLPQQCGLR
1091.5597	1090.5524	1090.5519	0.0005	151 -	158	1	QQEQQFKR
1726.6926	1725.6853	1725.6835	0.0019	118 -	130	0	CCNELNEFENNQR
2012.8281	2011.8208	2011.8220	-0.0012	131 -	146	0	CMCEALQQIMENQSDR
2028.8220	2027.8147	2027.8169	-0.0022	131 -	146	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8180	2043.8107	2043.8118	-0.0011	131 -	146	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1062.7854, 1074.5315, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1753.9185, 1940.9397, 2211.1025, 2225.1230, 2233.1162, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413

8. gi|118776566 **Mass:** 19009 **Score:** 49 **Expect:** 0.012 **Queries matched:** 8

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4590	934.4517	934.4508	0.0009	122 -	128	0	QQEQQFK
1056.4843	1055.4770	1055.4744	0.0026	79 -	88	0	GAGSSQHQER
1085.5533	1084.5460	1084.5447	0.0013	133 -	141	0	NLPQQCGLR
1091.5597	1090.5524	1090.5519	0.0005	122 -	129	1	QQEQQFKR
1726.6926	1725.6853	1725.6835	0.0019	89 -	101	0	CCNELNEFENNQR
2012.8281	2011.8208	2011.8220	-0.0012	102 -	117	0	CMCEALQQIMENQSDR
2028.8220	2027.8147	2027.8169	-0.0022	102 -	117	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8180	2043.8107	2043.8118	-0.0011	102 -	117	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1062.7854, 1074.5315, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1753.9185, 1940.9397, 2211.1025, 2225.1230, 2233.1162, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413

9. gi|14347293 **Mass:** 24390 **Score:** 47 **Expect:** 0.019 **Queries matched:** 8

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
935.4590	934.4517	934.4508	0.0009	124	-	130	0	QQEQQFK
1056.4843	1055.4770	1055.4744	0.0026	81	-	90	0	GAGSSQHQER
1085.5533	1084.5460	1084.5447	0.0013	135	-	143	0	NLPQQCGLR
1091.5597	1090.5524	1090.5519	0.0005	124	-	131	1	QQEQQFKR
1726.6926	1725.6853	1725.6835	0.0019	91	-	103	0	CCNELNEFENNQR
2012.8281	2011.8208	2011.8220	-0.0012	104	-	119	0	CMCEALQQIMENQSDR
2028.8220	2027.8147	2027.8169	-0.0022	104	-	119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8180	2043.8107	2043.8118	-0.0011	104	-	119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1062.7854, 1074.5315, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1753.9185, 1940.9397, 2211.1025, 2225.1230, 2233.1162, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413

10. gi|288479 **Mass:** 5059 **Score:** 13 **Expect:** 44 **Queries matched:** 1

chitinase [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
2233.1162	2232.1089	2232.1320	-0.0231	26	-	47	1	AANRTLGFGLVTNIINGGLDCG

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 935.4590, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1056.4843, 1062.7854, 1074.5315, 1085.5533, 1091.5597, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1726.6926, 1753.9185, 1940.9397, 2012.8281, 2028.8220, 2044.8180, 2211.1025, 2225.1230, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|15418705** Score: **54** Expect: **0.0033**
allergen II [Arachis hypogaea]

Nominal mass (M_r): **18612**; Calculated pI value: **5.67**
NCBI BLAST search of gi|15418705 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **8**
Sequence Coverage: **35%**

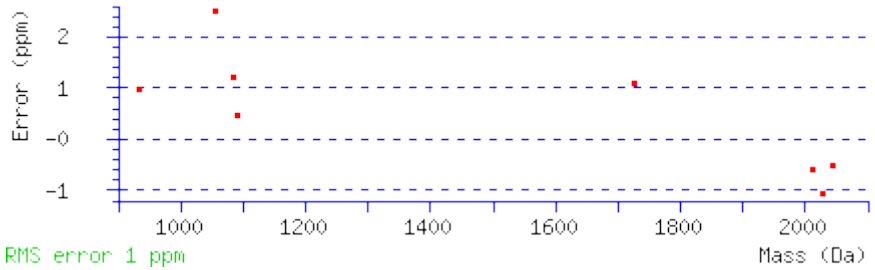
Matched peptides shown in **Bold Red**

```
     1 MAKLTILVAL ALFLLAAHAS ARQQWELQGD RRCQSQLERA NLRPCEQHLM
    51 QKIQRDEDSY ERDPYSPSQD PYSPSPYDRR GAGSSQHQER CCNELNEFEN
   101 NQRCMCEALQ QIMENQSDRL QGRQQEQQFK RELRNLPQQC GLRAPQRCDL
   151 DVESGG
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
81 - 90	1056.4843	1055.4770	1055.4744	0.0026	0	GAGSSQHQER	
91 - 103	1726.6926	1725.6853	1725.6835	0.0019	0	CCNELNEFENNQR	
104 - 119	2012.8281	2011.8208	2011.8220	-0.0012	0	CMCEALQQIMENQSDR	
104 - 119	2028.8220	2027.8147	2027.8169	-0.0022	0	CMCEALQQIMENQSDR	Oxidation (M)
104 - 119	2044.8180	2043.8107	2043.8118	-0.0011	0	CMCEALQQIMENQSDR	2 Oxidation (M)
124 - 130	935.4590	934.4517	934.4508	0.0009	0	QQEQQFK	
124 - 131	1091.5597	1090.5524	1090.5519	0.0005	1	QQEQQFKR	
135 - 143	1085.5533	1084.5460	1084.5447	0.0013	0	NLPQQCGLR	

No match to: 814.6308, 842.5090, 858.6428, 861.0711, 877.0372, 886.6819, 902.6690, 930.7084, 946.7036, 974.7318, 990.7215, 1018.7623, 1034.7548, 1045.5632, 1062.7854, 1074.5315, 1097.4985, 1106.8116, 1113.5231, 1122.8030, 1253.5918, 1269.5856, 1455.7162, 1566.7201, 1669.6691, 1709.6671, 1725.6654, 1753.9185, 1940.9397, 2211.1025, 2225.1230, 2233.1162, 2299.1733, 2408.0906, 2787.9653, 2788.4685, 2807.3247, 3338.7417, 3347.6775, 3348.6697, 3353.7537, 3809.8413



Spot 100

Database : Arachis 260207 (875 sequences; 195306 residues)
Timestamp : 20 Mar 2007 at 13:18:24 GMT
Top Score : 65 for gi|31322017, allergen Ara h 2 isoform [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|31322017	20212	65	allergen Ara h 2 isoform [Arachis hypogaea]
2.	gi|46560480	22229	62	seed storage protein SSP1 [Arachis hypogaea]
3.	gi|26245447	20558	62	allergen Ara h 2.02 [Arachis hypogaea]
4.	gi|118776566	19009	60	conglutin 7 [Arachis hypogaea]
5.	gi|46560482	20907	55	seed storage protein SSP2 [Arachis hypogaea]
6.	gi|15418705	18612	55	allergen II [Arachis hypogaea]
7.	gi|28912768	19765	54	seed storage protein [Arachis hypogaea]
8.	gi|52001227	21293	51	2S protein 1 [Arachis hypogaea]
9.	gi|14347293	24390	47	unnamed protein product [Arachis hypogaea]
10.	gi|66735602	10408	15	LEA protein [Arachis hypogaea]

Results List

1. gi|31322017 **Mass:** 20212 **Score:** 65 **Expect:** 0.00031 **Queries matched:** 9
allergen Ara h 2 isoform [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4477	934.4404	934.4508	-0.0104	133	139	0	QQEQQFK
1056.4827	1055.4754	1055.4744	0.0010	90	99	0	GAGSSQHQER
1085.5508	1084.5435	1084.5447	-0.0012	144	152	0	NLPQQCGLR
1091.5571	1090.5498	1090.5519	-0.0021	133	140	1	QQEQQFKR
1121.4917	1120.4844	1120.4818	0.0026	157	166	0	CDLEVESGGR
1726.6831	1725.6758	1725.6835	-0.0076	100	112	0	CCNELNEFENNQR
2012.8232	2011.8159	2011.8220	-0.0061	113	128	0	CMCEALQQIMENQSDR
2028.8177	2027.8104	2027.8169	-0.0065	113	128	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8174	2043.8101	2043.8118	-0.0017	113	128	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 1045.5605, 1050.1027, 1066.0758, 1072.0850, 1074.5371, 1101.5396, 1107.5262, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1339.6627, 1368.6128, 1384.6101, 1455.7256, 1513.6506, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1742.6757, 1748.6643, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517

2. gi|46560480 **Mass:** 22229 **Score:** 62 **Expect:** 0.00053 **Queries matched:** 9

seed storage protein SSP1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4477	934.4404	934.4508	-0.0104	151	157	0	QQEQQFK
1056.4827	1055.4754	1055.4744	0.0010	108	117	0	GAGSSQHQER
1085.5508	1084.5435	1084.5447	-0.0012	162	170	0	NLPQQCGLR
1091.5571	1090.5498	1090.5519	-0.0021	151	158	1	QQEQQFKR
1121.4917	1120.4844	1120.4818	0.0026	175	184	0	CDLEVESGGR
1726.6831	1725.6758	1725.6835	-0.0076	118	130	0	CCNELNEFENNQR
2012.8232	2011.8159	2011.8220	-0.0061	131	146	0	CMCEALQQIMENQSDR
2028.8177	2027.8104	2027.8169	-0.0065	131	146	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8174	2043.8101	2043.8118	-0.0017	131	146	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 1045.5605, 1050.1027, 1066.0758, 1072.0850, 1074.5371, 1101.5396, 1107.5262, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1339.6627, 1368.6128, 1384.6101, 1455.7256, 1513.6506, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1742.6757, 1748.6643, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517

3. gi|26245447 **Mass:** 20558 **Score:** 62 **Expect:** 0.00054 **Queries matched:** 9

allergen Ara h 2.02 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4477	934.4404	934.4508	-0.0104	136	142	0	QQEQQFK
1056.4827	1055.4754	1055.4744	0.0010	93	102	0	GAGSSQHQER
1085.5508	1084.5435	1084.5447	-0.0012	147	155	0	NLPQQCGLR
1091.5571	1090.5498	1090.5519	-0.0021	136	143	1	QQEQQFKR
1121.4917	1120.4844	1120.4818	0.0026	160	169	0	CDLEVESGGR
1726.6831	1725.6758	1725.6835	-0.0076	103	115	0	CCNELNEFENNQR
2012.8232	2011.8159	2011.8220	-0.0061	116	131	0	CMCEALQQIMENQSDR
2028.8177	2027.8104	2027.8169	-0.0065	116	131	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8174	2043.8101	2043.8118	-0.0017	116	131	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 1045.5605, 1050.1027, 1066.0758, 1072.0850, 1074.5371, 1101.5396, 1107.5262, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1339.6627, 1368.6128, 1384.6101, 1455.7256, 1513.6506, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1742.6757, 1748.6643, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517

4. gi|118776566 **Mass:** 19009 **Score:** 60 **Expect:** 0.00082 **Queries matched:** 9

conglutin 7 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

935.4477	934.4404	934.4508	-0.0104	122 - 128	0	QQEQQFK
1056.4827	1055.4754	1055.4744	0.0010	79 - 88	0	GAGSSQHQER
1085.5508	1084.5435	1084.5447	-0.0012	133 - 141	0	NLPQQCGLR
1091.5571	1090.5498	1090.5519	-0.0021	122 - 129	1	QQEQQFKR
1121.4917	1120.4844	1120.4818	0.0026	146 - 155	0	CDLEVESGGR
1726.6831	1725.6758	1725.6835	-0.0076	89 - 101	0	CCNELNEFENNQR
2012.8232	2011.8159	2011.8220	-0.0061	102 - 117	0	CMCEALQQIMENQSDR
2028.8177	2027.8104	2027.8169	-0.0065	102 - 117	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8174	2043.8101	2043.8118	-0.0017	102 - 117	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 1045.5605, 1050.1027, 1066.0758, 1072.0850, 1074.5371, 1101.5396, 1107.5262, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1339.6627, 1368.6128, 1384.6101, 1455.7256, 1513.6506, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1742.6757, 1748.6643, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517

5. gi|46560482 **Mass:** 20907 **Score:** 55 **Expect:** 0.0026 **Queries matched:** 8

seed storage protein SSP2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4477	934.4404	934.4508	-0.0104	139	145	0	QQEQQFK
1056.4827	1055.4754	1055.4744	0.0010	96	105	0	GAGSSQHQER
1085.5508	1084.5435	1084.5447	-0.0012	150	158	0	NLPQQCGLR
1091.5571	1090.5498	1090.5519	-0.0021	139	146	1	QQEQQFKR
1726.6831	1725.6758	1725.6835	-0.0076	106	118	0	CCNELNEFENNQR
2012.8232	2011.8159	2011.8220	-0.0061	119	134	0	CMCEALQQIMENQSDR
2028.8177	2027.8104	2027.8169	-0.0065	119	134	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8174	2043.8101	2043.8118	-0.0017	119	134	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 1045.5605, 1050.1027, 1066.0758, 1072.0850, 1074.5371, 1101.5396, 1107.5262, 1121.4917, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1339.6627, 1368.6128, 1384.6101, 1455.7256, 1513.6506, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1742.6757, 1748.6643, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517

6. gi|15418705 **Mass:** 18612 **Score:** 55 **Expect:** 0.0031 **Queries matched:** 8

allergen II [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4477	934.4404	934.4508	-0.0104	124	130	0	QQEQQFK
1056.4827	1055.4754	1055.4744	0.0010	81	90	0	GAGSSQHQER
1085.5508	1084.5435	1084.5447	-0.0012	135	143	0	NLPQQCGLR
1091.5571	1090.5498	1090.5519	-0.0021	124	131	1	QQEQQFKR
1726.6831	1725.6758	1725.6835	-0.0076	91	103	0	CCNELNEFENNQR
2012.8232	2011.8159	2011.8220	-0.0061	104	119	0	CMCEALQQIMENQSDR
2028.8177	2027.8104	2027.8169	-0.0065	104	119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8174	2043.8101	2043.8118	-0.0017	104	119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 1045.5605, 1050.1027, 1066.0758, 1072.0850, 1074.5371, 1101.5396, 1107.5262, 1121.4917, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1339.6627, 1368.6128, 1384.6101, 1455.7256, 1513.6506, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1742.6757, 1748.6643, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517

7. gi|28912768 **Mass:** 19765 **Score:** 54 **Expect:** 0.0039 **Queries matched:** 8

seed storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4477	934.4404	934.4508	-0.0104	134	140	0	QQEQQFK
1056.4827	1055.4754	1055.4744	0.0010	91	100	0	GAGSSQHQER
1085.5508	1084.5435	1084.5447	-0.0012	145	153	0	NLPQQCGLR
1091.5571	1090.5498	1090.5519	-0.0021	134	141	1	QQEQQFKR
1726.6831	1725.6758	1725.6835	-0.0076	101	113	0	CCNELNEFENNQR
2012.8232	2011.8159	2011.8220	-0.0061	114	129	0	CMCEALQQIMENQSDR
2028.8177	2027.8104	2027.8169	-0.0065	114	129	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8174	2043.8101	2043.8118	-0.0017	114	129	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 1045.5605, 1050.1027, 1066.0758, 1072.0850, 1074.5371, 1101.5396, 1107.5262, 1121.4917, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1339.6627, 1368.6128, 1384.6101, 1455.7256, 1513.6506, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1742.6757, 1748.6643, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517

8. gi|52001227 **Mass:** 21293 **Score:** 51 **Expect:** 0.0078 **Queries matched:** 8

2S protein 1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4477	934.4404	934.4508	-0.0104	143	149	0	QQEQQFK
1056.4827	1055.4754	1055.4744	0.0010	100	109	0	GAGSSQHQER
1085.5508	1084.5435	1084.5447	-0.0012	154	162	0	NLPQQCGLR
1091.5571	1090.5498	1090.5519	-0.0021	143	150	1	QQEQQFKR
1726.6831	1725.6758	1725.6835	-0.0076	110	122	0	CCNELNEFENNQR
2012.8232	2011.8159	2011.8220	-0.0061	123	138	0	CMCEALQQIMENQSDR
2028.8177	2027.8104	2027.8169	-0.0065	123	138	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8174	2043.8101	2043.8118	-0.0017	123	138	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 1045.5605, 1050.1027, 1066.0758, 1072.0850, 1074.5371, 1101.5396, 1107.5262, 1121.4917, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1339.6627, 1368.6128, 1384.6101, 1455.7256, 1513.6506, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1742.6757, 1748.6643, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517

9. gi|14347293 **Mass:** 24390 **Score:** 47 **Expect:** 0.018 **Queries matched:** 8

unnamed protein product [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
935.4477	934.4404	934.4508	-0.0104	124	130	0	QQEQQFK
1056.4827	1055.4754	1055.4744	0.0010	81	90	0	GAGSSQHQER

1085.5508	1084.5435	1084.5447	-0.0012	135 - 143	0	NLPQQCGLR
1091.5571	1090.5498	1090.5519	-0.0021	124 - 131	1	QQEQQFKR
1726.6831	1725.6758	1725.6835	-0.0076	91 - 103	0	CCNELNEFENNQR
2012.8232	2011.8159	2011.8220	-0.0061	104 - 119	0	CMCEALQQIMENQSDR
2028.8177	2027.8104	2027.8169	-0.0065	104 - 119	0	CMCEALQQIMENQSDR + Oxidation (M)
2044.8174	2043.8101	2043.8118	-0.0017	104 - 119	0	CMCEALQQIMENQSDR + 2 Oxidation (M)

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 1045.5605, 1050.1027, 1066.0758, 1072.0850, 1074.5371, 1101.5396, 1107.5262, 1121.4917, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1339.6627, 1368.6128, 1384.6101, 1455.7256, 1513.6506, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1742.6757, 1748.6643, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517

10. gi|66735602 **Mass:** 10408 **Score:** 15 **Expect:** 29 **Queries matched:** 2

LEA protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1339.6627	1338.6554	1338.6527	0.0027	29 -	40	0	SLEAQEHLAEGR
1513.6506	1512.6433	1512.6514	-0.0081	49 -	61	0	EQLGTEGYQEMGR + Oxidation (M)

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 935.4477, 1045.5605, 1050.1027, 1056.4827, 1066.0758, 1072.0850, 1074.5371, 1085.5508, 1091.5571, 1101.5396, 1107.5262, 1121.4917, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1368.6128, 1384.6101, 1455.7256, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1726.6831, 1742.6757, 1748.6643, 2012.8232, 2028.8177, 2044.8174, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|31322017** Score: **65** Expect: **0.00031**
allergen Ara h 2 isoform [Arachis hypogaea]

Nominal mass (M_r): **20212**; Calculated pI value: **5.69**
NCBI BLAST search of gi|31322017 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **9**
Sequence Coverage: **39%**

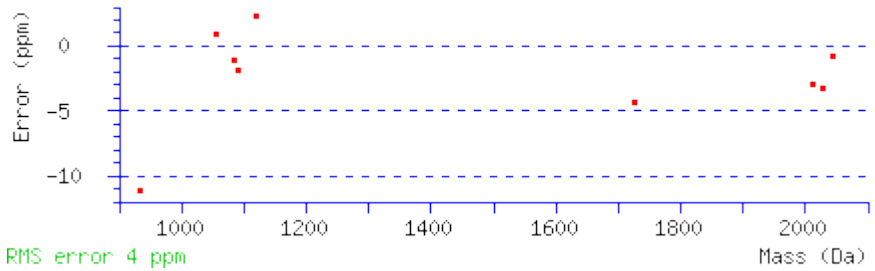
Matched peptides shown in **Bold Red**

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     1 LTILVAPALF LLAAHASARQ QWELQGDRRC QSQLERANLR PCEQHLMQKI
    51 QRDEDSYGRD PYSPSQDPYS PSQDPDRRDP YSPSPYDRRG AGSSQHQERC
   101 CNELNEFENN QRCMCEALQQ IMENQSDRLQ GRQQEQQFKR ELRNLPQQCG
   151 LRAPQRCDLE VESGGRDRY
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
90 - 99	1056.4827	1055.4754	1055.4744	0.0010	0	GAGSSQHQER	
100 - 112	1726.6831	1725.6758	1725.6835	-0.0076	0	CCNELNEFENNQR	
113 - 128	2012.8232	2011.8159	2011.8220	-0.0061	0	CMCEALQQIMENQSDR	
113 - 128	2028.8177	2027.8104	2027.8169	-0.0065	0	CMCEALQQIMENQSDR	Oxidation (M)
113 - 128	2044.8174	2043.8101	2043.8118	-0.0017	0	CMCEALQQIMENQSDR	2 Oxidation (M)
133 - 139	935.4477	934.4404	934.4508	-0.0104	0	QQEQQFK	
133 - 140	1091.5571	1090.5498	1090.5519	-0.0021	1	QQEQQFKR	
144 - 152	1085.5508	1084.5435	1084.5447	-0.0012	0	NLPQQCGLR	
157 - 166	1121.4917	1120.4844	1120.4818	0.0026	0	CDLEVESGGR	

No match to: 839.0886, 842.5093, 845.0953, 847.0999, 854.0487, 855.0571, 861.0718, 864.4905, 867.0737, 870.5328, 877.0423, 1045.5605, 1050.1027, 1066.0758, 1072.0850, 1074.5371, 1101.5396, 1107.5262, 1147.4852, 1212.5306, 1228.5132, 1277.0865, 1339.6627, 1368.6128, 1384.6101, 1455.7256, 1513.6506, 1555.6886, 1638.7924, 1669.6917, 1709.6641, 1725.6661, 1742.6757, 1748.6643, 2211.1038, 2225.1213, 2233.1108, 2299.1768, 3338.7554, 3348.7280, 3353.7517



Spot 101

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **20 Mar 2007 at 13:19:56 GMT**
Top Score : **74 for gi|17225991, conglutin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|17225991	17349	74	conglutin [Arachis hypogaea]
2.	gi|57014074	17479	72	conglutin [Arachis hypogaea]
3.	gi|52001229	17479	72	conglutin [Arachis hypogaea]
4.	gi|75114094	17479	72	Conglutin precursor (Allergen Ara h 6)
5.	gi|57669906	17480	72	conglutin [Arachis hypogaea]
6.	gi|57118278	15280	35	Ara h 6 allergen [Arachis hypogaea]
7.	gi|83753503	15575	26	Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)
8.	gi|5923742	15489	21	allergen Arah6 [Arachis hypogaea]
9.	gi|2498261	2416	14	33.0 kDa cold shock protein (AHCSP33)
10.	gi|230338	23975	13	Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Results List

1. gi|17225991 **Mass:** 17349 **Score:** 74 **Expect:** 3.7e-005 **Queries matched:** 11
conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3949	847.3876	847.3784	0.0092	71	77	0	SSDQQQR
924.4707	923.4634	923.4534	0.0100	111	117	0	QMVQQFK + Oxidation (M)
1064.5563	1063.5490	1063.5596	-0.0106	111	118	1	QMVQQFKR
1080.5641	1079.5568	1079.5546	0.0023	111	118	1	QMVQQFKR + Oxidation (M)
1138.4757	1137.4684	1137.4543	0.0142	135	144	1	CDLDVSGGRC
1430.6862	1429.6789	1429.6732	0.0058	131	143	1	APQRCDLDVSGGR
1549.7236	1548.7163	1548.7177	-0.0014	119	130	0	ELMNLPQQCNFR
1565.7150	1564.7077	1564.7126	-0.0049	119	130	0	ELMNLPQQCNFR + Oxidation (M)
1715.6316	1714.6243	1714.6233	0.0011	78	90	0	CCDELDQMENTER + Oxidation (M)

2001.9717	2000.9644	2000.9672	-0.0028	119 - 134	1	ELMNLPQQCNFRAPQR
2017.9648	2016.9575	2016.9621	-0.0046	119 - 134	1	ELMNLPQQCNFRAPQR + Oxidation (M)

No match to: 805.4813, 882.5616, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1046.6052, 1047.5533, 1062.5430, 1063.5394, 1079.5305, 1096.5496, 1105.5477, 1152.4860, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1547.7068, 1563.7257, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1714.6346, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2031.9774, 2273.1594, 2597.0518

2. gi|57014074 **Mass:** 17479 **Score:** 72 **Expect:** 5.3e-005 **Queries matched:** 11

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3949	847.3876	847.3784	0.0092	72 -	78	0	SSDQQQR
924.4707	923.4634	923.4534	0.0100	112 -	118	0	QMVQQFK + Oxidation (M)
1064.5563	1063.5490	1063.5596	-0.0106	112 -	119	1	QMVQQFKR
1080.5641	1079.5568	1079.5546	0.0023	112 -	119	1	QMVQQFKR + Oxidation (M)
1138.4757	1137.4684	1137.4543	0.0142	136 -	145	1	CDLDVSGGRC
1430.6862	1429.6789	1429.6732	0.0058	132 -	144	1	APQRCDLDVSGGR
1549.7236	1548.7163	1548.7177	-0.0014	120 -	131	0	ELMNLPQQCNFR
1565.7150	1564.7077	1564.7126	-0.0049	120 -	131	0	ELMNLPQQCNFR + Oxidation (M)
1714.6346	1713.6273	1713.6392	-0.0119	79 -	91	0	CCDELNEMENTQR + Oxidation (M)
2001.9717	2000.9644	2000.9672	-0.0028	120 -	135	1	ELMNLPQQCNFRAPQR
2017.9648	2016.9575	2016.9621	-0.0046	120 -	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)

No match to: 805.4813, 882.5616, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1046.6052, 1047.5533, 1062.5430, 1063.5394, 1079.5305, 1096.5496, 1105.5477, 1152.4860, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1547.7068, 1563.7257, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1715.6316, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2031.9774, 2273.1594, 2597.0518

3. gi|52001229 **Mass:** 17479 **Score:** 72 **Expect:** 5.3e-005 **Queries matched:** 11

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3949	847.3876	847.3784	0.0092	72 -	78	0	SSDQQQR
924.4707	923.4634	923.4534	0.0100	112 -	118	0	QMVQQFK + Oxidation (M)
1064.5563	1063.5490	1063.5596	-0.0106	112 -	119	1	QMVQQFKR
1080.5641	1079.5568	1079.5546	0.0023	112 -	119	1	QMVQQFKR + Oxidation (M)
1138.4757	1137.4684	1137.4543	0.0142	136 -	145	1	CDLDVSGGRC
1430.6862	1429.6789	1429.6732	0.0058	132 -	144	1	APQRCDLDVSGGR
1549.7236	1548.7163	1548.7177	-0.0014	120 -	131	0	ELMNLPQQCNFR
1565.7150	1564.7077	1564.7126	-0.0049	120 -	131	0	ELMNLPQQCNFR + Oxidation (M)
1714.6346	1713.6273	1713.6392	-0.0119	79 -	91	0	CCDELNEMENTQR + Oxidation (M)
2001.9717	2000.9644	2000.9672	-0.0028	120 -	135	1	ELMNLPQQCNFRAPQR
2017.9648	2016.9575	2016.9621	-0.0046	120 -	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)

No match to: 805.4813, 882.5616, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1046.6052, 1047.5533,

1062.5430, 1063.5394, 1079.5305, 1096.5496, 1105.5477, 1152.4860, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1547.7068, 1563.7257, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1715.6316, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2031.9774, 2273.1594, 2597.0518

4. gi|75114094 **Mass:** 17479 **Score:** 72 **Expect:** 5.3e-005 **Queries matched:** 11

Conglutin precursor (Allergen Ara h 6)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3949	847.3876	847.3784	0.0092	72	78	0	SSDQQQR
924.4707	923.4634	923.4534	0.0100	112	118	0	QMVQQFK + Oxidation (M)
1064.5563	1063.5490	1063.5596	-0.0106	112	119	1	QMVQQFKR
1080.5641	1079.5568	1079.5546	0.0023	112	119	1	QMVQQFKR + Oxidation (M)
1138.4757	1137.4684	1137.4543	0.0142	136	145	1	CDLDVSGGRC
1430.6862	1429.6789	1429.6732	0.0058	132	144	1	APQRCDLDVSGGR
1549.7236	1548.7163	1548.7177	-0.0014	120	131	0	ELMNLPQQCNFR
1565.7150	1564.7077	1564.7126	-0.0049	120	131	0	ELMNLPQQCNFR + Oxidation (M)
1714.6346	1713.6273	1713.6392	-0.0119	79	91	0	CCDELNEMENTQR + Oxidation (M)
2001.9717	2000.9644	2000.9672	-0.0028	120	135	1	ELMNLPQQCNFRAPQR
2017.9648	2016.9575	2016.9621	-0.0046	120	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)

No match to: 805.4813, 882.5616, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1046.6052, 1047.5533, 1062.5430, 1063.5394, 1079.5305, 1096.5496, 1105.5477, 1152.4860, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1547.7068, 1563.7257, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1715.6316, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2031.9774, 2273.1594, 2597.0518

5. gi|57669906 **Mass:** 17480 **Score:** 72 **Expect:** 5.3e-005 **Queries matched:** 11

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3949	847.3876	847.3784	0.0092	72	78	0	SSDQQQR
924.4707	923.4634	923.4534	0.0100	112	118	0	QMVQQFK + Oxidation (M)
1064.5563	1063.5490	1063.5596	-0.0106	112	119	1	QMVQQFKR
1080.5641	1079.5568	1079.5546	0.0023	112	119	1	QMVQQFKR + Oxidation (M)
1138.4757	1137.4684	1137.4543	0.0142	136	145	1	CDLDVSGGRC
1430.6862	1429.6789	1429.6732	0.0058	132	144	1	APQRCDLDVSGGR
1549.7236	1548.7163	1548.7177	-0.0014	120	131	0	ELMNLPQQCNFR
1565.7150	1564.7077	1564.7126	-0.0049	120	131	0	ELMNLPQQCNFR + Oxidation (M)
1715.6316	1714.6243	1714.6233	0.0011	79	91	0	CCDELDQMENTER + Oxidation (M)
2001.9717	2000.9644	2000.9672	-0.0028	120	135	1	ELMNLPQQCNFRAPQR
2017.9648	2016.9575	2016.9621	-0.0046	120	135	1	ELMNLPQQCNFRAPQR + Oxidation (M)

No match to: 805.4813, 882.5616, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1046.6052, 1047.5533, 1062.5430, 1063.5394, 1079.5305, 1096.5496, 1105.5477, 1152.4860, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1547.7068, 1563.7257, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1714.6346, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2031.9774, 2273.1594, 2597.0518

6. gi|57118278 **Mass:** 15280 **Score:** 35 **Expect:** 0.26 **Queries matched:** 6

Ara h 6 allergen [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3949	847.3876	847.3784	0.0092	51	57	0	SSDQQQR
924.4707	923.4634	923.4534	0.0100	91	97	0	QMVQQFK + Oxidation (M)
1064.5563	1063.5490	1063.5596	-0.0106	91	98	1	QMVQQFKR
1080.5641	1079.5568	1079.5546	0.0023	91	98	1	QMVQQFKR + Oxidation (M)
1138.4757	1137.4684	1137.4543	0.0142	115	124	1	CDLDVSGGRC
1430.6862	1429.6789	1429.6732	0.0058	111	123	1	APQRCDLDVSGGR

No match to: 805.4813, 882.5616, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1046.6052, 1047.5533, 1062.5430, 1063.5394, 1079.5305, 1096.5496, 1105.5477, 1152.4860, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1547.7068, 1549.7236, 1563.7257, 1565.7150, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1714.6346, 1715.6316, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2001.9717, 2017.9648, 2031.9774, 2273.1594, 2597.0518

7. gi|83753503 **Mass:** 15575 **Score:** 26 **Expect:** 2.3 **Queries matched:** 5

Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3949	847.3876	847.3784	0.0092	53	59	0	SSDQQQR
924.4707	923.4634	923.4534	0.0100	93	99	0	QMVQQFK + Oxidation (M)
1064.5563	1063.5490	1063.5596	-0.0106	93	100	1	QMVQQFKR
1080.5641	1079.5568	1079.5546	0.0023	93	100	1	QMVQQFKR + Oxidation (M)
1430.6862	1429.6789	1429.6732	0.0058	113	125	1	APQRCDLDVSGGR

No match to: 805.4813, 882.5616, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1046.6052, 1047.5533, 1062.5430, 1063.5394, 1079.5305, 1096.5496, 1105.5477, 1138.4757, 1152.4860, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1547.7068, 1549.7236, 1563.7257, 1565.7150, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1714.6346, 1715.6316, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2001.9717, 2017.9648, 2031.9774, 2273.1594, 2597.0518

8. gi|5923742 **Mass:** 15489 **Score:** 21 **Expect:** 7.8 **Queries matched:** 3

allergen Arah6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
848.3949	847.3876	847.3784	0.0092	56	62	0	SSDQQQR
1138.4757	1137.4684	1137.4543	0.0142	120	129	1	CDLDVSGGRC
1714.6346	1713.6273	1713.6392	-0.0119	63	75	0	CCDELNEMENTQR + Oxidation (M)

No match to: 805.4813, 882.5616, 924.4707, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1046.6052, 1047.5533, 1062.5430, 1063.5394, 1064.5563, 1079.5305, 1080.5641, 1096.5496, 1105.5477, 1152.4860, 1430.6862, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1547.7068, 1549.7236, 1563.7257, 1565.7150, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1715.6316, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2001.9717, 2017.9648, 2031.9774, 2273.1594, 2597.0518

9. gi|2498261 **Mass:** 2416 **Score:** 14 **Expect:** 39 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1547.7068	1546.6995	1546.7263	-0.0268	9	-	24	0	ASYTVTPPAQANAADA

No match to: 805.4813, 848.3949, 882.5616, 924.4707, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1046.6052, 1047.5533, 1062.5430, 1063.5394, 1064.5563, 1079.5305, 1080.5641, 1096.5496, 1105.5477, 1138.4757, 1152.4860, 1430.6862, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1549.7236, 1563.7257, 1565.7150, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1714.6346, 1715.6316, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2001.9717, 2017.9648, 2031.9774, 2273.1594, 2597.0518

10. gi|230338 **Mass:** 23975 **Score:** 13 **Expect:** 47 **Queries matched:** 2

Chain E, Trypsin (E.C.3.4.21.4) Complex With Bowman-Birk Inhibitor (AB-I)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1046.6052	1045.5979	1045.5880	0.0100	90	-	99	1	LKSAASLNSR
2273.1594	2272.1521	2272.1521	0.0000	70	-	89	0	SIVHPSYNSNTLNNDIMLIK

No match to: 805.4813, 848.3949, 882.5616, 924.4707, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1047.5533, 1062.5430, 1063.5394, 1064.5563, 1079.5305, 1080.5641, 1096.5496, 1105.5477, 1138.4757, 1152.4860, 1430.6862, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1547.7068, 1549.7236, 1563.7257, 1565.7150, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1714.6346, 1715.6316, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2001.9717, 2017.9648, 2031.9774, 2597.0518

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|17225991** Score: **74** Expect: **3.7e-005**
conglutin [Arachis hypogaea]

Nominal mass (M_r): **17349**; Calculated pI value: **5.74**
NCBI BLAST search of gi|17225991 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **11**
Sequence Coverage: **37%**

Matched peptides shown in **Bold Red**

```
     1 AKSTILVALL ALVLVAHASA MRRERGRQGD SSSCERQVDR VNLKPCEQHI
    51 MQRIMGEQEQ YDSYDIRSTR SSDQQQRCCD ELDQMENTER CMCEALQQIM
   101 ENQCDRLQDR QMVQQFKREL MNLPQQCNFR APQRCDLDVS GGRC
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
71 - 77	848.3949	847.3876	847.3784	0.0092	0	**SSDQQQR**
78 - 90	1715.6316	1714.6243	1714.6233	0.0011	0	**CCDELDQMENTER** Oxidation (M)
111 - 117	924.4707	923.4634	923.4534	0.0100	0	**QMVQQFK** Oxidation (M)
111 - 118	1064.5563	1063.5490	1063.5596	-0.0106	1	**QMVQQFKR**
111 - 118	1080.5641	1079.5568	1079.5546	0.0023	1	**QMVQQFKR** Oxidation (M)
119 - 130	1549.7236	1548.7163	1548.7177	-0.0014	0	**ELMNLPQQCNFR**
119 - 130	1565.7150	1564.7077	1564.7126	-0.0049	0	**ELMNLPQQCNFR** Oxidation (M)
119 - 134	2001.9717	2000.9644	2000.9672	-0.0028	1	**ELMNLPQQCNFRAPQR**
119 - 134	2017.9648	2016.9575	2016.9621	-0.0046	1	**ELMNLPQQCNFRAPQR** Oxidation (M)
131 - 143	1430.6862	1429.6789	1429.6732	0.0058	1	**APQRCDLDVSGGR**
135 - 144	1138.4757	1137.4684	1137.4543	0.0142	1	**CDLDVSGGRC**

No match to: 805.4813, 882.5616, 1001.4954, 1009.4846, 1016.5751, 1018.5085, 1032.5624, 1046.6052, 1047.5533, 1062.5430, 1063.5394, 1079.5305, 1096.5496, 1105.5477, 1152.4860, 1474.6982, 1477.8436, 1501.7156, 1503.7671, 1517.7606, 1547.7068, 1563.7257, 1579.7307, 1581.7192, 1590.7147, 1636.6807, 1653.6744, 1682.6195, 1697.6201, 1698.6068, 1712.6244, 1714.6346, 1727.6641, 1729.6455, 1743.6643, 1955.9982, 2031.9774, 2273.1594, 2597.0518

Spot 102

Database : **Arachis 260207 (875 sequences; 195306 residues)**
Timestamp : **20 Mar 2007 at 13:20:13 GMT**
Top Score : **91 for gi|57014074, conglutin [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|57014074	17479	91	conglutin [Arachis hypogaea]
2.	gi|52001229	17479	91	conglutin [Arachis hypogaea]
3.	gi|75114094	17479	91	Conglutin precursor (Allergen Ara h 6)
4.	gi|17225991	17349	64	conglutin [Arachis hypogaea]
5.	gi|57669906	17480	63	conglutin [Arachis hypogaea]
6.	gi|57118278	15280	26	Ara h 6 allergen [Arachis hypogaea]
7.	gi|5923742	15489	23	allergen Arah6 [Arachis hypogaea]
8.	gi|83753503	15575	17	Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)
9.	gi|2498261	2416	14	33.0 kDa cold shock protein (AHCSP33)
10.	gi|118776568	17335	13	conglutin 8 [Arachis hypogaea]

Results List

1. gi|57014074 **Mass:** 17479 **Score:** 91 **Expect:** 6.5e-007 **Queries matched:** 13
conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
924.4742	923.4669	923.4534	0.0135	112	118	0	QMVQQFK + Oxidation (M)
1064.5656	1063.5583	1063.5596	-0.0013	112	119	1	QMVQQFKR
1080.5720	1079.5647	1079.5546	0.0102	112	119	1	QMVQQFKR + Oxidation (M)
1138.4830	1137.4757	1137.4543	0.0215	136	145	1	CDLDVSGGRC
1430.6873	1429.6800	1429.6732	0.0069	132	144	1	APQRCDLDVSGGR
1549.7211	1548.7138	1548.7177	-0.0039	120	131	0	ELMNLPQQCNFR
1565.7173	1564.7100	1564.7126	-0.0026	120	131	0	ELMNLPQQCNFR + Oxidation (M)
1714.6356	1713.6283	1713.6392	-0.0109	79	91	0	CCDELNEMENTQR + Oxidation (M)
2001.9681	2000.9608	2000.9672	-0.0064	120	135	1	ELMNLPQQCNFRAPQR

2017.9640	2016.9567	2016.9621	-0.0054	120 - 135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2544.0388	2543.0315	2543.0071	0.0244	72 - 91	1	SSDQQQRCCDELNEMENTQR + Oxidation (M)
2598.1150	2597.1077	2597.0913	0.0164	92 - 111	1	CMCEALQQIMENQCDRLQDR
2614.1182	2613.1109	2613.0862	0.0247	92 - 111	1	CMCEALQQIMENQCDRLQDR + Oxidation (M)

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1079.5472, 1096.5691, 1105.5515, 1121.4552, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1547.7035, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217, 1697.6129, 1712.6302, 1713.6121, 1728.6515, 1956.0344, 2185.0408, 2273.1641, 2581.0764, 2597.1111, 3137.4888

2. gi|52001229 **Mass:** 17479 **Score:** 91 **Expect:** 6.5e-007 **Queries matched:** 13

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
924.4742	923.4669	923.4534	0.0135	112 - 118		0	QMVQQFK + Oxidation (M)
1064.5656	1063.5583	1063.5596	-0.0013	112 - 119		1	QMVQQFKR
1080.5720	1079.5647	1079.5546	0.0102	112 - 119		1	QMVQQFKR + Oxidation (M)
1138.4830	1137.4757	1137.4543	0.0215	136 - 145		1	CDLDVSGGRC
1430.6873	1429.6800	1429.6732	0.0069	132 - 144		1	APQRCDLDVSGGR
1549.7211	1548.7138	1548.7177	-0.0039	120 - 131		0	ELMNLPQQCNFR
1565.7173	1564.7100	1564.7126	-0.0026	120 - 131		0	ELMNLPQQCNFR + Oxidation (M)
1714.6356	1713.6283	1713.6392	-0.0109	79 - 91		0	CCDELNEMENTQR + Oxidation (M)
2001.9681	2000.9608	2000.9672	-0.0064	120 - 135		1	ELMNLPQQCNFRAPQR
2017.9640	2016.9567	2016.9621	-0.0054	120 - 135		1	ELMNLPQQCNFRAPQR + Oxidation (M)
2544.0388	2543.0315	2543.0071	0.0244	72 - 91		1	SSDQQQRCCDELNEMENTQR + Oxidation (M)
2598.1150	2597.1077	2597.0913	0.0164	92 - 111		1	CMCEALQQIMENQCDRLQDR
2614.1182	2613.1109	2613.0862	0.0247	92 - 111		1	CMCEALQQIMENQCDRLQDR + Oxidation (M)

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1079.5472, 1096.5691, 1105.5515, 1121.4552, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1547.7035, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217, 1697.6129, 1712.6302, 1713.6121, 1728.6515, 1956.0344, 2185.0408, 2273.1641, 2581.0764, 2597.1111, 3137.4888

3. gi|75114094 **Mass:** 17479 **Score:** 91 **Expect:** 6.5e-007 **Queries matched:** 13

Conglutin precursor (Allergen Ara h 6)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
924.4742	923.4669	923.4534	0.0135	112 - 118		0	QMVQQFK + Oxidation (M)
1064.5656	1063.5583	1063.5596	-0.0013	112 - 119		1	QMVQQFKR
1080.5720	1079.5647	1079.5546	0.0102	112 - 119		1	QMVQQFKR + Oxidation (M)
1138.4830	1137.4757	1137.4543	0.0215	136 - 145		1	CDLDVSGGRC
1430.6873	1429.6800	1429.6732	0.0069	132 - 144		1	APQRCDLDVSGGR
1549.7211	1548.7138	1548.7177	-0.0039	120 - 131		0	ELMNLPQQCNFR
1565.7173	1564.7100	1564.7126	-0.0026	120 - 131		0	ELMNLPQQCNFR + Oxidation (M)
1714.6356	1713.6283	1713.6392	-0.0109	79 - 91		0	CCDELNEMENTQR + Oxidation (M)

2001.9681	2000.9608	2000.9672	-0.0064	120 - 135	1	ELMNLPQQCNFRAPQR
2017.9640	2016.9567	2016.9621	-0.0054	120 - 135	1	ELMNLPQQCNFRAPQR + Oxidation (M)
2544.0388	2543.0315	2543.0071	0.0244	72 - 91	1	SSDQQQRCCDELNEMENTQR + Oxidation (M)
2598.1150	2597.1077	2597.0913	0.0164	92 - 111	1	CMCEALQQIMENQCDRLQDR
2614.1182	2613.1109	2613.0862	0.0247	92 - 111	1	CMCEALQQIMENQCDRLQDR + Oxidation (M)

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1079.5472, 1096.5691, 1105.5515, 1121.4552, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1547.7035, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217, 1697.6129, 1712.6302, 1713.6121, 1728.6515, 1956.0344, 2185.0408, 2273.1641, 2581.0764, 2597.1111, 3137.4888

4. gi|17225991 **Mass:** 17349 **Score:** 64 **Expect:** 0.00033 **Queries matched:** 11

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
924.4742	923.4669	923.4534	0.0135	111 - 117		0	QMVQQFK + Oxidation (M)
1064.5656	1063.5583	1063.5596	-0.0013	111 - 118		1	QMVQQFKR
1080.5720	1079.5647	1079.5546	0.0102	111 - 118		1	QMVQQFKR + Oxidation (M)
1138.4830	1137.4757	1137.4543	0.0215	135 - 144		1	CDLDVSGGRC
1430.6873	1429.6800	1429.6732	0.0069	131 - 143		1	APQRCDLDVSGGR
1549.7211	1548.7138	1548.7177	-0.0039	119 - 130		0	ELMNLPQQCNFR
1565.7173	1564.7100	1564.7126	-0.0026	119 - 130		0	ELMNLPQQCNFR + Oxidation (M)
2001.9681	2000.9608	2000.9672	-0.0064	119 - 134		1	ELMNLPQQCNFRAPQR
2017.9640	2016.9567	2016.9621	-0.0054	119 - 134		1	ELMNLPQQCNFRAPQR + Oxidation (M)
2598.1150	2597.1077	2597.0913	0.0164	91 - 110		1	CMCEALQQIMENQCDRLQDR
2614.1182	2613.1109	2613.0862	0.0247	91 - 110		1	CMCEALQQIMENQCDRLQDR + Oxidation (M)

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1079.5472, 1096.5691, 1105.5515, 1121.4552, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1547.7035, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217, 1697.6129, 1712.6302, 1713.6121, 1714.6356, 1728.6515, 1956.0344, 2185.0408, 2273.1641, 2544.0388, 2581.0764, 2597.1111, 3137.4888

5. gi|57669906 **Mass:** 17480 **Score:** 63 **Expect:** 0.00046 **Queries matched:** 11

conglutin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
924.4742	923.4669	923.4534	0.0135	112 - 118		0	QMVQQFK + Oxidation (M)
1064.5656	1063.5583	1063.5596	-0.0013	112 - 119		1	QMVQQFKR
1080.5720	1079.5647	1079.5546	0.0102	112 - 119		1	QMVQQFKR + Oxidation (M)
1138.4830	1137.4757	1137.4543	0.0215	136 - 145		1	CDLDVSGGRC
1430.6873	1429.6800	1429.6732	0.0069	132 - 144		1	APQRCDLDVSGGR
1549.7211	1548.7138	1548.7177	-0.0039	120 - 131		0	ELMNLPQQCNFR
1565.7173	1564.7100	1564.7126	-0.0026	120 - 131		0	ELMNLPQQCNFR + Oxidation (M)
2001.9681	2000.9608	2000.9672	-0.0064	120 - 135		1	ELMNLPQQCNFRAPQR
2017.9640	2016.9567	2016.9621	-0.0054	120 - 135		1	ELMNLPQQCNFRAPQR + Oxidation (M)

2598.1150	2597.1077	2597.0913	0.0164	92 - 111	1	CMCEALQQIMENQCDRLQDR
2614.1182	2613.1109	2613.0862	0.0247	92 - 111	1	CMCEALQQIMENQCDRLQDR + Oxidation (M)

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1079.5472, 1096.5691, 1105.5515, 1121.4552, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1547.7035, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217, 1697.6129, 1712.6302, 1713.6121, 1714.6356, 1728.6515, 1956.0344, 2185.0408, 2273.1641, 2544.0388, 2581.0764, 2597.1111, 3137.4888

6. gi|57118278 **Mass:** 15280 **Score:** 26 **Expect:** 2.2 **Queries matched:** 5

Ara h 6 allergen [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
924.4742	923.4669	923.4534	0.0135	91 -	97	0	QMVQQFK + Oxidation (M)
1064.5656	1063.5583	1063.5596	-0.0013	91 -	98	1	QMVQQFKR
1080.5720	1079.5647	1079.5546	0.0102	91 -	98	1	QMVQQFKR + Oxidation (M)
1138.4830	1137.4757	1137.4543	0.0215	115 -	124	1	CDLDVSGGRC
1430.6873	1429.6800	1429.6732	0.0069	111 -	123	1	APQRCDLDVSGGR

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1079.5472, 1096.5691, 1105.5515, 1121.4552, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1547.7035, 1549.7211, 1565.7173, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217, 1697.6129, 1712.6302, 1713.6121, 1714.6356, 1728.6515, 1956.0344, 2001.9681, 2017.9640, 2185.0408, 2273.1641, 2544.0388, 2581.0764, 2597.1111, 2598.1150, 2614.1182, 3137.4888

7. gi|5923742 **Mass:** 15489 **Score:** 23 **Expect:** 4.9 **Queries matched:** 3

allergen Arah6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1138.4830	1137.4757	1137.4543	0.0215	120 -	129	1	CDLDVSGGRC
1714.6356	1713.6283	1713.6392	-0.0109	63 -	75	0	CCDELNEMENTQR + Oxidation (M)
2544.0388	2543.0315	2543.0071	0.0244	56 -	75	1	SSDQQQRCCDELNEMENTQR + Oxidation (M)

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 924.4742, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1064.5656, 1079.5472, 1080.5720, 1096.5691, 1105.5515, 1121.4552, 1430.6873, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1547.7035, 1549.7211, 1565.7173, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217, 1697.6129, 1712.6302, 1713.6121, 1728.6515, 1956.0344, 2001.9681, 2017.9640, 2185.0408, 2273.1641, 2581.0764, 2597.1111, 2598.1150, 2614.1182, 3137.4888

8. gi|83753503 **Mass:** 15575 **Score:** 17 **Expect:** 16 **Queries matched:** 4

Chain A, Allergen Arah6 From Peanut (Arachis Hypogaea)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
924.4742	923.4669	923.4534	0.0135	93 -	99	0	QMVQQFK + Oxidation (M)
1064.5656	1063.5583	1063.5596	-0.0013	93 -	100	1	QMVQQFKR
1080.5720	1079.5647	1079.5546	0.0102	93 -	100	1	QMVQQFKR + Oxidation (M)
1430.6873	1429.6800	1429.6732	0.0069	113 -	125	1	APQRCDLDVSGGR

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1079.5472, 1096.5691, 1105.5515, 1121.4552, 1138.4830, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1547.7035, 1549.7211, 1565.7173, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217,

1697.6129, 1712.6302, 1713.6121, 1714.6356, 1728.6515, 1956.0344, 2001.9681, 2017.9640, 2185.0408, 2273.1641, 2544.0388, 2581.0764, 2597.1111, 2598.1150, 2614.1182, 3137.4888

9. gi|2498261 **Mass:** 2416 **Score:** 14 **Expect:** 39 **Queries matched:** 1

33.0 kDa cold shock protein (AHCSP33)

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1547.7035	1546.6962	1546.7263	-0.0301	9	-	24	0	ASYTVTPPAQANAADA

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 924.4742, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1064.5656, 1079.5472, 1080.5720, 1096.5691, 1105.5515, 1121.4552, 1138.4830, 1430.6873, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1549.7211, 1565.7173, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217, 1697.6129, 1712.6302, 1713.6121, 1714.6356, 1728.6515, 1956.0344, 2001.9681, 2017.9640, 2185.0408, 2273.1641, 2544.0388, 2581.0764, 2597.1111, 2598.1150, 2614.1182, 3137.4888

10. gi|118776568 **Mass:** 17335 **Score:** 13 **Expect:** 46 **Queries matched:** 2

conglutin 8 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1714.6356	1713.6283	1713.6392	-0.0109	79	-	91	0	CCDELNEMENTQR + Oxidation (M)
2544.0388	2543.0315	2543.0071	0.0244	72	-	91	1	SSDQQQRCCDELNEMENTQR + Oxidation (M)

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 924.4742, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1064.5656, 1079.5472, 1080.5720, 1096.5691, 1105.5515, 1121.4552, 1138.4830, 1430.6873, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1547.7035, 1549.7211, 1565.7173, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217, 1697.6129, 1712.6302, 1713.6121, 1728.6515, 1956.0344, 2001.9681, 2017.9640, 2185.0408, 2273.1641, 2581.0764, 2597.1111, 2598.1150, 2614.1182, 3137.4888

Search Parameters

Type of search	**: Peptide Mass Fingerprint**
Enzyme	**: Trypsin**
Fixed modifications	**: Carbamidomethyl (C)**
Variable modifications	**: Oxidation (M)**
Mass values	**: MONOISOTOPIC**
Protein Mass	**: Unrestricted**
Peptide Mass Tolerance	**: ± 20 ppm**
Peptide Charge State	**: 1+**
Max Missed Cleavages	: 1
Number of queries	: 50

Protein View

Match to: **gi|52001229** Score: **91** Expect: **6.5e-007**
conglutin [Arachis hypogaea]

Nominal mass (M_r): **17479**; Calculated pI value: **6.13**
NCBI BLAST search of gi|52001229 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **13**
Sequence Coverage: **51%**

Matched peptides shown in **Bold Red**

```
     1 MAKSTILVAL LALVLVAHAS AMRRERGRQG DSSSCERQVD RVNLKPCEQH
    51 IMQRIMGEQE QYDSYDIRST RSSDQQQRCC DELNEMENTQ RCMCEALQQI
   101 MENQCDRLQD RQMVQQFKRE LMNLPQQCNF RAPQRCDLDV SGGRC
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
72 - 91	2544.0388	2543.0315	2543.0071	0.0244	1	SSDQQQRCCDELNEMENTQR Oxidation (M)
79 - 91	1714.6356	1713.6283	1713.6392	-0.0109	0	CCDELNEMENTQR Oxidation (M)
92 - 111	2598.1150	2597.1077	2597.0913	0.0164	1	CMCEALQQIMENQCDRLQDR
92 - 111	2614.1182	2613.1109	2613.0862	0.0247	1	CMCEALQQIMENQCDRLQDR Oxidation (M)
112 - 118	924.4742	923.4669	923.4534	0.0135	0	QMVQQFK Oxidation (M)
112 - 119	1064.5656	1063.5583	1063.5596	-0.0013	1	QMVQQFKR
112 - 119	1080.5720	1079.5647	1079.5546	0.0102	1	QMVQQFKR Oxidation (M)
120 - 131	1549.7211	1548.7138	1548.7177	-0.0039	0	ELMNLPQQCNFR
120 - 131	1565.7173	1564.7100	1564.7126	-0.0026	0	ELMNLPQQCNFR Oxidation (M)
120 - 135	2001.9681	2000.9608	2000.9672	-0.0064	1	ELMNLPQQCNFRAPQR
120 - 135	2017.9640	2016.9567	2016.9621	-0.0054	1	ELMNLPQQCNFRAPQR Oxidation (M)
132 - 144	1430.6873	1429.6800	1429.6732	0.0069	1	APQRCDLDVSGGR
136 - 145	1138.4830	1137.4757	1137.4543	0.0215	1	CDLDVSGGRC

No match to: 805.4683, 848.4067, 861.0908, 868.5688, 882.5792, 1001.4973, 1016.5799, 1018.5278, 1032.5719, 1046.6112, 1047.5594, 1063.5465, 1079.5472, 1096.5691, 1105.5515, 1121.4552, 1477.8527, 1501.7327, 1503.7538, 1508.6838, 1547.7035, 1581.7039, 1590.7034, 1624.6246, 1635.6865, 1652.6952, 1681.6217, 1697.6129, 1712.6302, 1713.6121, 1728.6515, 1956.0344, 2185.0408, 2273.1641, 2581.0764, 2597.1111, 3137.4888

Spot 103

User :
Email :
Search title : SampleSetID: 2401, AnalysisID: 3097, MaldiWellID: 55839, SpectrumID: 110041, Path=\Janssen\Arachis_300708_1\MS+MSMS Arachis 70 ppm
Database : Arachis 260207 (876 sequences; 195471 residues)
Timestamp : 31 Jul 2008 at 06:46:28 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 291 for gi|22135348, trypsin inhibitor [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|22135348	25768	291	trypsin inhibitor [Arachis hypogaea]
2.	gi|9864777	60754	276	Gly1 [Arachis hypogaea]
3.	gi|118776570	60681	276	arachin 6 [Arachis hypogaea]
4.	gi|5712199	61430	276	glycinin [Arachis hypogaea]
5.	gi|57669861	61041	276	arachin Ahy-4 [Arachis hypogaea]
6.	gi|108595573	61041	276	arachin Ahy-4 [Arachis hypogaea]
7.	gi|52001219	61810	276	arachin Ahy-1 [Arachis hypogaea]
8.	gi|52001221	61836	276	arachin Ahy-2 [Arachis hypogaea]
9.	gi|21314465	62042	276	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|3703107	58543	177	glycinin [Arachis hypogaea]

Results List

1. gi|22135348 **Mass:** 25768 **Score:** 291 **Expect:** 7e-027 **Queries matched:** 7
trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5499	1082.5426	1082.5581	-0.0154	39	47	0	---	LNAQRPDNR
1534.6493	1533.6420	1533.6630	-0.0210	27	38	0	61	QQPEENACQFQR
1534.6493	1533.6420	1533.6630	-0.0210	27	38	0	---	QQPEENACQFQR
2051.0203	2050.0130	2050.0384	-0.0254	84	100	0	91	RPFYSNAPQEIFIQQGR
2051.0203	2050.0130	2050.0384	-0.0254	84	100	0	---	RPFYSNAPQEIFIQQGR
2474.1123	2473.1050	2473.1371	-0.0321	101	122	0	---	GYFGLIFPGCPSTYEEPAQQGR

2474.1123	2473.1050	2473.1371	-0.0321	101 - 122	0	86	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.0056, 1026.5101, 1151.7046, 1434.8832, 1517.6248, 1517.6248, 1618.0503, 2909.3987, 3074.3435, 3074.3435

2. gi|9864777 **Mass:** 60754 **Score:** 276 **Expect:** 2.2e-025 **Queries matched:** 7

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5499	1082.5426	1082.5581	-0.0154	38 -	46	0	---	LNAQRPDNR
1534.6493	1533.6420	1533.6630	-0.0210	26 -	37	0	61	QQPEENACQFQR
1534.6493	1533.6420	1533.6630	-0.0210	26 -	37	0	---	QQPEENACQFQR
2051.0203	2050.0130	2050.0384	-0.0254	83 -	99	0	91	RPFYSNAPQEIFIQQGR
2051.0203	2050.0130	2050.0384	-0.0254	83 -	99	0	---	RPFYSNAPQEIFIQQGR
2474.1123	2473.1050	2473.1371	-0.0321	100 - 121	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1123	2473.1050	2473.1371	-0.0321	100 - 121	0	86	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.0056, 1026.5101, 1151.7046, 1434.8832, 1517.6248, 1517.6248, 1618.0503, 2909.3987, 3074.3435, 3074.3435

3. gi|118776570 **Mass:** 60681 **Score:** 276 **Expect:** 2.2e-025 **Queries matched:** 7

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5499	1082.5426	1082.5581	-0.0154	37 -	45	0	---	LNAQRPDNR
1534.6493	1533.6420	1533.6630	-0.0210	25 -	36	0	61	QQPEENACQFQR
1534.6493	1533.6420	1533.6630	-0.0210	25 -	36	0	---	QQPEENACQFQR
2051.0203	2050.0130	2050.0384	-0.0254	82 -	98	0	91	RPFYSNAPQEIFIQQGR
2051.0203	2050.0130	2050.0384	-0.0254	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99 - 120	0	86	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.0056, 1026.5101, 1151.7046, 1434.8832, 1517.6248, 1517.6248, 1618.0503, 2909.3987, 3074.3435, 3074.3435

4. gi|5712199 **Mass:** 61430 **Score:** 276 **Expect:** 2.2e-025 **Queries matched:** 7

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5499	1082.5426	1082.5581	-0.0154	37 -	45	0	---	LNAQRPDNR
1534.6493	1533.6420	1533.6630	-0.0210	25 -	36	0	61	QQPEENACQFQR
1534.6493	1533.6420	1533.6630	-0.0210	25 -	36	0	---	QQPEENACQFQR
2051.0203	2050.0130	2050.0384	-0.0254	82 -	98	0	91	RPFYSNAPQEIFIQQGR
2051.0203	2050.0130	2050.0384	-0.0254	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99 - 120	0	86	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.0056, 1026.5101, 1151.7046, 1434.8832, 1517.6248, 1517.6248, 1618.0503, 2909.3987, 3074.3435,

3074.3435

5. gi|57669861 **Mass:** 61041 **Score:** 276 **Expect:** 2.2e-025 **Queries matched:** 7

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1083.5499	1082.5426	1082.5581	-0.0154	37	-	45	0	---	LNAQRPDNR
1534.6493	1533.6420	1533.6630	-0.0210	25	-	36	0	61	QQPEENACQFQR
1534.6493	1533.6420	1533.6630	-0.0210	25	-	36	0	---	QQPEENACQFQR
2051.0203	2050.0130	2050.0384	-0.0254	82	-	98	0	91	RPFYSNAPQEIFIQQGR
2051.0203	2050.0130	2050.0384	-0.0254	82	-	98	0	---	RPFYSNAPQEIFIQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99	-	120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99	-	120	0	86	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.0056, 1026.5101, 1151.7046, 1434.8832, 1517.6248, 1517.6248, 1618.0503, 2909.3987, 3074.3435, 3074.3435

6. gi|108595573 **Mass:** 61041 **Score:** 276 **Expect:** 2.2e-025 **Queries matched:** 7

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1083.5499	1082.5426	1082.5581	-0.0154	37	-	45	0	---	LNAQRPDNR
1534.6493	1533.6420	1533.6630	-0.0210	25	-	36	0	61	QQPEENACQFQR
1534.6493	1533.6420	1533.6630	-0.0210	25	-	36	0	---	QQPEENACQFQR
2051.0203	2050.0130	2050.0384	-0.0254	82	-	98	0	91	RPFYSNAPQEIFIQQGR
2051.0203	2050.0130	2050.0384	-0.0254	82	-	98	0	---	RPFYSNAPQEIFIQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99	-	120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99	-	120	0	86	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.0056, 1026.5101, 1151.7046, 1434.8832, 1517.6248, 1517.6248, 1618.0503, 2909.3987, 3074.3435, 3074.3435

7. gi|52001219 **Mass:** 61810 **Score:** 276 **Expect:** 2.2e-025 **Queries matched:** 7

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1083.5499	1082.5426	1082.5581	-0.0154	37	-	45	0	---	LNAQRPDNR
1534.6493	1533.6420	1533.6630	-0.0210	25	-	36	0	61	QQPEENACQFQR
1534.6493	1533.6420	1533.6630	-0.0210	25	-	36	0	---	QQPEENACQFQR
2051.0203	2050.0130	2050.0384	-0.0254	82	-	98	0	91	RPFYSNAPQEIFIQQGR
2051.0203	2050.0130	2050.0384	-0.0254	82	-	98	0	---	RPFYSNAPQEIFIQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99	-	120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99	-	120	0	86	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.0056, 1026.5101, 1151.7046, 1434.8832, 1517.6248, 1517.6248, 1618.0503, 2909.3987, 3074.3435, 3074.3435

8. gi|52001221 **Mass:** 61836 **Score:** 276 **Expect:** 2.2e-025 **Queries matched:** 7

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1083.5499	1082.5426	1082.5581	-0.0154	37	-	45	0	---	LNAQRPDNR
1534.6493	1533.6420	1533.6630	-0.0210	25	-	36	0	61	QQPEENACQFQR
1534.6493	1533.6420	1533.6630	-0.0210	25	-	36	0	---	QQPEENACQFQR
2051.0203	2050.0130	2050.0384	-0.0254	82	-	98	0	91	RPFYSNAPQEIFIQQGR
2051.0203	2050.0130	2050.0384	-0.0254	82	-	98	0	---	RPFYSNAPQEIFIQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99	-	120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99	-	120	0	86	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.0056, 1026.5101, 1151.7046, 1434.8832, 1517.6248, 1517.6248, 1618.0503, 2909.3987, 3074.3435, 3074.3435

9. gi|21314465 **Mass:** 62042 **Score:** 276 **Expect:** 2.2e-025 **Queries matched:** 7

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1083.5499	1082.5426	1082.5581	-0.0154	37	-	45	0	---	LNAQRPDNR
1534.6493	1533.6420	1533.6630	-0.0210	25	-	36	0	61	QQPEENACQFQR
1534.6493	1533.6420	1533.6630	-0.0210	25	-	36	0	---	QQPEENACQFQR
2051.0203	2050.0130	2050.0384	-0.0254	82	-	98	0	91	RPFYSNAPQEIFIQQGR
2051.0203	2050.0130	2050.0384	-0.0254	82	-	98	0	---	RPFYSNAPQEIFIQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99	-	120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.1123	2473.1050	2473.1371	-0.0321	99	-	120	0	86	GYFGLIFPGCPSTYEEPAQQGR

No match to: 1026.0056, 1026.5101, 1151.7046, 1434.8832, 1517.6248, 1517.6248, 1618.0503, 2909.3987, 3074.3435, 3074.3435

10. gi|3703107 **Mass:** 58543 **Score:** 177 **Expect:** 1.7e-015 **Queries matched:** 5

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Ions	Peptide
1083.5499	1082.5426	1082.5581	-0.0154	14	-	22	0	---	LNAQRPDNR
1534.6493	1533.6420	1533.6630	-0.0210	2	-	13	0	61	QQPEENACQFQR
1534.6493	1533.6420	1533.6630	-0.0210	2	-	13	0	---	QQPEENACQFQR
2051.0203	2050.0130	2050.0384	-0.0254	59	-	75	0	91	RPFYSNAPQEIFIQQGR
2051.0203	2050.0130	2050.0384	-0.0254	59	-	75	0	---	RPFYSNAPQEIFIQQGR

No match to: 1026.0056, 1026.5101, 1151.7046, 1434.8832, 1517.6248, 1517.6248, 1618.0503, 2474.1123, 2474.1123, 2909.3987, 3074.3435, 3074.3435

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Number of Queries: 17

Protein View

Match to: **gi|22135348** Score: **291** Expect: **7e-027**
trypsin inhibitor [Arachis hypogaea]

Nominal mass (M_r): **25768**; Calculated pI value: **6.66**
NCBI BLAST search of gi|22135348 against nr
Unformatted sequence string for pasting into other applications

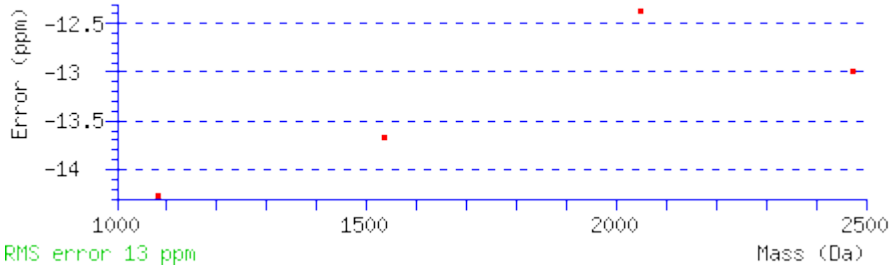
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **27%**

Matched peptides shown in **Bold Red**

```
   1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES
  51 EGGYIETWNP NNQEFECAGV ALSRLVLRRN ALRRPFYSNA PQEIFIQQGR
 101 GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH
 151 RFDEGDLIAV PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
 201 AGNHEQEFLR YQQQSRRRS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
27 - 38	1534.6493	1533.6420	1533.6630	-0.0210	0	QQPEENACQFQR	(Ions score 61)
27 - 38	1534.6493	1533.6420	1533.6630	-0.0210	0	QQPEENACQFQR	(No match)
39 - 47	1083.5499	1082.5426	1082.5581	-0.0154	0	LNAQRPDNR	(No match)
84 - 100	2051.0203	2050.0130	2050.0384	-0.0254	0	RPFYSNAPQEIFIQQGR	(Ions score 91)
84 - 100	2051.0203	2050.0130	2050.0384	-0.0254	0	RPFYSNAPQEIFIQQGR	(No match)
101 - 122	2474.1123	2473.1050	2473.1371	-0.0321	0	GYFGLIFPGCPSTYEEPAQQGR	(No match)
101 - 122	2474.1123	2473.1050	2473.1371	-0.0321	0	GYFGLIFPGCPSTYEEPAQQGR	(Ions score 86)



N terminus of Arachin 6

Match to: **gi|118776570** Score: **276** Expect: **2.2e-025**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
  1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
 51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Spot 104

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:43:42 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **175 for gi|22135348, trypsin inhibitor [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|22135348	25768	175	trypsin inhibitor [Arachis hypogaea]
2.	gi|9864777	60754	160	Gly1 [Arachis hypogaea]
3.	gi|118776570	60681	160	arachin 6 [Arachis hypogaea]
4.	gi|5712199	61430	160	glycinin [Arachis hypogaea]
5.	gi|57669861	61041	160	arachin Ahy-4 [Arachis hypogaea]
6.	gi|108595573	61041	160	arachin Ahy-4 [Arachis hypogaea]
7.	gi|52001219	61810	160	arachin Ahy-1 [Arachis hypogaea]
8.	gi|52001221	61836	160	arachin Ahy-2 [Arachis hypogaea]
9.	gi|21314465	62042	160	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|3703107	58543	147	glycinin [Arachis hypogaea]

Results List

1. gi|22135348 **Mass:** 25768 **Score:** 175 **Expect:** 2.8e-015 **Queries matched:** 6
trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5283	1082.5210	1082.5581	-0.0370	39	47	0	---	LNAQRPDNR
1083.5283	1082.5210	1082.5581	-0.0370	39	47	0	23	LNAQRPDNR
1534.6188	1533.6115	1533.6630	-0.0515	27	38	0	---	QQPEENACQFQR
2050.9771	2049.9698	2050.0384	-0.0686	84	100	0	---	RPFYSNAPQEIFIQQGR
2050.9771	2049.9698	2050.0384	-0.0686	84	100	0	99	RPFYSNAPQEIFIQQGR
2474.0564	2473.0491	2473.1371	-0.0880	101	122	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5404, 1151.6840, 1464.5323, 1464.5323, 1481.5590, 1481.5590, 1517.5984, 1651.7716, 3073.2922, 3073.2922

2. gi|9864777 **Mass:** 60754 **Score:** 160 **Expect:** 8.8e-014 **Queries matched:** 6

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5283	1082.5210	1082.5581	-0.0370	38	46	0	---	LNAQRPDNR
1083.5283	1082.5210	1082.5581	-0.0370	38	46	0	23	LNAQRPDNR
1534.6188	1533.6115	1533.6630	-0.0515	26	37	0	---	QQPEENACQFQR
2050.9771	2049.9698	2050.0384	-0.0686	83	99	0	---	RPFYSNAPQEIFIQQGR
2050.9771	2049.9698	2050.0384	-0.0686	83	99	0	99	RPFYSNAPQEIFIQQGR
2474.0564	2473.0491	2473.1371	-0.0880	100	121	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5404, 1151.6840, 1464.5323, 1464.5323, 1481.5590, 1481.5590, 1517.5984, 1651.7716, 3073.2922, 3073.2922

3. gi|118776570 **Mass:** 60681 **Score:** 160 **Expect:** 8.8e-014 **Queries matched:** 6

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5283	1082.5210	1082.5581	-0.0370	37	45	0	---	LNAQRPDNR
1083.5283	1082.5210	1082.5581	-0.0370	37	45	0	23	LNAQRPDNR
1534.6188	1533.6115	1533.6630	-0.0515	25	36	0	---	QQPEENACQFQR
2050.9771	2049.9698	2050.0384	-0.0686	82	98	0	---	RPFYSNAPQEIFIQQGR
2050.9771	2049.9698	2050.0384	-0.0686	82	98	0	99	RPFYSNAPQEIFIQQGR
2474.0564	2473.0491	2473.1371	-0.0880	99	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5404, 1151.6840, 1464.5323, 1464.5323, 1481.5590, 1481.5590, 1517.5984, 1651.7716, 3073.2922, 3073.2922

4. gi|5712199 **Mass:** 61430 **Score:** 160 **Expect:** 8.8e-014 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5283	1082.5210	1082.5581	-0.0370	37	45	0	---	LNAQRPDNR
1083.5283	1082.5210	1082.5581	-0.0370	37	45	0	23	LNAQRPDNR
1534.6188	1533.6115	1533.6630	-0.0515	25	36	0	---	QQPEENACQFQR
2050.9771	2049.9698	2050.0384	-0.0686	82	98	0	---	RPFYSNAPQEIFIQQGR
2050.9771	2049.9698	2050.0384	-0.0686	82	98	0	99	RPFYSNAPQEIFIQQGR
2474.0564	2473.0491	2473.1371	-0.0880	99	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5404, 1151.6840, 1464.5323, 1464.5323, 1481.5590, 1481.5590, 1517.5984, 1651.7716, 3073.2922, 3073.2922

5. gi|57669861 **Mass:** 61041 **Score:** 160 **Expect:** 8.8e-014 **Queries matched:** 6

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5283	1082.5210	1082.5581	-0.0370	37	45	0	---	LNAQRPDNR
1083.5283	1082.5210	1082.5581	-0.0370	37	45	0	23	LNAQRPDNR
1534.6188	1533.6115	1533.6630	-0.0515	25	36	0	---	QQPEENACQFQR

2050.9771	2049.9698	2050.0384	-0.0686	82 - 98	0	---	RPFYSNAPQEIFIQQGR
2050.9771	2049.9698	2050.0384	-0.0686	82 - 98	0	99	RPFYSNAPQEIFIQQGR
2474.0564	2473.0491	2473.1371	-0.0880	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5404, 1151.6840, 1464.5323, 1464.5323, 1481.5590, 1481.5590, 1517.5984, 1651.7716, 3073.2922, 3073.2922

6. gi|108595573 **Mass:** 61041 **Score:** 160 **Expect:** 8.8e-014 **Queries matched:** 6

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5283	1082.5210	1082.5581	-0.0370	37 -	45	0	---	LNAQRPDNR
1083.5283	1082.5210	1082.5581	-0.0370	37 -	45	0	23	LNAQRPDNR
1534.6188	1533.6115	1533.6630	-0.0515	25 -	36	0	---	QQPEENACQFQR
2050.9771	2049.9698	2050.0384	-0.0686	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2050.9771	2049.9698	2050.0384	-0.0686	82 -	98	0	99	RPFYSNAPQEIFIQQGR
2474.0564	2473.0491	2473.1371	-0.0880	99 -	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5404, 1151.6840, 1464.5323, 1464.5323, 1481.5590, 1481.5590, 1517.5984, 1651.7716, 3073.2922, 3073.2922

7. gi|52001219 **Mass:** 61810 **Score:** 160 **Expect:** 8.8e-014 **Queries matched:** 6

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5283	1082.5210	1082.5581	-0.0370	37 -	45	0	---	LNAQRPDNR
1083.5283	1082.5210	1082.5581	-0.0370	37 -	45	0	23	LNAQRPDNR
1534.6188	1533.6115	1533.6630	-0.0515	25 -	36	0	---	QQPEENACQFQR
2050.9771	2049.9698	2050.0384	-0.0686	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2050.9771	2049.9698	2050.0384	-0.0686	82 -	98	0	99	RPFYSNAPQEIFIQQGR
2474.0564	2473.0491	2473.1371	-0.0880	99 -	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5404, 1151.6840, 1464.5323, 1464.5323, 1481.5590, 1481.5590, 1517.5984, 1651.7716, 3073.2922, 3073.2922

8. gi|52001221 **Mass:** 61836 **Score:** 160 **Expect:** 8.8e-014 **Queries matched:** 6

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5283	1082.5210	1082.5581	-0.0370	37 -	45	0	---	LNAQRPDNR
1083.5283	1082.5210	1082.5581	-0.0370	37 -	45	0	23	LNAQRPDNR
1534.6188	1533.6115	1533.6630	-0.0515	25 -	36	0	---	QQPEENACQFQR
2050.9771	2049.9698	2050.0384	-0.0686	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2050.9771	2049.9698	2050.0384	-0.0686	82 -	98	0	99	RPFYSNAPQEIFIQQGR
2474.0564	2473.0491	2473.1371	-0.0880	99 -	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5404, 1151.6840, 1464.5323, 1464.5323, 1481.5590, 1481.5590, 1517.5984, 1651.7716, 3073.2922, 3073.2922

9. gi|21314465 **Mass:** 62042 **Score:** 160 **Expect:** 8.8e-014 **Queries matched:** 6

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide

1083.5283	1082.5210	1082.5581	-0.0370	37 - 45	0	---	LNAQRPDNR
1083.5283	1082.5210	1082.5581	-0.0370	37 - 45	0	23	LNAQRPDNR
1534.6188	1533.6115	1533.6630	-0.0515	25 - 36	0	---	QQPEENACQFQR
2050.9771	2049.9698	2050.0384	-0.0686	82 - 98	0	---	RPFYSNAPQEIFIQQGR
2050.9771	2049.9698	2050.0384	-0.0686	82 - 98	0	99	RPFYSNAPQEIFIQQGR
2474.0564	2473.0491	2473.1371	-0.0880	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5404, 1151.6840, 1464.5323, 1464.5323, 1481.5590, 1481.5590, 1517.5984, 1651.7716, 3073.2922, 3073.2922

10. gi|3703107 **Mass:** 58543 **Score:** 147 **Expect:** 1.7e-012 **Queries matched:** 5

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5283	1082.5210	1082.5581	-0.0370	14 -	22	0	---	LNAQRPDNR
1083.5283	1082.5210	1082.5581	-0.0370	14 -	22	0	23	LNAQRPDNR
1534.6188	1533.6115	1533.6630	-0.0515	2 -	13	0	---	QQPEENACQFQR
2050.9771	2049.9698	2050.0384	-0.0686	59 -	75	0	---	RPFYSNAPQEIFIQQGR
2050.9771	2049.9698	2050.0384	-0.0686	59 -	75	0	99	RPFYSNAPQEIFIQQGR

No match to: 982.5404, 1151.6840, 1464.5323, 1464.5323, 1481.5590, 1481.5590, 1517.5984, 1651.7716, 2474.0564, 3073.2922, 3073.2922

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Number of Queries: 16

Protein View

Match to: **gi|22135348** Score: **175** Expect: **2.8e-015**
trypsin inhibitor [Arachis hypogaea]

Nominal mass (M_r): **25768**; Calculated pI value: **6.66**
NCBI BLAST search of gi|22135348 against nr
Unformatted sequence string for pasting into other applications

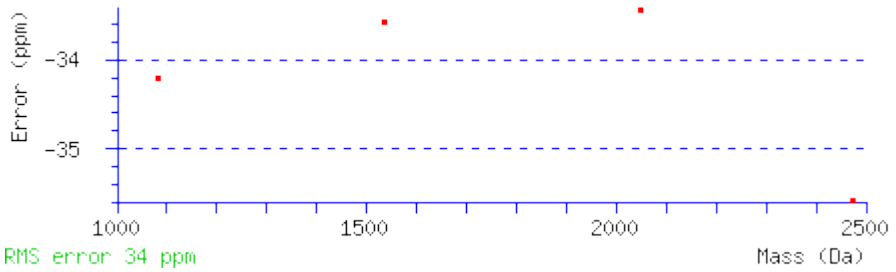
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **27%**

Matched peptides shown in **Bold Red**

```
   1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES
  51 EGGYIETWNP NNQEFECAGV ALSRLVLRRN ALRRPFYSNA PQEIFIQQGR
 101 GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH
 151 RFDEGDLIAV PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
 201 AGNHEQEFLR YQQQSRRRS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
27 - 38	1534.6188	1533.6115	1533.6630	-0.0515	0	QQPEENACQFQR	(No match)
39 - 47	1083.5283	1082.5210	1082.5581	-0.0370	0	LNAQRPDNR	(No match)
39 - 47	1083.5283	1082.5210	1082.5581	-0.0370	0	LNAQRPDNR	(Ions score 23)
84 - 100	2050.9771	2049.9698	2050.0384	-0.0686	0	RPFYSNAPQEIFIQQGR	(No match)
84 - 100	2050.9771	2049.9698	2050.0384	-0.0686	0	RPFYSNAPQEIFIQQGR	(Ions score 99)
101 - 122	2474.0564	2473.0491	2473.1371	-0.0880	0	GYFGLIFPGCPSTYEEPAQQGR	(No match)



N terminus of Arachin 6

Match to: **gi|118776570** Score: **160** Expect: **8.8e-014**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
   1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
  51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
 101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
 151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
 201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
 251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
 301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
 351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
 401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
 451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
 501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Spot 105

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:46:09 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **347 for gi|22135348, trypsin inhibitor [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|22135348	25768	347	trypsin inhibitor [Arachis hypogaea]
2.	gi|5712199	61430	333	glycinin [Arachis hypogaea]
3.	gi|9864777	60754	332	Gly1 [Arachis hypogaea]
4.	gi|118776570	60681	332	arachin 6 [Arachis hypogaea]
5.	gi|57669861	61041	332	arachin Ahy-4 [Arachis hypogaea]
6.	gi|108595573	61041	332	arachin Ahy-4 [Arachis hypogaea]
7.	gi|52001219	61810	332	arachin Ahy-1 [Arachis hypogaea]
8.	gi|52001221	61836	332	arachin Ahy-2 [Arachis hypogaea]
9.	gi|21314465	62042	332	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|3703107	58543	217	glycinin [Arachis hypogaea]

Results List

1. gi|22135348 **Mass:** 25768 **Score:** 347 **Expect:** 1.7e-032 **Queries matched:** 8
trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5546	1082.5473	1082.5581	-0.0107	39	47	0	---	LNAQRPDNR
1083.5546	1082.5473	1082.5581	-0.0107	39	47	0	24	LNAQRPDNR
1534.6558	1533.6485	1533.6630	-0.0145	27	38	0	74	QQPEENACQFQR
1534.6558	1533.6485	1533.6630	-0.0145	27	38	0	---	QQPEENACQFQR
2051.0320	2050.0247	2050.0384	-0.0137	84	100	0	96	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	84	100	0	---	RPFYSNAPQEIFIQQGR
2474.1267	2473.1194	2473.1371	-0.0177	101	122	0	102	GYFGLIFPGCPSTYEEPAQQGR
2474.1267	2473.1194	2473.1371	-0.0177	101	122	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 886.9755, 934.4769, 1026.0146, 1026.5161, 1517.6334, 1517.6334, 1533.6227, 1650.8179, 2034.4802, 2491.1338, 3075.3486

2. gi|5712199 **Mass:** 61430 **Score:** 333 **Expect:** 4.4e-031 **Queries matched:** 8

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5546	1082.5473	1082.5581	-0.0107	37	45	0	---	LNAQRPDNR
1083.5546	1082.5473	1082.5581	-0.0107	37	45	0	24	LNAQRPDNR
1534.6558	1533.6485	1533.6630	-0.0145	25	36	0	74	QQPEENACQFQR
1534.6558	1533.6485	1533.6630	-0.0145	25	36	0	---	QQPEENACQFQR
2051.0320	2050.0247	2050.0384	-0.0137	82	98	0	96	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82	98	0	---	RPFYSNAPQEIFIQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99	120	0	102	GYFGLIFPGCPSTYEEPAQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 886.9755, 934.4769, 1026.0146, 1026.5161, 1517.6334, 1517.6334, 1533.6227, 1650.8179, 2034.4802, 2491.1338, 3075.3486

3. gi|9864777 **Mass:** 60754 **Score:** 332 **Expect:** 5.5e-031 **Queries matched:** 8

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5546	1082.5473	1082.5581	-0.0107	38	46	0	---	LNAQRPDNR
1083.5546	1082.5473	1082.5581	-0.0107	38	46	0	24	LNAQRPDNR
1534.6558	1533.6485	1533.6630	-0.0145	26	37	0	74	QQPEENACQFQR
1534.6558	1533.6485	1533.6630	-0.0145	26	37	0	---	QQPEENACQFQR
2051.0320	2050.0247	2050.0384	-0.0137	83	99	0	96	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	83	99	0	---	RPFYSNAPQEIFIQQGR
2474.1267	2473.1194	2473.1371	-0.0177	100	121	0	102	GYFGLIFPGCPSTYEEPAQQGR
2474.1267	2473.1194	2473.1371	-0.0177	100	121	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 886.9755, 934.4769, 1026.0146, 1026.5161, 1517.6334, 1517.6334, 1533.6227, 1650.8179, 2034.4802, 2491.1338, 3075.3486

4. gi|118776570 **Mass:** 60681 **Score:** 332 **Expect:** 5.5e-031 **Queries matched:** 8

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5546	1082.5473	1082.5581	-0.0107	37	45	0	---	LNAQRPDNR
1083.5546	1082.5473	1082.5581	-0.0107	37	45	0	24	LNAQRPDNR
1534.6558	1533.6485	1533.6630	-0.0145	25	36	0	74	QQPEENACQFQR
1534.6558	1533.6485	1533.6630	-0.0145	25	36	0	---	QQPEENACQFQR
2051.0320	2050.0247	2050.0384	-0.0137	82	98	0	96	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82	98	0	---	RPFYSNAPQEIFIQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99	120	0	102	GYFGLIFPGCPSTYEEPAQQGR

2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 886.9755, 934.4769, 1026.0146, 1026.5161, 1517.6334, 1517.6334, 1533.6227, 1650.8179, 2034.4802, 2491.1338, 3075.3486

5. gi|57669861 **Mass:** 61041 **Score:** 332 **Expect:** 5.5e-031 **Queries matched:** 8

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5546	1082.5473	1082.5581	-0.0107	37 -	45	0	---	LNAQRPDNR
1083.5546	1082.5473	1082.5581	-0.0107	37 -	45	0	24	LNAQRPDNR
1534.6558	1533.6485	1533.6630	-0.0145	25 -	36	0	74	QQPEENACQFQR
1534.6558	1533.6485	1533.6630	-0.0145	25 -	36	0	---	QQPEENACQFQR
2051.0320	2050.0247	2050.0384	-0.0137	82 -	98	0	96	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	102	GYFGLIFPGCPSTYEEPAQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 886.9755, 934.4769, 1026.0146, 1026.5161, 1517.6334, 1517.6334, 1533.6227, 1650.8179, 2034.4802, 2491.1338, 3075.3486

6. gi|108595573 **Mass:** 61041 **Score:** 332 **Expect:** 5.5e-031 **Queries matched:** 8

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5546	1082.5473	1082.5581	-0.0107	37 -	45	0	---	LNAQRPDNR
1083.5546	1082.5473	1082.5581	-0.0107	37 -	45	0	24	LNAQRPDNR
1534.6558	1533.6485	1533.6630	-0.0145	25 -	36	0	74	QQPEENACQFQR
1534.6558	1533.6485	1533.6630	-0.0145	25 -	36	0	---	QQPEENACQFQR
2051.0320	2050.0247	2050.0384	-0.0137	82 -	98	0	96	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	102	GYFGLIFPGCPSTYEEPAQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 886.9755, 934.4769, 1026.0146, 1026.5161, 1517.6334, 1517.6334, 1533.6227, 1650.8179, 2034.4802, 2491.1338, 3075.3486

7. gi|52001219 **Mass:** 61810 **Score:** 332 **Expect:** 5.5e-031 **Queries matched:** 8

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5546	1082.5473	1082.5581	-0.0107	37 -	45	0	---	LNAQRPDNR
1083.5546	1082.5473	1082.5581	-0.0107	37 -	45	0	24	LNAQRPDNR
1534.6558	1533.6485	1533.6630	-0.0145	25 -	36	0	74	QQPEENACQFQR
1534.6558	1533.6485	1533.6630	-0.0145	25 -	36	0	---	QQPEENACQFQR
2051.0320	2050.0247	2050.0384	-0.0137	82 -	98	0	96	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 -	98	0	---	RPFYSNAPQEIFIQQGR

2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	102	GYFGLIFPGCPSTYEEPAQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 886.9755, 934.4769, 1026.0146, 1026.5161, 1517.6334, 1517.6334, 1533.6227, 1650.8179, 2034.4802, 2491.1338, 3075.3486

8. gi|52001221 **Mass:** 61836 **Score:** 332 **Expect:** 5.5e-031 **Queries matched:** 8

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5546	1082.5473	1082.5581	-0.0107	37 -	45	0	---	LNAQRPDNR
1083.5546	1082.5473	1082.5581	-0.0107	37 -	45	0	24	LNAQRPDNR
1534.6558	1533.6485	1533.6630	-0.0145	25 -	36	0	74	QQPEENACQFQR
1534.6558	1533.6485	1533.6630	-0.0145	25 -	36	0	---	QQPEENACQFQR
2051.0320	2050.0247	2050.0384	-0.0137	82 -	98	0	96	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	102	GYFGLIFPGCPSTYEEPAQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 886.9755, 934.4769, 1026.0146, 1026.5161, 1517.6334, 1517.6334, 1533.6227, 1650.8179, 2034.4802, 2491.1338, 3075.3486

9. gi|21314465 **Mass:** 62042 **Score:** 332 **Expect:** 5.5e-031 **Queries matched:** 8

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5546	1082.5473	1082.5581	-0.0107	37 -	45	0	---	LNAQRPDNR
1083.5546	1082.5473	1082.5581	-0.0107	37 -	45	0	24	LNAQRPDNR
1534.6558	1533.6485	1533.6630	-0.0145	25 -	36	0	74	QQPEENACQFQR
1534.6558	1533.6485	1533.6630	-0.0145	25 -	36	0	---	QQPEENACQFQR
2051.0320	2050.0247	2050.0384	-0.0137	82 -	98	0	96	RPFYSNAPQEIFIQQGR
2051.0320	2050.0247	2050.0384	-0.0137	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	102	GYFGLIFPGCPSTYEEPAQQGR
2474.1267	2473.1194	2473.1371	-0.0177	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR

No match to: 886.9755, 934.4769, 1026.0146, 1026.5161, 1517.6334, 1517.6334, 1533.6227, 1650.8179, 2034.4802, 2491.1338, 3075.3486

10. gi|3703107 **Mass:** 58543 **Score:** 217 **Expect:** 1.7e-019 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5546	1082.5473	1082.5581	-0.0107	14 -	22	0	---	LNAQRPDNR
1083.5546	1082.5473	1082.5581	-0.0107	14 -	22	0	24	LNAQRPDNR
1534.6558	1533.6485	1533.6630	-0.0145	2 -	13	0	74	QQPEENACQFQR
1534.6558	1533.6485	1533.6630	-0.0145	2 -	13	0	---	QQPEENACQFQR
2051.0320	2050.0247	2050.0384	-0.0137	59 -	75	0	96	RPFYSNAPQEIFIQQGR

2051.0320 2050.0247 2050.0384 -0.0137 59 - 75 0 --- RPFYSNAPQEIFIQQGR

No match to: 886.9755, 934.4769, 1026.0146, 1026.5161, 1517.6334, 1517.6334, 1533.6227, 1650.8179, 2034.4802, 2474.1267, 2474.1267, 2491.1338, 3075.3486

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Number of Queries: 16

Protein View

Match to: **gi|22135348** Score: **347** Expect: **1.7e-032**
trypsin inhibitor [Arachis hypogaea]

Nominal mass (M_r): **25768**; Calculated pI value: **6.66**
NCBI BLAST search of gi|22135348 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **27%**

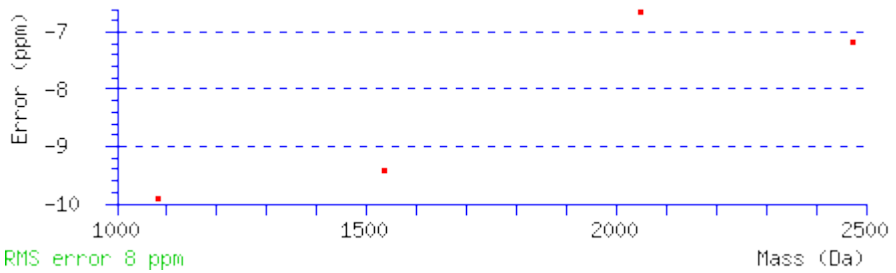
Matched peptides shown in **Bold Red**

```
   1 NYLHMLLALS VCFCFLVLGA SSISFRQQPE ENACQFQRLN AQRPDNRIES
  51 EGGYIETWNP NNQEFECAGV ALSRLVLRRN ALRRPFYSNA PQEIFIQQGR
 101 GYFGLIFPGC PSTYEEPAQQ GRRHQSQRPP RRFQGQDQSQ QQQDSHQKVH
 151 RFDEGDLIAV PTGVAFWMYN DHDTDVVAVS LTDTNNNDNQ LDQFPRRFNL
 201 AGNHEQEFLR YQQQSRRRS
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
27 - 38	1534.6558	1533.6485	1533.6630	-0.0145	0	QQPEENACQFQR	(Ions score 74)
27 - 38	1534.6558	1533.6485	1533.6630	-0.0145	0	QQPEENACQFQR	(No match)
39 - 47	1083.5546	1082.5473	1082.5581	-0.0107	0	LNAQRPDNR	(No match)

39 - 47	1083.5546	1082.5473	1082.5581	-0.0107	0	**LNAQRPDNR**	(Ions score 24)
84 - 100	2051.0320	2050.0247	2050.0384	-0.0137	0	**RPFYSNAPQEIFIQQGR**	(Ions score 96)
84 - 100	2051.0320	2050.0247	2050.0384	-0.0137	0	**RPFYSNAPQEIFIQQGR**	(No match)
101 - 122	2474.1267	2473.1194	2473.1371	-0.0177	0	**GYFGLIFPGCPSTYEEPAQQGR**	(Ions score 102)
101 - 122	2474.1267	2473.1194	2473.1371	-0.0177	0	**GYFGLIFPGCPSTYEEPAQQGR**	(No match)



N-terminus of Arachin 6

Match to: **gi|118776570** Score: **332** Expect: **5.5e-031**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

```
   1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
  51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
 101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
 151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
 201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
 251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
 301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
 351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
 401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
 451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
 501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Spot 106

Database : **Arachis 260207 (876 sequences; 195471 residues)**
Timestamp : **31 Jul 2008 at 06:46:02 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **376 for gi|118776570, arachin 6 [Arachis hypogaea]**

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|118776570	60681	376	arachin 6 [Arachis hypogaea]
2.	gi|5712199	61430	376	glycinin [Arachis hypogaea]
3.	gi|22135348	25768	349	trypsin inhibitor [Arachis hypogaea]
4.	gi|9864777	60754	335	Gly1 [Arachis hypogaea]
5.	gi|57669861	61041	335	arachin Ahy-4 [Arachis hypogaea]
6.	gi|108595573	61041	335	arachin Ahy-4 [Arachis hypogaea]
7.	gi|52001219	61810	335	arachin Ahy-1 [Arachis hypogaea]
8.	gi|52001221	61836	335	arachin Ahy-2 [Arachis hypogaea]
9.	gi|21314465	62042	335	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|3703107	58543	215	glycinin [Arachis hypogaea]

Results List

1. gi|118776570 **Mass:** 60681 **Score:** 376 **Expect:** 2.2e-035 **Queries matched:** 10
arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.4928	1030.4855	1030.5308	-0.0453	122	129	0	17	YQSQRPPR
1031.4928	1030.4855	1030.5308	-0.0453	122	129	0	---	YQSQRPPR
1083.5197	1082.5124	1082.5581	-0.0456	37	45	0	---	LNAQRPDNR
1187.5874	1186.5801	1186.6319	-0.0518	122	130	1	---	YQSQRPPRR
1534.6082	1533.6009	1533.6630	-0.0621	25	36	0	80	QQPEENACQFQR
1534.6082	1533.6009	1533.6630	-0.0621	25	36	0	---	QQPEENACQFQR
2050.9683	2049.9610	2050.0384	-0.0774	82	98	0	---	RPFYSNAPQEIFIQQGR
2050.9683	2049.9610	2050.0384	-0.0774	82	98	0	115	RPFYSNAPQEIFIQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99	120	0	---	GYFGLIFPGCPSTYEEPAQQGR

2474.0500	2473.0427	2473.1371	-0.0944	99 - 120	0	108	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5316, 1026.4862, 1151.6750, 1434.8538, 1517.5850, 1517.5850, 1618.0083, 1650.7631, 2034.4226, 2490.0771, 2506.2244, 3074.2690

2. gi|5712199 **Mass:** 61430 **Score:** 376 **Expect:** 2.2e-035 **Queries matched:** 10

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1031.4928	1030.4855	1030.5308	-0.0453	122 -	129	0	17	YQSQRPPR
1031.4928	1030.4855	1030.5308	-0.0453	122 -	129	0	---	YQSQRPPR
1083.5197	1082.5124	1082.5581	-0.0456	37 -	45	0	---	LNAQRPDNR
1187.5874	1186.5801	1186.6319	-0.0518	122 -	130	1	---	YQSQRPPRR
1534.6082	1533.6009	1533.6630	-0.0621	25 -	36	0	80	QQPEENACQFQR
1534.6082	1533.6009	1533.6630	-0.0621	25 -	36	0	---	QQPEENACQFQR
2050.9683	2049.9610	2050.0384	-0.0774	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2050.9683	2049.9610	2050.0384	-0.0774	82 -	98	0	115	RPFYSNAPQEIFIQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99 -	120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99 -	120	0	108	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5316, 1026.4862, 1151.6750, 1434.8538, 1517.5850, 1517.5850, 1618.0083, 1650.7631, 2034.4226, 2490.0771, 2506.2244, 3074.2690

3. gi|22135348 **Mass:** 25768 **Score:** 349 **Expect:** 1.1e-032 **Queries matched:** 7

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5197	1082.5124	1082.5581	-0.0456	39 -	47	0	---	LNAQRPDNR
1534.6082	1533.6009	1533.6630	-0.0621	27 -	38	0	80	QQPEENACQFQR
1534.6082	1533.6009	1533.6630	-0.0621	27 -	38	0	---	QQPEENACQFQR
2050.9683	2049.9610	2050.0384	-0.0774	84 -	100	0	---	RPFYSNAPQEIFIQQGR
2050.9683	2049.9610	2050.0384	-0.0774	84 -	100	0	115	RPFYSNAPQEIFIQQGR
2474.0500	2473.0427	2473.1371	-0.0944	101 -	122	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.0500	2473.0427	2473.1371	-0.0944	101 -	122	0	108	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5316, 1026.4862, 1031.4928, 1031.4928, 1151.6750, 1187.5874, 1434.8538, 1517.5850, 1517.5850, 1618.0083, 1650.7631, 2034.4226, 2490.0771, 2506.2244, 3074.2690

4. gi|9864777 **Mass:** 60754 **Score:** 335 **Expect:** 2.8e-031 **Queries matched:** 7

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5197	1082.5124	1082.5581	-0.0456	38 -	46	0	---	LNAQRPDNR
1534.6082	1533.6009	1533.6630	-0.0621	26 -	37	0	80	QQPEENACQFQR
1534.6082	1533.6009	1533.6630	-0.0621	26 -	37	0	---	QQPEENACQFQR
2050.9683	2049.9610	2050.0384	-0.0774	83 -	99	0	---	RPFYSNAPQEIFIQQGR
2050.9683	2049.9610	2050.0384	-0.0774	83 -	99	0	115	RPFYSNAPQEIFIQQGR

2474.0500	2473.0427	2473.1371	-0.0944	100 - 121	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.0500	2473.0427	2473.1371	-0.0944	100 - 121	0	108	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5316, 1026.4862, 1031.4928, 1031.4928, 1151.6750, 1187.5874, 1434.8538, 1517.5850, 1517.5850, 1618.0083, 1650.7631, 2034.4226, 2490.0771, 2506.2244, 3074.2690

5. gi|57669861 **Mass:** 61041 **Score:** 335 **Expect:** 2.8e-031 **Queries matched:** 7

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5197	1082.5124	1082.5581	-0.0456	37 -	45	0	---	LNAQRPDNR
1534.6082	1533.6009	1533.6630	-0.0621	25 -	36	0	80	QQPEENACQFQR
1534.6082	1533.6009	1533.6630	-0.0621	25 -	36	0	---	QQPEENACQFQR
2050.9683	2049.9610	2050.0384	-0.0774	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2050.9683	2049.9610	2050.0384	-0.0774	82 -	98	0	115	RPFYSNAPQEIFIQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99 - 120	0	108	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5316, 1026.4862, 1031.4928, 1031.4928, 1151.6750, 1187.5874, 1434.8538, 1517.5850, 1517.5850, 1618.0083, 1650.7631, 2034.4226, 2490.0771, 2506.2244, 3074.2690

6. gi|108595573 **Mass:** 61041 **Score:** 335 **Expect:** 2.8e-031 **Queries matched:** 7

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5197	1082.5124	1082.5581	-0.0456	37 -	45	0	---	LNAQRPDNR
1534.6082	1533.6009	1533.6630	-0.0621	25 -	36	0	80	QQPEENACQFQR
1534.6082	1533.6009	1533.6630	-0.0621	25 -	36	0	---	QQPEENACQFQR
2050.9683	2049.9610	2050.0384	-0.0774	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2050.9683	2049.9610	2050.0384	-0.0774	82 -	98	0	115	RPFYSNAPQEIFIQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99 - 120	0	108	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5316, 1026.4862, 1031.4928, 1031.4928, 1151.6750, 1187.5874, 1434.8538, 1517.5850, 1517.5850, 1618.0083, 1650.7631, 2034.4226, 2490.0771, 2506.2244, 3074.2690

7. gi|52001219 **Mass:** 61810 **Score:** 335 **Expect:** 2.8e-031 **Queries matched:** 7

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5197	1082.5124	1082.5581	-0.0456	37 -	45	0	---	LNAQRPDNR
1534.6082	1533.6009	1533.6630	-0.0621	25 -	36	0	80	QQPEENACQFQR
1534.6082	1533.6009	1533.6630	-0.0621	25 -	36	0	---	QQPEENACQFQR
2050.9683	2049.9610	2050.0384	-0.0774	82 -	98	0	---	RPFYSNAPQEIFIQQGR
2050.9683	2049.9610	2050.0384	-0.0774	82 -	98	0	115	RPFYSNAPQEIFIQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99 - 120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99 - 120	0	108	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5316, 1026.4862, 1031.4928, 1031.4928, 1151.6750, 1187.5874, 1434.8538, 1517.5850, 1517.5850, 1618.0083, 1650.7631, 2034.4226, 2490.0771, 2506.2244, 3074.2690

8. gi|52001221 **Mass:** 61836 **Score:** 335 **Expect:** 2.8e-031 **Queries matched:** 7

arachin Ahy-2 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5197	1082.5124	1082.5581	-0.0456	37	45	0	---	LNAQRPDNR
1534.6082	1533.6009	1533.6630	-0.0621	25	36	0	80	QQPEENACQFQR
1534.6082	1533.6009	1533.6630	-0.0621	25	36	0	---	QQPEENACQFQR
2050.9683	2049.9610	2050.0384	-0.0774	82	98	0	---	RPFYSNAPQEIFIQQGR
2050.9683	2049.9610	2050.0384	-0.0774	82	98	0	115	RPFYSNAPQEIFIQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99	120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99	120	0	108	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5316, 1026.4862, 1031.4928, 1031.4928, 1151.6750, 1187.5874, 1434.8538, 1517.5850, 1517.5850, 1618.0083, 1650.7631, 2034.4226, 2490.0771, 2506.2244, 3074.2690

9. gi|21314465 **Mass:** 62042 **Score:** 335 **Expect:** 2.8e-031 **Queries matched:** 7

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5197	1082.5124	1082.5581	-0.0456	37	45	0	---	LNAQRPDNR
1534.6082	1533.6009	1533.6630	-0.0621	25	36	0	80	QQPEENACQFQR
1534.6082	1533.6009	1533.6630	-0.0621	25	36	0	---	QQPEENACQFQR
2050.9683	2049.9610	2050.0384	-0.0774	82	98	0	---	RPFYSNAPQEIFIQQGR
2050.9683	2049.9610	2050.0384	-0.0774	82	98	0	115	RPFYSNAPQEIFIQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99	120	0	---	GYFGLIFPGCPSTYEEPAQQGR
2474.0500	2473.0427	2473.1371	-0.0944	99	120	0	108	GYFGLIFPGCPSTYEEPAQQGR

No match to: 982.5316, 1026.4862, 1031.4928, 1031.4928, 1151.6750, 1187.5874, 1434.8538, 1517.5850, 1517.5850, 1618.0083, 1650.7631, 2034.4226, 2490.0771, 2506.2244, 3074.2690

10. gi|3703107 **Mass:** 58543 **Score:** 215 **Expect:** 2.8e-019 **Queries matched:** 5

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1083.5197	1082.5124	1082.5581	-0.0456	14	22	0	---	LNAQRPDNR
1534.6082	1533.6009	1533.6630	-0.0621	2	13	0	80	QQPEENACQFQR
1534.6082	1533.6009	1533.6630	-0.0621	2	13	0	---	QQPEENACQFQR
2050.9683	2049.9610	2050.0384	-0.0774	59	75	0	---	RPFYSNAPQEIFIQQGR
2050.9683	2049.9610	2050.0384	-0.0774	59	75	0	115	RPFYSNAPQEIFIQQGR

No match to: 982.5316, 1026.4862, 1031.4928, 1031.4928, 1151.6750, 1187.5874, 1434.8538, 1517.5850, 1517.5850, 1618.0083, 1650.7631, 2034.4226, 2474.0500, 2474.0500, 2490.0771, 2506.2244, 3074.2690

Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 70 ppm
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages : 1
Number of Queries: 22

Protein View

Match to: **gi|118776570** Score: **376** Expect: **2.2e-035**
arachin 6 [Arachis hypogaea]

Nominal mass (M_r): **60681**; Calculated pI value: **5.40**
NCBI BLAST search of gi|118776570 against nr
Unformatted sequence string for pasting into other applications

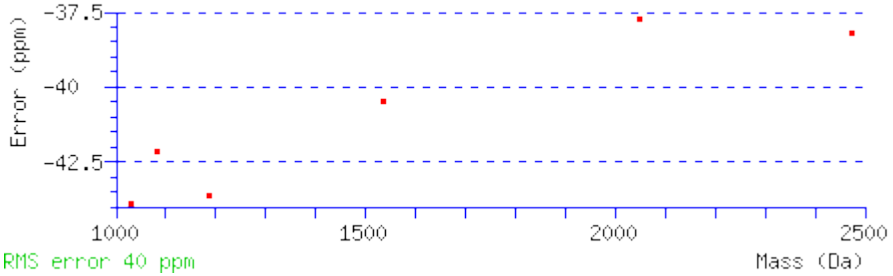
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **13%**

Matched peptides shown in **Bold Red**

```
    1 MAKLLELSFC FCFLVLGASS ISFRQQPEEN ACQFQRLNAQ RPDNRIESEG
   51 GYIETWNPNN QEFECAGVAL SRLVLRRNAL RRPFYSNAPQ EIFIQQGRGY
  101 FGLIFPGCPS TYEEPAQQGR RYQSQRPPRR LQEEDQSQQQ QDSHQKVHRF
  151 NEGDLIAVPT GVAFWLYNDH DTDVVAVSLT DTNNNDNQLD QFPRRFNLAG
  201 NHEQEFLRYQ QQSRQSRRRS LPLSPYSPQP GQEDREFSPQ GQHGRRERAG
  251 QEQENEGGNI FSGFTSEFLA QAFQVDDRQI VQNLRGENES EEQGAIVTVK
  301 GGLRILSPDR KSPDEEEEYD EDEYAEEERQ QDRRRGRGSR GSGNGIEETI
  351 CTATVKKNIG RNRSPDIYNP QAGSLKTANE LNLLILRWLG LSAEYGNLYR
  401 NALFVPHYNT NAHSIIYALR GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ
  451 NFAVAGKSQS ENFEYVAFKT DSRPSIANLA GENSFIDNLP EEVVANSYGL
  501 PREQARQLKN NNPFKFFVPP FQQSPRAVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence	
25 - 36	1534.6082	1533.6009	1533.6630	-0.0621	0	QQPEENACQFQR	(Ions score 80)
25 - 36	1534.6082	1533.6009	1533.6630	-0.0621	0	QQPEENACQFQR	(No match)
37 - 45	1083.5197	1082.5124	1082.5581	-0.0456	0	LNAQRPDNR	(No match)
82 - 98	2050.9683	2049.9610	2050.0384	-0.0774	0	RPFYSNAPQEIFIQQGR	(No match)
82 - 98	2050.9683	2049.9610	2050.0384	-0.0774	0	RPFYSNAPQEIFIQQGR	(Ions score 115)
99 - 120	2474.0500	2473.0427	2473.1371	-0.0944	0	GYFGLIFPGCPSTYEEPAQQGR	(No match)
99 - 120	2474.0500	2473.0427	2473.1371	-0.0944	0	GYFGLIFPGCPSTYEEPAQQGR	(Ions score 108)
122 - 129	1031.4928	1030.4855	1030.5308	-0.0453	0	YQSQRPPR	(Ions score 17)
122 - 129	1031.4928	1030.4855	1030.5308	-0.0453	0	YQSQRPPR	(No match)
122 - 130	1187.5874	1186.5801	1186.6319	-0.0518	1	YQSQRPPRR	(No match)



Spot 107

Top Score : 81 for gi|47933675, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	81	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	81	iso-Ara h3 [Arachis hypogaea]
3.	gi|118776570	60681	40	arachin 6 [Arachis hypogaea]
4.	gi|9864777	60754	31	Gly1 [Arachis hypogaea]
5.	gi|5712199	61430	31	glycinin [Arachis hypogaea]
6.	gi|52001219	61810	31	arachin Ahy-1 [Arachis hypogaea]
7.	gi|37789212	61803	31	storage protein [Arachis hypogaea]
8.	gi|21314465	62042	31	allergen Arah3/Arah4 [Arachis hypogaea]
9.	gi|22135348	25768	29	trypsin inhibitor [Arachis hypogaea]
10.	gi|57669861	61041	24	arachin Ahy-4 [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 81 **Expect:** 7.1e-006 **Queries matched:** 11

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
859.4529	858.4456	858.4559	-0.0103	256	262	0	QTVENLR
939.3672	938.3599	938.3617	-0.0018	300	306	0	EEFDEDR
1083.5680	1082.5607	1082.5581	0.0027	35	43	0	LNAQRPDNR
1149.6223	1148.6150	1148.6050	0.0100	120	128	1	YQSQKPSRR
1481.6250	1480.6177	1480.6000	0.0177	23	34	0	QGGEENECQFQR
1547.7661	1546.7588	1546.7389	0.0199	209	220	0	YQQQQGSRPHYR
1614.8114	1613.8041	1613.7837	0.0204	196	208	0	FYLAGNQEQEFLR
1618.7943	1617.7870	1617.7746	0.0124	342	356	0	SSNPDIYNPQAGSLR
1658.8419	1657.8346	1657.8270	0.0076	263	277	1	GENEREEQGAIVTVK
1770.9109	1769.9036	1769.8848	0.0188	195	208	1	RFYLAGNQEQEFLR
2438.2527	2437.2454	2437.2688	-0.0234	381	402	0	NAMFVPHYTLNAHTIVVALNGR

No match to: 771.4036, 855.0451, 906.4902, 916.4388, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1174.6469,

1296.6290, 1305.7103, 1349.7247, 1375.7299, 1464.6042, 1534.7006, 1541.7936, 1636.7788, 1638.8101, 1652.7897, 1730.8856, 1756.8555, 1774.8636, 2051.0437, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

2. gi|112380623 **Mass:** 58570 **Score:** 81 **Expect:** 7.4e-006 **Queries matched:** 11

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
859.4529	858.4456	858.4559	-0.0103	258	264	0	QTVENLR
939.3672	938.3599	938.3617	-0.0018	302	308	0	EEFDEDR
1083.5680	1082.5607	1082.5581	0.0027	37	45	0	LNAQRPDNR
1149.6223	1148.6150	1148.6050	0.0100	122	130	1	YQSQKPSRR
1481.6250	1480.6177	1480.6000	0.0177	25	36	0	QGGEENECQFQR
1547.7661	1546.7588	1546.7389	0.0199	211	222	0	YQQQQGSRPHYR
1614.8114	1613.8041	1613.7837	0.0204	198	210	0	FYLAGNQEQEFLR
1618.7943	1617.7870	1617.7746	0.0124	344	358	0	SSNPDIYNPQAGSLR
1658.8419	1657.8346	1657.8270	0.0076	265	279	1	GENEREEQGAIVTVK
1770.9109	1769.9036	1769.8848	0.0188	197	210	1	RFYLAGNQEQEFLR
2438.2527	2437.2454	2437.2688	-0.0234	383	404	0	NAMFVPHYTLNAHTIVVALNGR

No match to: 771.4036, 855.0451, 906.4902, 916.4388, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1174.6469, 1296.6290, 1305.7103, 1349.7247, 1375.7299, 1464.6042, 1534.7006, 1541.7936, 1636.7788, 1638.8101, 1652.7897, 1730.8856, 1756.8555, 1774.8636, 2051.0437, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

3. gi|118776570 **Mass:** 60681 **Score:** 40 **Expect:** 0.087 **Queries matched:** 7

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5680	1082.5607	1082.5581	0.0027	37	45	0	LNAQRPDNR
1349.7247	1348.7174	1348.6927	0.0247	516	526	0	FFVPPFQQSPR
1534.7006	1533.6933	1533.6630	0.0303	25	36	0	QQPEENACQFQR
1541.7936	1540.7863	1540.7673	0.0190	388	400	0	WLGLSAEYGNLYR
1636.7788	1635.7715	1635.7773	-0.0058	341	356	0	GSGNGIEETICTATVK
1730.8856	1729.8783	1729.8648	0.0136	195	208	1	RFNLAGNHEQEFLR
2051.0437	2050.0364	2050.0384	-0.0020	82	98	0	RPFYSNAPQEIFIQQGR

No match to: 771.4036, 855.0451, 859.4529, 906.4902, 916.4388, 939.3672, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1149.6223, 1174.6469, 1296.6290, 1305.7103, 1375.7299, 1464.6042, 1481.6250, 1547.7661, 1614.8114, 1618.7943, 1638.8101, 1652.7897, 1658.8419, 1756.8555, 1770.9109, 1774.8636, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2438.2527, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

4. gi|9864777 **Mass:** 60754 **Score:** 31 **Expect:** 0.71 **Queries matched:** 6

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide

1083.5680	1082.5607	1082.5581	0.0027	38 - 46	0	LNAQRPDNR
1305.7103	1304.7030	1304.6877	0.0154	516 - 526	0	FFVPPSQQSLR
1534.7006	1533.6933	1533.6630	0.0303	26 - 37	0	QQPEENACQFQR
1541.7936	1540.7863	1540.7673	0.0190	388 - 400	0	WLGLSAEYGNLYR
1730.8856	1729.8783	1729.8648	0.0136	197 - 210	1	RFNLAGNHEQEFLR
2051.0437	2050.0364	2050.0384	-0.0020	83 - 99	0	RPFYSNAPQEIFIQQGR

No match to: 771.4036, 855.0451, 859.4529, 906.4902, 916.4388, 939.3672, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1149.6223, 1174.6469, 1296.6290, 1349.7247, 1375.7299, 1464.6042, 1481.6250, 1547.7661, 1614.8114, 1618.7943, 1636.7788, 1638.8101, 1652.7897, 1658.8419, 1756.8555, 1770.9109, 1774.8636, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2438.2527, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

5. gi|5712199 **Mass:** 61430 **Score:** 31 **Expect:** 0.71 **Queries matched:** 6

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
1083.5680	1082.5607	1082.5581	0.0027	37 - 45	0	LNAQRPDNR
1349.7247	1348.7174	1348.6927	0.0247	517 - 527	0	FFVPPFQQSPR
1534.7006	1533.6933	1533.6630	0.0303	25 - 36	0	QQPEENACQFQR
1541.7936	1540.7863	1540.7673	0.0190	389 - 401	0	WLGLSAEYGNLYR
1730.8856	1729.8783	1729.8648	0.0136	195 - 208	1	RFNLAGNHEQEFLR
2051.0437	2050.0364	2050.0384	-0.0020	82 - 98	0	RPFYSNAPQEIFIQQGR

No match to: 771.4036, 855.0451, 859.4529, 906.4902, 916.4388, 939.3672, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1149.6223, 1174.6469, 1296.6290, 1305.7103, 1375.7299, 1464.6042, 1481.6250, 1547.7661, 1614.8114, 1618.7943, 1636.7788, 1638.8101, 1652.7897, 1658.8419, 1756.8555, 1770.9109, 1774.8636, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2438.2527, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

6. gi|52001219 **Mass:** 61810 **Score:** 31 **Expect:** 0.73 **Queries matched:** 6

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start - End	Miss	Peptide
1083.5680	1082.5607	1082.5581	0.0027	37 - 45	0	LNAQRPDNR
1296.6290	1295.6217	1295.6218	-0.0000	430 - 441	0	AHVQVVDSNGDR
1534.7006	1533.6933	1533.6630	0.0303	25 - 36	0	QQPEENACQFQR
1541.7936	1540.7863	1540.7673	0.0190	395 - 407	0	WLGLSAEYGNLYR
1730.8856	1729.8783	1729.8648	0.0136	195 - 208	1	RFNLAGNHEQEFLR
2051.0437	2050.0364	2050.0384	-0.0020	82 - 98	0	RPFYSNAPQEIFIQQGR

No match to: 771.4036, 855.0451, 859.4529, 906.4902, 916.4388, 939.3672, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1149.6223, 1174.6469, 1305.7103, 1349.7247, 1375.7299, 1464.6042, 1481.6250, 1547.7661, 1614.8114, 1618.7943, 1636.7788, 1638.8101, 1652.7897, 1658.8419, 1756.8555, 1770.9109, 1774.8636, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2438.2527, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

7. gi|37789212 **Mass:** 61803 **Score:** 31 **Expect:** 0.73 **Queries matched:** 6

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5680	1082.5607	1082.5581	0.0027	37	45	0	LNAQRPDNR
1296.6290	1295.6217	1295.6218	-0.0000	430	441	0	AHVQVVDSNGDR
1534.7006	1533.6933	1533.6630	0.0303	25	36	0	QQPEENACQFQR
1541.7936	1540.7863	1540.7673	0.0190	395	407	0	WLGLSAEYGNLYR
1730.8856	1729.8783	1729.8648	0.0136	195	208	1	RFNLAGNHEQEFLR
2051.0437	2050.0364	2050.0384	-0.0020	82	98	0	RPFYSNAPQEIFIQQGR

No match to: 771.4036, 855.0451, 859.4529, 906.4902, 916.4388, 939.3672, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1149.6223, 1174.6469, 1305.7103, 1349.7247, 1375.7299, 1464.6042, 1481.6250, 1547.7661, 1614.8114, 1618.7943, 1636.7788, 1638.8101, 1652.7897, 1658.8419, 1756.8555, 1770.9109, 1774.8636, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2438.2527, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

8. gi|21314465 **Mass:** 62042 **Score:** 31 **Expect:** 0.74 **Queries matched:** 6

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5680	1082.5607	1082.5581	0.0027	37	45	0	LNAQRPDNR
1296.6290	1295.6217	1295.6218	-0.0000	432	443	0	AHVQVVDSNGDR
1534.7006	1533.6933	1533.6630	0.0303	25	36	0	QQPEENACQFQR
1541.7936	1540.7863	1540.7673	0.0190	397	409	0	WLGLSAEYGNLYR
1730.8856	1729.8783	1729.8648	0.0136	195	208	1	RFNLAGNHEQEFLR
2051.0437	2050.0364	2050.0384	-0.0020	82	98	0	RPFYSNAPQEIFIQQGR

No match to: 771.4036, 855.0451, 859.4529, 906.4902, 916.4388, 939.3672, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1149.6223, 1174.6469, 1305.7103, 1349.7247, 1375.7299, 1464.6042, 1481.6250, 1547.7661, 1614.8114, 1618.7943, 1636.7788, 1638.8101, 1652.7897, 1658.8419, 1756.8555, 1770.9109, 1774.8636, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2438.2527, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

9. gi|22135348 **Mass:** 25768 **Score:** 29 **Expect:** 1 **Queries matched:** 4

trypsin inhibitor [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5680	1082.5607	1082.5581	0.0027	39	47	0	LNAQRPDNR
1534.7006	1533.6933	1533.6630	0.0303	27	38	0	QQPEENACQFQR
1730.8856	1729.8783	1729.8648	0.0136	197	210	1	RFNLAGNHEQEFLR
2051.0437	2050.0364	2050.0384	-0.0020	84	100	0	RPFYSNAPQEIFIQQGR

No match to: 771.4036, 855.0451, 859.4529, 906.4902, 916.4388, 939.3672, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1149.6223, 1174.6469, 1296.6290, 1305.7103, 1349.7247, 1375.7299, 1464.6042, 1481.6250, 1541.7936, 1547.7661, 1614.8114, 1618.7943, 1636.7788, 1638.8101, 1652.7897, 1658.8419, 1756.8555, 1770.9109, 1774.8636, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2438.2527, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

10. gi|57669861 **Mass:** 61041 **Score:** 24 **Expect:** 3.9 **Queries matched:** 5

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1083.5680	1082.5607	1082.5581	0.0027	37	-	45	0	LNAQRPDNR
1534.7006	1533.6933	1533.6630	0.0303	25	-	36	0	QQPEENACQFQR
1541.7936	1540.7863	1540.7673	0.0190	389	-	401	0	WLGLSAEYGNLYR
1730.8856	1729.8783	1729.8648	0.0136	195	-	208	1	RFNLAGNHEQEFLR
2051.0437	2050.0364	2050.0384	-0.0020	82	-	98	0	RPFYSNAPQEIFIQQGR

No match to: 771.4036, 855.0451, 859.4529, 906.4902, 916.4388, 939.3672, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1149.6223, 1174.6469, 1296.6290, 1305.7103, 1349.7247, 1375.7299, 1464.6042, 1481.6250, 1547.7661, 1614.8114, 1618.7943, 1636.7788, 1638.8101, 1652.7897, 1658.8419, 1756.8555, 1770.9109, 1774.8636, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2438.2527, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Match to: **gi|47933675** Score: **81** Expect: **7.1e-006**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **11**
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

```
   1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
  51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
 101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
 151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
 201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
 251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
 301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
 351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
 401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
 451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
 501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6250	1480.6177	1480.6000	0.0177	0	QGGEENECQFQR
35 - 43	1083.5680	1082.5607	1082.5581	0.0027	0	LNAQRPDNR
120 - 128	1149.6223	1148.6150	1148.6050	0.0100	1	YQSQKPSRR
195 - 208	1770.9109	1769.9036	1769.8848	0.0188	1	RFYLAGNQEQEFLR
196 - 208	1614.8114	1613.8041	1613.7837	0.0204	0	FYLAGNQEQEFLR
209 - 220	1547.7661	1546.7588	1546.7389	0.0199	0	YQQQQGSRPHYR
256 - 262	859.4529	858.4456	858.4559	-0.0103	0	QTVENLR
263 - 277	1658.8419	1657.8346	1657.8270	0.0076	1	GENEREEQGAIVTVK
300 - 306	939.3672	938.3599	938.3617	-0.0018	0	EEFDEDR
342 - 356	1618.7943	1617.7870	1617.7746	0.0124	0	SSNPDIYNPQAGSLR
381 - 402	2438.2527	2437.2454	2437.2688	-0.0234	0	NAMFVPHYTLNAHTIVVALNGR

No match to: 771.4036, 855.0451, 906.4902, 916.4388, 1046.6019, 1073.6079, 1080.5299, 1111.5608, 1174.6469, 1296.6290, 1305.7103, 1349.7247, 1375.7299, 1464.6042, 1534.7006, 1541.7936, 1636.7788, 1638.8101, 1652.7897, 1730.8856, 1756.8555, 1774.8636, 2051.0437, 2146.6196, 2185.0371, 2192.9963, 2208.0330, 2256.7148, 2273.1594, 2295.1326, 2307.0955, 2311.1245, 2612.1404, 3069.2764, 3136.3320, 3153.3386, 3211.3855, 3227.3894, 3300.6055

Spot 108

Top Score : 82 for gi|47933675, glycinin [Arachis hypogaea]

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 42 are significant (p<0.05).

Index

	Accession	Mass	Score	Description
1.	gi|47933675	58368	82	glycinin [Arachis hypogaea]
2.	gi|112380623	58570	82	iso-Ara h3 [Arachis hypogaea]
3.	gi|118776570	60681	32	arachin 6 [Arachis hypogaea]
4.	gi|37221903	19440	26	resistance protein [Arachis stenosperma]
5.	gi|52001219	61810	16	arachin Ahy-1 [Arachis hypogaea]
6.	gi|37789212	61803	16	storage protein [Arachis hypogaea]
7.	gi|9864777	60754	16	Gly1 [Arachis hypogaea]
8.	gi|5712199	61430	16	glycinin [Arachis hypogaea]
9.	gi|21314465	62042	16	allergen Arah3/Arah4 [Arachis hypogaea]
10.	gi|57669861	61041	16	arachin Ahy-4 [Arachis hypogaea]

Results List

1. gi|47933675 **Mass:** 58368 **Score:** 82 **Expect:** 5.4e-006 **Queries matched:** 11

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
939.3727	938.3654	938.3617	0.0037	300	306	0	EEFDEDR
1083.5603	1082.5530	1082.5581	-0.0050	35	43	0	LNAQRPDNR
1462.6815	1461.6742	1461.6775	-0.0033	438	449	0	AQSENYEYLAFK
1481.6262	1480.6189	1480.6000	0.0189	23	34	0	QGGEENECQFQR
1507.7275	1506.7202	1506.7078	0.0125	496	507	0	FFVPPFDHQSMR
1547.7620	1546.7547	1546.7389	0.0158	209	220	0	YQQQQGSRPHYR
1614.8080	1613.8007	1613.7837	0.0170	196	208	0	FYLAGNQEQEFLR
1618.7930	1617.7857	1617.7746	0.0111	342	356	0	SSNPDIYNPQAGSLR
1658.8438	1657.8365	1657.8270	0.0095	263	277	1	GENEREEQGAIVTVK
1770.8956	1769.8883	1769.8848	0.0035	195	208	1	RFYLAGNQEQEFLR
2438.2446	2437.2373	2437.2688	-0.0315	381	402	0	NAMFVPHYTLNAHTIVVALNGR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 1080.5332, 1111.5609, 1174.6504, 1289.6808, 1296.6310, 1305.7078, 1349.7169, 1365.7046, 1375.7458, 1376.7343, 1464.6086, 1541.7844, 1636.7700, 1652.7709, 1756.8481, 1774.8533, 2051.0208, 2146.5798, 2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535, 3211.3992

2. gi|112380623 **Mass:** 58570 **Score:** 82 **Expect:** 5.6e-006 **Queries matched:** 11

iso-Ara h3 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
939.3727	938.3654	938.3617	0.0037	302	-	308	0	EEFDEDR
1083.5603	1082.5530	1082.5581	-0.0050	37	-	45	0	LNAQRPDNR
1462.6815	1461.6742	1461.6775	-0.0033	440	-	451	0	AQSENYEYLAFK
1481.6262	1480.6189	1480.6000	0.0189	25	-	36	0	QGGEENECQFQR
1507.7275	1506.7202	1506.7078	0.0125	498	-	509	0	FFVPPFDHQSMR
1547.7620	1546.7547	1546.7389	0.0158	211	-	222	0	YQQQQGSRPHYR
1614.8080	1613.8007	1613.7837	0.0170	198	-	210	0	FYLAGNQEQEFLR
1618.7930	1617.7857	1617.7746	0.0111	344	-	358	0	SSNPDIYNPQAGSLR
1658.8438	1657.8365	1657.8270	0.0095	265	-	279	1	GENEREEQGAIVTVK
1770.8956	1769.8883	1769.8848	0.0035	197	-	210	1	RFYLAGNQEQEFLR
2438.2446	2437.2373	2437.2688	-0.0315	383	-	404	0	NAMFVPHYTLNAHTIVVALNGR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 1080.5332, 1111.5609, 1174.6504, 1289.6808, 1296.6310, 1305.7078, 1349.7169, 1365.7046, 1375.7458, 1376.7343, 1464.6086, 1541.7844, 1636.7700, 1652.7709, 1756.8481, 1774.8533, 2051.0208, 2146.5798, 2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535, 3211.3992

3. gi|118776570 **Mass:** 60681 **Score:** 32 **Expect:** 0.54 **Queries matched:** 6

arachin 6 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide
1083.5603	1082.5530	1082.5581	-0.0050	37	-	45	0	LNAQRPDNR
1349.7169	1348.7096	1348.6927	0.0169	516	-	526	0	FFVPPFQQSPR
1541.7844	1540.7771	1540.7673	0.0098	388	-	400	0	WLGLSAEYGNLYR
1636.7700	1635.7627	1635.7773	-0.0146	341	-	356	0	GSGNGIEETICTATVK
1770.8956	1769.8883	1769.8584	0.0299	220	-	235	0	SLPLSPYSPQPGQEDR
2051.0208	2050.0135	2050.0384	-0.0249	82	-	98	0	RPFYSNAPQEIFIQQGR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 939.3727, 1080.5332, 1111.5609, 1174.6504, 1289.6808, 1296.6310, 1305.7078, 1365.7046, 1375.7458, 1376.7343, 1462.6815, 1464.6086, 1481.6262, 1507.7275, 1547.7620, 1614.8080, 1618.7930, 1652.7709, 1658.8438, 1756.8481, 1774.8533, 2146.5798, 2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2438.2446, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535, 3211.3992

4. gi|37221903 **Mass:** 19440 **Score:** 26 **Expect:** 2.3 **Queries matched:** 4

resistance protein [Arachis stenosperma]

Observed	Mr(expt)	Mr(calc)	Delta	Start		End	Miss	Peptide

1349.7169	1348.7096	1348.6908	0.0189	53 - 64	1	SVEEGISMIKEK
1365.7046	1364.6973	1364.6857	0.0117	53 - 64	1	SVEEGISMIKEK + Oxidation (M)
1462.6815	1461.6742	1461.6533	0.0210	13 - 23	0	FECACFLFNVR
3211.3992	3210.3919	3210.4062	-0.0143	80 - 105	1	IEQLKALAGECDWFTGECDWFSYETR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 939.3727, 1080.5332, 1083.5603, 1111.5609, 1174.6504, 1289.6808, 1296.6310, 1305.7078, 1375.7458, 1376.7343, 1464.6086, 1481.6262, 1507.7275, 1541.7844, 1547.7620, 1614.8080, 1618.7930, 1636.7700, 1652.7709, 1658.8438, 1756.8481, 1770.8956, 1774.8533, 2051.0208, 2146.5798, 2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2438.2446, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535

5. gi|52001219 **Mass:** 61810 **Score:** 16 **Expect:** 21 **Queries matched:** 4

arachin Ahy-1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5603	1082.5530	1082.5581	-0.0050	37 -	45	0	LNAQRPDNR
1296.6310	1295.6237	1295.6218	0.0020	430 -	441	0	AHVQVVDSNGDR
1541.7844	1540.7771	1540.7673	0.0098	395 -	407	0	WLGLSAEYGNLYR
2051.0208	2050.0135	2050.0384	-0.0249	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 939.3727, 1080.5332, 1111.5609, 1174.6504, 1289.6808, 1305.7078, 1349.7169, 1365.7046, 1375.7458, 1376.7343, 1462.6815, 1464.6086, 1481.6262, 1507.7275, 1547.7620, 1614.8080, 1618.7930, 1636.7700, 1652.7709, 1658.8438, 1756.8481, 1770.8956, 1774.8533, 2146.5798, 2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2438.2446, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535, 3211.3992

6. gi|37789212 **Mass:** 61803 **Score:** 16 **Expect:** 21 **Queries matched:** 4

storage protein [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5603	1082.5530	1082.5581	-0.0050	37 -	45	0	LNAQRPDNR
1296.6310	1295.6237	1295.6218	0.0020	430 -	441	0	AHVQVVDSNGDR
1541.7844	1540.7771	1540.7673	0.0098	395 -	407	0	WLGLSAEYGNLYR
2051.0208	2050.0135	2050.0384	-0.0249	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 939.3727, 1080.5332, 1111.5609, 1174.6504, 1289.6808, 1305.7078, 1349.7169, 1365.7046, 1375.7458, 1376.7343, 1462.6815, 1464.6086, 1481.6262, 1507.7275, 1547.7620, 1614.8080, 1618.7930, 1636.7700, 1652.7709, 1658.8438, 1756.8481, 1770.8956, 1774.8533, 2146.5798, 2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2438.2446, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535, 3211.3992

7. gi|9864777 **Mass:** 60754 **Score:** 16 **Expect:** 21 **Queries matched:** 4

Gly1 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5603	1082.5530	1082.5581	-0.0050	38 -	46	0	LNAQRPDNR
1305.7078	1304.7005	1304.6877	0.0129	516 -	526	0	FFVPPSQQSLR
1541.7844	1540.7771	1540.7673	0.0098	388 -	400	0	WLGLSAEYGNLYR

2051.0208	2050.0135	2050.0384	-0.0249	83 - 99	0	RPFYSNAPQEIFIQQGR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 939.3727, 1080.5332, 1111.5609, 1174.6504, 1289.6808, 1296.6310, 1349.7169, 1365.7046, 1375.7458, 1376.7343, 1462.6815, 1464.6086, 1481.6262, 1507.7275, 1547.7620, 1614.8080, 1618.7930, 1636.7700, 1652.7709, 1658.8438, 1756.8481, 1770.8956, 1774.8533, 2146.5798, 2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2438.2446, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535, 3211.3992

8. gi|5712199 **Mass:** 61430 **Score:** 16 **Expect:** 21 **Queries matched:** 4

glycinin [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5603	1082.5530	1082.5581	-0.0050	37 -	45	0	LNAQRPDNR
1349.7169	1348.7096	1348.6927	0.0169	517 -	527	0	FFVPPFQQSPR
1541.7844	1540.7771	1540.7673	0.0098	389 -	401	0	WLGLSAEYGNLYR
2051.0208	2050.0135	2050.0384	-0.0249	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 939.3727, 1080.5332, 1111.5609, 1174.6504, 1289.6808, 1296.6310, 1305.7078, 1365.7046, 1375.7458, 1376.7343, 1462.6815, 1464.6086, 1481.6262, 1507.7275, 1547.7620, 1614.8080, 1618.7930, 1636.7700, 1652.7709, 1658.8438, 1756.8481, 1770.8956, 1774.8533, 2146.5798, 2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2438.2446, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535, 3211.3992

9. gi|21314465 **Mass:** 62042 **Score:** 16 **Expect:** 21 **Queries matched:** 4

allergen Arah3/Arah4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5603	1082.5530	1082.5581	-0.0050	37 -	45	0	LNAQRPDNR
1296.6310	1295.6237	1295.6218	0.0020	432 -	443	0	AHVQVVDSNGDR
1541.7844	1540.7771	1540.7673	0.0098	397 -	409	0	WLGLSAEYGNLYR
2051.0208	2050.0135	2050.0384	-0.0249	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 939.3727, 1080.5332, 1111.5609, 1174.6504, 1289.6808, 1305.7078, 1349.7169, 1365.7046, 1375.7458, 1376.7343, 1462.6815, 1464.6086, 1481.6262, 1507.7275, 1547.7620, 1614.8080, 1618.7930, 1636.7700, 1652.7709, 1658.8438, 1756.8481, 1770.8956, 1774.8533, 2146.5798, 2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2438.2446, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535, 3211.3992

10. gi|57669861 **Mass:** 61041 **Score:** 16 **Expect:** 21 **Queries matched:** 4

arachin Ahy-4 [Arachis hypogaea]

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1083.5603	1082.5530	1082.5581	-0.0050	37 -	45	0	LNAQRPDNR
1289.6808	1288.6735	1288.6564	0.0172	518 -	528	0	FFVPPSQQSPR
1541.7844	1540.7771	1540.7673	0.0098	389 -	401	0	WLGLSAEYGNLYR
2051.0208	2050.0135	2050.0384	-0.0249	82 -	98	0	RPFYSNAPQEIFIQQGR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 939.3727, 1080.5332, 1111.5609, 1174.6504, 1296.6310, 1305.7078, 1349.7169, 1365.7046, 1375.7458, 1376.7343, 1462.6815, 1464.6086, 1481.6262, 1507.7275, 1547.7620, 1614.8080, 1618.7930, 1636.7700, 1652.7709, 1658.8438, 1756.8481, 1770.8956, 1774.8533, 2146.5798,

2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2438.2446, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535, 3211.3992

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 20 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Protein View

Match to: **gi|47933675** Score: **82** Expect: **5.4e-006**
glycinin [Arachis hypogaea]

Nominal mass (M_r): **58368**; Calculated pI value: **5.41**
NCBI BLAST search of gi|47933675 against nr
Unformatted sequence string for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **11**
Sequence Coverage: **25%**

Matched peptides shown in **Bold Red**

```
   1 KLLALSLCFC VLVLGASSVT FRQGGEENEC QFQRLNAQRP DNRIESEGGY
  51 IETWNPNNQE FQCAGVALSR TVLRRNALRR PFYSNAPLEI YVQQGSGYFG
 101 LIFPGCPSTY EEPAQEGRRY QSQKPSRRFQ VGQDDPSQQQ QDSHQKVHRF
 151 DEGDLIAVPT GVAFWMYNDE DTDVVTVTLS DTSSIHNQLD QFPRRFYLAG
 201 NQEQEFLRYQ QQQGSRPHYR QISPRVRGDE QENEGSNIFS GFAQEFLQHA
 251 FQVDRQTVEN LRGENEREEQ GAIVTVKGGL RILSPDEEDE SSRSPPSRRE
 301 EFDEDRSRPQ QRGKYDENRR GYKNGIEETI CSASVKKNLG RSSNPDIYNP
 351 QAGSLRSVNE LDLPILGWLG LSAQHGTIYR NAMFVPHYTL NAHTIVVALN
 401 GRAHVQVVDS NGNRVYDEEL QEGHVLVVPQ NFAVAAKAQS ENYEYLAFKT
 451 DSRPSIANLA GENSIIDNLP EEVVANSYRL PREQARQLKN NNPFKFFVPP
 501 FDHQSMREVA
```

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
23 - 34	1481.6262	1480.6189	1480.6000	0.0189	0	QGGEENECQFQR
35 - 43	1083.5603	1082.5530	1082.5581	-0.0050	0	LNAQRPDNR
195 - 208	1770.8956	1769.8883	1769.8848	0.0035	1	RFYLAGNQEQEFLR
196 - 208	1614.8080	1613.8007	1613.7837	0.0170	0	FYLAGNQEQEFLR
209 - 220	1547.7620	1546.7547	1546.7389	0.0158	0	YQQQQGSRPHYR
263 - 277	1658.8438	1657.8365	1657.8270	0.0095	1	GENEREEQGAIVTVK
300 - 306	939.3727	938.3654	938.3617	0.0037	0	EEFDEDR
342 - 356	1618.7930	1617.7857	1617.7746	0.0111	0	SSNPDIYNPQAGSLR
381 - 402	2438.2446	2437.2373	2437.2688	-0.0315	0	NAMFVPHYTLNAHTIVVALNGR
438 - 449	1462.6815	1461.6742	1461.6775	-0.0033	0	AQSENYEYLAFK
496 - 507	1507.7275	1506.7202	1506.7078	0.0125	0	FFVPPFDHQSMR

No match to: 771.3975, 855.0331, 859.4409, 861.0486, 906.4902, 1080.5332, 1111.5609, 1174.6504, 1289.6808, 1296.6310, 1305.7078, 1349.7169, 1365.7046, 1375.7458, 1376.7343, 1464.6086, 1541.7844, 1636.7700, 1652.7709, 1756.8481, 1774.8533, 2051.0208, 2146.5798, 2185.0313, 2192.9951, 2227.1523, 2256.6870, 2273.1597, 2295.1406, 2311.1130, 2315.1895, 2335.0801, 2379.0735, 2612.1450, 2926.2581, 3069.2505, 3137.2969, 3153.3535, 3211.3992