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Shotgun proteomics of *Brassica rapa* seed proteins identifies vicilin as a major seed storage protein in the mature seed

Mahmudur Rahman[1], **Qi Guo**[1], **Abdul Baten**[1,2], **Ramil Mauleon**[1], **Amina Khatun**[1], **Lei Liu**[1], **Bronwyn J. Barkla**[1]*

1 Southern Cross Plant Science, Faculty of Science and Engineering, Southern Cross University, Lismore, New South Wales, Australia, **2** Institute of Precision Medicine & Bioinformatics, Sydney Local Health District, Royal Prince Alfred Hospital, Camperdown, New South Wales, Australia

* bronwyn.barkla@scu.edu.au

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Abstract

Proteins make up a large percentage of the Brassica seed and are second only to the oil in economic importance with uses for both animal and human nutrition. The most abundant proteins reported in the seeds of Brassica are the seed storage proteins cruciferin and napin, belonging to the 12S globulin and 2S albumin families of proteins, respectively. To gain insight into the *Brassica rapa* seed proteome and to confirm the presence and relative quantity of proteins encoded by candidate seed storage genes in the mature seed, shotgun proteomics was carried out on protein extracts from seeds of *B. rapa* inbred line R-o-18. Following liquid chromatography tandem mass spectrometry, a total of 34016 spectra were mapped to 323 proteins, where 233 proteins were identified in 3 out of 4 biological replicates by at least 2 unique peptides. 2S albumin like napin seed storage proteins (SSPs), 11/12S globulin like cruciferin SSPs and 7S globulin like vicilin SSPs were identified in the samples, along with other notable proteins including oil body proteins, namely ten oleosins and two oil body-associated proteins. The identification of vicilin like proteins in the mature *B. rapa* seed represents the first account of these proteins in the Brassicaceae and analysis indicates high conservation of sequence motifs to other 7S vicilin-like allergenic proteins as well as conservation of major allergenic epitopes in the proteins. This study enriches our existing knowledge on rapeseed seed proteins and provides a robust foundation and rational basis for plant bioengineering of seed storage proteins.

Introduction

It is estimated that up to a billion people worldwide, from both developing and developed nations, do not have an adequate intake of protein in their diet which leads to impaired growth and increased risk of disease [1, 2]. To overcome this deficiency there is a push to identify sustainable supplies of both animal and plant protein for human consumption in order to lower greenhouse gas emissions and improve the protein supply chain in agriculture.

Competing interests: The authors have declared that no competing interests exist.

Abbreviations: 1-D-SDS-PAGE, One-Dimensional Sodium Dodecyl Sulfate -Polyacrylamide Gel Electrophoresis; 1H NMR, Proton Nuclear Magnetic Resonance; 3D-structure, Three Dimensional Structure; BLAST, Basic Local Alignment Search Tool; BP, Biological Process; CC, Cellular Component; cDNA, Complementary Deoxyribonucleic Acid; COV, Sequence Coverage; CRISPR/Cas9, Clustered Regularly Interspaced Short Palindromic Repeats-Associated Protein-9 Nuclease; DNA, Deoxyribonucleic Acid; ESI, Electron Spray Ionization; EST, Expressed Sequence Tag; FASTA, Fast Adaptive Shrinkage Threshold Algorithm; FDR, False Discovery Rate; g, Relative Centrifugal Force, Gravity; GM, Genetically Modified; GMQE, Global Model Quality Estimation; GO, Gene Ontology; HPLC, High Performance Liquid Chromatography; IDA, Information Dependent Acquisition; IgE, Immunoglobulin E; kDa, Kilo Dalton; LC-MS/MS, Liquid Chromatography Coupled to Tandem Mass Spectrometry; MF, Molecular Function; min, Minute; mL, Mili Litre; mm, Milli Metre; MS, Mass Spectrometry, Mass Spectrometer; MSA, Multiple Sequence Alignment; NCBI, National Center for Biotechnology Infromation; PID, Percent Sequence Identity, Pairwise Identity; QMEAN, Qualitative Model Energy Analysis; RNA, Ribonucleic Acid; SDS-PAGE, Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis; SSP, SSPs, Seed Storage Protein, Seed Storage Proteins; TCA, Trichloroacetic Acid; TOF, Time-of-Flight; wiff, File Extension of Applied Biosystems Raw Data Files; μg, Micro Gram; μL, Micro Litre.

Rapeseed is the second-most abundantly cultivated oilseed crop globally [3–5]. After extraction of oil, about 1.2 million tons of defatted rapeseed meal is produced globally on an annual basis. This meal contains about 35–45% protein (dry weight) bringing it close to soybean for protein value [6–8]. This protein rich by-product has a nutritional content comparable to milk casein [9], egg protein [10] and animal proteins [7], with a balanced amino acid profile high in methionine and cysteine [10], providing important sulphur containing amino acids. However, the meal is primarily used to boost the nutritional value of animal or aquaculture feed or as a soil supplementation product [11, 12], rather than as a source of proteins for human consumption. This is primarily due to the presence of proteins that may cause allergenic responses as they pass through the human digestive system [13–15].

B. rapa is the highest oil-bearing species and therefore one of the economically most important species in the tribe Brassiceae belonging to the crucifer family [16]. In contrast to allopolyploid *B. napus* (AC genome), *B. juncea* (AB genome) and *B. carinata* (BC genome), *B. rapa* is a diploid species and contains only the Brassica A genome [17, 18]. In addition to oilseed crops (subsp. *Trilocularis* and *oleifera*), *B. rapa* encompasses edible leafy vegetables like bok choy or pak choi (subsp. *chinensis*), bomdong (var. *glabra*), Chinese cabbage (subsp. *pekinensis*), choy sum (subsp. *parachinensis*), komatsuna (subsp. *perviridis*), napa cabbage (subsp. *pekinensis*), rapini or broccoli rabe (var. *ruvo*) and tatosi, spoon mustard or tat choy (subsp. *narinosa*); root and tuber crops like Japanese vegetable turnip (subsp. *rapa*) [19–22]. Although some seed storage proteins have been partially characterised and allergenicity studies have been carried out on a few proteins from *B. napus* and *S. alba*, seed storage proteins and their potential allergenicity have not been well explored for *B. rapa* [23–31].

The Brassica seed storage proteins napin and cruciferin, two of the most abundant proteins in the seed, have been identified as the most likely candidates for triggering allergies, with key epitopes identified in their sequences [15, 32–35], however evidence shows other seed proteins present in other species outside the Brassica family, namely 7S globulin type vicilins, and oil-body proteins like oleosins and non-specific lipid transfer proteins may also elicit an allergenic response [36, 37].

More information is needed on the protein sequence, structure and biochemistry of *Brassica rapa* allergens. This would allow for biotechnological approaches which could manipulate the quantities of these proteins in the seed and lower the amount of allergenic proteins while not compromising the total amount of protein. This approach has recently been carried out using CRISPR/Cas9 (clustered regularly interspaced short palindromic repeat-associated protein-9 nuclease) gene editing technology in the Brassica, *Camelina sativa* whereby deletions were generated in three of the 12 genes encoding cruciferin to successfully improve seed protein composition [38].

Recent sequencing of the genomes of *Brassica rapa* inbred lines Chifu-401 v3 [39] and R-o-18 v2.2 [40], two of the most widely cultivated genotypes of rapeseed and Canola, has provided important information on the gene families for the seed storage proteins and their similarity to known allergenic proteins [12]. In this study a proteomics approach using LC-MS/MS was carried out on single seeds of *B. rapa* R-o-18 to validate the presence of predicted seed storage protein-coding genes, and to catalogue the proteins in the seed which will further understanding of their functions and identify regulatory proteins that may be targeted to alter the amount of proteins of interest including those involved in oil accumulation, disease and pest sensitivity/resistance and those considered allergenic. Using this approach, we were able to identify the presence of the seed storage protein vicilin for the first time within the Brassica family.

Materials and methods

Seed materials

Non-genetically modified seeds of *Brassica rapa* inbred line R-o-18, were collected from the Southern Cross Plant Science seed repository. In this study, four pooled populations, each consisting of seeds from 4 different plants were used.

Extraction of protein from seeds

Protein was extracted from seeds according to the method described in [41] with some modifications. In summary, seeds were placed in 2.0 mL PCR grade Safe Lock microcentrifuge tubes (Eppendorf AG, Germany, Lot: D15893R) with a single 5 mm stainless steel bead (Qiagen GmbH, D-40724, Hilden, Cat. No. 69989). Methanol (200 μL of 100%) was added as solvent and seeds were macerated using a ball grinder/homogeniser (TissueLyser Qiagen, Retsch GmbH, Germany) by shaking in a precooled adapter for 20 cycles per second for two min with a one min rest interval. Extracts were then centrifuged at 4˚C in a Sigma 4K15 Laboratory centrifuge (Sigma Laboratory Centrifuge 4K15, Germany), at 10,000g for 20 min, followed by drying in a speed vacuum dryer (Eppendorf concentrator plus 5301 Eppendorf, USA) at 30˚C under vacuum.

TCA precipitation

Trichloroacetic acid (TCA) precipitation of the dried samples was carried out according to the protocol of Barkla et al. [42] with minor modification. In summary, 500 μl MilliQ water (Advantage A 10, Millipore, USA) was added to the dried samples and vortexed lightly. This was followed by addition of 100 μl of 10X TE (standard Tris-EDTA buffer) [43] and 100 μl of 0.3% NaDoC (Sodium deoxycholate). Finally, 100 μl of 72% TCA was added, and the samples were vortexed and incubated on ice for one hour. The samples were then centrifuged at 4˚C for 20 min at 11000*g*. The supernatant was carefully aspirated, and the pellet was resuspended in 500 μl of 90% methanol. The sample was incubated in a -20˚C freezer overnight. The samples were then centrifuged at 4˚C for 20 min at 11000*g* and the supernatant aspirated. The pellets were air dried and then stored at -80˚C.

NanoHPLC, mass spectrometry and protein identification

Mass spectroscopic analysis was carried out on the protein samples at the Institute for Molecular Biosciences proteomics facility at the University of Queensland, Brisbane. The extracts were analysed by Shimadzu Prominence NanoHPLC- MS/MS on an Eksigent, Ekspert nano LC400 uHPLC (SCIEX, Canada) coupled to a Triple Time of Flight (TOF) 6600 mass spectrometer (SCIEX, Canada) equipped with a PicoView nanoflow (New Objective, USA) ion source. Five μL of each trypsin digested extract was injected onto a 75μm x 150mm ChromXP C18 CL 3 μm column (SCIEX, Canada) at 400 nL/min and a column temperature of 45˚C. Mobile phase contained two solvents, solvent A and solvent B. Solvent A consisted of 0.1% formic acid in water and solvent B contained 0.1% formic acid in acetonitrile. Linear gradients of 5–30% solvent B were run over 120 min at 400 nL/minute flow rate, followed by a steeper gradient of 30% to 90% solvent B for 3 min, then 90% solvent B for 17 min, for peptide elution. The gradient was then returned to 5% solvent B for equilibration prior to the next sample injection. The ion spray voltage was set to 2600V, declustering potential (DP) 80V, curtain gas flow 25 psi, nebuliser gas 1 (GS1) 30 psi, interface heater at 150˚C. The mass spectrometer acquired 100ms full scan TOF-MS data followed by up to fifty 50ms full scan product ion data in an Information Dependent Acquisition (IDA) mode. Full scan TOF-MS data was acquired

over the mass range 350–1500 *m/z* and for product ion MS/MS, 100–1500 *m/z*. Ions observed in the TOF-MS scan exceeding a threshold of 100 counts and a charge state of +2 to +5 were set to trigger the acquisition of product ion MS/MS spectra of the resultant 50 most intense ions followed by data acquisition. Raw spectral data was submitted to the Southern Cross University research portal (https://researchportal.scu.edu.au/) and is available under 10.25918/data.133.

Analysis of proteomic data

Spectral data from the mass spectrometer was acquired and processed using Analyst TF 1.7 software (SCIEX, Canada). A combined database was generated from the *B. rapa* R-o-18 v2.2 database annotated in house at Southern Cross Plant Science, Southern Cross University [43, 245 proteins) [40], merged with previously reported sequences publicly available in the Uniprot and NCBI protein databases including (a) 1.7/2S albumin or napin (b) 11/12S globulin or cruciferin (c) 7S globulin or vicilin (d) oleosin, and (e) putative napin sequences characterised in *B. rapa* [15], (S1 and S2 Tables in S1 File) (f) putative napin, cruciferin and vicilin sequences characterised in *B. rapa* determined by performing BLASTP analysis with the corresponding cruciferin and vicilin sequences from *A. thaliana* [15]. ProteinPilot 5.0.2 (SCIEX, Canada) was used to search spectra against the combined database, visualize fragmentation evidence of identified peptides, process qualitative and quantitative proteomics data and encode the output mzIdentML file (Fig 1) [44]. To interpret, organize, validate and visualize the information, Scaffold 4.8.7 (Proteome Science) was used [45, 46].

Gene ontology enrichment analysis

Proteins identified in at least 3 out of 4 biological replicates with at least 2 unique peptides were selected for downstream analysis. Sequences of identified proteins were compared against the UniprotKB *Arabidopsis thaliana* database using the Basic Local Alignment Search Tool (BLASTP). Uniprot IDs of matched Arabidopsis homologs were then submitted to DAVID v6.8 (Functional Annotation Bioinformatics Microarray Analysis database https://david.ncifcrf.gov/, 20.04.2020) [47] for functional annotation of identified proteins and Gene

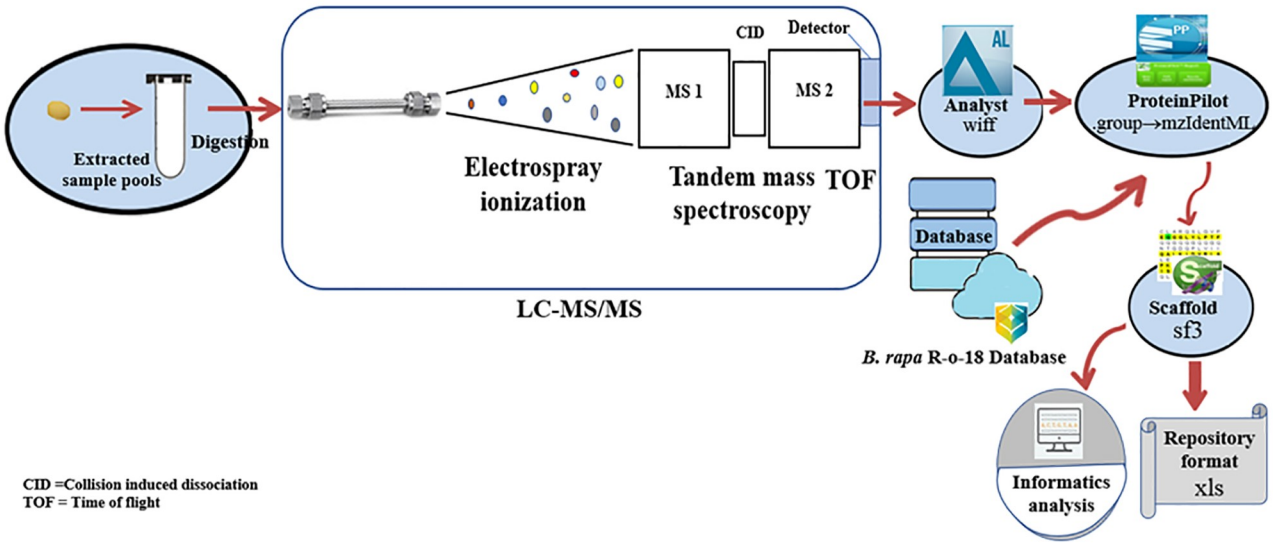


Fig 1. Overview graph of proteomics pipeline. The LC-MS/MS proteomics workflow is illustrated using ovals to represent the key steps within the workflow and the arrows connecting them.

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Ontology (GO) enrichment analysis using the hypergeometric method with Benjamini false discovery rate (FDR) correction.

Multiple sequence alignment and phylogenetic analysis

Multiple sequence alignment was performed using Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo/) (S1 Table in S1 File) [48]. Aligned sequences were formatted using MView [49]. Evolutionary relationships were determined by phylogenetic analysis using the online NGPhylogeny.fr web resource (https://ngphylogeny.fr/workflows/oneclick/, 30/05/2020).

Sequence analysis and epitope mapping and of vicilin proteins

To obtain more insight into the allergenicity of vicilin like proteins, epitope mapping was performed according to the method described in [15, 50]. In summary, previously documented vicilin proteins from diverse species representing known allergens reported in the protein databases (S1 Table in S1 File) were mapped to the sequences identified in this study (S5 Table in S1 File), to determine conservation of IgE-binding epitopes [50–52].

Results

Mass spectrometric data was searched against a database made up of the *Brassica rapa* R-o-18 genome annotation version 2.2 comprising 43,245 protein entries [53] which was combined with putative and published sequences of seed storage and oil body proteins [15] (S1 and S2 Tables in S1 File). The data obtained were analysed with ProteinPilot 5.0.2 software (SCIEX), then visualized and validated using Scaffold 4.8.7 (Proteome Science) employing a minimum protein threshold of 99.9% and peptide threshold of 95% (S3 Table in S1 File).

A total of 34016 spectra were mapped to 323 proteins (S3 Table in S1 File). These proteins ranged in theoretical molecular weight from 7 kDa (Bra000692) to 175 kDa (Bra026064) (S4 Table in S1 File). A Venn diagram was constructed (Fig 2) to show how the proteins were distributed between the biological replicates (Pool 1 to 4). A total of 233 proteins were identified as present in at least 3 out of 4 biological replicates with at least 2 unique peptides (S4 Table in S1 File) as indicated by the numbers within the red outline (Fig 2). Of these 164 were identified in all four biological replicates as indicated by the middle square inside the red outline (Fig 2).

Gene ontology (GO) terms for the identified proteins were initially obtained by BLASTP search against protein sequences in the Arabidopsis database in NCBI. This was refined using manual curation taking into account both experimental evidence available in the literature for protein homologs, detailed sequence analysis, as well as verified information from the Uniprot database [54]. The characterised proteins were then grouped according to their gene ontology (GO) terms within the categories of cellular component and molecular function. Ten different cellular component categories were mapped to the identified proteins (Fig 3). The majority of the proteins identified were associated to the cytoplasm (50.6%), while 8.1% were associated to lipid/oil bodies and 6.4% to vacuoles. Fourteen of the identified proteins were unable to be assigned to any cellular component.

Identified proteins were then grouped according to their molecular function [55], and the percent contribution of proteins to each functional group compared in Fig 4. The majority of these were directly linked to cellular metabolic processes, including carbohydrate and lipid metabolic processes, as well as cellular homeostasis. There was also a considerable grouping of proteins in the category of response to stress and translation. Proteins grouped in the nutrient reservoir category were all classified as seed storage proteins (SSP), representing 4.72% of all non-redundant proteins identified. This group was made up of 2S albumin like napins, 11/12S

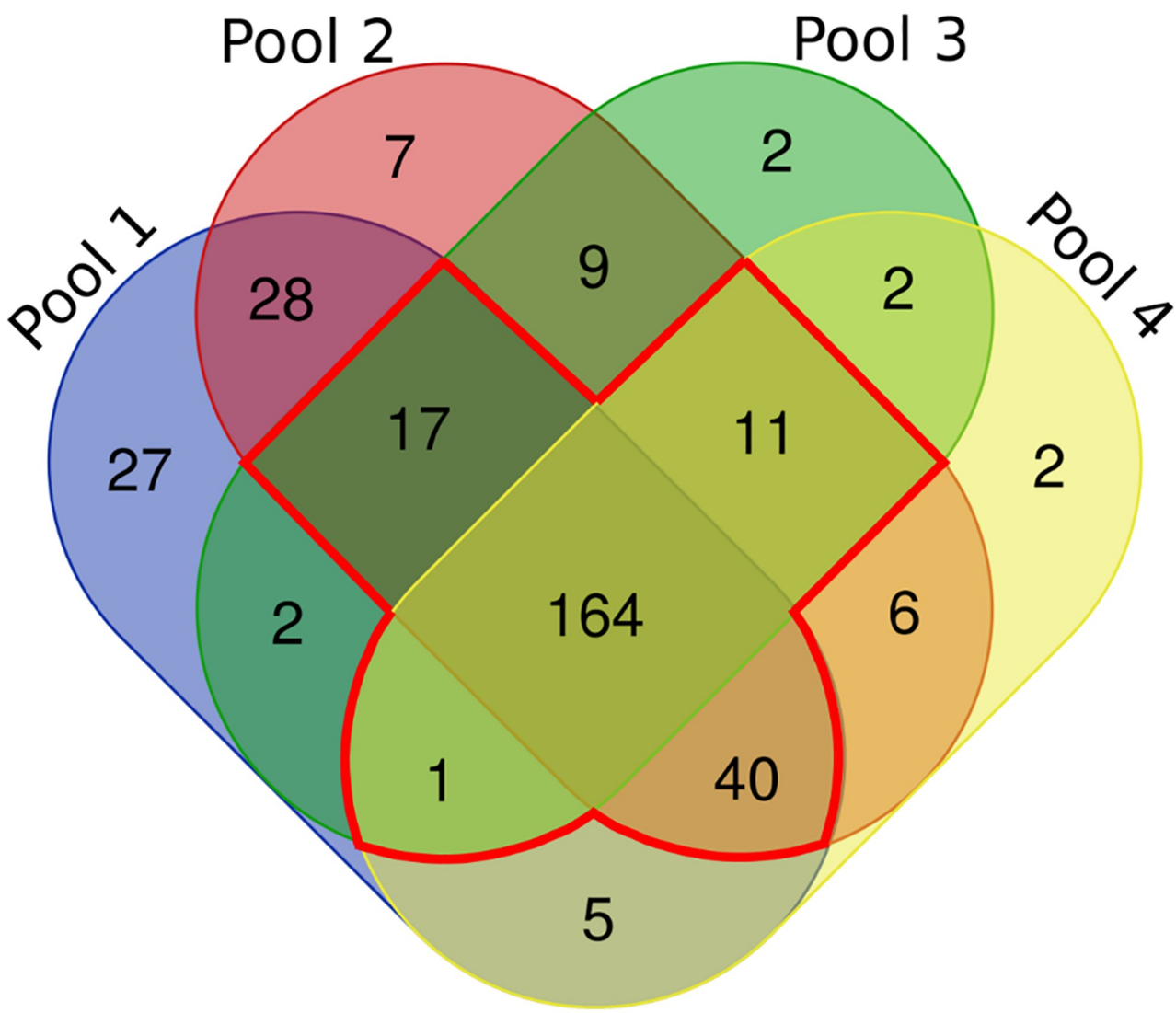


Fig 2. Venn diagram showing the distribution of unique and common non-redundant proteins among the four biological replicates. The overlapping regions show numbers demonstrating the proteins that were expressed in at least three biological replicates with 2 unique peptides Proteins within the red outline are those present in all biological replicates (Pool 1 to 4). The identities of the expressed proteins are detailed in S4 Table in S1 File.

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globulin-like cruciferins and 7S globulin like vicilins [56]. In addition to the napins Bra041165, BraA03000889 and BraA01001883, all previously predicted *Brassica rapa* napin gene products [15] were found to have high percent identity and coverage with the napins identified by LC-MS/MS at the protein level, and the percent identity and coverage for these are reported in S8 Table in S1 File. In total, seed storage proteins made up on average 20.3% of the total spectra identified, with 14.8% of the spectra associated to cruciferins, and 2.6% associated with napins. Another 2.8% of the seed storage protein spectra were associated with 7S-globulin like vicilins, suggesting that these proteins are also a major seed storage protein in the seeds of *Brassica rapa*.

As expected for an oil seed crop, a large number of oil/lipid body proteins, namely oleosins and oil-body associated proteins as well as lipid transfer proteins were identified (Fig 3 and S5

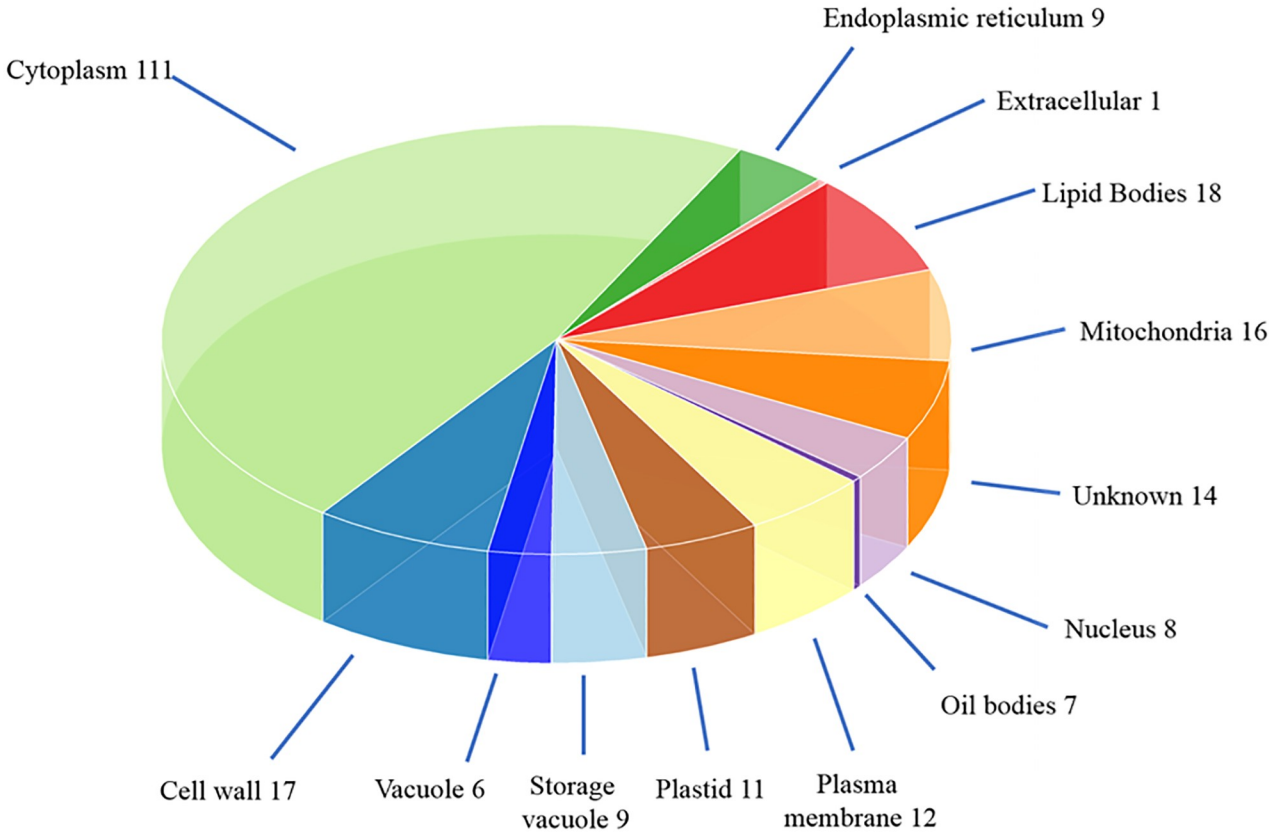


Fig 3. Distribution of proteins identified from *Brassica rapa* R-o-18 seed extract according to GO cellular component annotations. The proteins identified from *Brassica rapa* R-o-18 seed extract using LC-MS/MS were categorized based on Gene Ontology (GO) annotation as described in Material and Methods. Ten 'cellular component' categories were assigned to 219 proteins with 14 unknown proteins remaining uncategorized.

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Table in S1 File) [57–59]. Oleosins and other oil body associated proteins accounted for 19.8 and 1.3%, respectively of the total spectra in the seed.

Gene Ontology (GO) term enrichment analysis using the DAVID functional annotation tool, was undertaken to test the over-representation of GO terms within the list of identified proteins compared to the natural abundance in the reference background Arabidopsis dataset to gain insight into their biological significance in the seed proteome. A total of 181, 189, and 157 proteins from the identified proteome were assigned to a biological process, cellular component, or molecular function GO annotation term, respectively. GO enrichment of molecular function identified 14 categories showing enrichment (Fig 5) with the most significantly enriched in our dataset being structural constituent of ribosome (*p*-value: 6.4E-17), copper ion binding (*p*-value: 2.2E-14), nutrient reservoir activity (*p*-value: 0.000000011), mRNA binding (*p*-value: 0.000000061) and glutathione transferase activity (*p*-value: 0.00019). The enriched GO terms associated with biological processes totaled 46 (Fig 5B), with those relating to stress responses showing the most significant enrichment compared to the background dataset, including response to cadmium ion (*p*-value: 1.10E-24), response to salt stress (*p*-value: 2.1E-13), response to heat (*p*-value: 3E-13), response to cytokinin (*p*-value: 3.3E-10), response to abscisic acid (*p*-value: 1.8E-09); and response to cold (*p*-value: 5.9E-09). Translation and oxidation-reduction processes were also enriched significantly (*p*-value: 0.0000013 and *p*-value: 0.019, respectively). Cellular component GO terms significantly enriched totaled 32 (Fig 5), and included the most enriched related terms of cytosol (*p*-value: 2.2E-46), and cytoplasm

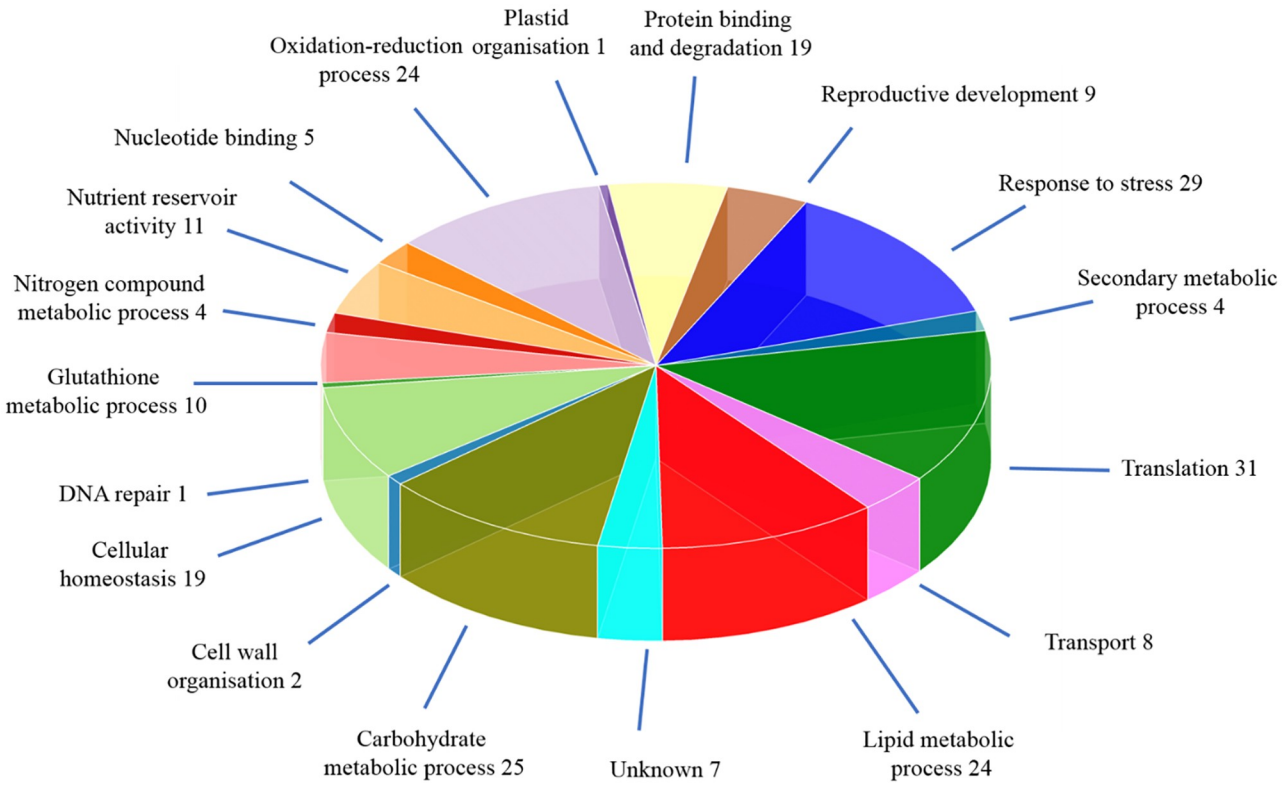


Fig 4. Distribution of proteins identified from *Brassica rapa* R-o-18 seed extract according to GO molecular function annotations. The proteins identified from *B. rapa* R-o-18 seed extract using LC-MS/MS were categorized based on Gene Ontology (GO) annotation as described in Material and Methods. Seventeen 'molecular function' categories were assigned to 226 proteins with 7 unknown proteins remaining uncategorized.

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(*p*-value: 1.5E-22) as well as membrane and plasma membrane (*p*-value: 1.6E-12 and 6.6E-10, respectively).

The identification of five 7S globulin-like vicilin proteins provides the first experimental evidence of these proteins in Brassica (S5 Table in S1 File), fragmentation evidence for all high confidence peptides (>95%) that matched the vicilin sequences in all four pooled populations are shown in S1 Fig. Previously vicilin proteins in the *B. rapa* R-o-18 genome had only been inferred from partial complementary DNA (cDNA) sequences, RNAseq data or expressed sequence tags (ESTs), and based on sequence similarities to known legume vicilins [59, 60]. Multiple sequence alignment of the five identified *B. rapa* vicilins with vicilin and vicilin-like protein sequences from *Arabidopsis thaliana*, *Cannabis sativa*, cashew (*Anacardium occidental*), narrow-leaf blue lupine (*Lupinus angustifolius*), *w*hite lupine (*Lupinus albus*), sesame (*Sesamum indicum*), pistachio (*Pistacia vera*), European hazel (*Corylus avellana*) and peanut (*Arachis hypogaea*) can be seen in (Fig 6). The alignment indicates significant sequence identity of the five identified *B. rapa* vicilins with other vicilin and vicilin like proteins [51, 61, 62]. To confirm this, a pairwise sequence comparison analyses for percent sequence identities (PIDs) was performed comparing the known vicilin sequences in S1 Table in S1 File with the identified 7S globulin like vicilins using CLC Genomics Workbench v3.6.5 (QIAGEN Bioinformatics). A distance matrix, expressing the nearest neighbour distance was created from a multiple sequence alignment with the sequences of similar length using the distmat server (https://www.bioinformatics.nl/cgi-bin/emboss/distmat, 3, 08, 2020). The pairwise comparison shows that there are high sequence similarities among the identified *B. rapa* 7S globulin

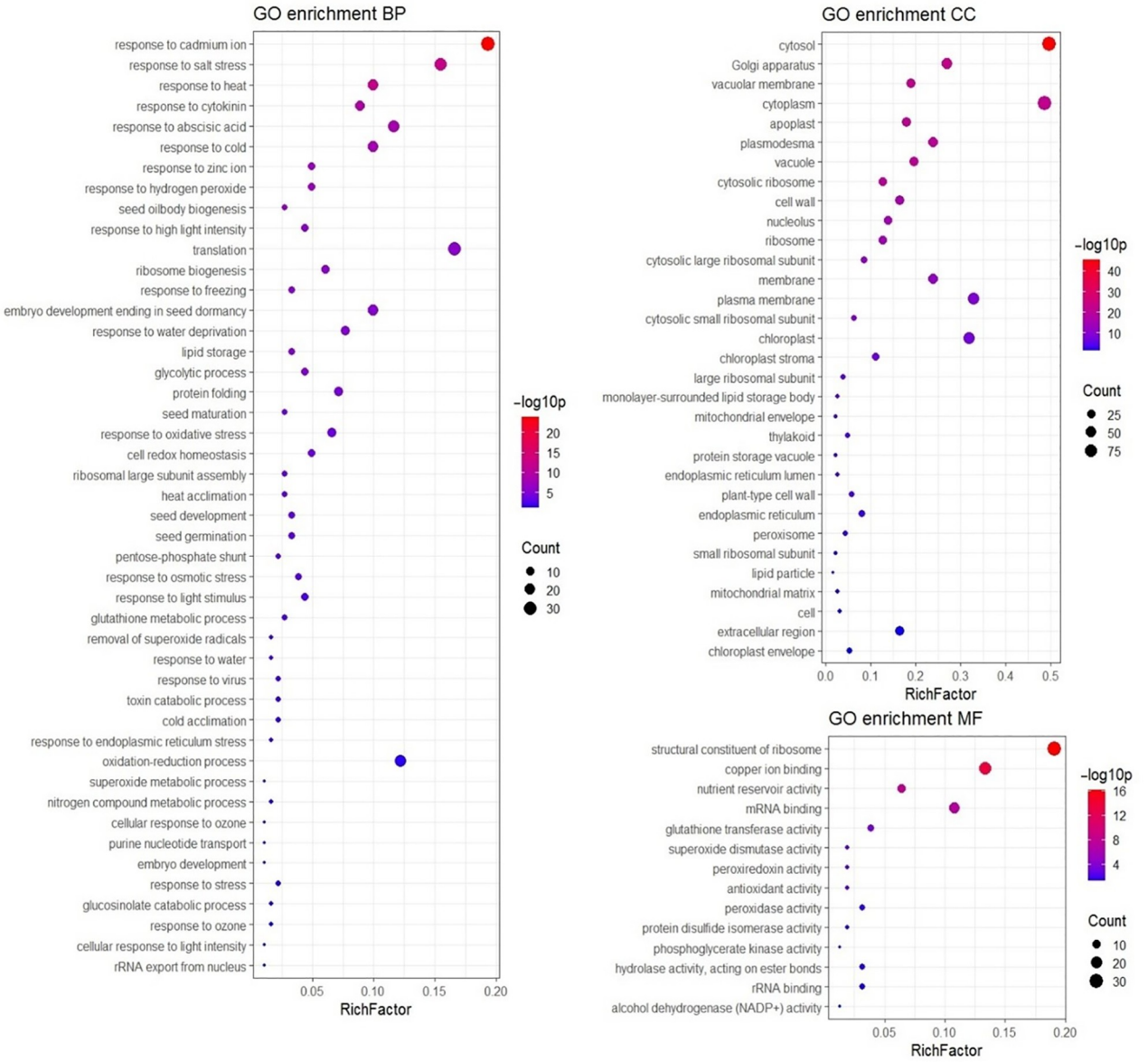


Fig 5. Gene Ontology (GO) term enrichment analysis of identified *Brassica rapa* seed proteins by DAVID. Gene Ontology (GO) term enrichment analysis was carried out using the hypergeometric method with Benjamini false discovery rate (FDR) correction. MF, CC and BP represents molecular functions, cellular components and biological processes, respectively. Rich factor is the ratio of the number of identified proteins annotated in the given GO term pathway to the number of all proteins from the database annotated in the pathway.

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like vicilins and previously identified vicilin sequences suggesting there are close evolutionary relationships between members of this cupin superfamily [15, 63, 64]. A distance matrix was constructed based on the score of the evolutionary distance between each pair of sequences (S2 and S3 Figs) [65, 66].

Crystallographic studies suggest that all vicilin proteins are composed of two domains, consisting of 11 β-sheets within the N-terminal region, and 3 to 4 α-helices at the C-terminus of the protein [51, 61, 67]. To confirm the presence of these domains in the *B. rapa*, vicilin proteins identified in this study, the full-length sequences of identified vicilins were analysed using SWISS-MODEL (https://swissmodel.expasy.org/, 20.06.20) to perform tertiary structure



Fig 6. Multiple sequence alignment of the 7S globulin-like vicilin protein sequences identified in *Brassica rapa*. 7S globulin-like vicilin protein sequences from *B. rapa* R-o-18 seed proteome were aligned with sequences from *Arabidopsis thaliana*, *Cannabis sativa*, cashew (*Anacardium occidental*), narrow-leaved blue lupine (*Lupinus angustifolius*), *w*hite lupine (*Lupinus albus*), sesame (*Sesamum indicum*), pistachio (*Pistacia vera*), European hazel (*Corylus avellana*) and peanut (*Arachis hypogaea*) available in public domain databases. Ep = epitopes. The orange boxes delineate known Ara h 1 epitopes [50], dark blue boxes outline known Ana o 1 epitopes [52], grey boxes

delineate known olive vicilin T-cell epitopes abbreviated as OVTE and yellow boxes bound the known olive vicilin B-cell epitopes abbreviated as OVBE [51]. All the epitopes are listed in Table 1 and the corresponding sequences identified in the vicilin-like proteins in *B. rapa*. pid = percent sequence identity. Blue boxes show the location of the conserved proline and glycine residues.

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prediction. High-resolution three-dimensional structure models of the identified vicilin proteins were drawn without ligands, as homo-trimers, based on the available crystal structures of vicilins (https://www.rcsb.org/) as template. Details of the 3D models with the quality scores and global model quality estimate (GMQE) and qualitative model energy analysis (QMEAN) values are presented in S6 Table in S1 File [15, 68]. The best models from the tertiary structure analysis based on GMQE and QMEAN values confirmed that the identified vicilin proteins in the *B. rapa* R-o-18 seed proteome possess this uniquely shared characteristic property of vicilins, with β-sheets in the N-terminal region and α-helices at the C-terminus (Fig 7) [51].

Within these two domains vicilin proteins show conserved glycine and proline residues located 15 amino acid residues apart [67, 69]. This motif is conserved in the *B. rapa* vicilins (Fig 6, blue boxes). Additionally, as noted in other vicilins, there was a lack of cysteine residues and a high abundance of glycine, lysine, glutamic and aspartic acid residues [70–72].

Phylogenetic analysis carried out with well characterized full length vicilin proteins [50–52] showed the evolutionary relationship of the five identified vicilin proteins from *B. rapa* to vicilins from other species (Fig 8). *B. rapa* vicilin Bra014536 was observed to cluster with the *A. thaliana* vicilin (At3g22640), whereas vicilin Bra 025745 was more closely related to the *Cannabis sativa* 7S vicilin-like protein (Cs7S, A0A219D1T7) (Fig 8, S1 Table in S1 File). The other

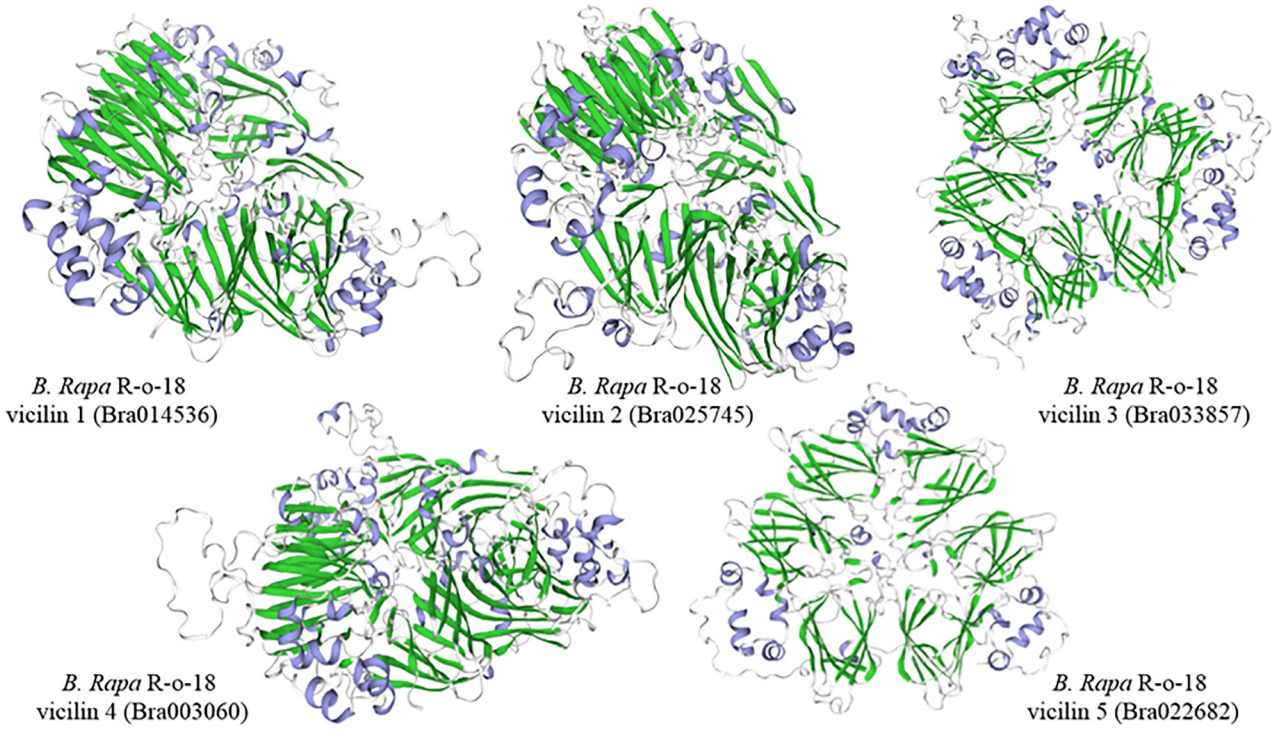


Fig 7. Three-dimensional structure of the vicilin like seed storage proteins identified in *Brassica rapa*. Structural modelling was carried out using the SWISS-MODEL program and was based on the available crystal structures of vicilin (S6 Table in S1 File). The green shading indicates the location of β-sheets in the N-terminal region and the blue shading indicates α-helices at the C-terminus.

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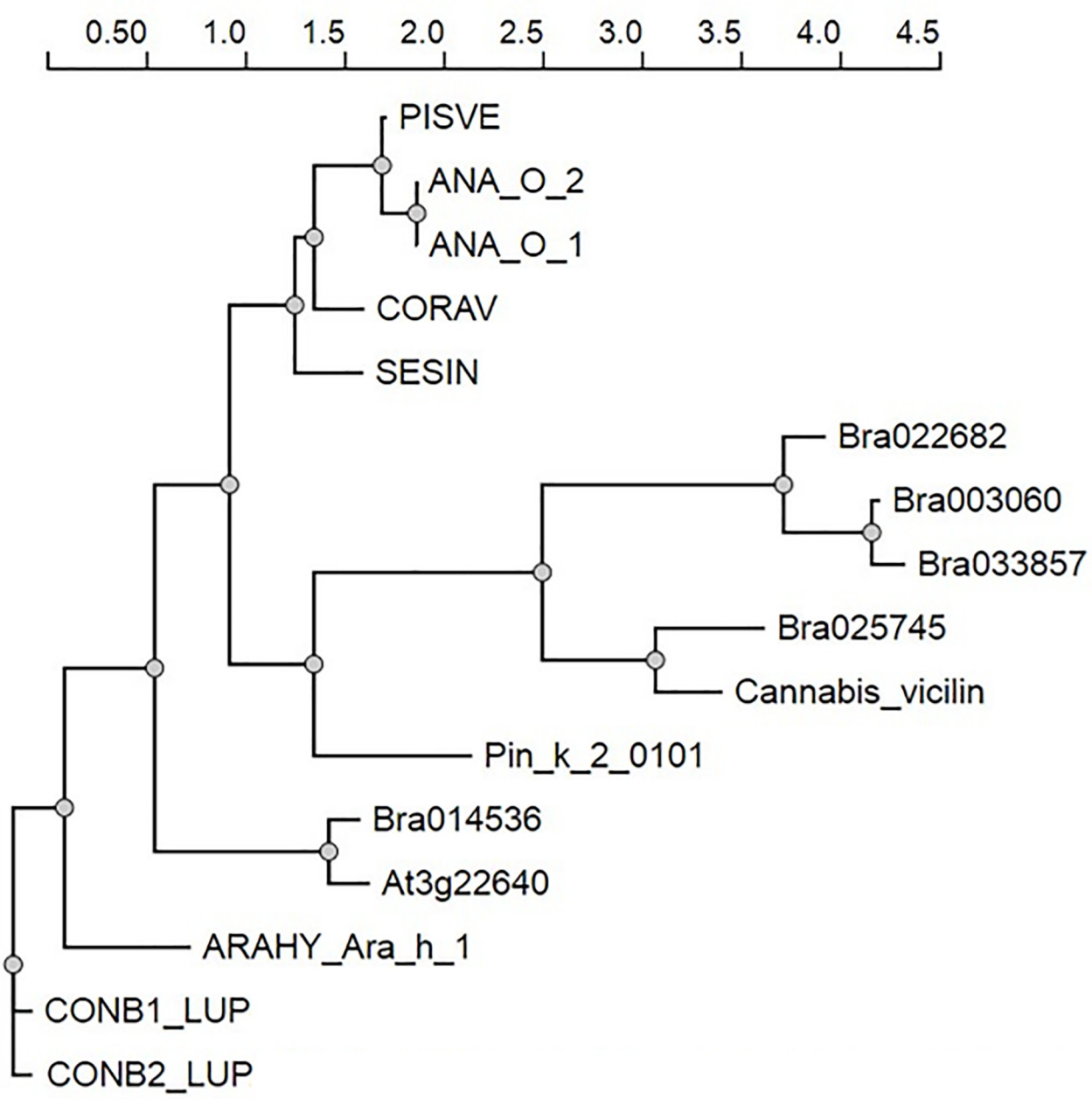


Fig 8. Phylogenetic tree of vicilin-like proteins. The phylogenetic tree was constructed using the maximum likelihood method in NGPhylogeny.fr web resource (https://ngphylogeny.fr/workflows/oneclick/, 30/05/2020). The tree was constructed using the five 7S globulin-like vicilin protein sequences identified in *Brassica rapa* R-o-18, as well as 7S globulin like vicilin protein sequences reported in different plant species including *Arabidopsis thaliana* (At3g22640), *Cannabis sativa* (Cannabis_vicilin), cashew (*Anacardium occidental*) (ANA_O-1 and ANA_O_2), narrow-leaved blue lupine (*Lupinus angustifolius*) (CONB1_LUP), *w*hite lupine (*Lupinus albus*) (CONB2_LUP), sesame (*Sesamum indicum*) (SESIN), *Korean pine (Pinus koraiensis) (Pin_k_2_0101)*, pistachio (*Pistacia vera*) (PISVE), European hazel (*Corylus avellana*) (CORAV) and peanut (*Arachis hypogaea*) (ARAHY_Ara_h_1), all available in public domain databases. The full-length sequences of identified vicilins are presented in S5 Table in S1 File, while the other sequences are presented in S1 Table in S1 File. The scale above the tree represents the in-built distance matrix employed in NGPhylogeny.fr web resource and indicates the distance based on the sequence similarity of their features.

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B. *rapa* vicilin proteins identified (Bra 033857, Bra 003060 and Bra022682), clustered together in a branch distinct from vicilins from other species.

Vicilins have been shown to induce allergenic responses in humans [36, 50, 52, 73, 74]. To investigate potential allergenicity of the *B*. *rapa* vicilin proteins, epitope mapping was performed using the sequences of *B*. *rapa* vicilins and comparing them to the twenty-three reported epitopes of the well-studied peanut vicilin allergen Ara h 1 [50], eleven epitopes of a cashew allergen Ana o 1 [52] and T- and B- cell epitopes characterized in olive 7S vicilins corresponding to lupine Lup 1, sesame Ses i 3, pistachio Pis v 3 and European hazel Cor a 11 [51] (Table 1, Fig 6, deep blue, orange, grey and yellow boxes, respectively).

Epitope mapping to compare the known epitope sequences of Ara h 1, Ana o 1, Olive 7S vicilin T and B-cell epitopes and the linear epitopes in lupine and sesame with corresponding sequence motifs in the *B*. *rapa* vicilin proteins indicates that a large number (13 out of 23) of the peanut vicilin epitopes are highly conserved, while others, including cashew and olive vicilin B-cell epitopes are partially conserved based on the degree of amino acid similarity and identity (Fig 6, S5 Table in S1 File). Most of the highly conserved Ara h 1 epitopes are found in the second half of the proteins comprising epitopes 10 to 23. This corresponds to the region of the protein that contains the α-helices at the C-terminus [50, 51, 67]. Sequence analysis of the identified 7S globulin-like vicilins is presented in S9 Table in S1 File.

Discussion

A shotgun proteomic approach was carried out on extracts from *B*. *rapa* mature seeds to profile seed proteins with a specific focus to identify and catalogue SSP. From a total of 34016 spectra, 323 proteins were identified (Fig 2). This number is similar to protein numbers reported for shotgun seed proteomics of soybean and quinoa seeds, (243 and 352 respectively) [75, 76], although less than the number of proteins identified in seeds from the tree *Camellia oleifera* (1691 proteins) [77], or from rice and barley grains (822 and 1168 proteins, respectively) [78, 79].

Previous seed focused proteomic studies in Brassica oil-seed crops have primarily employed gel-based approaches to identify proteins showing changes in abundance through seed development or under changing conditions [31, 80–86]. While these studies have advanced understanding of specific biological processes important for the seed, they have not provided a general overview of the proteins in the seed that can be obtained by a bottom-up type approach.

In this study five cruciferin (Bra022801, Bra035434, Bra002906, BraA09006896 and P15456], and three napin proteins (Bra041165, BraA03000889 and BraA01001883] were identified in the proteome of the *B*. *rapa* R-o-18 seed extracts (S4 Table in S1 File). Molecular genetic analysis indicated the presence of five genes encoding napin proteins in the *B*. *rapa* R-o-18 genome and 10 genes encoding napin proteins in the Chiifu genome [15] (S8 Table in S1 File). Direct identification of three of these in this study provides protein-level evidence of gene expression which can help to refine gene models.

Previous studies have reported that in Brassica, 12S globulin type cruciferins and 2S albumin type napins together constitute approximately 85%–90% of the total protein in the seed [59, 87]. Cruciferin is the most abundant of these, roughly accounting for 60% of the total protein in the seed. Napin is reported as the second most abundant SSP, representing 20–30% of the total protein [88]. Generally, the ratio of cruciferin to napin, although variable, is in the range of 0.6 to 0.2 [58, 59]. In this study, based on spectral counting of identified proteins, cruciferin accounted for 14.8% of the seed proteome and napin accounted for an additional 2.6%.

Table 1. Epitope mapping of *Brassica rapa* vicilin sequences with the twenty-three reported epitopes of the well-studied peanut vicilin allergen Ara h 1.

Epitope number	A.A. sequences	A.A. position	Identified *B. rapa* vicilins				
			Bra 025745	Bra 022682	Bra 033857	Bra 003060	Bra 014536
Ara h 1 epitopes (peanut, *Arachis hypogaea*)							
1	*AKSSPYQKKT*	25–34	x	x	x	x	x
2	QEPDDLKQKA	48–57	x	x	x	x	x
3	*LEYDPRCVYD*	65–74	x	x	x	x	x
4	*GERTRGRQPG*	89–98	x	x	x	x	x
5	PGDYDDDRRQ	97–105	x	x	x	x	x
6	PRREEGGRWG	107–116	x	x	x	x	x
7	REREEDWRQP	123–132	x	x	x	x	x
8	EDWRRPSHQQ	134–143	PC	PC	PC	PC	PC
9	QPRKIRPEGR	143–152	PC	PC	PC	PC	PC
10	TPGQFEDFFP	294–303	HC	HC	HC	HC	HC
11	SYLQEFSRNT	311–320	HC	HC	HC	HC	HC
12	FNAEFNEIRR	325–334	HC	HC	HC	HC	HC
13	*EQEERGQRRW*	344–353	x	x	x	x	x
14	DITNPINLRE	393–402	HC	x	HC	HC	HC
15	DNFGRLFEVK	409–418	HC	x	HC	HC	HC
16	GTGNLELVAV	461–470	HC	HC	HC	HC	HC
17	*RRYTARLKEG*	498–507	HC	HC	HC	HC	HC
18	ELHLLGFGIN	525–534	HC	HC	HC	HC	HC
19	HRIFLAGDKD	539–548	HC	HC	HC	HC	HC
20	VDQIEKQAKD	551–560	HC	HC	HC	HC	HC
21	KDLAFPGSGE	559–568	HC	HC	HC	HC	HC
22	*RESHFVSARP*	578–587	HC	PC	HC	HC	HC
23	QSPSSPEKED	597–606	HC	PC	HC	HC	HC
Ana o 1 epitopes (cashew, *Anacardium occidental*)							
1	MGPPTKFSFSLFL	1–15	x	x	x	x	x
2	CKVQRQYDEQQKEQC	41–55	x	x	x	x	x
3	EQQKEQCVKECEKYY	49–53	x	x	x	x	x
4	**KECEKYYKEKKGRER**	57–71	x	x	x	x	x
5	EKKGREREHEEEEEE	65–79	x	x	x	x	x
6	DEAEEEDENPYVFED	145–159	x	x	x	x	x
7	RRGEGPKIWPFTEES	337–351	x	x	x	x	x
8	NITKGGMSVPFYNSR	393–407	PC	PC	PC	PC	PC
9	TKIAIVVSGEGCVEI	409–423	PC	PC	PC	PC	PC
10	SSHPSYKKLRARIRK	433–447	x	x	x	x	x
11	**EEFFFQGPEWRKEKE**	521–535	PC	PC	PC	PC	PC
Olive 7S vicilin T-cell epitopes (OVTE)							
T1, T5	LVIAKLLQP	140–148	x	x	x	x	x
T2	FEMACPHLS	297–305	x	x	x	x	x
T3	INIHDQRPS	231–239	x	x	x	x	x
T4	YVAVASNNQ	336–345	x	x	x	x	x
T6	YVAQGMGTV	194–102	x	x	x	x	x
T7	VVLLPKFTQ		x	x	x	x	x
T8	DSPGMKYRV	63–71	x	x	x	x	x
T9	LVSVLVLCL (in AANOC)	13–22					
Olive 7S vicilin B-cell epitopes (OBVE)							

(*Continued*)

Table 1. (Continued)

Epitope number	A.A. sequences	A.A. position	Identified *B. rapa* vicilins				
			Bra 025745	**Bra 022682**	**Bra 033857**	**Bra 003060**	**Bra 014536**
B1	KHQGEHGRGGGDIL	Sesame	x	x	x	x	x
B2	DQRPSQFNQ	Olive	x	x	x	x	x
B3	QGAMTTPYYNSKA	Olive	PC	PC	PC	PC	PC
B4	EITPDRNPQVQ	Lupine	x	x	x	x	PC
B5	KNNKRYPLA	Olive	PC	PC	PC	PC	PC

The sequences of Ara h 1 and corresponding sequences identified as vicilin-like proteins in *B. rapa*. are taken from Fig 6. X = not conserved, PC = partially conserved (≥50% identity in corresponding sequence alignment), HC = highly conserved (>90% identity in corresponding sequence alignment) depending on the degree of amino acid similarity and identity among the Ara h 1 and corresponding *Brassica rapa* vicilin sequences. The italicized epitopes were the most commonly recognised peptides in Ara h 1 sequence by IgE in at least 80% of the sera from sensitive individuals [50]. Peptides reported as immunodominant epitopes are shown in bold [52].

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This represented a napin to cruciferin ratio of 1 to 5 and agrees with the range previously reported.

Identification of vicilin SSP in the *B. rapa* seed provides evidence for an important role for this family of SSP in Brassica. Vicilins have been predominantly mentioned as SSP in legumes [70] and tree nuts [36, 52, 89], with only partial gene sequences corresponding to incomplete clones identified in Arabidopsis [59].

Previously it was assumed that cruciferins and napins were the main seed storage proteins in the Brassica seed [59]. However, based on spectral counts, vicilins appear to be close in abundance to napins in the seeds of *B. rapa*. The molecular weight of identified vicilins ranges from 52–83 kDa (S5 Table in S1 File), and analysis of seed extract protein profiles from 1D-SDS-PAGE identified a strong band within this range (S4 Fig). Western blotting with a vicilin specific antibody would help to confirm this.

The identification of vicilins in the seed extract of *Brassica rapa* is an important finding, as vicilin-like seed storage proteins are one of the major allergens in tree nuts, including almond (*Prunus dulcis*) [73, 74], cashew (*Anacardium occidental*) [52], *Pinus koraiensis* (Pinaceae) [90, 91] and walnut (*Juglans regia*) [36]. Vicilins from pulses and legumes, including peanut (*Arachis hypogaea*) [50], pea [92], chickpea [93], and lentils [62] have also been shown to elicit strong allergenic responses in humans. Sequence analysis revealed that sequence identity of the *B. rapa* vicilins to those of other species ranged from 9.4% to 25.5%, with the highest value obtained for Bra014536 with reference to peanut vicilin Ara h 1 (Fig 6) [51]. Sequence comparisons reported among other vicilins also show quite low sequence identity, for example, cashew vicilin and the peanut vicilin have 27% sequence identity although both are predominant allergens [61]. Similarly, the identity between lentil Len c 1.0101 and sesame Ses i 3 is only 31% [62]. Despite low overall sequence identity, a number of epitopes identified in the peanut Ara h 1 vicilin protein were highly conserved in the vicilins from *B. rapa*, including epitopes 10, 11, 12 and 14–24, inclusive (Table 1) [50], with two of these, 17 and 22 corresponding to peptides in the Ara h 1 sequence recognised by IgE antibodies in at least 80% of the sera from sensitive individuals [50]. The epitope modelling shows that identified *B. rapa* R-o-18 vicilin like proteins have higher epitope conservation with the Ara h 1 epitopes than that of Ano a 1 and olive vicilin and its homologues. Further clinical testing would need to be carried out to determine the *B. rapa* R-o-18 vicilin epitopes which elicit the strongest immune response.

Phylogenetic analysis showed the evolutionary relationship among the identified *B. rapa* R-o-18 vicilins to known vicilins and vicilin like proteins (Fig 8). The *B. rapa* R-o-18 vicilins which have demonstrated higher sequence conservation of allergenic epitopes with Ara h 1

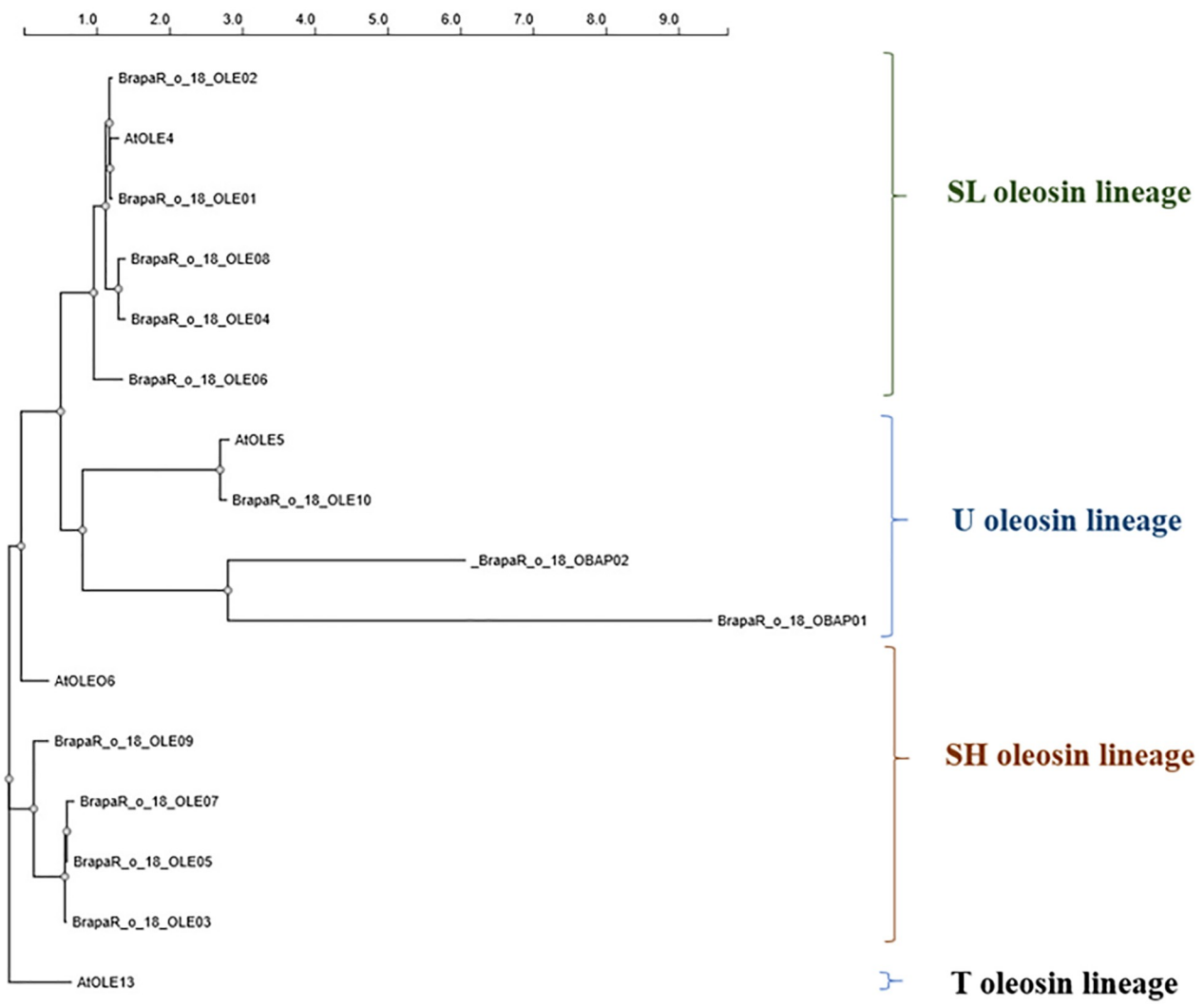


Fig 9. Phylogenetic analysis of identified *Brassica rapa* oleosin and oil body associated proteins. The linear phylogram was built using PRESTO-Phylogenetic tReE viSualisaTiOn server (https://ngphylogeny.fr/data/displaytree//, 29/09/2020) and shows the relationship to the Arabidopsis oleosin genes (S7 Table in S1 File). The branch length scale at the top of the figure indicates the distance between the sequences based on the sequence similarity of their features. The identified oleosin proteins Bra019493, Bra000167, A0A078GHK4, M4E9X1, A0A397KW15, A0A397ZZI8, M4DBK6, M4EI43, Bra035756, Bra032113 and oil-body associated proteins Bra036039 and Bra036039 are designated as OLE01, OLE02, OLE03, OLE04, OLE05, OLE06, OLE07, OLE08, OLE09, OLE10, OBAP 01 and OBAP 02 respectively.

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(Table 1), were found to be rooted from the same evolutionary ancestor and distant from the Ano a 1 vicilin which shared fewer epitopes (Fig 8).

A number of proteins associated with lipid biosynthesis and oil body structure were also identified in the *B. rapa* proteome (S5 Table in S1 File) including ten oleosins and two oil body associated proteins. Previous studies have identified up to 30 oleosin genes in *B. rapa* after analysis of the draft genome sequence of inbred line Chiifu-401-42 [94], and in this study we were able to identify 12 proteins corresponding to these genes in the seeds. Identified proteins can be placed into three out of the five oleosin lineages described by Huang and Huang, 2015 (Fig 9) [95]. These described lineages include primitive (in green algae, mosses and ferns); universal (U) encompassing all land plants; seed low-molecular weight (SL) from seed plants; seed high molecular weight (SH) from angiosperms and tapetum (T) from Brassicaceae.

B. *rapa* oil body associated protein Bra0360391, 2 and Bra036099, designated as OBAP01 and OBAP02, respectively, and oleosin Bra032113 (designated as OLE10) originate from U lineage, *B*. *rapa* oleosin Bra0194931, Bra0001672, M4E9X1, A0A397ZZI8, M4EI43, (designated as OLE01, OLE02, OLE04, OLE06 and OLE08, respectively) from SL lineage, *B*. *rapa* oleosin A0A078GHK4, A0A397KW15, M4DBK6 and Bra035756 (designated as OLE03, OLE05, OLE07 and OLE09, respectively) from SH lineage (Fig 8, S6 Table in S1 File) [94]. No oleosin from the T lineage was detected in *B*. *rapa*. Oleosins have been shown to have important roles in determining oil body size, seed size and seed weight which in turn would likely influence oil production [96].

Many of the proteins identified relate to well-studied seed physiological processes. Brassicaceae crops have been reported to synthesize many unique S-containing secondary metabolites which play an important role in oxidative stress signalling and resistance to herbivores [97, 98], the most notable of these is glutathione. In this study six glutathione S-transferases were identified in the seed extracts along with proteins involved in glutathione-linked responses including but not limited to glutathione peroxidase, thioredoxin. and S-formylglutathione hydrolase as well as a sulphur transporter. Several enzymes involved in the cysteine/methionine metabolism were also identified (O-acetylserine (thiol) lyase, cysteine synthase, adenosylhomocysteinase, gltaredoxin, sulfotransferase, sulfate transporter, 5-methyltetrahydropteroyltriglutamate—homocysteine methyltransferase, glutathione S-transferase, adenylate kinate).

There was also a large number of proteins identified in the seed associated with translation (Fig 4). These proteins would likely play a key role in translation of stored mRNA's during the initial stages of seed imbibition, and evidence has shown that stored translational machinery is already effective during the very first hours upon imbibition [99]. There were also numerous proteins related to desiccation tolerance identified in the seed, including late embryogenesis related proteins (LEA), dehydrins, seed maturation protein (SMP), as well as embryonic maturation protein (EM). These proteins, as well as being important for seed desiccation, play a key role in the early stages of seed imbibition leading to germination [99]. We also identified the repair protein l-isoaspartyl methyltransferase (PIMT) which has been shown to be involved in isoAsp protein repair functions in the seed which functions to increase seed longevity and germination vigour [100, 101].

Conclusion

This study has catalogued the proteins in *B*. *rapa* R-o-18 seeds which can serve as a reference for future rapeseed protein analyses and provides information that can help to gain insight into the regulation, molecular mechanism and subcellular localization of the identified proteins. Major seed storage proteins were identified, including for the first time in *B*. *rapa*, proteins belonging to the 7S vicilin family of SSPs. Analysis of the sequences of the identified vicilin proteins provided evidence for their potential allergenicity due to high conservation of sequences that have shown to be major allergenic epitopes in vicilins of other species. This epitope identification could be used in the development of recombinant proteins for diagnosis and therapeutic purposes against rapeseed allergy [50, 102].

This study enriches our existing knowledge on rapeseed seed proteins and because of the close evolutionary relationship of *B*. *rapa* with other Brassicas, the knowledge obtained from this study should be useful to further understanding of the proteins of its other progenitors [103, 104], as well as construct a robust foundation and rational basis for plant bioengineering of seed storage proteins to allow improvement of seed protein which will allow the utilization of such an abundant and low cost rapeseed by-product for human consumption.

Supporting information

S1 Fig. Fragmentation evidence of high confidence peptides matching vicilin sequences in all four pooled populations.
(DOCX)

S2 Fig. Pairwise analysis of full length 7S vicilin sequences.
(DOCX)

S3 Fig. Distance matrix of the 18 full length vicilin sequences aligned in Supplementary Tables 1 and 5 in S1 File.
(DOCX)

S4 Fig. SDS-PAGE of proteins extracted from single seeds to demonstrate quality of protein used for MS analysis.
(DOCX)

S1 Raw image.
(PPTX)

S1 File. Supplementary tables.
(DOCX)

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Author Contributions

Conceptualization: Mahmudur Rahman, Bronwyn J. Barkla.

Formal analysis: Mahmudur Rahman, Qi Guo, Abdul Baten, Ramil Mauleon.

Funding acquisition: Mahmudur Rahman.

Investigation: Mahmudur Rahman, Amina Khatun.

Methodology: Mahmudur Rahman, Bronwyn J. Barkla.

Project administration: Bronwyn J. Barkla.

Resources: Bronwyn J. Barkla.

Supervision: Lei Liu, Bronwyn J. Barkla.

Writing – original draft: Mahmudur Rahman.

Writing – review & editing: Qi Guo, Lei Liu, Bronwyn J. Barkla.

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Fragmentation evidence of all the high confidence peptide (95%) that matched the vicilin sequences in all four pooled populations

*The **Protein Sequence Coverage** map shows the protein sequence with matching peptides indicated in color: green for highest confidence, yellow for moderate confidence, and red for lowest confidence. Gray text indicates portions of the protein sequence for which no peptides are identified. The **Fragmentation Evidence** lists the theoretical fragment ions for the peptide sequence, with matching ions shown in **bold** text in the table. The matched ions are drawn on the MS/MS spectrum at the *m/z* for the theoretical ion.

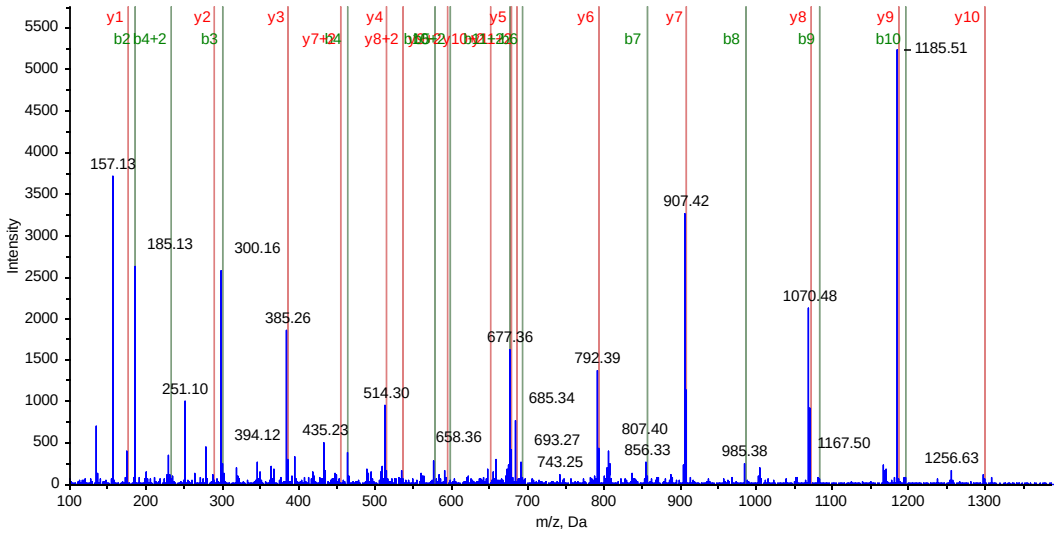
Sample Pool 1

Protein: B.rapa.Ro18.Candidate-1, 12 peptides (95%)

Protein sequence coverage

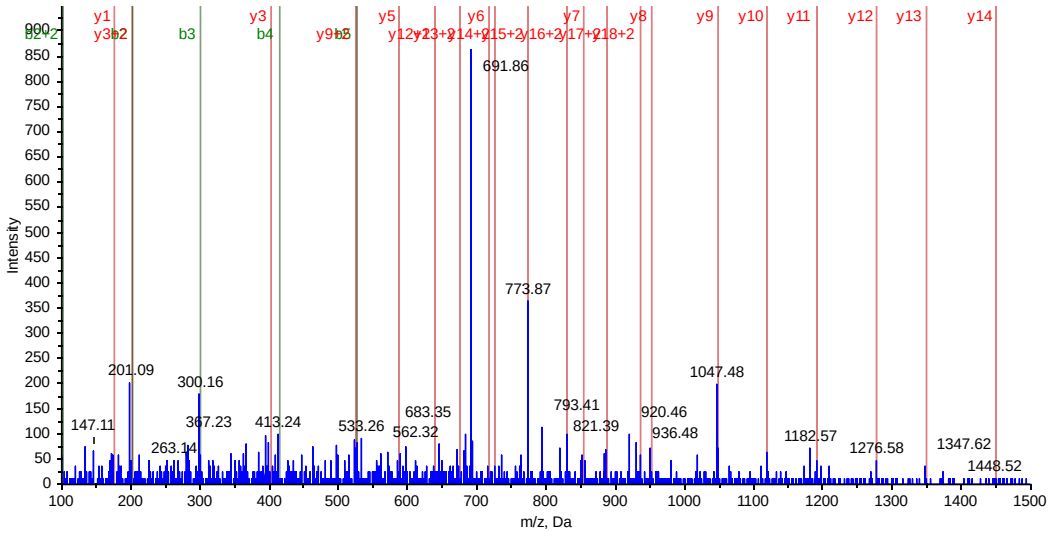
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Peptide sequence 1: ALDYDDYEPLR



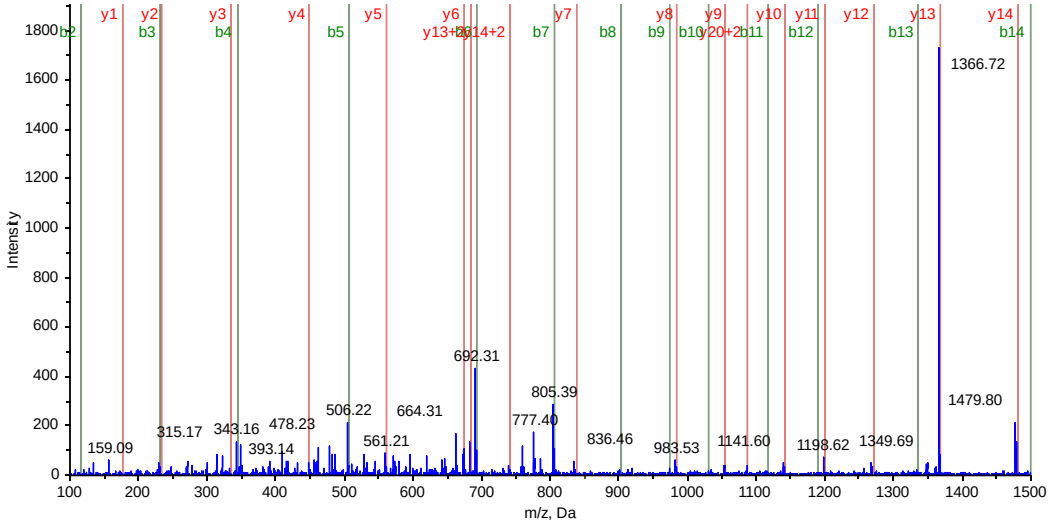
Residue	b	b+2	y	y+2
A	72.0444	36.5258	1369.6270	**685.3172**
L	**185.1285**	93.0679	**1298.5899**	**649.7986**
D	**300.1554**	150.5813	**1185.5059**	**593.2566**
Y	**463.2187**	**232.1130**	**1070.4789**	**535.7431**
D	**578.2457**	289.6265	**907.4156**	**454.2114**
D	**693.2726**	347.1399	**792.3886**	396.6980
Y	**856.3359**	428.6716	**677.3617**	339.1845
E	**985.3785**	493.1929	**514.2984**	257.6528
P	**1082.4313**	541.7193	**385.2558**	193.1315
L	**1195.5154**	**598.2613**	**288.2030**	144.6051
R	1351.6165	**676.3119**	**175.1190**	88.0631

Peptide sequence 2: EAVILPTASAAPPHEGEPER



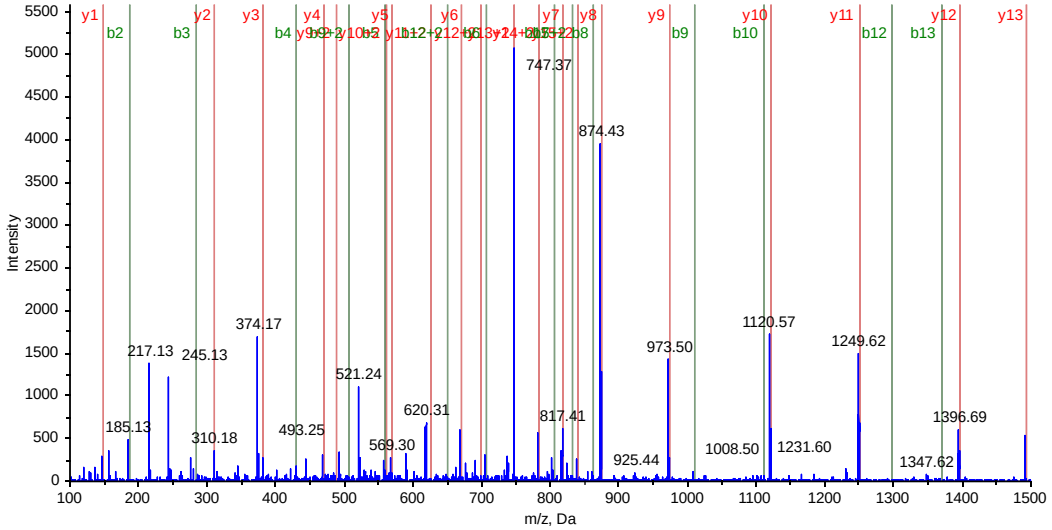
Residue	b	b+2	y	y+2
E	130.0499	65.5286	2071.0455	1036.0264
A	**201.0870**	**101.0471**	1942.0029	971.5051
V	**300.1554**	150.5813	1870.9658	**935.9865**
I	**413.2395**	207.1234	1771.8973	**886.4523**
L	**526.3235**	263.6654	1658.8133	**829.9103**
P	623.3763	312.1918	1545.7292	**773.3682**
T	724.4240	362.7156	**1448.6764**	**724.8419**
A	795.4611	398.2342	**1347.6288**	**674.3180**
S	882.4931	441.7502	**1276.5917**	**638.7995**
A	953.5302	477.2688	**1189.5596**	595.2835
A	1024.5673	512.7873	**1118.5225**	559.7649
P	1121.6201	561.3137	**1047.4854**	**524.2463**
P	1218.6729	609.8401	**950.4326**	475.7200
H	1355.7318	678.3695	**853.3799**	427.1936
E	1484.7744	742.8908	**716.3210**	358.6641
G	1541.7958	771.4016	**587.2784**	294.1428
E	1670.8384	835.9229	530.2569	265.6321
P	1767.8912	884.4492	**401.2143**	**201.1108**
E	1896.9338	948.9705	304.1615	152.5844
R	2053.0349	1027.0211	**175.1190**	88.0631

Peptide sequence 3: GGDIYWIPAGSAFYLLNTGR



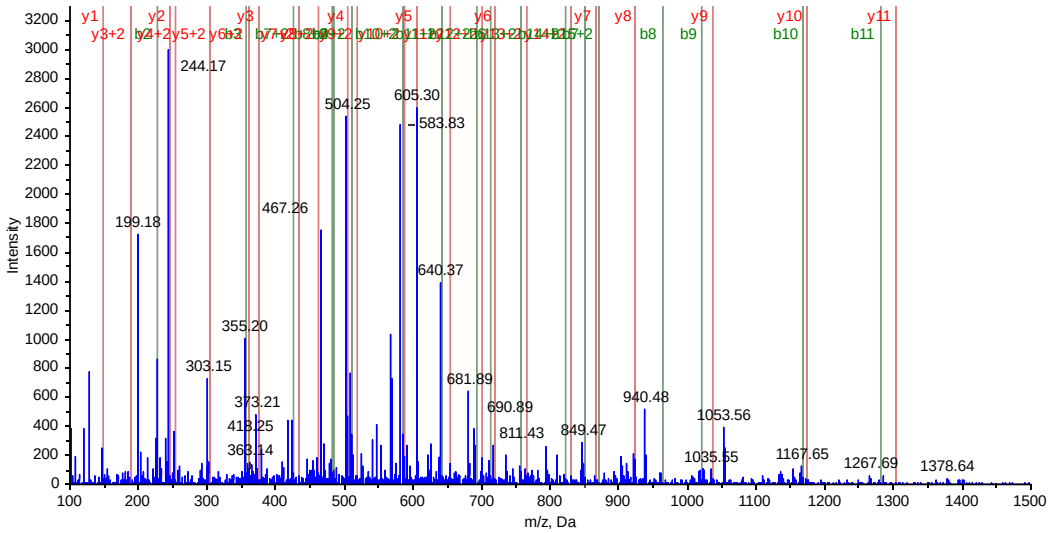
Residue	b	b+2	y	y+2
G	58.0287	29.5180	2171.0920	**1086.0496**
G	**115.0502**	58.0287	2114.0706	1057.5389
D	**230.0771**	115.5422	2057.0491	1029.0282
I	**343.1612**	172.0842	1942.0221	971.5147
Y	**506.2245**	253.6159	1828.9381	914.9727
W	**692.3039**	346.6556	1665.8748	833.4410
I	**805.3879**	403.1976	**1479.7954**	**740.4014**
P	**902.4407**	451.7240	**1366.7114**	**683.8593**
A	**973.4778**	487.2425	**1269.6586**	635.3329
G	**1030.4993**	515.7533	**1198.6215**	599.8144
S	**1117.5313**	559.2693	**1141.6000**	571.3037
A	**1188.5684**	594.7878	**1054.5680**	527.7876
F	**1335.6368**	668.3220	**983.5309**	492.2691
Y	**1498.7001**	749.8537	**836.4625**	418.7349
L	1611.7842	806.3957	**673.3991**	337.2032
L	1724.8683	862.9378	**560.3151**	280.6612
N	1838.9112	919.9592	**447.2310**	224.1191
T	1939.9589	970.4831	**333.1881**	167.0977
G	1996.9803	998.9938	**232.1404**	116.5738
R	2153.0815	1077.0444	**175.1190**	88.0631

Peptide sequence 4: IAPFEFVGFTTSAYK



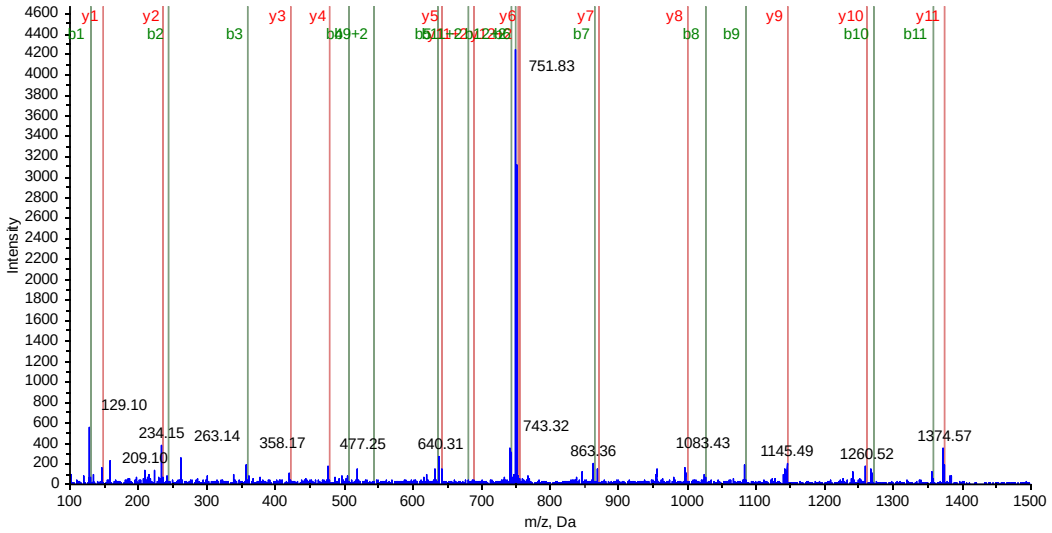
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1677.8523	**839.4298**
A	**185.1285**	93.0679	1564.7682	**782.8877**
P	**282.1812**	141.5942	**1493.7311**	**747.3692**
F	**429.2496**	215.1285	**1396.6783**	**698.8428**
E	**558.2922**	279.6498	**1249.6099**	**625.3086**
F	**705.3606**	353.1840	**1120.5673**	**560.7873**
V	**804.4291**	402.7182	**973.4989**	**487.2531**
G	**861.4505**	431.2289	**874.4305**	437.7189
F	**1008.5189**	**504.7631**	**817.4090**	409.2082
T	**1109.5666**	555.2869	**670.3406**	335.6740
T	1210.6143	605.8108	**569.2930**	285.1501
S	**1297.6463**	**649.3268**	**468.2453**	234.6263
A	**1368.6834**	684.8454	**381.2132**	191.1103
Y	1531.7468	766.3770	**310.1761**	155.5917
K	1659.8417	**830.4245**	**147.1128**	74.0600

Peptide sequence 5: IIEKPMHIGFLTMEPK



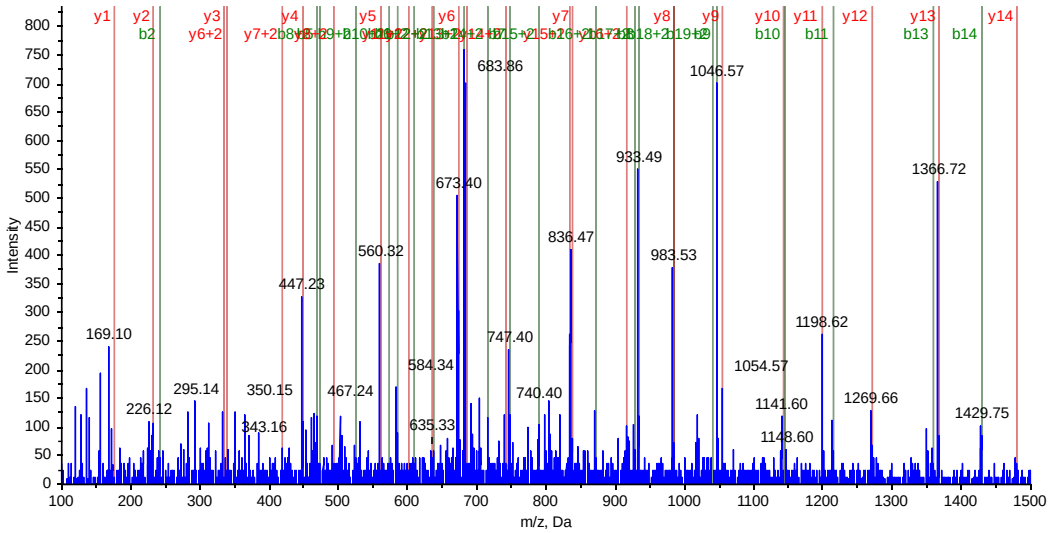
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1884.0122	942.5097
I	**227.1754**	114.0913	1770.9281	885.9677
E	**356.2180**	178.6126	1657.8440	**829.4257**
K	**484.3130**	242.6601	1528.8015	**764.9044**
P	581.3657	291.1865	1400.7065	**700.8569**
M	**712.4062**	356.7067	**1303.6537**	**652.3305**
H	**849.4651**	**425.2362**	**1172.6132**	**586.8103**
I	**962.5492**	**481.7782**	**1035.5543**	**518.2808**
G	**1019.5706**	**510.2890**	**922.4703**	**461.7388**
F	**1166.6391**	**583.8232**	**865.4488**	**433.2280**
L	**1279.7231**	**640.3652**	**718.3804**	**359.6938**
T	1380.7708	**690.8890**	**605.2963**	**303.1518**
M	1511.8113	**756.4093**	**504.2486**	**252.6280**
E	1640.8539	**820.9306**	**373.2082**	**187.1077**
P	1737.9066	**869.4570**	**244.1656**	122.5864
K	1866.0016	933.5044	**147.1128**	74.0600

Peptide sequence 6: KNDFENDYGWSK



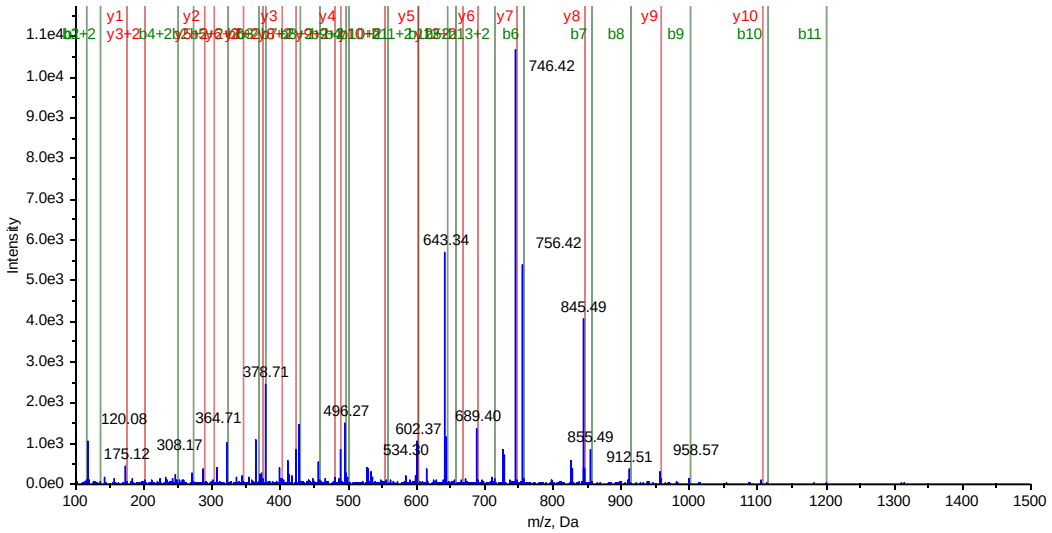
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	1502.6546	**751.8310**
N	**243.1452**	122.0762	**1374.5597**	**687.7835**
D	**358.1721**	179.5897	**1260.5168**	630.7620
F	**505.2405**	253.1239	**1145.4898**	573.2485
E	**634.2831**	317.6452	**998.4214**	499.7143
N	**748.3260**	374.6667	**869.3788**	435.1930
D	**863.3530**	432.1801	**755.3359**	378.1716
Y	**1026.4163**	513.7118	**640.3089**	320.6581
G	**1083.4378**	**542.2225**	**477.2456**	239.1264
W	**1269.5171**	635.2622	**420.2241**	210.6157
S	**1356.5491**	**678.7782**	**234.1448**	117.5761
K	1484.6441	**742.8257**	**147.1128**	74.0600

Peptide sequence 7: LKGGDIYWIPAGSAFYLLNTGR



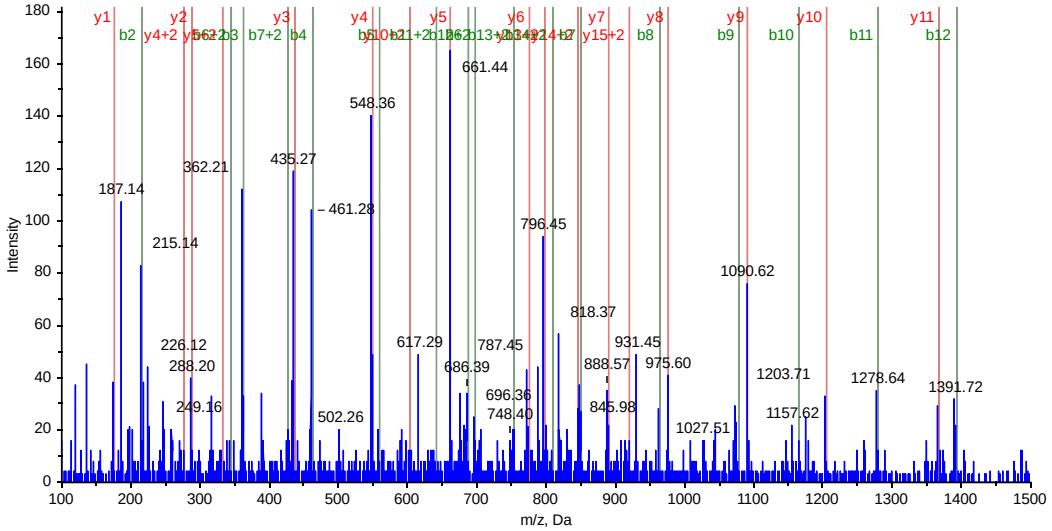
Residue	b	b+2	y	y+2
L	114.0913	57.5493	2412.2710	1206.6392
K	**242.1863**	121.5968	2299.1870	1150.0971
G	299.2078	150.1075	2171.0920	1086.0496
G	356.2292	178.6183	2114.0706	1057.5389
D	**471.2562**	236.1317	2057.0491	1029.0282
I	**584.3402**	292.6738	1942.0221	971.5147
Y	**747.4036**	374.2054	1828.9381	**914.9727**
W	**933.4829**	**467.2451**	1665.8748	**833.4410**
I	**1046.5669**	**523.7871**	**1479.7954**	**740.4014**
P	**1143.6197**	**572.3135**	**1366.7114**	**683.8593**
A	**1214.6568**	**607.8320**	**1269.6586**	**635.3329**
G	1271.6783	**636.3428**	**1198.6215**	**599.8144**
S	**1358.7103**	**679.8588**	**1141.6000**	571.3037
A	**1429.7474**	**715.3774**	**1054.5680**	527.7876
F	1576.8158	**788.9116**	**983.5309**	**492.2691**
Y	1739.8792	**870.4432**	**836.4625**	**418.7349**
L	1852.9632	**926.9853**	**673.3991**	**337.2032**
L	1966.0473	**983.5273**	**560.3151**	280.6612
N	2080.0902	**1040.5488**	**447.2310**	224.1191
T	2181.1379	1091.0726	**333.1881**	167.0977
G	2238.1594	1119.5833	**232.1404**	116.5738
R	2394.2605	1197.6339	**175.1190**	88.0631

Peptide sequence 8: NRPQFLVGSNSLLR



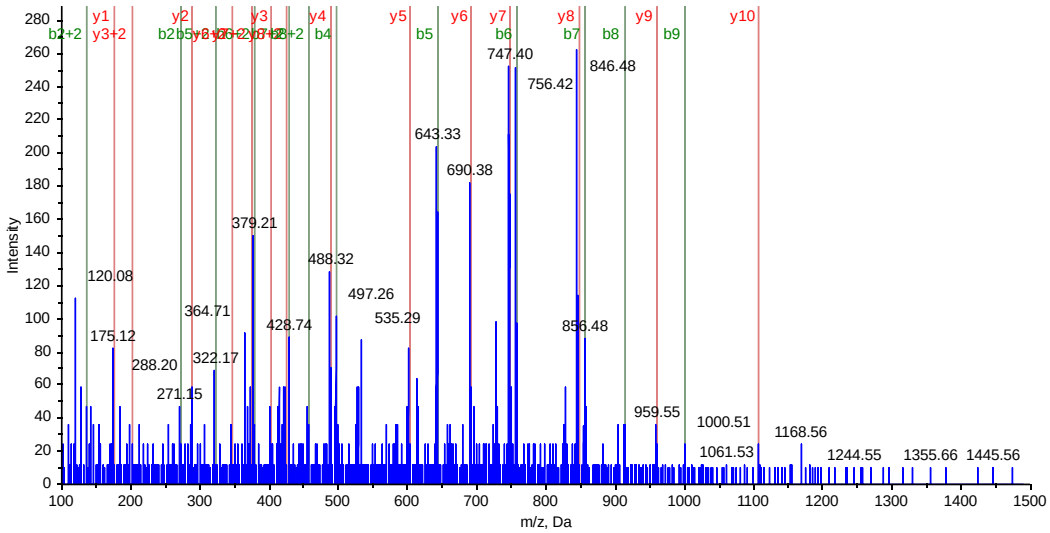
Residue	b	b+2	y	y+2
N	**115.0502**	58.0287	1600.8918	800.9495
R	**271.1513**	**136.0793**	1486.8489	743.9281
P	**368.2041**	184.6057	1330.7478	**665.8775**
Q	**496.2627**	**248.6350**	1233.6950	617.3511
F	**643.3311**	**322.1692**	**1105.6364**	**553.3218**
L	**756.4151**	**378.7112**	**958.5680**	**479.7876**
V	**855.4835**	**428.2454**	**845.4839**	**423.2456**
G	**912.5050**	**456.7561**	**746.4155**	**373.7114**
S	**999.5370**	**500.2722**	**689.3941**	**345.2007**
N	**1113.5800**	**557.2936**	**602.3620**	**301.6847**
S	**1200.6120**	**600.8096**	**488.3191**	244.6632
L	1313.6961	**657.3517**	**401.2871**	**201.1472**
L	1426.7801	**713.8937**	**288.2030**	144.6051
R	1582.8812	791.9443	**175.1190**	88.0631

Peptide sequence 9: TLFVPQYLDSNLLIFIR



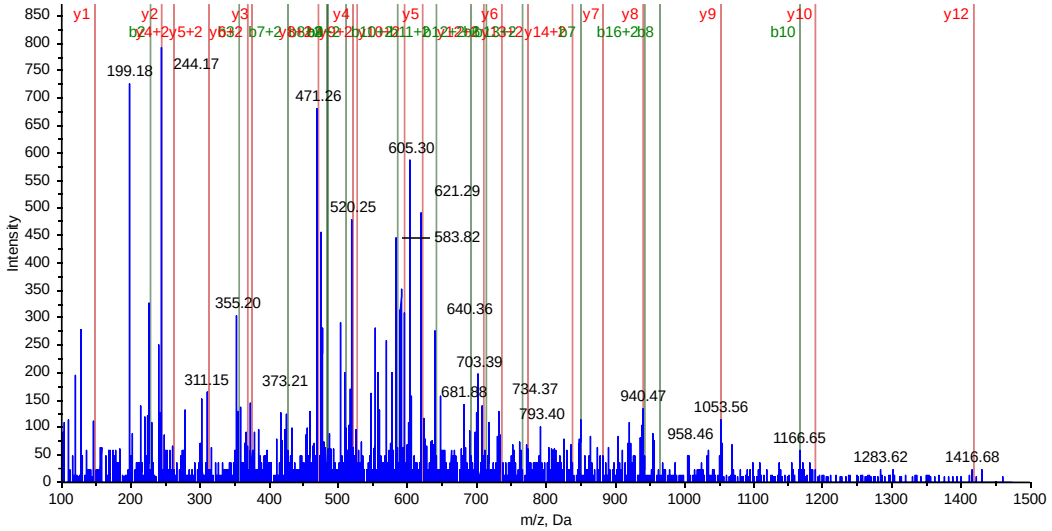
Residue	b	b+2	y	y+2
T	102.0550	51.5311	2052.1528	1026.5801
L	**215.1390**	108.0731	1951.1051	976.0562
F	**362.2074**	181.6074	1838.0211	**919.5142**
V	**461.2758**	231.1416	1690.9527	**845.9800**
P	**558.3286**	279.6679	1591.8843	**796.4458**
Q	**686.3872**	**343.6972**	1494.8315	747.9194
Y	**849.4505**	**425.2289**	**1366.7729**	683.8901
L	**962.5346**	481.7709	**1203.7096**	**602.3584**
D	**1077.5615**	539.2844	**1090.6255**	545.8164
S	**1164.5936**	582.8004	**975.5986**	488.3029
N	**1278.6365**	**639.8219**	**888.5665**	444.7869
L	**1391.7205**	**696.3639**	**774.5236**	387.7654
L	1504.8046	**752.9059**	**661.4396**	**331.2234**
I	1617.8887	**809.4480**	**548.3555**	**274.6814**
F	1764.9571	882.9822	**435.2714**	218.1394
I	1878.0411	939.5242	**288.2030**	144.6051
R	2034.1423	1017.5748	**175.1190**	88.0631

Peptide sequence 10: NRPQFLVGSN[Dea]SLLR



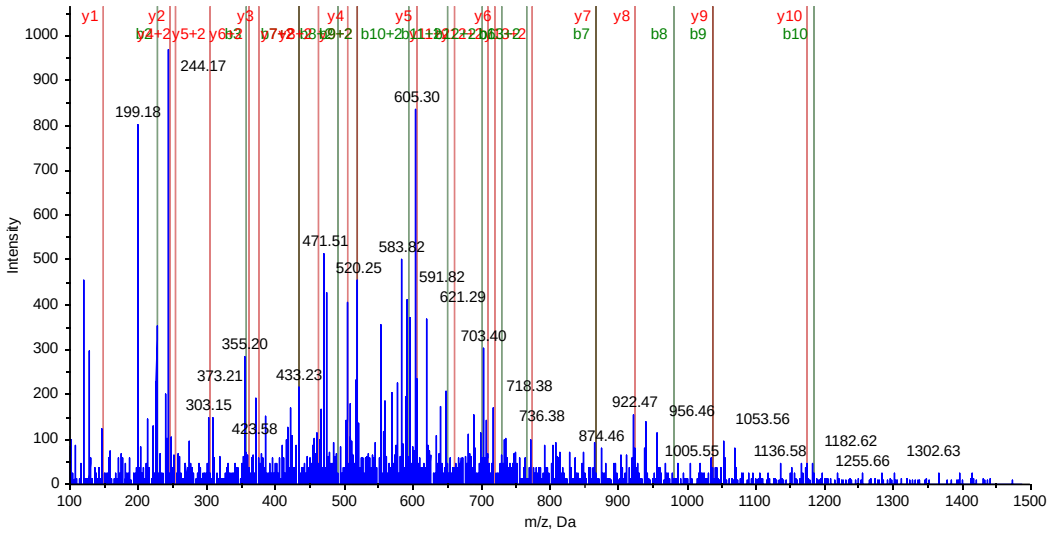
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1601.8758	801.4415
R	**271.1513**	**136.0793**	1487.8329	744.4201
P	368.2041	184.6057	1331.7318	666.3695
Q	**496.2627**	248.6350	1234.6790	617.8431
F	**643.3311**	**322.1692**	**1106.6204**	553.8139
L	**756.4151**	**378.7112**	**959.5520**	480.2796
V	**855.4835**	**428.2454**	**846.4680**	**423.7376**
G	**912.5050**	**456.7561**	**747.3995**	**374.2034**
S	**999.5370**	500.2722	**690.3781**	**345.6927**
N[Dea]	1114.5640	557.7856	**603.3461**	302.1767
S	1201.5960	601.3016	**488.3191**	244.6632
L	1314.6801	657.8437	**401.2871**	**201.1472**
L	1427.7641	714.3857	**288.2030**	144.6051
R	1583.8653	792.4363	**175.1190**	88.0631

Peptide sequence 11: IIEKPMHIGFLTM[Oxi]EPK



Residue	b	b+2	y	y+2
I	114.0913	57.5493	1900.0071	950.5072
I	**227.1754**	114.0913	1786.9230	893.9652
E	**356.2180**	178.6126	1673.8390	**837.4231**
K	**484.3130**	242.6601	1544.7964	**772.9018**
P	581.3657	291.1865	**1416.7014**	**708.8543**
M	**712.4062**	356.7067	1319.6486	660.3280
H	**849.4651**	**425.2362**	**1188.6082**	**594.8077**
I	**962.5492**	**481.7782**	**1051.5492**	**526.2783**
G	1019.5706	**510.2890**	**938.4652**	**469.7362**
F	**1166.6391**	**583.8232**	**881.4437**	441.2255
L	1279.7231	**640.3652**	**734.3753**	**367.6913**
T	1380.7708	**690.8890**	**621.2912**	**311.1493**
M[Oxi]	1527.8062	**764.4067**	**520.2436**	**260.6254**
E	1656.8488	828.9280	**373.2082**	187.1077
P	1753.9016	877.4544	**244.1656**	122.5864
K	1881.9965	**941.5019**	**147.1128**	74.0600

Peptide sequence 12: IIEKPM[Oxi]HIGFLTMEPK



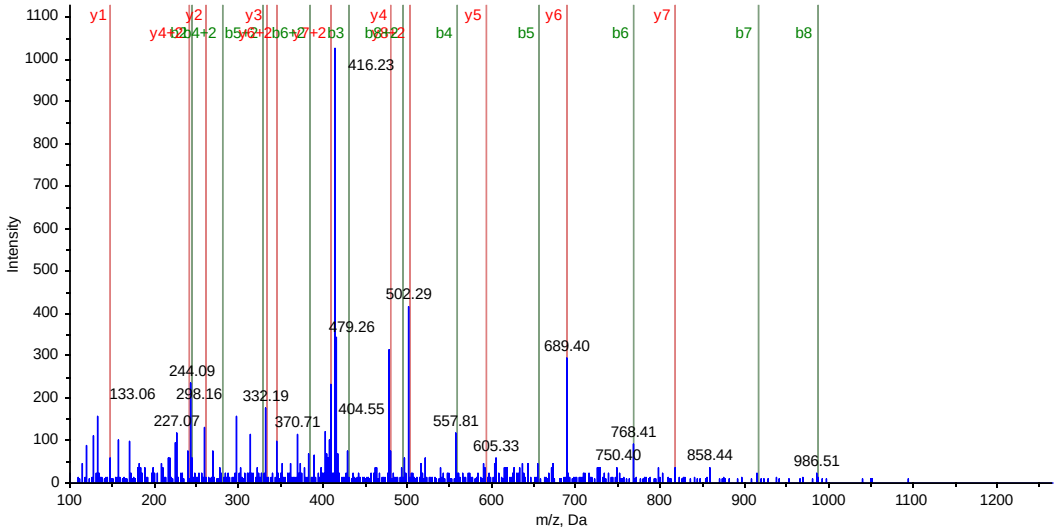
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1900.0071	950.5072
I	**227.1754**	114.0913	1786.9230	893.9652
E	**356.2180**	178.6126	1673.8390	837.4231
K	484.3130	242.6601	1544.7964	**772.9018**
P	581.3657	291.1865	1416.7014	**708.8543**
M[Oxi]	**728.4011**	364.7042	1319.6486	**660.3280**
H	**865.4600**	**433.2337**	**1172.6132**	586.8103
I	**978.5441**	**489.7757**	**1035.5543**	**518.2808**
G	**1035.5656**	**518.2864**	**922.4703**	**461.7388**
F	**1182.6340**	**591.8206**	**865.4488**	**433.2280**
L	1295.7180	**648.3627**	**718.3804**	**359.6938**
T	1396.7657	**698.8865**	**605.2963**	**303.1518**
M	1527.8062	**764.4067**	**504.2486**	**252.6280**
E	1656.8488	828.9280	**373.2082**	187.1077
P	1753.9016	877.4544	**244.1656**	122.5864
K	1881.9965	941.5019	**147.1128**	74.0600

Protein: B.rapa.Ro18.Candidate-2, 14 peptides (95%)

Protein sequence coverage

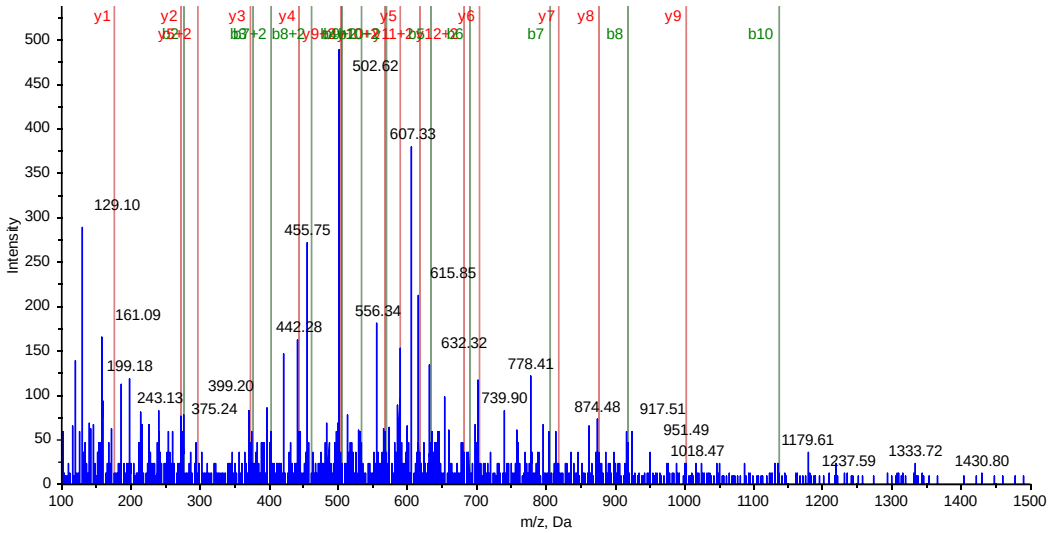
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GQISTVQIGDGCGGMGPYKIHSITLEPNALMLPLLLHSDMVFFVDSGSGILNWVEAQATSTEIRLGDVY
R**LRPGTVFYLQSKPVDIFLGTK**LKIYAIFSNSQECLHDPCFGAYSSVTDLLFGFDETILK**SAFGVPEEI**
IGLMRNRTQPPLIVHDMLTTPGEANTDTDTNTWPLQTRLLKLFSGDASADSVENKKVKKEKKEKKEKKK
KPK**KATTFNVFESEPDFQSPNGQTITINRK**DLKVLQGSMVGVSMVNLTQGSMMGPHWNPWACEISVVVR
GSGMVRVLRNSISRSSSECKNMR**FKVEKGDIFAVPR**LHPMAQMSFLNDSLVFVGFTTSAK**NNEPQFLAG**
KNSALWSLDREVLAASFNVSSFMIAGLLEAQKEAAVLGCPACAEGELEKLKEDEEKKESPPQQPPQPFQ
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Peptide sequence 1: DQWKPIFANK



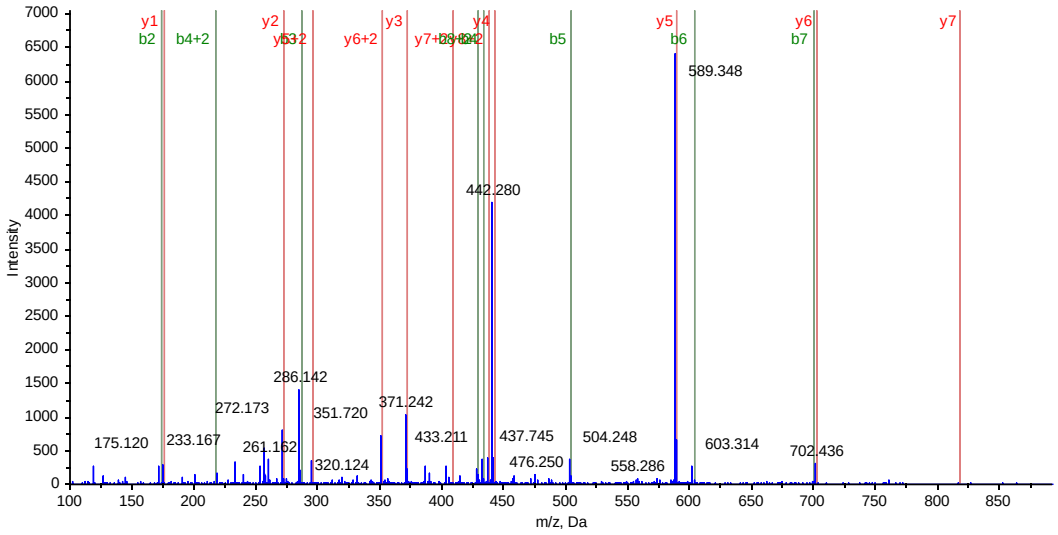
Residue	b	b+2	y	y+2
D	116.0342	58.5207	1246.6579	623.8326
Q	**244.0928**	122.5500	1131.6309	566.3191
W	**430.1721**	215.5897	1003.5724	**502.2898**
K	**558.2671**	**279.6372**	**817.4931**	**409.2502**
P	**655.3198**	**328.1636**	**689.3981**	**345.2027**
I	**768.4039**	**384.7056**	**592.3453**	296.6763
F	**915.4723**	458.2398	**479.2613**	**240.1343**
A	**986.5094**	**493.7584**	**332.1928**	166.6001
N	1100.5524	550.7798	**261.1557**	131.0815
K	1228.6473	614.8273	**147.1128**	74.0600

Peptide sequence 2: FKVEKGDIFAVPR



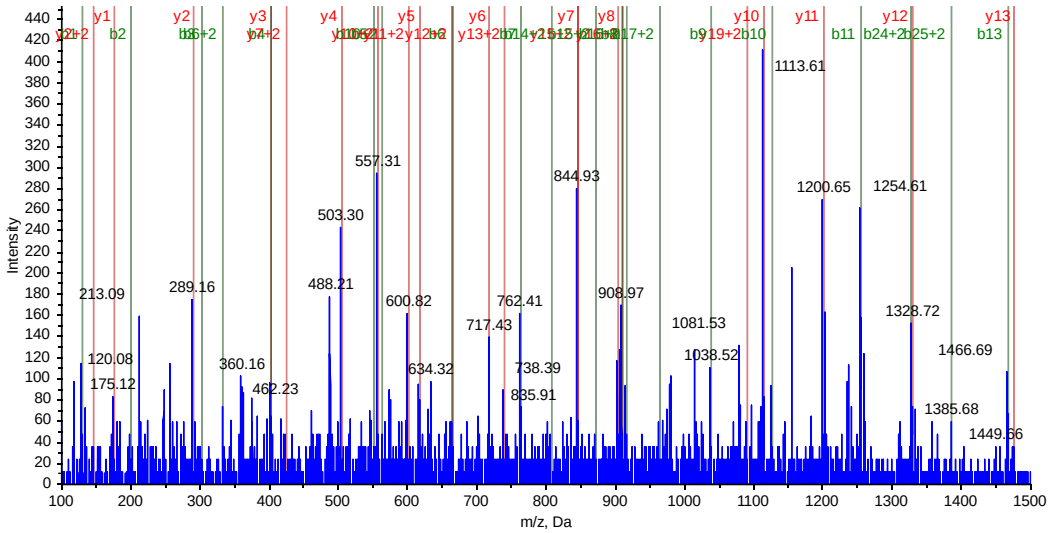
Residue	b	b+2	y	y+2
F	148.0757	74.5415	1505.8475	753.4274
K	**276.1707**	138.5890	1358.7791	**679.8932**
V	**375.2391**	188.1232	1230.6841	**615.8457**
E	**504.2817**	252.6445	1131.6157	**566.3115**
K	**632.3766**	316.6919	**1002.5731**	**501.7902**
G	**689.3981**	345.2027	**874.4781**	437.7427
D	**804.4250**	**402.7162**	**817.4567**	409.2320
I	**917.5091**	**459.2582**	**702.4297**	351.7185
F	1064.5775	**532.7924**	**589.3457**	**295.1765**
A	**1135.6146**	**568.3109**	**442.2772**	221.6423
V	1234.6830	617.8452	**371.2401**	186.1237
P	1331.7358	666.3715	**272.1717**	136.5895
R	1487.8369	744.4221	**175.1190**	88.0631

Peptide sequence 3: GDIFAVPR



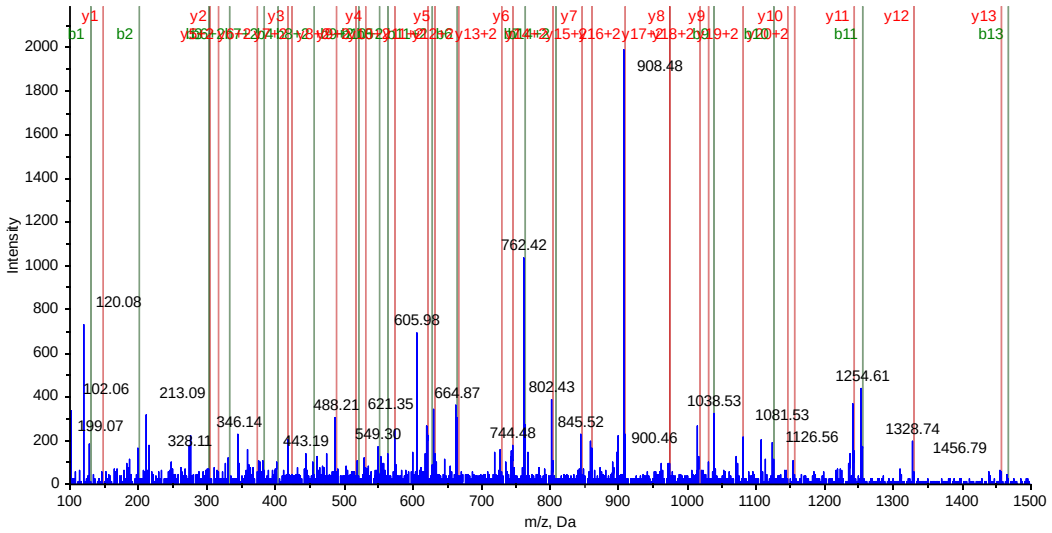
Residue	b	b+2	y	y+2
G	58.0287	29.5180	874.4781	**437.7427**
D	**173.0557**	87.0315	**817.4567**	**409.2320**
I	**286.1397**	143.5735	**702.4297**	**351.7185**
F	**433.2082**	**217.1077**	**589.3457**	**295.1765**
A	**504.2453**	252.6263	**442.2772**	221.6423
V	**603.3137**	302.1605	**371.2401**	186.1237
P	**700.3665**	350.6869	**272.1717**	136.5895
R	856.4676	**428.7374**	**175.1190**	88.0631

Peptide sequence 4: KATTFNVFESEPDFQSPNGQTITINR



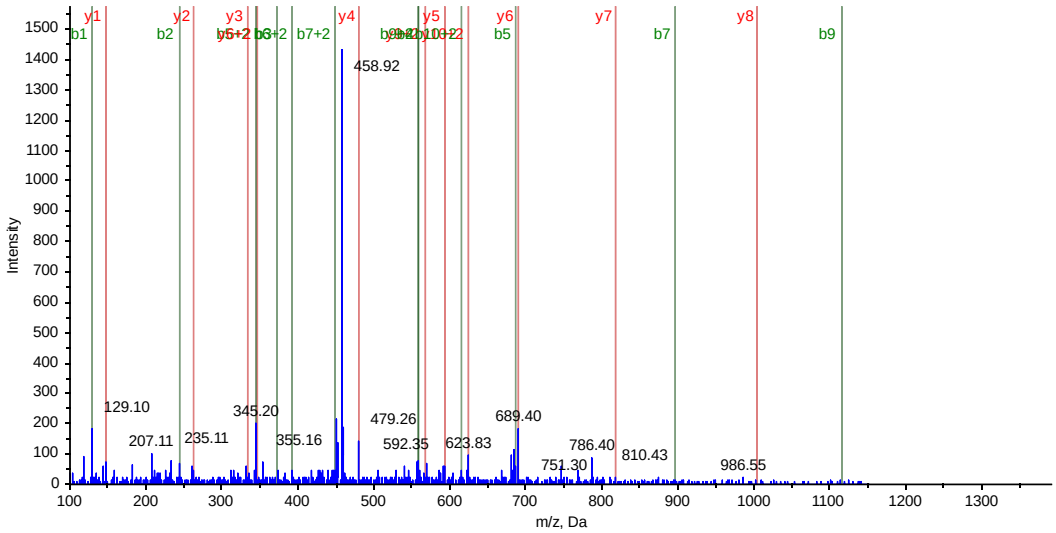
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	2941.4326	1471.2200
A	**200.1394**	100.5733	2813.3377	1407.1725
T	**301.1870**	151.0972	2742.3006	1371.6539
T	**402.2347**	201.6210	2641.2529	1321.1301
F	**549.3031**	275.1552	2540.2052	1270.6062
N	**663.3461**	**332.1767**	2393.1368	1197.0720
V	**762.4145**	381.7109	2279.0939	1140.0506
F	**909.4829**	455.2451	2180.0255	**1090.5164**
E	**1038.5255**	519.7664	2032.9570	1016.9822
S	**1125.5575**	**563.2824**	1903.9144	952.4609
E	**1254.6001**	627.8037	1816.8824	**908.9448**
P	1351.6529	676.3301	1687.8398	**844.4236**
D	**1466.6798**	733.8435	1590.7871	795.8972
F	1613.7482	**807.3777**	**1475.7601**	**738.3837**
Q	1741.8068	**871.4070**	**1328.6917**	**664.8495**
S	1828.8388	**914.9230**	**1200.6331**	**600.8202**
P	1925.8916	**963.4494**	**1113.6011**	**557.3042**
N	2039.9345	1020.4709	1016.5483	508.7778
G	2096.9560	1048.9816	**902.5054**	451.7563
Q	2225.0146	1113.0109	**845.4839**	**423.2456**
T	2326.0622	1163.5348	**717.4254**	359.2163
I	2439.1463	1220.0768	616.3777	308.6925
T	2540.1940	1270.6006	503.2936	252.1504
I	2653.2780	1327.1427	402.2459	201.6266
N	2767.3210	1384.1641	289.1619	145.0846
R	2923.4221	1462.2147	175.1190	88.0631

Peptide sequence 5: KATTFNVFESEPDFQSPNGQTITINRK



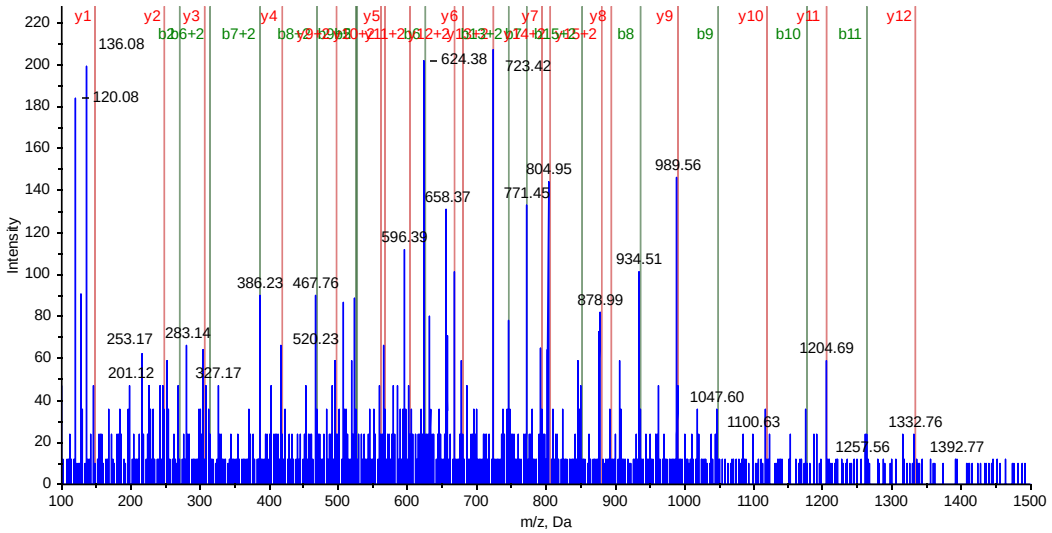
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	3069.5276	1535.2674
A	**200.1394**	100.5733	2941.4326	1471.2200
T	**301.1870**	151.0972	2870.3955	1435.7014
T	**402.2347**	201.6210	2769.3478	1385.1776
F	**549.3031**	275.1552	2668.3002	1334.6537
N	**663.3461**	**332.1767**	2521.2318	1261.1195
V	**762.4145**	**381.7109**	2407.1888	1204.0981
F	909.4829	**455.2451**	2308.1204	**1154.5638**
E	**1038.5255**	**519.7664**	2161.0520	**1081.0296**
S	**1125.5575**	**563.2824**	2032.0094	**1016.5083**
E	**1254.6001**	**627.8037**	1944.9774	**972.9923**
P	1351.6529	676.3301	1815.9348	**908.4710**
D	**1466.6798**	733.8435	1718.8820	**859.9446**
F	1613.7482	**807.3777**	1603.8551	**802.4312**
Q	1741.8068	871.4070	**1456.7867**	**728.8970**
S	1828.8388	914.9230	**1328.7281**	**664.8677**
P	1925.8916	963.4494	**1241.6961**	**621.3517**
N	2039.9345	1020.4709	**1144.6433**	**572.8253**
G	2096.9560	1048.9816	**1030.6004**	**515.8038**
Q	2225.0146	1113.0109	**973.5789**	**487.2931**
T	2326.0622	1163.5348	**845.5203**	**423.2638**
I	2439.1463	1220.0768	**744.4726**	**372.7400**
T	2540.1940	1270.6006	**631.3886**	**316.1979**
I	2653.2780	1327.1427	**530.3409**	265.6741
N	2767.3210	1384.1641	**417.2568**	209.1321
R	2923.4221	1462.2147	**303.2139**	152.1106
K	3051.5170	1526.2622	**147.1128**	74.0600

Peptide sequence 6: KDQWKPIFANK



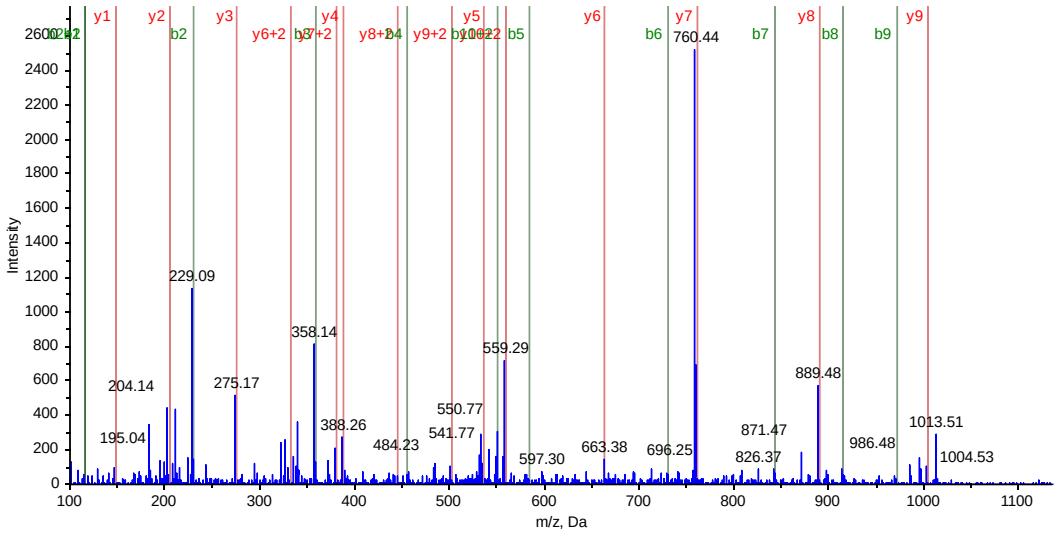
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	1374.7528	687.8801
D	**244.1292**	122.5682	1246.6579	**623.8326**
Q	**372.1878**	186.5975	1131.6309	**566.3191**
W	**558.2671**	279.6372	**1003.5724**	502.2898
K	**686.3620**	**343.6847**	**817.4931**	409.2502
P	783.4148	**392.2110**	**689.3981**	**345.2027**
I	**896.4989**	**448.7531**	**592.3453**	296.6763
F	1043.5673	522.2873	**479.2613**	240.1343
A	**1114.6044**	**557.8058**	**332.1928**	166.6001
N	1228.6473	**614.8273**	**261.1557**	131.0815
K	1356.7423	678.8748	**147.1128**	74.0600

Peptide sequence 7: LRPGTVFYLQSKPVDIFLGTK



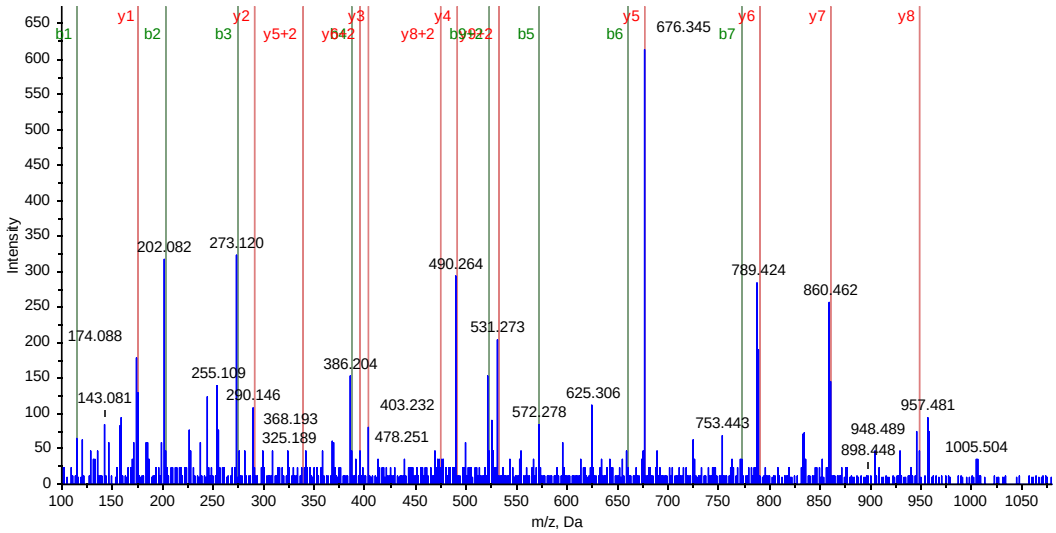
Residue	b	b+2	y	y+2
L	114.0913	57.5493	2379.3435	1190.1754
R	**270.1925**	135.5999	2266.2594	1133.6333
P	367.2452	184.1262	2110.1583	1055.5828
G	424.2667	212.6370	2013.1055	1007.0564
T	**525.3144**	263.1608	1956.0841	978.5457
V	**624.3828**	**312.6950**	1855.0364	928.0218
F	**771.4512**	**386.2292**	1755.9680	**878.4876**
Y	**934.5145**	**467.7609**	1608.8996	**804.9534**
L	**1047.5986**	**524.3029**	1445.8362	**723.4218**
Q	**1175.6572**	588.3322	**1332.7522**	**666.8797**
S	**1262.6892**	631.8482	**1204.6936**	**602.8504**
K	1390.7841	695.8957	**1117.6616**	**559.3344**
P	1487.8369	**744.4221**	**989.5666**	**495.2869**
V	1586.9053	793.9563	**892.5138**	446.7606
D	1701.9323	**851.4698**	**793.4454**	397.2264
I	1815.0163	908.0118	**678.4185**	339.7129
F	1962.0847	981.5460	**565.3344**	283.1709
L	2075.1688	1038.0880	**418.2660**	209.6366
G	2132.1903	1066.5988	**305.1819**	153.0946
T	2233.2380	1117.1226	**248.1605**	124.5839
K	2361.3329	1181.1701	**147.1128**	74.0600

Peptide sequence 8: NNEPQFLAGK



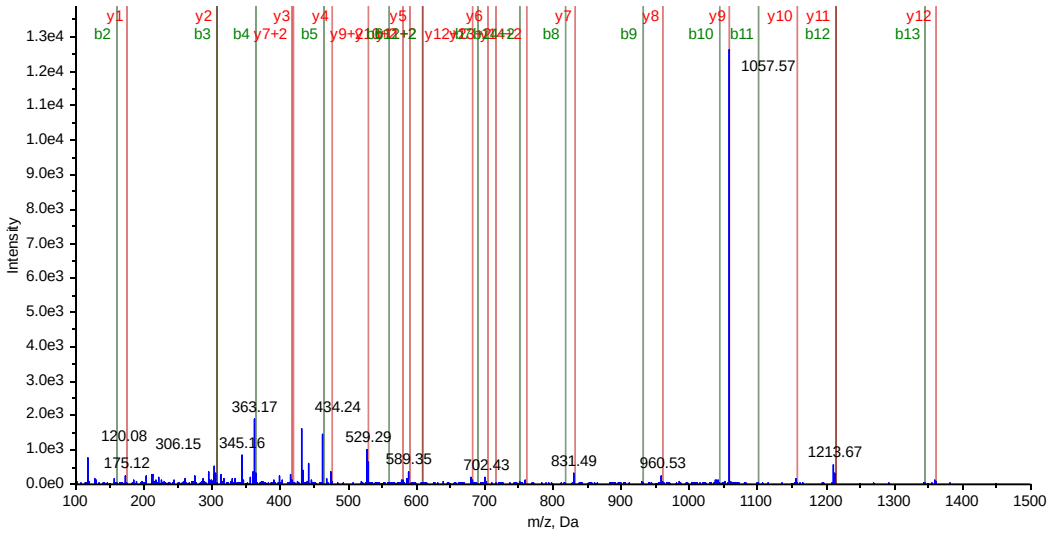
Residue	b	b+2	y	y+2
N	**115.0502**	58.0287	1117.5636	**559.2855**
N	**229.0931**	**115.0502**	**1003.5207**	**502.2640**
E	**358.1357**	179.5715	**889.4778**	**445.2425**
P	**455.1885**	228.0979	**760.4352**	**380.7212**
Q	**583.2471**	292.1272	**663.3824**	**332.1949**
F	**730.3155**	365.6614	**535.3239**	268.1656
L	**843.3995**	422.2034	**388.2554**	194.6314
A	**914.4367**	457.7220	**275.1714**	138.0893
G	**971.4581**	486.2327	**204.1343**	102.5708
K	1099.5531	**550.2802**	**147.1128**	74.0600

Peptide sequence 9: NSALWSLDR



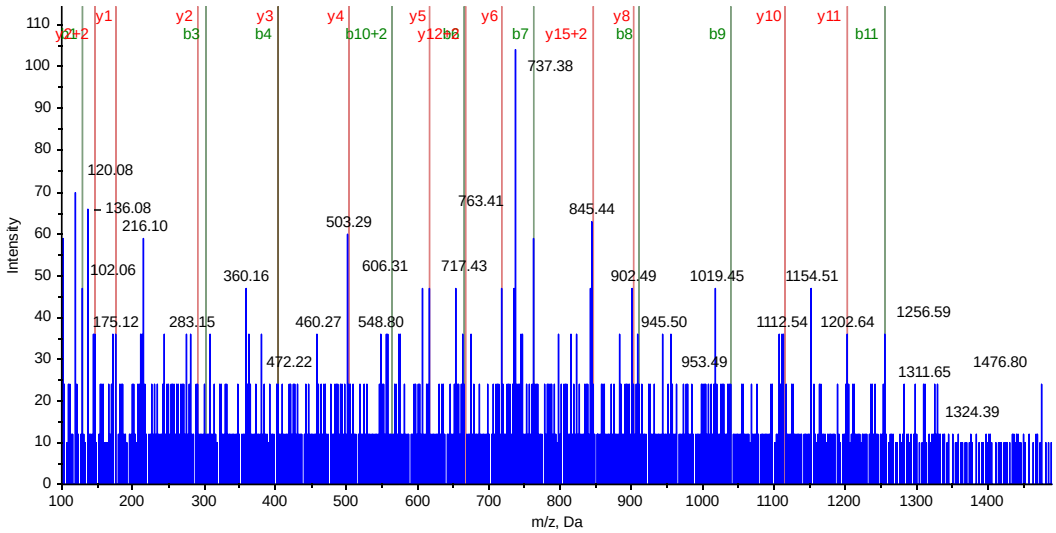
Residue	b	b+2	y	y+2
N	**115.0502**	58.0287	1061.5374	**531.2724**
S	**202.0822**	101.5448	**947.4945**	**474.2509**
A	**273.1193**	137.0633	**860.4625**	430.7349
L	**386.2034**	193.6053	**789.4254**	**395.2163**
W	**572.2827**	286.6450	**676.3413**	**338.6743**
S	**659.3148**	330.1610	**490.2620**	245.6346
L	**772.3988**	386.7030	**403.2300**	202.1186
D	887.4258	444.2165	**290.1459**	145.5766
R	1043.5269	**522.2671**	**175.1190**	88.0631

Peptide sequence 10: SAFGVPEEIIGLMR



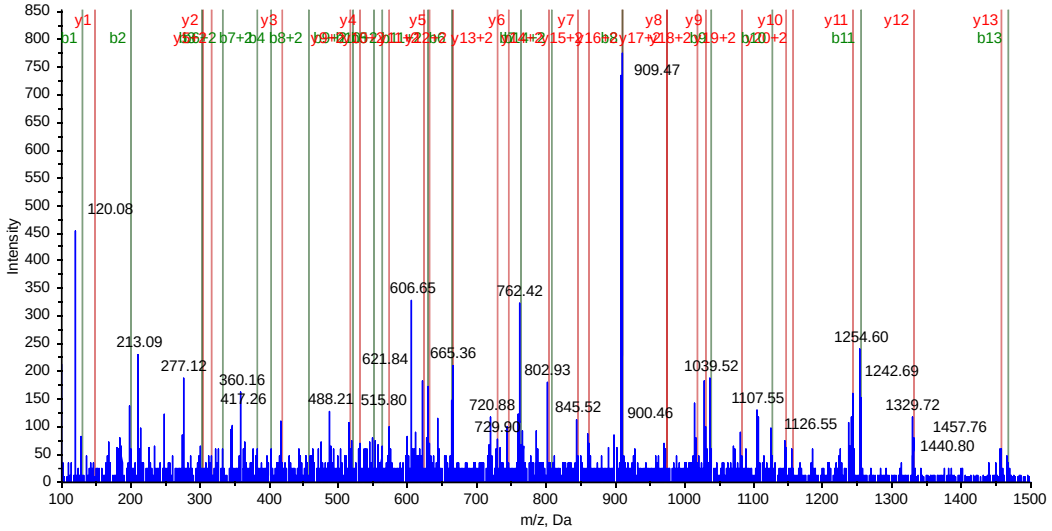
Residue	b	b+2	y	y+2
S	88.0393	44.5233	1518.7985	**759.9029**
A	**159.0764**	80.0418	1431.7664	**716.3869**
F	**306.1448**	153.5761	**1360.7293**	**680.8683**
G	**363.1663**	182.0868	**1213.6609**	**607.3341**
V	**462.2347**	231.6210	**1156.6395**	**578.8234**
P	**559.2875**	280.1474	**1057.5710**	**529.2892**
E	**688.3301**	344.6687	**960.5183**	480.7628
E	**817.3727**	409.1900	**831.4757**	**416.2415**
I	**930.4567**	465.7320	**702.4331**	351.7202
I	**1043.5408**	522.2740	**589.3490**	295.1782
G	**1100.5623**	550.7848	**476.2650**	238.6361
L	**1213.6463**	**607.3268**	**419.2435**	210.1254
M	**1344.6868**	672.8470	**306.1594**	153.5834
R	1500.7879	**750.8976**	**175.1190**	88.0631

Peptide sequence 11: KATTFNVFESEPDFQSPN[Dea]GQTITINR



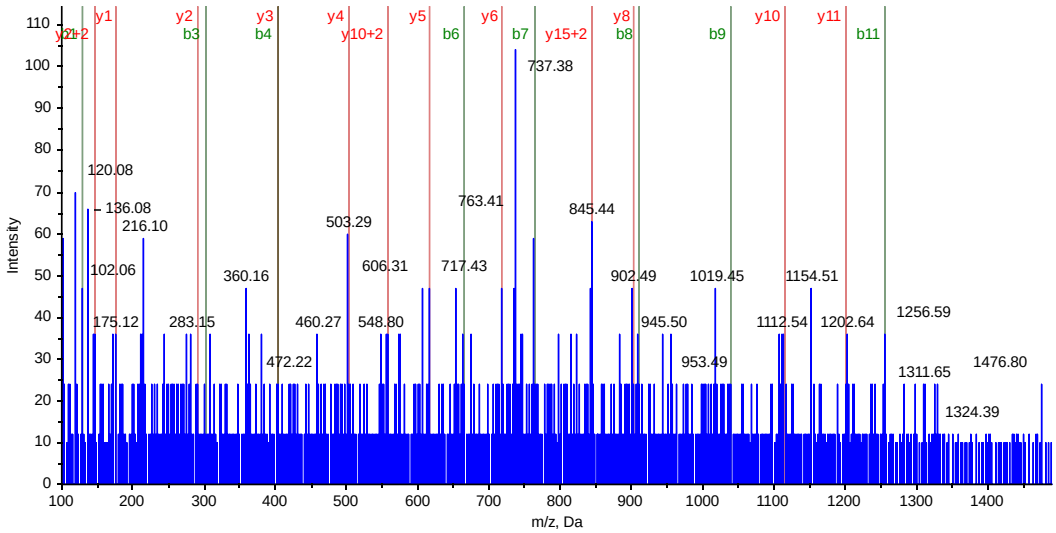
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	2942.4167	1471.7120
A	200.1394	100.5733	2814.3217	1407.6645
T	**301.1870**	151.0972	2743.2846	1372.1459
T	**402.2347**	201.6210	2642.2369	1321.6221
F	549.3031	275.1552	2541.1892	1271.0982
N	**663.3461**	332.1767	2394.1208	1197.5640
V	**762.4145**	381.7109	2280.0779	1140.5426
F	**909.4829**	455.2451	2181.0095	1091.0084
E	**1038.5255**	519.7664	2033.9411	1017.4742
S	1125.5575	**563.2824**	1904.8985	952.9529
E	**1254.6001**	627.8037	1817.8664	909.4369
P	1351.6529	676.3301	1688.8238	**844.9156**
D	1466.6798	733.8435	1591.7711	796.3892
F	1613.7482	807.3777	1476.7441	738.8757
Q	1741.8068	871.4070	1329.6757	**665.3415**
S	1828.8388	914.9230	**1201.6171**	601.3122
P	1925.8916	963.4494	**1114.5851**	557.7962
N[Dea]	2040.9185	1020.9629	1017.5323	509.2698
G	2097.9400	1049.4736	**902.5054**	451.7563
Q	2225.9986	1113.5029	845.4839	423.2456
T	2327.0462	1164.0268	**717.4254**	359.2163
I	2440.1303	1220.5688	**616.3777**	308.6925
T	2541.1780	1271.0926	**503.2936**	252.1504
I	2654.2621	1327.6347	**402.2459**	201.6266
N	2768.3050	1384.6561	**289.1619**	**145.0846**
R	2924.4061	1462.7067	**175.1190**	88.0631

Peptide sequence 12: KATTFNVFESEPDFQSPN[Dea]GQTITINRK



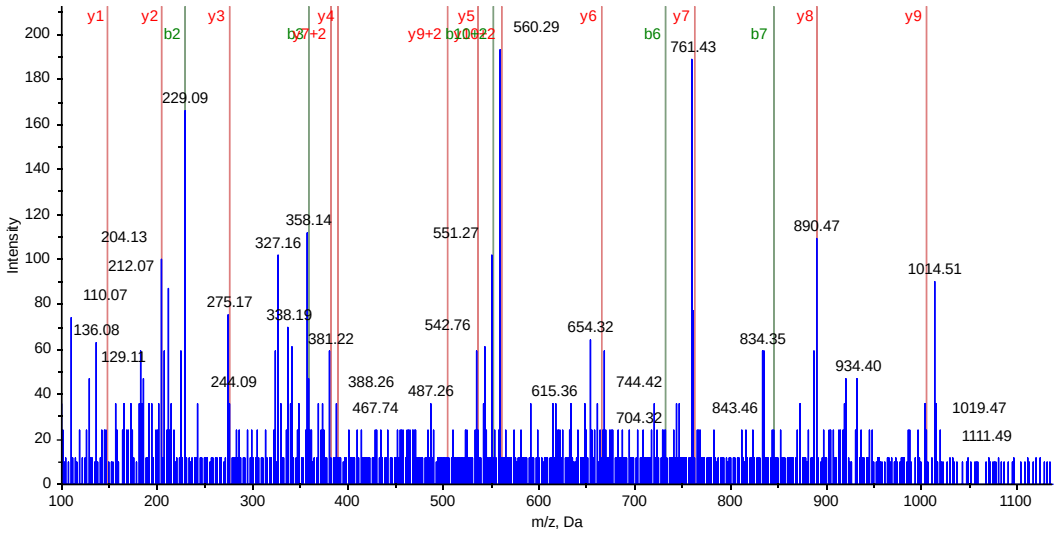
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	3070.5116	1535.7594
A	**200.1394**	100.5733	2942.4167	1471.7120
T	**301.1870**	151.0972	2871.3795	1436.1934
T	**402.2347**	201.6210	2770.3319	1385.6696
F	**549.3031**	275.1552	2669.2842	1335.1457
N	**663.3461**	**332.1767**	2522.2158	1261.6115
V	**762.4145**	**381.7109**	2408.1728	1204.5901
F	**909.4829**	**455.2451**	2309.1044	**1155.0559**
E	**1038.5255**	**519.7664**	2162.0360	**1081.5216**
S	**1125.5575**	**563.2824**	2032.9934	**1017.0004**
E	**1254.6001**	**627.8037**	1945.9614	**973.4843**
P	1351.6529	676.3301	1816.9188	**908.9630**
D	**1466.6798**	733.8435	1719.8660	**860.4367**
F	1613.7482	**807.3777**	1604.8391	**802.9232**
Q	1741.8068	871.4070	**1457.7707**	**729.3890**
S	1828.8388	914.9230	**1329.7121**	**665.3597**
P	1925.8916	963.4494	**1242.6801**	**621.8437**
N[Dea]	2040.9185	1020.9629	**1145.6273**	**573.3173**
G	2097.9400	1049.4736	**1030.6004**	515.8038
Q	2225.9986	1113.5029	**973.5789**	487.2931
T	2327.0462	1164.0268	**845.5203**	423.2638
I	2440.1303	1220.5688	**744.4726**	372.7400
T	2541.1780	1271.0926	**631.3886**	**316.1979**
I	2654.2621	1327.6347	**530.3409**	265.6741
N	2768.3050	1384.6561	**417.2568**	209.1321
R	2924.4061	1462.7067	**303.2139**	152.1106
K	3052.5011	1526.7542	**147.1128**	74.0600

Peptide sequence 13: KATTFN[Dea]VFESEPDFQSPNGQTITINR



Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	2942.4167	1471.7120
A	200.1394	100.5733	2814.3217	1407.6645
T	**301.1870**	151.0972	2743.2846	1372.1459
T	**402.2347**	201.6210	2642.2369	1321.6221
F	549.3031	275.1552	2541.1892	1271.0982
N[Dea]	**664.3301**	332.6687	2394.1208	1197.5640
V	**763.3985**	382.2029	2279.0939	1140.0506
F	**910.4669**	455.7371	2180.0255	1090.5164
E	**1039.5095**	520.2584	2032.9570	1016.9822
S	1126.5415	563.7744	1903.9144	952.4609
E	**1255.5841**	628.2957	1816.8824	908.9448
P	1352.6369	676.8221	1687.8398	**844.4236**
D	1467.6638	734.3355	1590.7871	795.8972
F	1614.7322	807.8698	1475.7601	738.3837
Q	1742.7908	871.8990	1328.6917	664.8495
S	1829.8228	915.4151	**1200.6331**	600.8202
P	1926.8756	963.9414	**1113.6011**	**557.3042**
N	2040.9185	1020.9629	1016.5483	508.7778
G	2097.9400	1049.4736	**902.5054**	451.7563
Q	2225.9986	1113.5029	845.4839	423.2456
T	2327.0462	1164.0268	**717.4254**	359.2163
I	2440.1303	1220.5688	**616.3777**	308.6925
T	2541.1780	1271.0926	**503.2936**	252.1504
I	2654.2621	1327.6347	**402.2459**	201.6266
N	2768.3050	1384.6561	**289.1619**	**145.0846**
R	2924.4061	1462.7067	**175.1190**	88.0631

Peptide sequence 14: NNEPQ[Dea]FLAGK



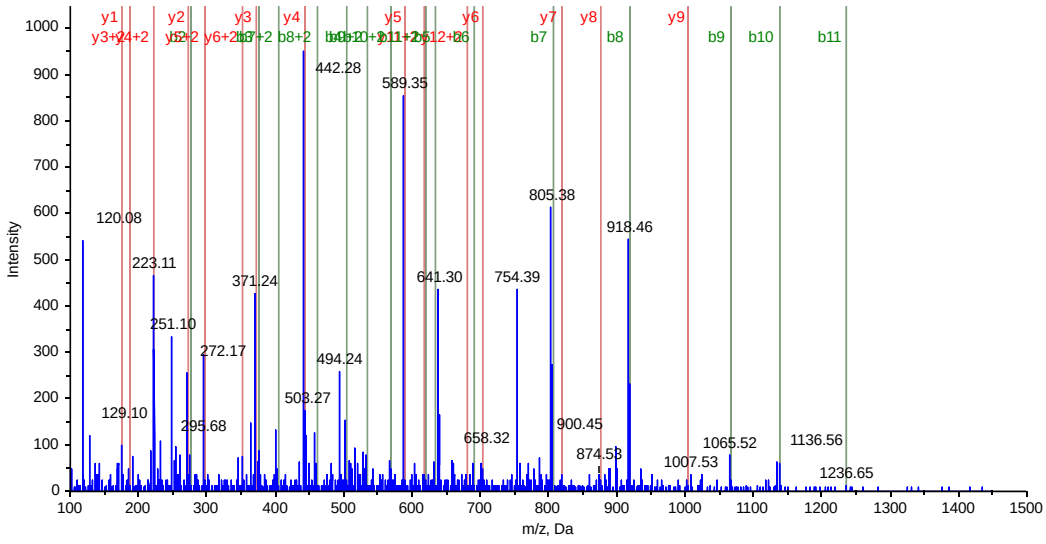
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1118.5477	**559.7775**
N	**229.0931**	115.0502	**1004.5047**	**502.7560**
E	**358.1357**	179.5715	**890.4618**	445.7345
P	455.1885	228.0979	**761.4192**	**381.2132**
Q[Dea]	584.2311	292.6192	**664.3665**	332.6869
F	**731.2995**	366.1534	**535.3239**	268.1656
L	**844.3836**	422.6954	**388.2554**	194.6314
A	915.4207	458.2140	**275.1714**	138.0893
G	972.4421	486.7247	**204.1343**	102.5708
K	1100.5371	**550.7722**	**147.1128**	74.0600

Protein: B.rapa.Ro18.Candidate-3, 2 peptides (95%)

Protein sequence coverage

MTKFTVLPLFVLLFLVLLCTKSWAKSEEFDESSDEENDVAAVPSCCGFSSPLLIKKDQWKPIFGTQFGQ
ISTVQIGEGCGGMGPYKIHSITLEPNALLLPLLLHSDMVFFVESGSGILNWVEAEPTSSEIRRGDVYRL
RPGTVFYLQSKPIDIFLGTKLRVYAIFSNTEECLHDPCFGAYSSITDLLFGFDEAILQSAFGVPEEIIG
LMTNRTQPPLIVHDMLSTPGEANTYTWQLQVQPRLLKLFAGYVSAAEKKKKEKKTKKAKTFNVFESEPD
FQSPSGRTITINRKDLEVLSGSMVGVSMVNLTQASMMGPHWNPWACEISIVLKGSGMVRVLRSSISSTS
SSSSSSECKNMR**FKVEEGDIFAVPR**LHPMAQMSFINESLVFIGFTTSARNNEPQFLAGQRSALRLLDQE
VLAASLNVSSVMIEGLLGAQKDAVVLGCPYCAEGELEKLKVETEMKKRDDERKREEEEAKKEEEERRKR
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Peptide sequence 1: FKVEEGDIFAVPR



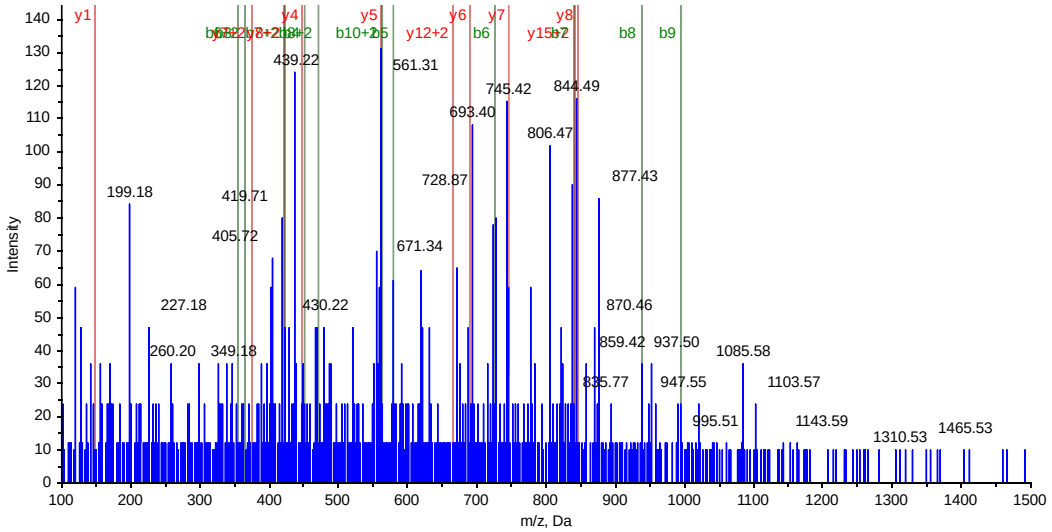
Residue	b	b+2	y	y+2
F	148.0757	74.5415	1506.7951	753.9012
K	**276.1707**	138.5890	1359.7267	**680.3670**
V	**375.2391**	188.1232	1231.6317	**616.3195**
E	**504.2817**	252.6445	1132.5633	566.7853
E	**633.3243**	317.1658	**1003.5207**	502.2640
G	**690.3457**	345.6765	**874.4781**	437.7427
D	**805.3727**	**403.1900**	**817.4567**	409.2320
I	**918.4567**	**459.7320**	**702.4297**	**351.7185**
F	**1065.5251**	**533.2662**	**589.3457**	**295.1765**
A	**1136.5623**	**568.7848**	**442.2772**	**221.6423**
V	**1235.6307**	**618.3190**	**371.2401**	**186.1237**
P	1332.6834	666.8454	**272.1717**	136.5895
R	1488.7845	744.8959	**175.1190**	88.0631

Protein: B.rapa.Ro18.Candidate-4, 2 peptides (95%)

Protein sequence coverage

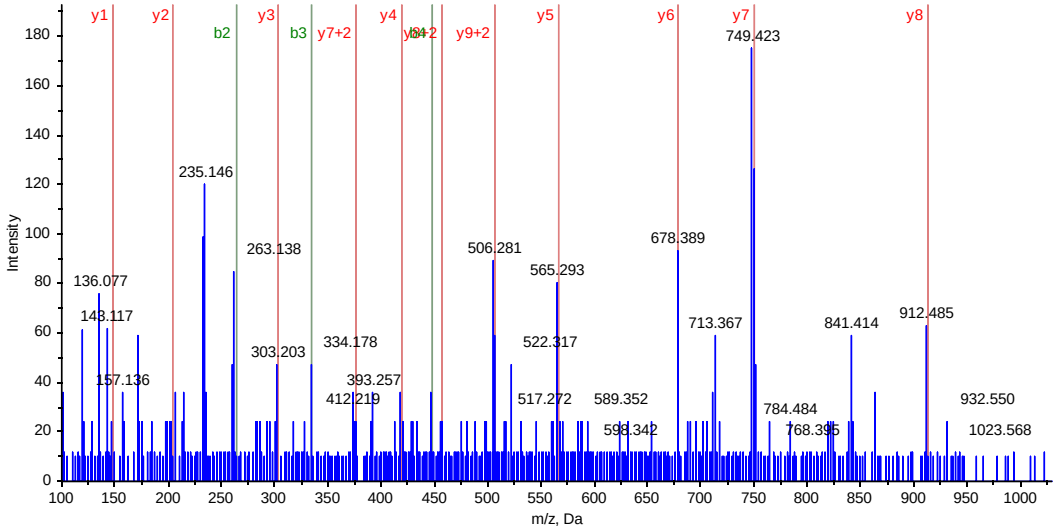
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VYAIFDVGKCLSDQCLGAYSSIRDLLWGFDEKTLRSAFAVPKDVFGRLRDAVKPPLITHAMPKNRTQGS
EEETWGSRLAKLFVRVEDVTDHLEMKPVVNKKKKKKKKSSAYNVFESDPDFENDNGQSIVVDEKDMDA
LKGSSFGVYMVNLTKGSMMGPHWNPNACEISIVLQGEGMIRVVNHPSYQSKNESERFMVEDGDVFVVPQ
FYPMAQLSFVNSSFMFMGFSTSAK**TNHPQFLVGQNSVLK**IFNRDVLATSFNMRYATVERLLGAQKDGLL
LECVSCAEVELSRLMREIEERRRREEEEIERRKREEEEAKRQEEERRRREEEEAERKKKAEEEARKREK
ERE REEEAAKRREEERRRREEEEAERKRKEEEEARKREEERKREEEAAKKREEERRKREKEEEEARKRE
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REEERQRKERE DVERKKREEEEERKRREEEAMRREEERKREEEAAKRAEEERRKREEEAEHKKRPPPQG
PQPPIHH

Peptide sequence 1: TNHPQFLVGQNSVLK



Residue	b	b+2	y	y+2
T	102.0550	51.5311	1681.9020	**841.4547**
N	216.0979	108.5526	1580.8544	790.9308
H	**353.1568**	177.0820	1466.8114	733.9094
P	**450.2096**	225.6084	1329.7525	**665.3799**
Q	**578.2681**	289.6377	1232.6997	616.8535
F	**725.3365**	**363.1719**	1104.6412	552.8242
L	**838.4206**	**419.7139**	957.5728	479.2900
V	**937.4890**	**469.2482**	**844.4887**	**422.7480**
G	**994.5105**	497.7589	**745.4203**	**373.2138**
Q	1122.5691	**561.7882**	**688.3988**	344.7030
N	1236.6120	618.8096	**560.3402**	280.6738
S	1323.6440	662.3257	**446.2973**	223.6523
V	1422.7124	711.8599	359.2653	180.1363
L	1535.7965	768.4019	260.1969	130.6021
K	1663.8915	832.4494	**147.1128**	74.0600

Peptide sequence 2: VYAIFDVGK



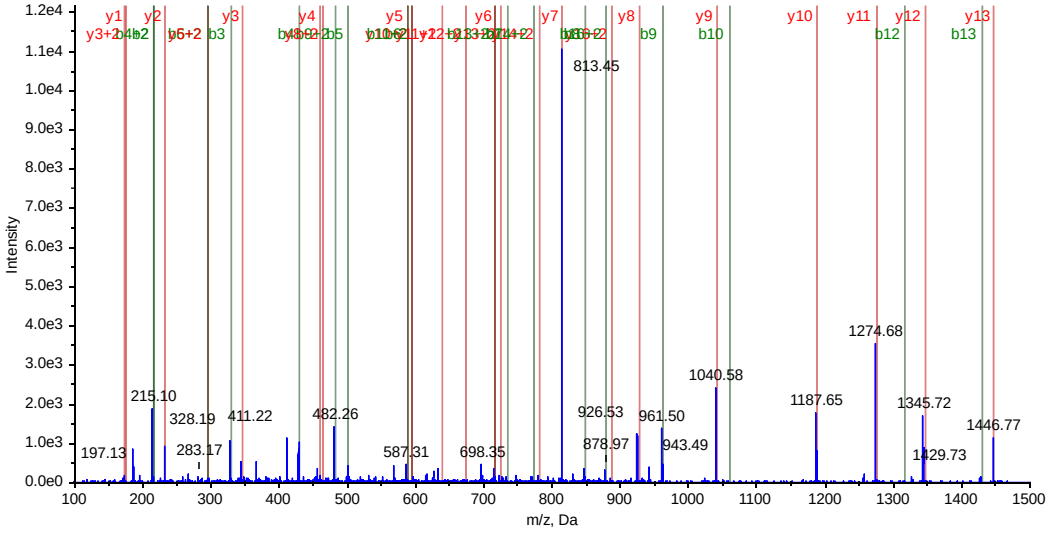
Residue	b	b+2	y	y+2
V	100.0757	50.5415	1011.5510	**506.2791**
Y	**263.1390**	132.0731	**912.4825**	**456.7449**
A	**334.1761**	167.5917	**749.4192**	**375.2132**
I	**447.2602**	224.1337	**678.3821**	339.6947
F	594.3286	297.6679	**565.2980**	283.1527
D	709.3556	355.1814	**418.2296**	209.6185
V	808.4240	404.7156	**303.2027**	152.1050
G	865.4454	433.2264	**204.1343**	102.5708
K	993.5404	497.2738	**147.1128**	74.0600

Protein: B.rapa.Ro18.Candidate-5, 21 peptides (95%)

Protein sequence coverage

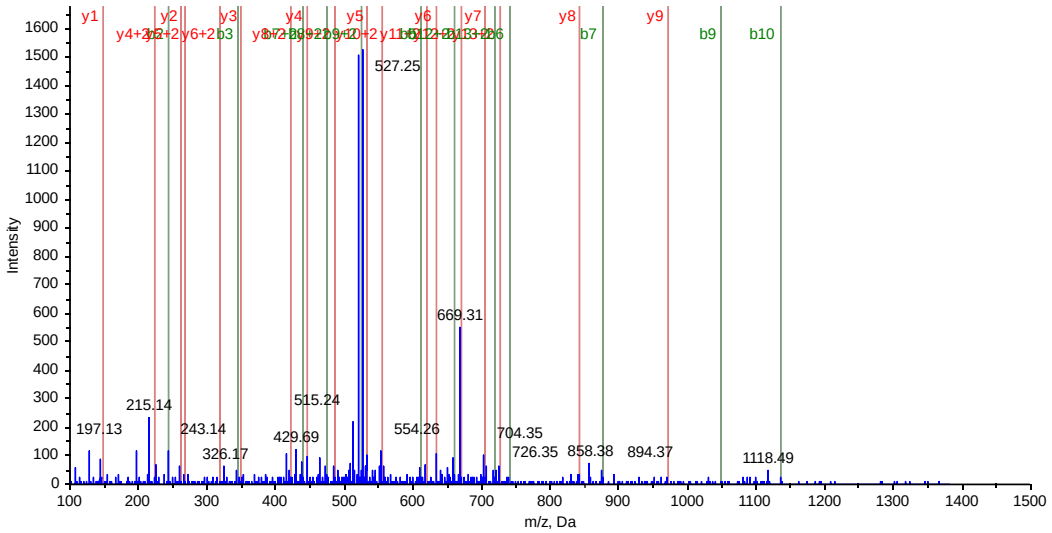
MAINKLTITLFLLISLAVFHCLAFRVEVQEFEPPRQEGQEGPGGGSGEGWDEEATK**NPYHFGQWSFK**NF
FQSKDGFVKMLPKFTKR**SSTLFR**GIENYR**FLFQEMQPNTFLVPHHLDADYVFLVVQGK**GVIGFVTDTAN
ESFQITKGDVVR**VPSSVTHFFANTNGTVPLR**LAK**IAVPANVPGHFQVFFPAHSGFHQSYFNGFSKDVLT**
ASFNIPEELLGRLIRGPQQEVGQGIIRRVSPEQIKELTEHEHATSPSNKHKDKKDKHKDKDR**STFGSPF**
NLLTQDAIYSNNFGRYHEAHPKRFSQLQDLDIAVGWVNMTQGSLFLPQYNSETTFVTFVENGCARYEMA
SPYTFQGEQQQPWFGPGQEEEVEEEMSGQVHKIVSRVCKGEVFILPAGHPFAILSQDENFVAVGFGIHA
SNSTR**TFLAGQDNMLSNINTVATRLSFGLGSK**MAEKLFTSQNYSHFAPTTPSHQFPEKPKPSFQSVFNL
VGF

Peptide sequence 1: DVLTASFNIPEELLGR



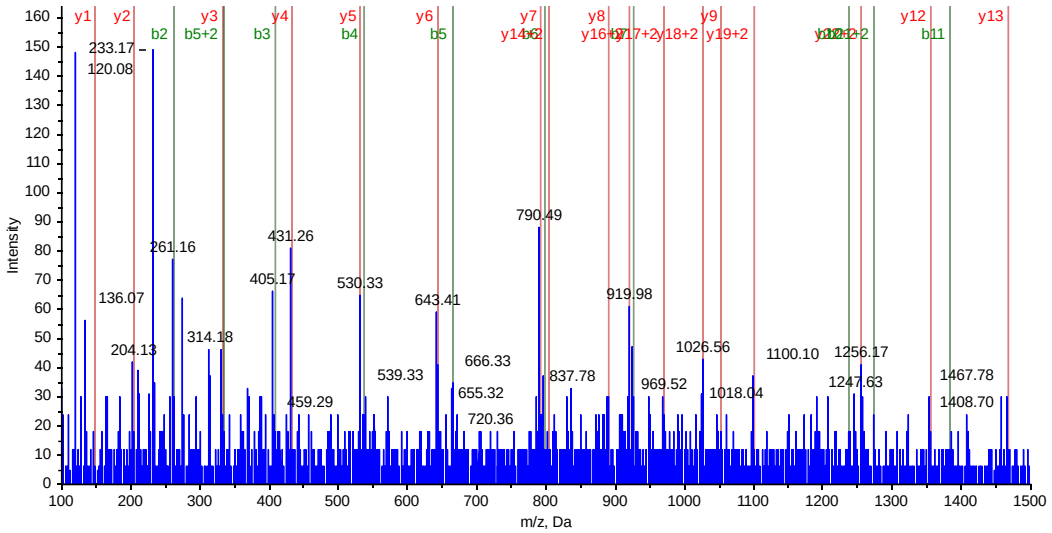
Residue	b	b+2	y	y+2
D	116.0342	58.5207	1773.9381	**887.4727**
V	**215.1026**	108.0550	1658.9112	829.9592
L	**328.1867**	164.5970	1559.8428	**780.4250**
T	**429.2344**	**215.1208**	**1446.7587**	**723.8830**
A	**500.2715**	250.6394	**1345.7110**	**673.3592**
S	**587.3035**	**294.1554**	**1274.6739**	**637.8406**
F	**734.3719**	367.6896	**1187.6419**	**594.3246**
N	**848.4149**	424.7111	**1040.5735**	520.7904
I	**961.4989**	**481.2531**	**926.5306**	**463.7689**
P	**1058.5517**	529.7795	**813.4465**	407.2269
E	1187.5943	594.3008	**716.3937**	358.7005
E	**1316.6369**	658.8221	**587.3511**	**294.1792**
L	**1429.7209**	**715.3641**	**458.3085**	229.6579
L	1542.8050	**771.9061**	**345.2245**	**173.1159**
G	1599.8265	800.4169	**232.1404**	116.5738
R	1755.9276	**878.4674**	**175.1190**	88.0631

Peptide sequence 2: ELTEHEHATSPSNK



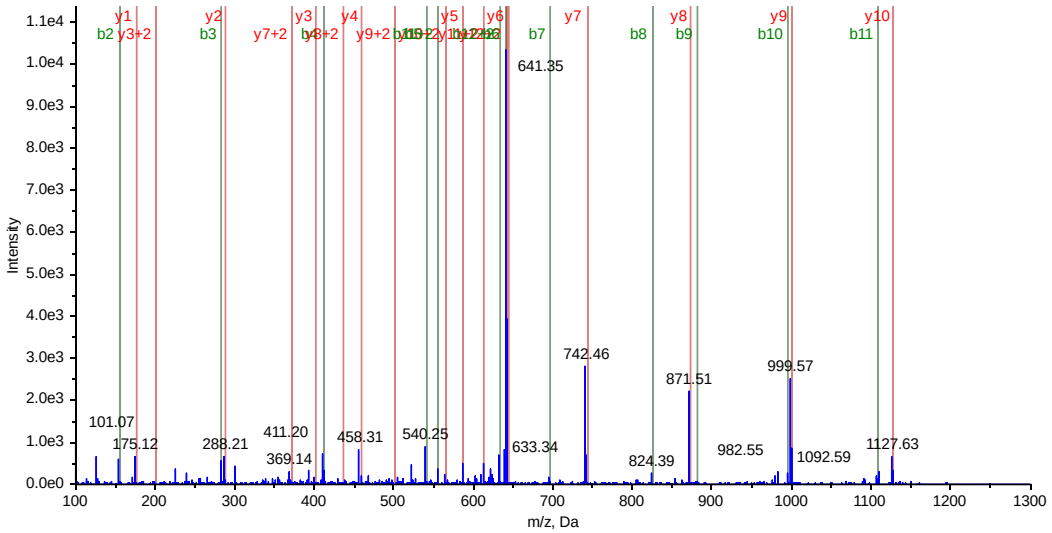
Residue	b	b+2	y	y+2
E	130.0499	65.5286	1579.7347	790.3710
L	**243.1339**	122.0706	1450.6921	**725.8497**
T	**344.1816**	172.5944	1337.6080	**669.3077**
E	473.2242	237.1157	1236.5604	**618.7838**
H	**610.2831**	305.6452	1107.5178	**554.2625**
E	**739.3257**	370.1665	**970.4588**	**485.7331**
H	**876.3846**	**438.6959**	**841.4163**	**421.2118**
A	947.4217	**474.2145**	**704.3573**	352.6823
T	**1048.4694**	**524.7383**	**633.3202**	**317.1638**
S	**1135.5014**	568.2544	**532.2726**	**266.6399**
P	1232.5542	616.7807	**445.2405**	**223.1239**
S	1319.5862	**660.2968**	**348.1878**	174.5975
N	1433.6292	**717.3182**	**261.1557**	131.0815
K	1561.7241	781.3657	**147.1128**	74.0600

Peptide sequence 3: FLFQEMQPNTFLVPHHLDADYVFLVVQGK



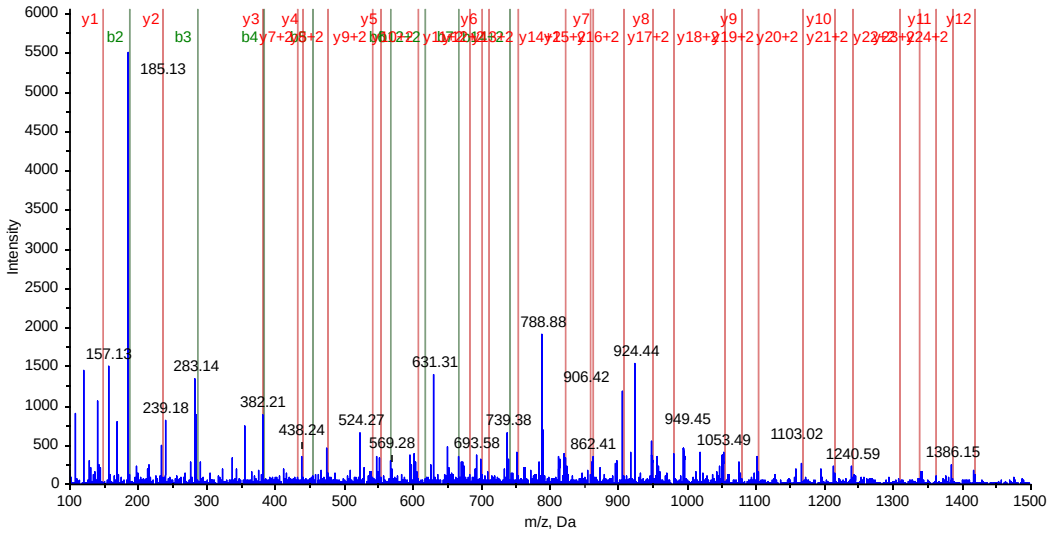
Residue	b	b+2	y	y+2
F	148.0757	74.5415	3432.7449	1716.8761
L	**261.1598**	131.0835	3285.6765	1643.3419
F	**408.2282**	204.6177	3172.5925	1586.7999
Q	**536.2867**	268.6470	3025.5240	1513.2657
E	**665.3293**	**333.1683**	2897.4655	1449.2364
M	**796.3698**	398.6885	2768.4229	1384.7151
Q	**924.4284**	462.7178	2637.3824	1319.1948
P	1021.4812	511.2442	2509.3238	**1255.1655**
N	1135.5241	568.2657	2412.2710	1206.6392
T	**1236.5718**	618.7895	2298.2281	1149.6177
F	**1383.6402**	692.3237	2197.1804	**1099.0939**
L	1496.7242	748.8658	2050.1120	**1025.5596**
V	1595.7927	798.4000	1937.0280	**969.0176**
P	1692.8454	846.9264	1837.9595	**919.4834**
H	1829.9043	915.4558	1740.9068	870.9570
H	1966.9633	983.9853	1603.8479	**802.4276**
L	2080.0473	1040.5273	**1466.7890**	733.8981
D	2195.0743	1098.0408	**1353.7049**	677.3561
A	2266.1114	1133.5593	1238.6780	619.8426
D	2381.1383	1191.0728	1167.6408	584.3241
Y	2544.2016	**1272.6045**	**1052.6139**	526.8106
V	2643.2701	1322.1387	**889.5506**	445.2789
F	2790.3385	1395.6729	**790.4822**	395.7447
L	2903.4225	1452.2149	**643.4137**	322.2105
V	3002.4909	1501.7491	**530.3297**	265.6685
V	3101.5594	1551.2833	**431.2613**	216.1343
Q	3229.6179	1615.3126	**332.1928**	166.6001
G	3286.6394	1643.8233	**204.1343**	102.5708
K	3414.7344	1707.8708	**147.1128**	74.0600

Peptide sequence 4: GPQQEVGQGIIR



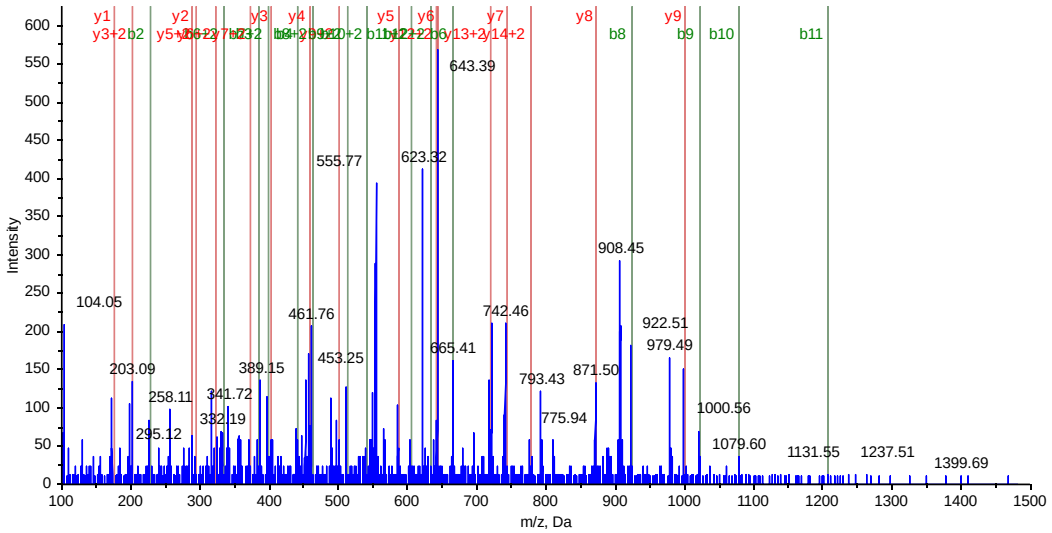
Residue	b	b+2	y	y+2
G	58.0287	29.5180	1281.6910	**641.3491**
P	**155.0815**	78.0444	1224.6695	**612.8384**
Q	**283.1401**	142.0737	**1127.6167**	**564.3120**
Q	**411.1987**	206.1030	**999.5582**	**500.2827**
E	**540.2413**	270.6243	**871.4996**	**436.2534**
V	**639.3097**	320.1585	**742.4570**	**371.7321**
G	**696.3311**	348.6692	**643.3886**	322.1979
Q	**824.3897**	412.6985	**586.3671**	293.6872
G	**881.4112**	441.2092	**458.3085**	229.6579
I	**994.4952**	497.7513	**401.2871**	**201.1472**
I	**1107.5793**	**554.2933**	**288.2030**	144.6051
R	1263.6804	**632.3438**	**175.1190**	88.0631

Peptide sequence 5: IAVPANVPGHFQVFFPAHSGFHQSYFNGFSK



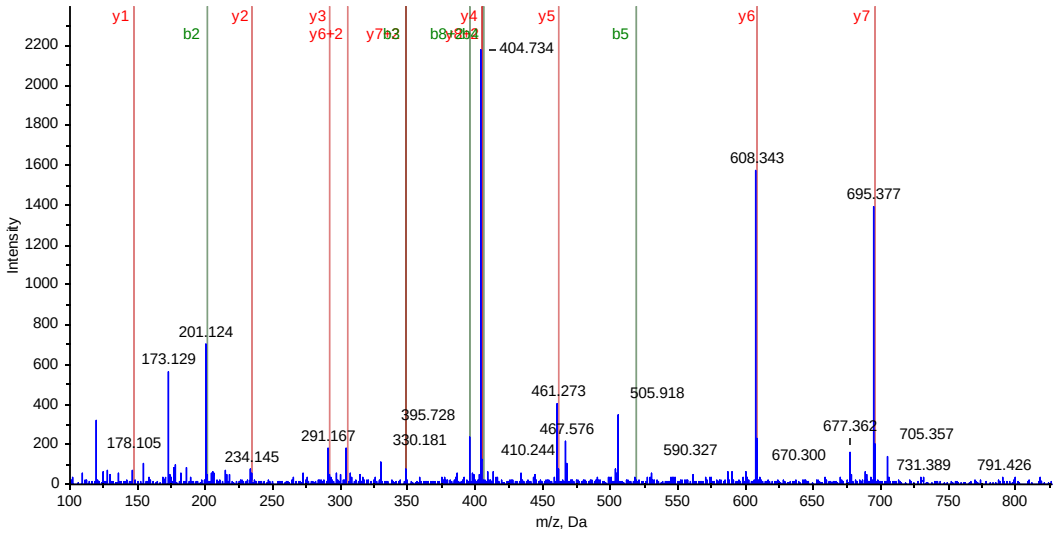
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3434.6858	1717.8465
A	**185.1285**	93.0679	3321.6017	1661.3045
V	**284.1969**	142.6021	3250.5646	1625.7859
P	**381.2496**	191.1285	3151.4962	1576.2517
A	**452.2867**	226.6470	3054.4434	1527.7253
N	**566.3297**	283.6685	2983.4063	1492.2068
V	**665.3981**	333.2027	2869.3634	1435.1853
P	762.4509	381.7291	2770.2950	**1385.6511**
G	819.4723	410.2398	2673.2422	**1337.1247**
H	956.5312	478.7693	2616.2207	**1308.6140**
F	1103.5996	552.3035	2479.1618	**1240.0846**
Q	1231.6582	**616.3327**	2332.0934	**1166.5503**
V	1330.7266	665.8670	2204.0348	**1102.5211**
F	1477.7950	**739.4012**	2104.9664	**1052.9868**
F	1624.8635	812.9354	1957.8980	**979.4526**
P	1721.9162	861.4618	1810.8296	**905.9184**
A	1792.9533	896.9803	1713.7768	**857.3921**
H	1930.0122	965.5098	1642.7397	**821.8735**
S	2017.0443	1009.0258	1505.6808	**753.3440**
G	2074.0657	1037.5365	**1418.6488**	**709.8280**
F	2221.1342	1111.0707	**1361.6273**	**681.3173**
H	2358.1931	1179.6002	**1214.5589**	**607.7831**
Q	2486.2516	1243.6295	**1077.5000**	**539.2536**
S	2573.2837	1287.1455	**949.4414**	**475.2243**
Y	2736.3470	1368.6771	**862.4094**	**431.7083**
F	2883.4154	1442.2113	**699.3461**	350.1767
N	2997.4583	1499.2328	**552.2776**	276.6425
G	3054.4798	1527.7435	**438.2347**	219.6210
F	3201.5482	1601.2777	**381.2132**	191.1103
S	3288.5802	1644.7938	**234.1448**	117.5761
K	3416.6752	1708.8412	**147.1128**	74.0600

Peptide sequence 6: LIRGPQQEVGQGIIR



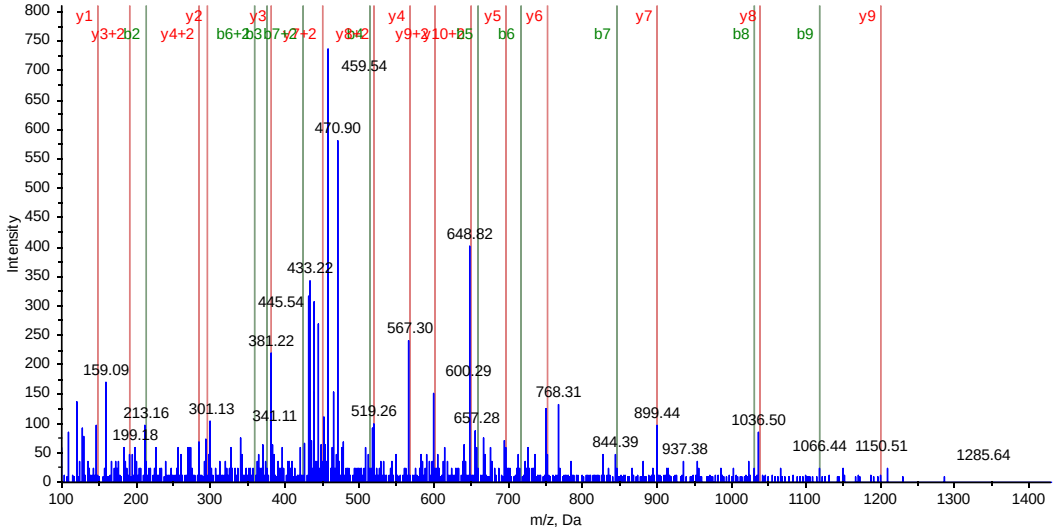
Residue	b	b+2	y	y+2
L	114.0913	57.5493	1663.9602	832.4837
I	**227.1754**	114.0913	1550.8761	**775.9417**
R	**383.2765**	192.1419	1437.7921	**719.3997**
G	**440.2980**	220.6526	1281.6910	**641.3491**
P	537.3507	269.1790	1224.6695	612.8384
Q	**665.4093**	333.2083	1127.6167	564.3120
Q	793.4679	397.2376	**999.5582**	**500.2827**
E	**922.5105**	461.7589	**871.4996**	436.2534
V	**1021.5789**	511.2931	**742.4570**	**371.7321**
G	**1078.6004**	539.8038	**643.3886**	**322.1979**
Q	**1206.6589**	603.8331	**586.3671**	**293.6872**
G	1263.6804	632.3438	**458.3085**	229.6579
I	1376.7645	688.8859	**401.2871**	**201.1472**
I	1489.8485	745.4279	**288.2030**	144.6051
R	1645.9496	823.4785	**175.1190**	88.0631

Peptide sequence 7: LSFGLGSK



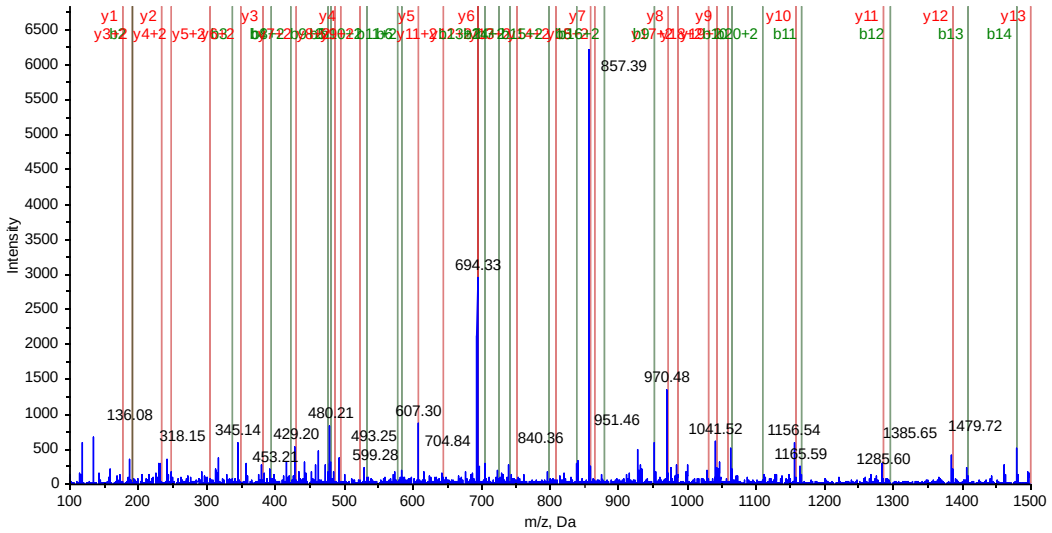
Residue	b	b+2	y	y+2
L	114.0913	57.5493	808.4563	**404.7318**
S	**201.1234**	101.0653	**695.3723**	**348.1898**
F	**348.1918**	174.5995	**608.3402**	**304.6738**
G	**405.2132**	203.1103	**461.2718**	231.1396
L	**518.2973**	259.6523	**404.2504**	202.6288
G	575.3188	288.1630	**291.1663**	146.0868
S	662.3508	331.6790	**234.1448**	117.5761
K	790.4458	**395.7265**	**147.1128**	74.0600

Peptide sequence 8: NPYHFGQWSFK



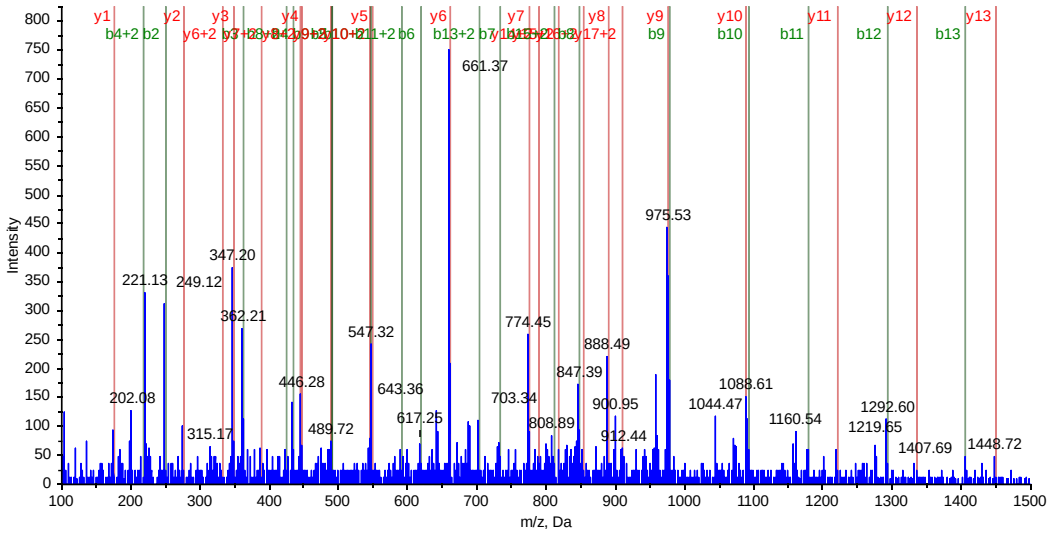
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1410.6589	705.8331
P	**212.1030**	106.5551	1296.6160	**648.8116**
Y	**375.1663**	188.0868	**1199.5633**	**600.2853**
H	**512.2252**	256.6162	**1036.4999**	**518.7536**
F	**659.2936**	330.1504	**899.4410**	**450.2241**
G	**716.3151**	**358.6612**	**752.3726**	376.6899
Q	**844.3737**	**422.6905**	**695.3511**	348.1792
W	**1030.4530**	515.7301	**567.2926**	**284.1499**
S	**1117.4850**	559.2461	**381.2132**	**191.1103**
F	1264.5534	632.7803	**294.1812**	147.5942
K	1392.6484	696.8278	**147.1128**	74.0600

Peptide sequence 9: STFGSPFNLLTQDAIYSNNFGR



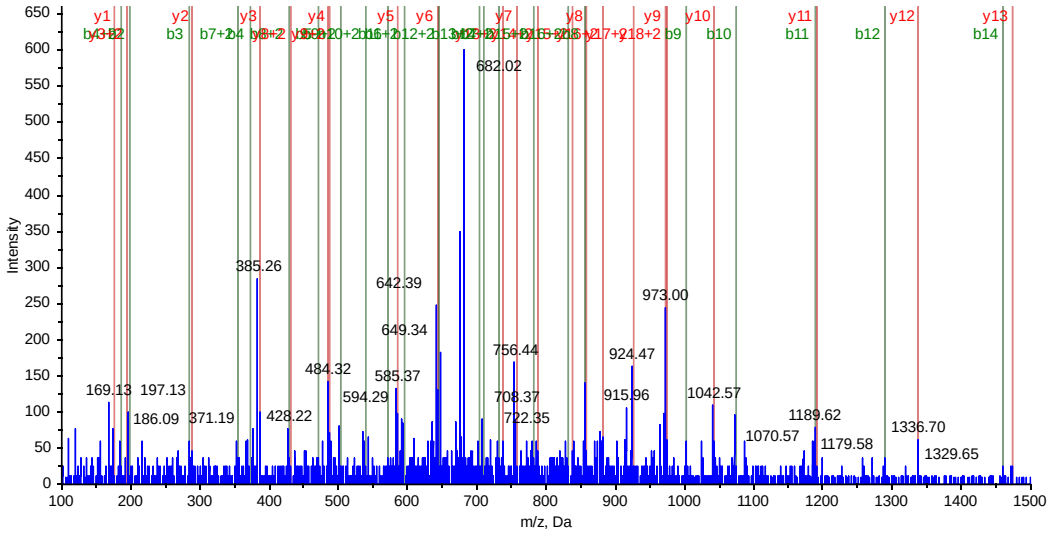
Residue	b	b+2	y	y+2
S	88.0393	44.5233	2449.1783	1225.0928
T	**189.0870**	95.0471	2362.1462	1181.5768
F	**336.1554**	168.5813	2261.0986	1131.0529
G	**393.1769**	197.0921	2114.0301	**1057.5187**
S	**480.2089**	240.6081	2057.0087	**1029.0080**
P	**577.2617**	289.1345	1969.9767	**985.4920**
F	**724.3301**	362.6687	1872.9239	936.9656
N	**838.3730**	**419.6901**	1725.8555	**863.4314**
L	**951.4571**	**476.2322**	1611.8125	**806.4099**
L	**1064.5411**	**532.7742**	**1498.7285**	**749.8679**
T	**1165.5888**	**583.2980**	**1385.6444**	**693.3258**
Q	**1293.6474**	647.3273	**1284.5967**	**642.8020**
D	**1408.6743**	**704.8408**	**1156.5382**	578.7727
A	**1479.7114**	**740.3594**	**1041.5112**	**521.2592**
I	1592.7955	**796.9014**	**970.4741**	**485.7407**
Y	1755.8588	**878.4331**	**857.3900**	**429.1987**
S	1842.8909	921.9491	**694.3267**	**347.6670**
N	1956.9338	978.9705	**607.2947**	**304.1510**
N	2070.9767	1035.9920	**493.2518**	**247.1295**
F	2218.0451	**1109.5262**	**379.2088**	**190.1081**
G	2275.0666	1138.0369	**232.1404**	116.5738
R	2431.1677	1216.0875	**175.1190**	88.0631

Peptide sequence 10: TFLAGQDNMLSNINTVATR



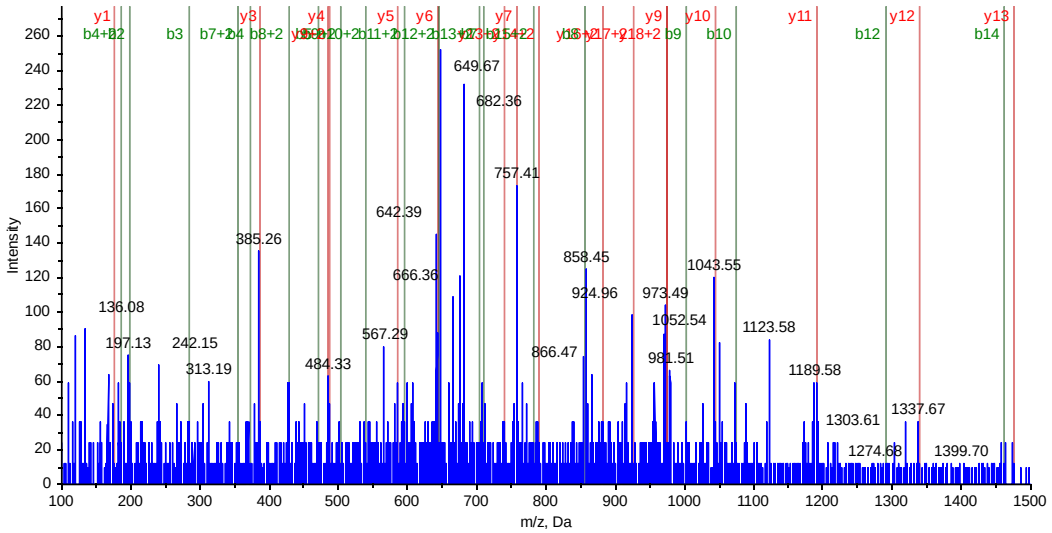
Residue	b	b+2	y	y+2
T	102.0550	51.5311	2066.0335	1033.5204
F	**249.1234**	125.0653	1964.9858	982.9966
L	**362.2074**	181.6074	1817.9174	**909.4623**
A	**433.2445**	**217.1259**	1704.8334	**852.9203**
G	**490.2660**	245.6366	1633.7962	**817.4018**
Q	**618.3246**	309.6659	1576.7748	**788.8910**
D	**733.3515**	367.1794	**1448.7162**	724.8617
N	**847.3945**	**424.2009**	**1333.6893**	667.3483
M	**978.4349**	**489.7211**	**1219.6463**	610.3268
L	**1091.5190**	**546.2631**	**1088.6058**	**544.8066**
S	**1178.5510**	**589.7792**	**975.5218**	**488.2645**
N	**1292.5940**	646.8006	**888.4898**	**444.7485**
I	**1405.6780**	**703.3427**	**774.4468**	**387.7271**
N	1519.7210	760.3641	**661.3628**	**331.1850**
T	1620.7686	**810.8880**	**547.3198**	274.1636
V	1719.8370	860.4222	**446.2722**	223.6397
A	1790.8742	895.9407	**347.2037**	174.1055
T	1891.9218	946.4646	**276.1666**	138.5870
R	2048.0229	1024.5151	**175.1190**	88.0631

Peptide sequence 11: VPSSVTHFFANTNGTVPLR



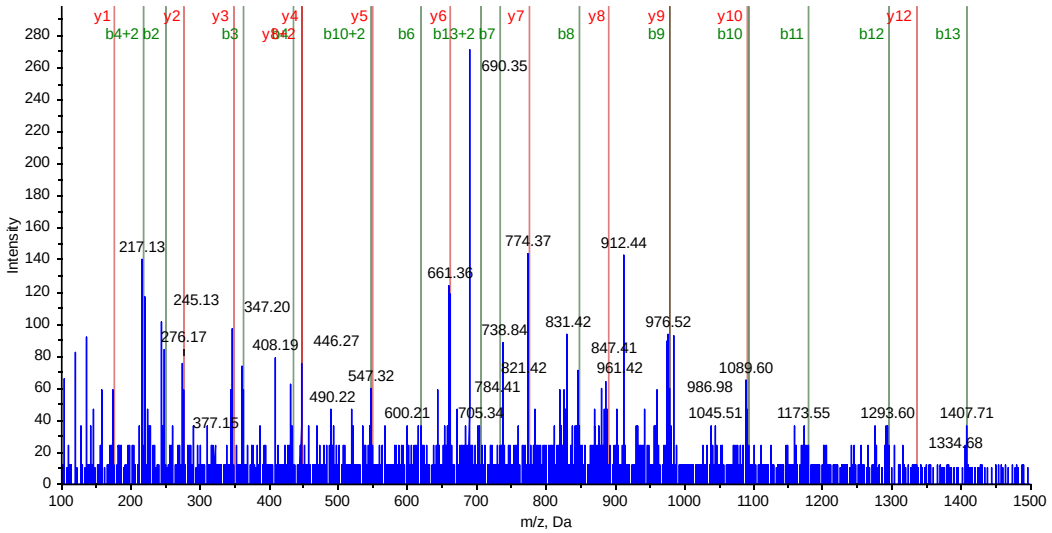
Residue	b	b+2	y	y+2
V	100.0757	50.5415	2044.0610	1022.5342
P	**197.1285**	99.0679	1944.9926	**973.0000**
S	**284.1605**	142.5839	1847.9399	**924.4736**
S	**371.1925**	**186.0999**	1760.9078	**880.9576**
V	**470.2609**	235.6341	1673.8758	**837.4415**
T	**571.3086**	286.1579	1574.8074	**787.9073**
H	**708.3675**	**354.6874**	**1473.7597**	**737.3835**
F	**855.4359**	**428.2216**	**1336.7008**	668.8540
F	**1002.5043**	**501.7558**	**1189.6324**	595.3198
A	**1073.5415**	**537.2744**	**1042.5640**	521.7856
N	**1187.5844**	**594.2958**	**971.5269**	**486.2671**
T	**1288.6321**	**644.8197**	**857.4839**	**429.2456**
N	1402.6750	**701.8411**	**756.4363**	378.7218
G	**1459.6965**	**730.3519**	**642.3933**	321.7003
T	1560.7441	**780.8757**	**585.3719**	293.1896
V	1659.8125	**830.4099**	**484.3242**	242.6657
P	1756.8653	878.9363	**385.2558**	**193.1315**
L	1869.9494	935.4783	**288.2030**	144.6051
R	2026.0505	1013.5289	**175.1190**	88.0631

Peptide sequence 12: VPSSVTHFFAN[Dea]TNGTVPLR



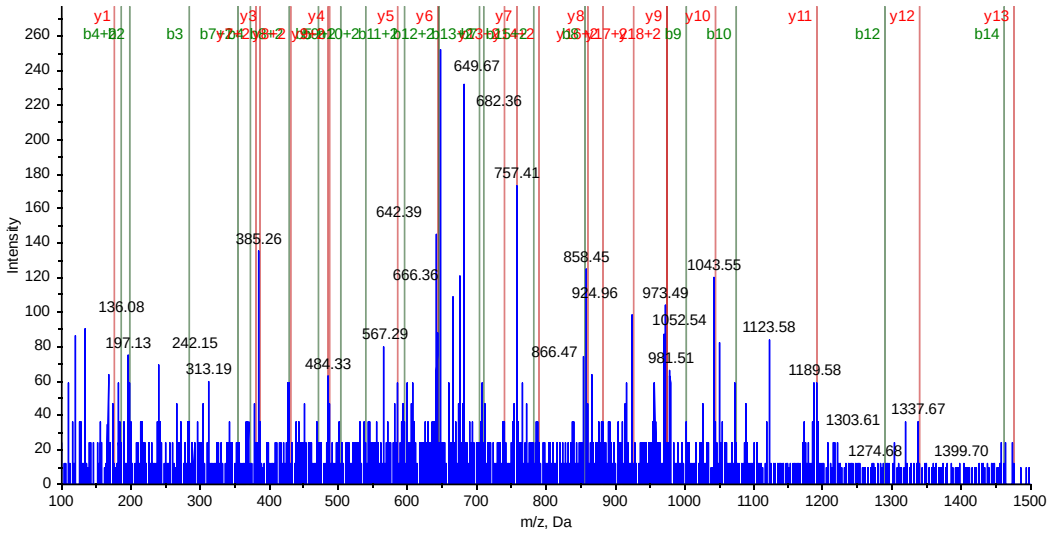
Residue	b	b+2	y	y+2
V	100.0757	50.5415	2045.0451	1023.0262
P	**197.1285**	99.0679	1945.9767	**973.4920**
S	**284.1605**	142.5839	1848.9239	**924.9656**
S	**371.1925**	**186.0999**	1761.8919	**881.4496**
V	**470.2609**	235.6341	1674.8598	837.9336
T	571.3086	286.1579	1575.7914	**788.3993**
H	**708.3675**	**354.6874**	**1474.7437**	**737.8755**
F	**855.4359**	**428.2216**	**1337.6848**	669.3461
F	**1002.5043**	**501.7558**	**1190.6164**	595.8118
A	**1073.5415**	**537.2744**	**1043.5480**	522.2776
N[Dea]	1188.5684	**594.7878**	**972.5109**	**486.7591**
T	**1289.6161**	**645.3117**	857.4839	429.2456
N	1403.6590	**702.3331**	**756.4363**	378.7218
G	**1460.6805**	730.8439	**642.3933**	321.7003
T	1561.7281	**781.3677**	**585.3719**	293.1896
V	1660.7966	830.9019	**484.3242**	242.6657
P	1757.8493	879.4283	**385.2558**	193.1315
L	1870.9334	935.9703	288.2030	144.6051
R	2027.0345	1014.0209	**175.1190**	88.0631

Peptide sequence 13: TFLAGQDNMLSN[Dea]INTVATR



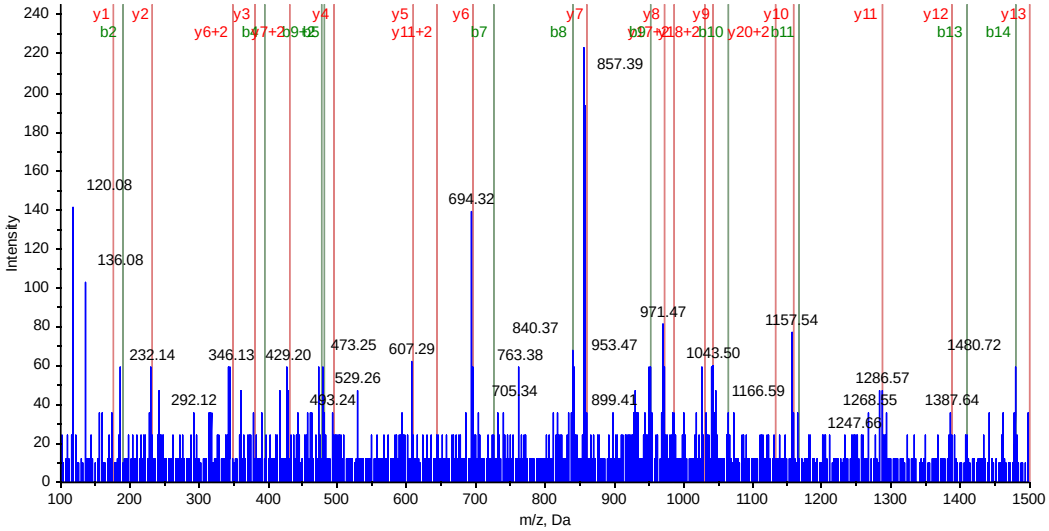
Residue	b	b+2	y	y+2
T	102.0550	51.5311	2067.0175	1034.0124
F	**249.1234**	125.0653	1965.9699	983.4886
L	**362.2074**	181.6074	1818.9014	909.9544
A	**433.2445**	**217.1259**	1705.8174	853.4123
G	490.2660	245.6366	1634.7803	817.8938
Q	**618.3246**	309.6659	1577.7588	789.3830
D	**733.3515**	367.1794	1449.7002	725.3537
N	**847.3945**	424.2009	**1334.6733**	667.8403
M	**978.4349**	489.7211	1220.6303	610.8188
L	**1091.5190**	**546.2631**	**1089.5899**	545.2986
S	**1178.5510**	589.7792	**976.5058**	488.7565
N[Dea]	**1293.5780**	647.2926	**889.4738**	**445.2405**
I	**1406.6620**	**703.8347**	**774.4468**	387.7271
N	1520.7050	760.8561	**661.3628**	331.1850
T	1621.7526	811.3800	**547.3198**	274.1636
V	1720.8211	860.9142	**446.2722**	223.6397
A	1791.8582	896.4327	**347.2037**	174.1055
T	1892.9059	946.9566	**276.1666**	138.5870
R	2049.0070	1025.0071	**175.1190**	88.0631

Peptide sequence 14: VPSSVTHFFANTN[Dea]GTVPLR



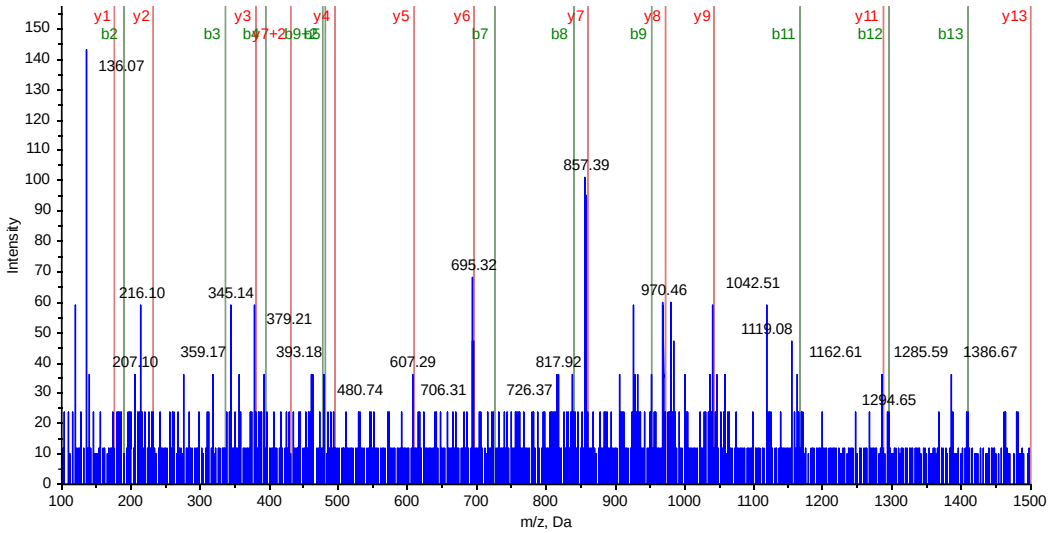
Residue	b	b+2	y	y+2
V	100.0757	50.5415	2045.0451	1023.0262
P	**197.1285**	99.0679	1945.9767	**973.4920**
S	**284.1605**	142.5839	1848.9239	**924.9656**
S	**371.1925**	**186.0999**	1761.8919	**881.4496**
V	**470.2609**	235.6341	1674.8598	837.9336
T	571.3086	286.1579	1575.7914	**788.3993**
H	**708.3675**	**354.6874**	**1474.7437**	**737.8755**
F	**855.4359**	**428.2216**	**1337.6848**	669.3461
F	**1002.5043**	**501.7558**	**1190.6164**	595.8118
A	**1073.5415**	**537.2744**	**1043.5480**	522.2776
N	1187.5844	**594.2958**	**972.5109**	**486.7591**
T	**1288.6321**	**644.8197**	**858.4680**	**429.7376**
N[Dea]	1403.6590	**702.3331**	**757.4203**	**379.2138**
G	**1460.6805**	730.8439	**642.3933**	321.7003
T	1561.7281	**781.3677**	**585.3719**	293.1896
V	1660.7966	830.9019	**484.3242**	242.6657
P	1757.8493	879.4283	**385.2558**	193.1315
L	1870.9334	935.9703	288.2030	144.6051
R	2027.0345	1014.0209	**175.1190**	88.0631

Peptide sequence 15: STFGSPFNLLTQDAIYSN[Dea]NFGR



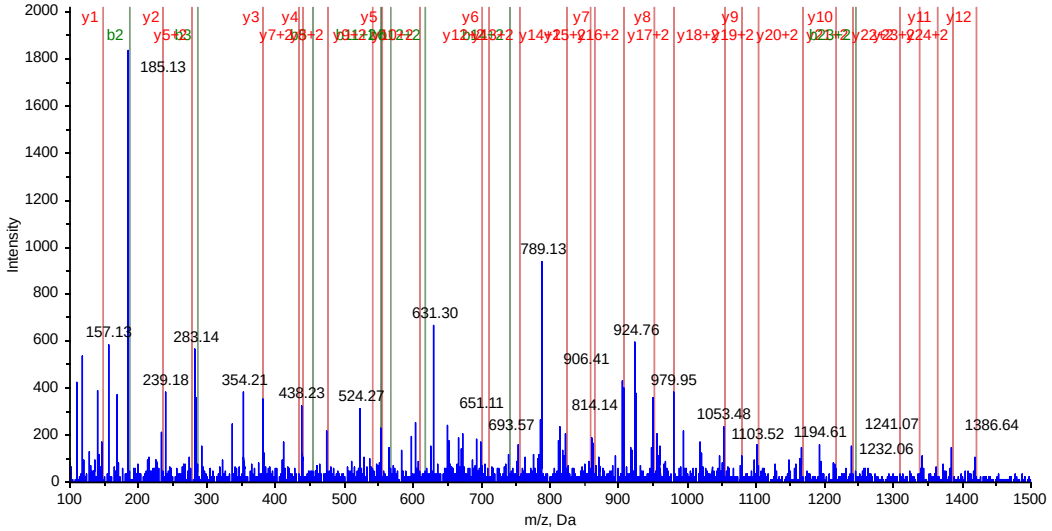
Residue	b	b+2	y	y+2
S	88.0393	44.5233	2450.1623	1225.5848
T	**189.0870**	95.0471	2363.1303	1182.0688
F	336.1554	168.5813	2262.0826	**1131.5449**
G	**393.1769**	197.0921	2115.0142	1058.0107
S	**480.2089**	240.6081	2057.9927	**1029.5000**
P	577.2617	289.1345	1970.9607	**985.9840**
F	**724.3301**	362.6687	1873.9079	937.4576
N	**838.3730**	419.6901	1726.8395	863.9234
L	**951.4571**	**476.2322**	1612.7966	806.9019
L	**1064.5411**	532.7742	**1499.7125**	750.3599
T	**1165.5888**	583.2980	**1386.6284**	693.8179
Q	1293.6474	647.3273	**1285.5808**	**643.2940**
D	**1408.6743**	704.8408	**1157.5222**	579.2647
A	**1479.7114**	740.3594	**1042.4952**	521.7513
I	1592.7955	796.9014	**971.4581**	486.2327
Y	1755.8588	878.4331	**858.3741**	**429.6907**
S	1842.8909	921.9491	**695.3107**	**348.1590**
N[Dea]	1957.9178	979.4625	**608.2787**	304.6430
N	2071.9607	1036.4840	**493.2518**	247.1295
F	2219.0291	1110.0182	**379.2088**	190.1081
G	2276.0506	1138.5289	**232.1404**	116.5738
R	2432.1517	1216.5795	**175.1190**	88.0631

Peptide sequence 16: STFGSPFNLLTQDAIYSNN[Dea]FGR



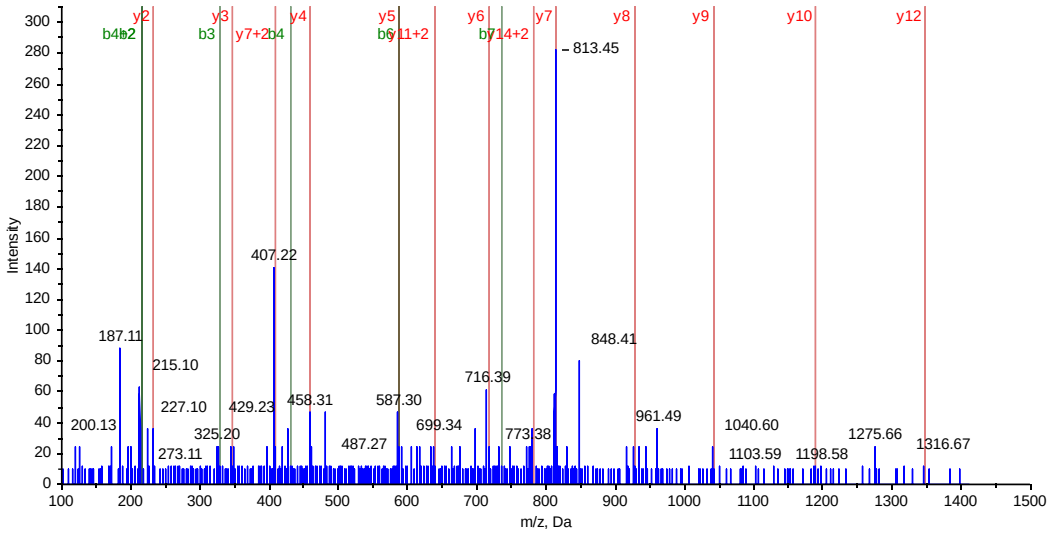
Residue	b	b+2	y	y+2
S	**88.0393**	44.5233	2450.1623	1225.5848
T	**189.0870**	95.0471	2363.1303	1182.0688
F	**336.1554**	168.5813	2262.0826	1131.5449
G	**393.1769**	197.0921	2115.0142	1058.0107
S	**480.2089**	240.6081	2057.9927	1029.5000
P	577.2617	289.1345	1970.9607	985.9840
F	**724.3301**	362.6687	1873.9079	937.4576
N	**838.3730**	419.6901	1726.8395	863.9234
L	**951.4571**	**476.2322**	1612.7966	806.9019
L	1064.5411	532.7742	**1499.7125**	750.3599
T	**1165.5888**	583.2980	1386.6284	693.8179
Q	**1293.6474**	647.3273	**1285.5808**	643.2940
D	**1408.6743**	704.8408	1157.5222	579.2647
A	1479.7114	740.3594	**1042.4952**	521.7513
I	1592.7955	796.9014	**971.4581**	486.2327
Y	1755.8588	878.4331	**858.3741**	**429.6907**
S	1842.8909	921.9491	**695.3107**	348.1590
N	1956.9338	978.9705	**608.2787**	304.6430
N[Dea]	2071.9607	1036.4840	**494.2358**	247.6215
F	2219.0291	1110.0182	**379.2088**	190.1081
G	2276.0506	1138.5289	**232.1404**	116.5738
R	2432.1517	1216.5795	**175.1190**	88.0631

Peptide sequence 17: IAVPANVPGHFQVFFPAHSGFHQSYFN[Dea]GFSK



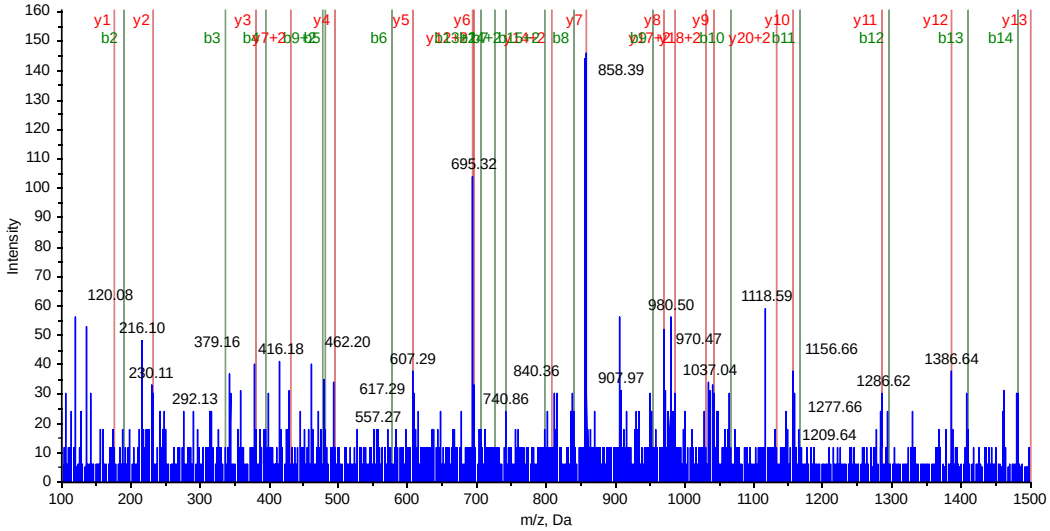
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3435.6698	1718.3385
A	**185.1285**	93.0679	3322.5857	1661.7965
V	**284.1969**	142.6021	3251.5486	1626.2779
P	381.2496	191.1285	3152.4802	1576.7437
A	**452.2867**	226.6470	3055.4274	1528.2174
N	**566.3297**	283.6685	2984.3903	1492.6988
V	665.3981	333.2027	2870.3474	1435.6773
P	762.4509	381.7291	2771.2790	**1386.1431**
G	819.4723	410.2398	2674.2262	**1337.6167**
H	956.5312	478.7693	2617.2048	**1309.1060**
F	1103.5996	**552.3035**	2480.1458	**1240.5766**
Q	1231.6582	**616.3327**	2333.0774	**1167.0424**
V	1330.7266	665.8670	2205.0189	**1103.0131**
F	1477.7950	**739.4012**	2105.9504	**1053.4789**
F	1624.8635	812.9354	1958.8820	**979.9446**
P	1721.9162	861.4618	1811.8136	**906.4104**
A	1792.9533	896.9803	1714.7608	**857.8841**
H	1930.0122	965.5098	1643.7237	**822.3655**
S	2017.0443	1009.0258	1506.6648	**753.8360**
G	2074.0657	1037.5365	**1419.6328**	**710.3200**
F	2221.1342	1111.0707	**1362.6113**	681.8093
H	2358.1931	1179.6002	**1215.5429**	**608.2751**
Q	2486.2516	**1243.6295**	**1078.4840**	**539.7456**
S	2573.2837	1287.1455	**950.4254**	**475.7164**
Y	2736.3470	1368.6771	**863.3934**	**432.2003**
F	2883.4154	1442.2113	**700.3301**	350.6687
N[Dea]	2998.4424	1499.7248	**553.2617**	**277.1345**
G	3055.4638	1528.2355	**438.2347**	219.6210
F	3202.5322	1601.7698	**381.2132**	191.1103
S	3289.5643	1645.2858	**234.1448**	117.5761
K	3417.6592	1709.3333	**147.1128**	74.0600

Peptide sequence 18: DVLTASFN[Dea]IPEELLGR



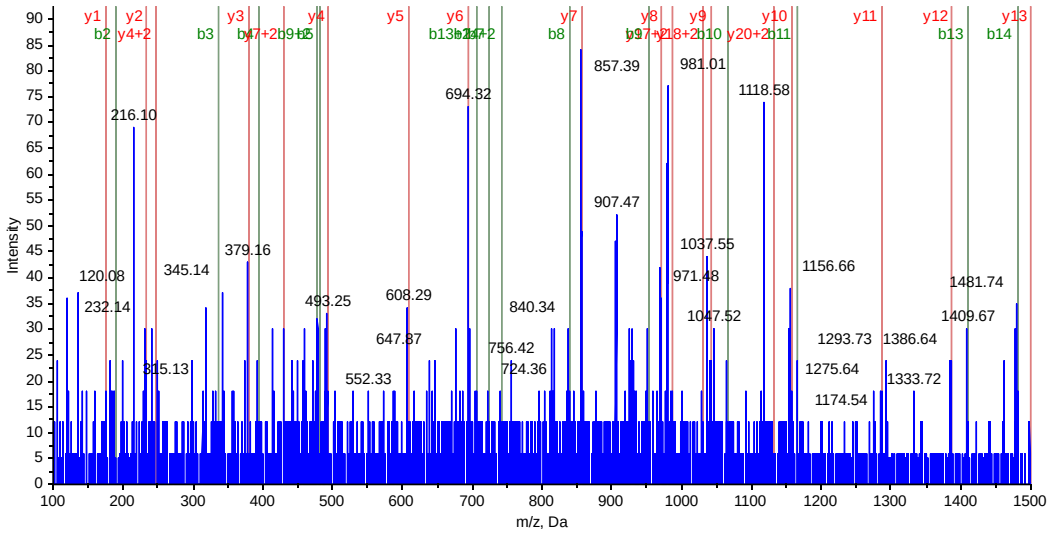
Residue	b	b+2	y	y+2
D	116.0342	58.5207	1774.9222	887.9647
V	**215.1026**	108.0550	1659.8952	830.4512
L	**328.1867**	164.5970	1560.8268	**780.9170**
T	**429.2344**	**215.1208**	1447.7427	724.3750
A	500.2715	250.6394	**1346.6951**	673.8512
S	**587.3035**	294.1554	1275.6579	**638.3326**
F	**734.3719**	367.6896	**1188.6259**	594.8166
N[Dea]	849.3989	425.2031	**1041.5575**	521.2824
I	962.4829	481.7451	**926.5306**	463.7689
P	1059.5357	530.2715	**813.4465**	**407.2269**
E	1188.5783	594.7928	**716.3937**	358.7005
E	1317.6209	659.3141	**587.3511**	294.1792
L	1430.7050	715.8561	**458.3085**	229.6579
L	1543.7890	772.3981	**345.2245**	173.1159
G	1600.8105	800.9089	**232.1404**	116.5738
R	1756.9116	878.9594	175.1190	88.0631

Peptide sequence 19: STFGSPFN[Dea]LLTQDAIYSNNFGR



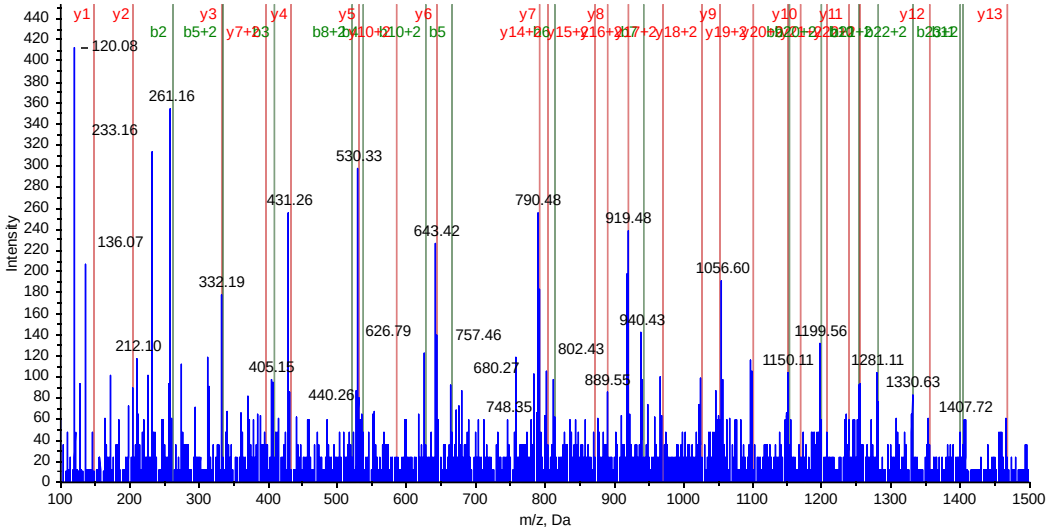
Residue	b	b+2	y	y+2
S	88.0393	44.5233	2450.1623	1225.5848
T	**189.0870**	95.0471	2363.1303	1182.0688
F	**336.1554**	168.5813	2262.0826	**1131.5449**
G	**393.1769**	197.0921	2115.0142	1058.0107
S	**480.2089**	240.6081	2057.9927	**1029.5000**
P	**577.2617**	289.1345	1970.9607	**985.9840**
F	**724.3301**	362.6687	1873.9079	937.4576
N[Dea]	**839.3570**	420.1821	1726.8395	863.9234
L	**952.4411**	**476.7242**	1611.8125	**806.4099**
L	**1065.5251**	533.2662	**1498.7285**	749.8679
T	**1166.5728**	583.7900	**1385.6444**	**693.3258**
Q	**1294.6314**	647.8193	**1284.5967**	642.8020
D	**1409.6583**	**705.3328**	**1156.5382**	578.7727
A	**1480.6955**	**740.8514**	**1041.5112**	521.2592
I	1593.7795	**797.3934**	**970.4741**	485.7407
Y	1756.8428	878.9251	**857.3900**	**429.1987**
S	1843.8749	922.4411	**694.3267**	347.6670
N	1957.9178	979.4625	**607.2947**	304.1510
N	2071.9607	1036.4840	**493.2518**	247.1295
F	2219.0291	1110.0182	**379.2088**	190.1081
G	2276.0506	1138.5289	**232.1404**	116.5738
R	2432.1517	1216.5795	**175.1190**	88.0631

Peptide sequence 20: STFGSPFNLLTQ[Dea]DAIYSNNFGR



Residue	b	b+2	y	y+2
S	88.0393	44.5233	2450.1623	1225.5848
T	**189.0870**	95.0471	2363.1303	1182.0688
F	**336.1554**	168.5813	2262.0826	**1131.5449**
G	**393.1769**	197.0921	2115.0142	1058.0107
S	**480.2089**	240.6081	2057.9927	**1029.5000**
P	577.2617	289.1345	1970.9607	**985.9840**
F	**724.3301**	362.6687	1873.9079	937.4576
N	**838.3730**	419.6901	1726.8395	863.9234
L	**951.4571**	**476.2322**	1612.7966	806.9019
L	**1064.5411**	532.7742	**1499.7125**	750.3599
T	**1165.5888**	583.2980	**1386.6284**	693.8179
Q[Dea]	1294.6314	647.8193	**1285.5808**	643.2940
D	**1409.6583**	**705.3328**	**1156.5382**	578.7727
A	**1480.6955**	**740.8514**	**1041.5112**	521.2592
I	1593.7795	797.3934	**970.4741**	485.7407
Y	1756.8428	878.9251	**857.3900**	**429.1987**
S	1843.8749	922.4411	**694.3267**	347.6670
N	1957.9178	979.4625	**607.2947**	304.1510
N	2071.9607	1036.4840	**493.2518**	**247.1295**
F	2219.0291	1110.0182	**379.2088**	190.1081
G	2276.0506	1138.5289	**232.1404**	116.5738
R	2432.1517	1216.5795	**175.1190**	88.0631

Peptide sequence 21: FLFQEM[Oxi]QPNTFLVPHHLDADYVFLVVQGK



Residue	b	b+2	y	y+2
F	148.0757	74.5415	3448.7398	1724.8736
L	**261.1598**	131.0835	3301.6714	1651.3394
F	**408.2282**	204.6177	3188.5874	1594.7973
Q	**536.2867**	268.6470	3041.5190	1521.2631
E	**665.3293**	**333.1683**	2913.4604	1457.2338
M[Oxi]	**812.3647**	406.6860	2784.4178	1392.7125
Q	**940.4233**	470.7153	2637.3824	1319.1948
P	1037.4761	**519.2417**	2509.3238	**1255.1655**
N	**1151.5190**	576.2631	2412.2710	**1206.6392**
T	**1252.5667**	**626.7870**	2298.2281	**1149.6177**
F	**1399.6351**	700.3212	2197.1804	**1099.0939**
L	1512.7192	756.8632	2050.1120	**1025.5596**
V	1611.7876	806.3974	1937.0280	**969.0176**
P	1708.8403	854.9238	1837.9595	**919.4834**
H	1845.8993	923.4533	1740.9068	**870.9570**
H	1982.9582	991.9827	1603.8479	**802.4276**
L	2096.0422	1048.5248	**1466.7890**	733.8981
D	2211.0692	1106.0382	**1353.7049**	677.3561
A	2282.1063	1141.5568	**1238.6780**	619.8426
D	2397.1332	**1199.0703**	**1167.6408**	**584.3241**
Y	2560.1966	**1280.6019**	**1052.6139**	526.8106
V	2659.2650	**1330.1361**	**889.5506**	445.2789
F	2806.3334	**1403.6703**	**790.4822**	**395.7447**
L	2919.4174	1460.2124	**643.4137**	322.2105
V	3018.4859	1509.7466	**530.3297**	265.6685
V	3117.5543	1559.2808	**431.2613**	216.1343
Q	3245.6129	1623.3101	**332.1928**	166.6001
G	3302.6343	1651.8208	**204.1343**	102.5708
K	3430.7293	1715.8683	**147.1128**	74.0600

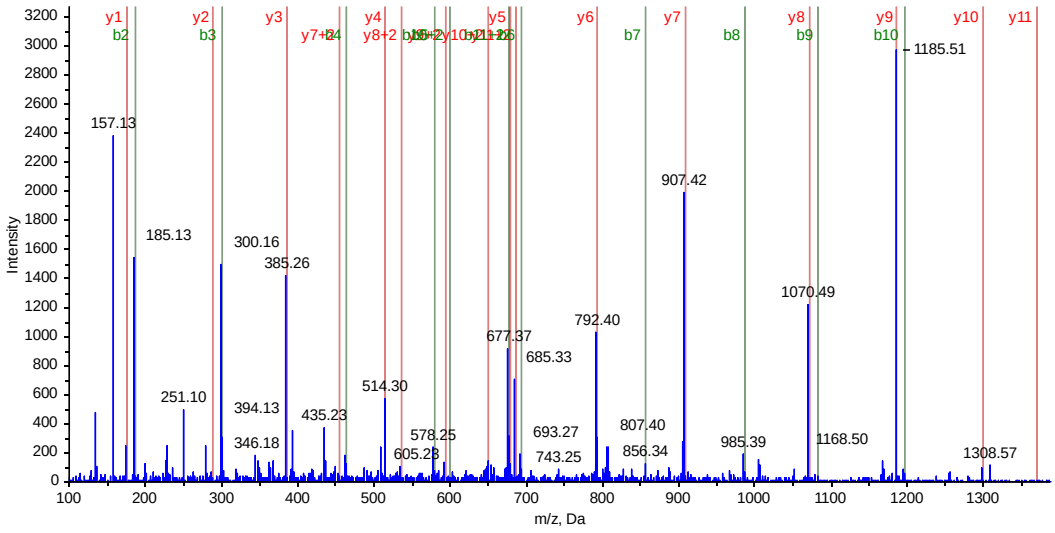
Sample Pool 2

Protein: B.rapa.Ro18.Candidate-1, 11 peptides (95%)

Protein sequence coverage

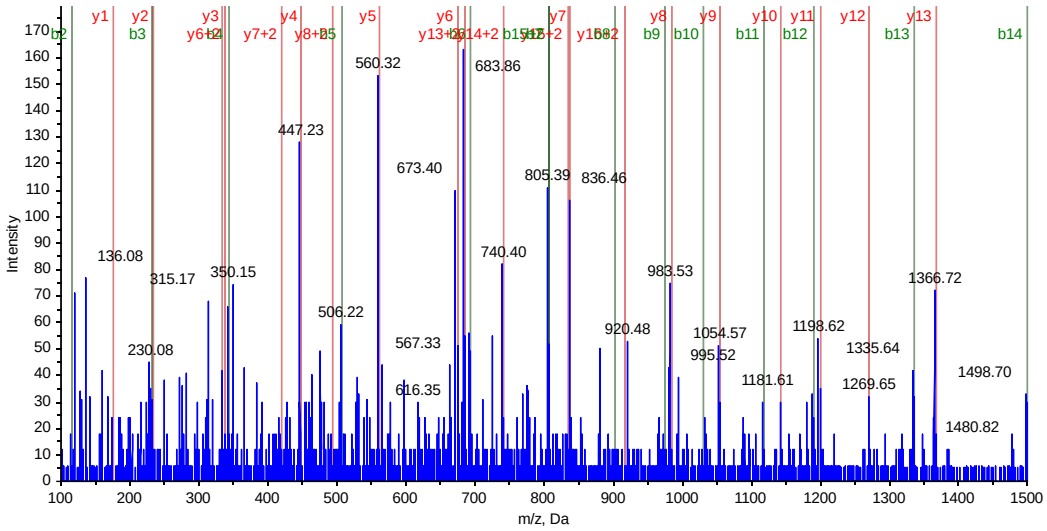
MEKNKRIFTFLLVIVFFHGVMMMRSIGYEGEEEQGGGGRERGGFMMKESRQVIKSEGGEMRVVISPR**GR**
IIEKPMHIGFLTMEPKTLFVPQYLDSNLLIFIRQGEATLGVICKDEFGEKR**LKGGDIYWIPAGSAFYLL**
NTGRGQRLHVICSIDPSQSLGFETFQPFYIGGGPSSVLAGFDPDTITSALNVSRPEVQQLMTSQVRGPI
VHITEHAPTMWTDFLGLRGEEKHKHLKKLLELKQGTSQEQEDNPWWSWKNIVSSILDVTGEKNRGSGSS
KCEDSYNIYDR**KNDFENDYGWSKALDYDDYEPLR**YSGVGVYLVNLTAGSMMAPHMNPTATEYGIVLSGS
GEIQVVLPNGTSAMNMRVSPGDVFWIPRYFAFCQIASR**IAPFEFVGFTTSAYKNRPQFLVGSNSLLR**SL
NLTSLAMAFGVDEGTMKRFVEAQREAVILPTASAAPPHEGEPERFGSDHIFT

Peptide sequence 1: ALDYDDYEPLR



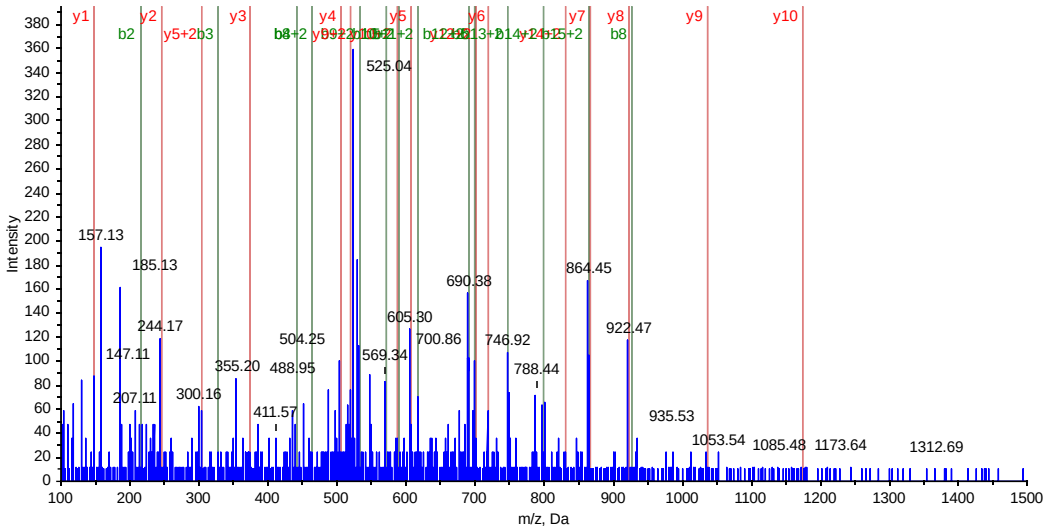
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1900.0071	950.5072
I	**227.1754**	114.0913	1786.9230	893.9652
E	**356.2180**	178.6126	1673.8390	837.4231
K	484.3130	242.6601	1544.7964	**772.9018**
P	581.3657	291.1865	**1416.7014**	**708.8543**
M[Oxi]	**728.4011**	364.7042	1319.6486	660.3280
H	**865.4600**	**433.2337**	**1172.6132**	586.8103
I	978.5441	**489.7757**	**1035.5543**	**518.2808**
G	**1035.5656**	**518.2864**	**922.4703**	**461.7388**
F	**1182.6340**	**591.8206**	**865.4488**	**433.2280**
L	1295.7180	**648.3627**	**718.3804**	**359.6938**
T	1396.7657	**698.8865**	**605.2963**	**303.1518**
M	1527.8062	**764.4067**	**504.2486**	**252.6280**
E	1656.8488	828.9280	**373.2082**	187.1077
P	1753.9016	877.4544	**244.1656**	122.5864
K	1881.9965	**941.5019**	**147.1128**	74.0600

Peptide sequence 2: GGDIYWIPAGSAFYLLNTGR



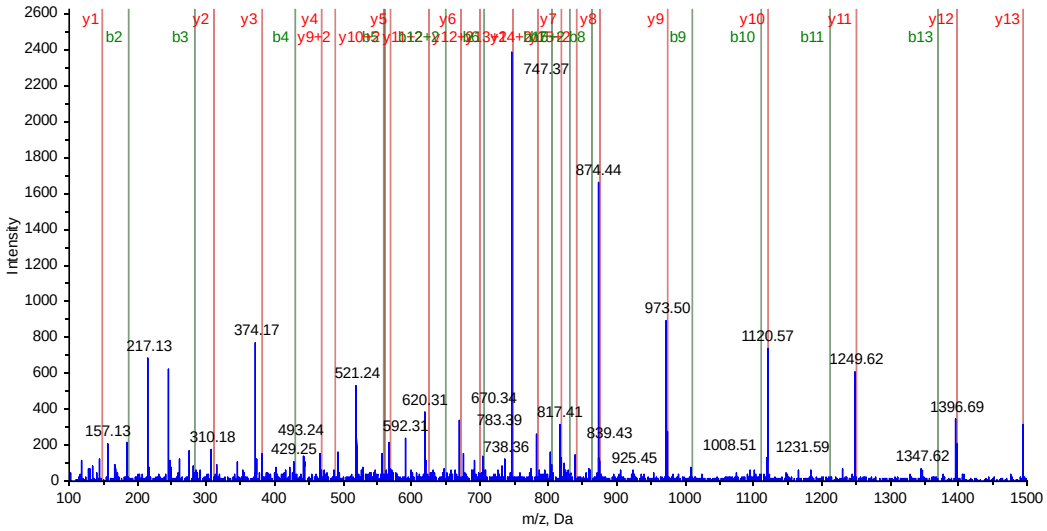
Residue	b	b+2	y	y+2
G	58.0287	29.5180	2171.0920	1086.0496
G	**115.0502**	58.0287	2114.0706	1057.5389
D	**230.0771**	115.5422	2057.0491	1029.0282
I	**343.1612**	172.0842	1942.0221	971.5147
Y	**506.2245**	253.6159	1828.9381	**914.9727**
W	**692.3039**	346.6556	1665.8748	**833.4410**
I	**805.3879**	403.1976	1479.7954	**740.4014**
P	**902.4407**	451.7240	**1366.7114**	**683.8593**
A	**973.4778**	487.2425	**1269.6586**	635.3329
G	**1030.4993**	515.7533	**1198.6215**	599.8144
S	**1117.5313**	559.2693	**1141.6000**	571.3037
A	**1188.5684**	594.7878	**1054.5680**	527.7876
F	**1335.6368**	668.3220	**983.5309**	**492.2691**
Y	**1498.7001**	749.8537	**836.4625**	**418.7349**
L	1611.7842	**806.3957**	**673.3991**	**337.2032**
L	1724.8683	862.9378	**560.3151**	280.6612
N	1838.9112	919.9592	**447.2310**	224.1191
T	1939.9589	970.4831	**333.1881**	167.0977
G	1996.9803	998.9938	**232.1404**	116.5738
R	2153.0815	1077.0444	**175.1190**	88.0631

Peptide sequence 3: GRIIEKPMHIGFLTMEPK



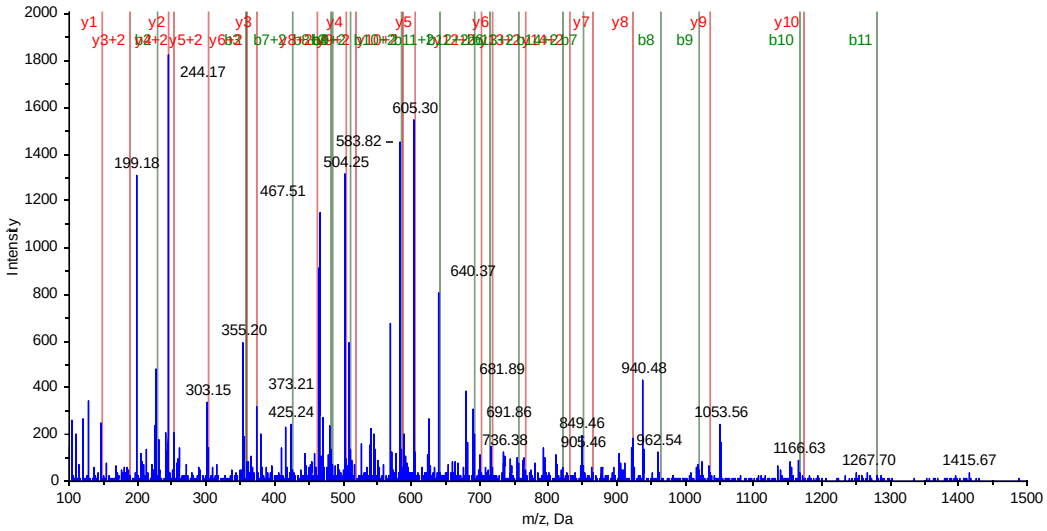
Residue	b	b+2	y	y+2
G	58.0287	29.5180	2097.1347	1049.0710
R	**214.1299**	107.5686	2040.1133	1020.5603
I	**327.2139**	164.1106	1884.0122	942.5097
I	**440.2980**	220.6526	1770.9281	885.9677
E	**569.3406**	285.1739	1657.8440	**829.4257**
K	**697.4355**	349.2214	1528.8015	764.9044
P	794.4883	397.7478	1400.7065	**700.8569**
M	**925.5288**	**463.2680**	1303.6537	652.3305
H	1062.5877	**531.7975**	**1172.6132**	**586.8103**
I	1175.6718	**588.3395**	**1035.5543**	**518.2808**
G	1232.6932	**616.8502**	**922.4703**	461.7388
F	1379.7616	**690.3845**	**865.4488**	433.2280
L	1492.8457	**746.9265**	**718.3804**	359.6938
T	1593.8934	**797.4503**	**605.2963**	**303.1518**
M	1724.9339	**862.9706**	**504.2486**	252.6280
E	1853.9765	927.4919	**373.2082**	187.1077
P	1951.0292	976.0182	**244.1656**	122.5864
K	2079.1242	1040.0657	**147.1128**	74.0600

Peptide sequence 4: IAPFEFVGFTTSAYK



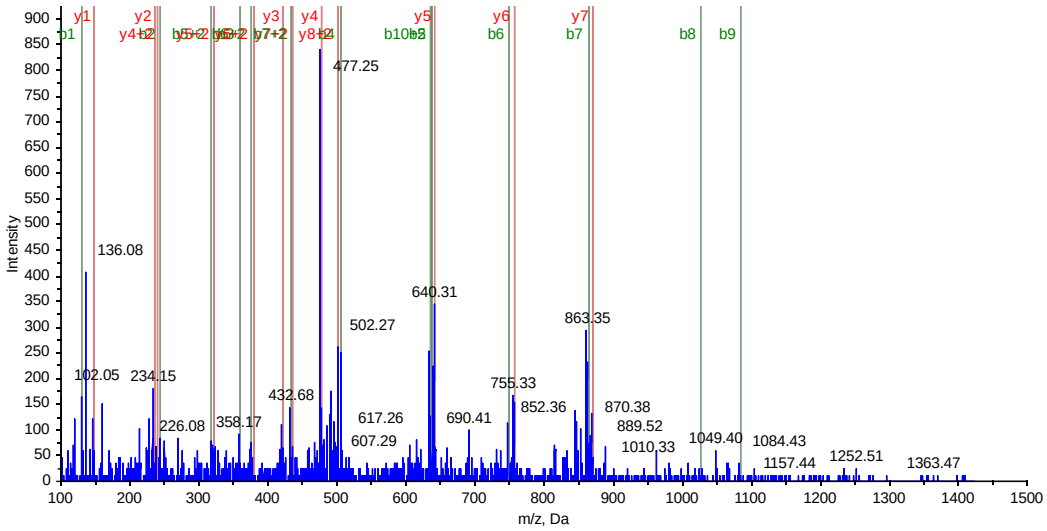
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1677.8523	**839.4298**
A	**185.1285**	93.0679	1564.7682	**782.8877**
P	**282.1812**	141.5942	**1493.7311**	**747.3692**
F	**429.2496**	215.1285	**1396.6783**	**698.8428**
E	**558.2922**	279.6498	**1249.6099**	**625.3086**
F	**705.3606**	353.1840	**1120.5673**	**560.7873**
V	**804.4291**	402.7182	**973.4989**	**487.2531**
G	**861.4505**	431.2289	**874.4305**	437.7189
F	**1008.5189**	504.7631	**817.4090**	409.2082
T	**1109.5666**	555.2869	**670.3406**	335.6740
T	**1210.6143**	605.8108	**569.2930**	285.1501
S	1297.6463	**649.3268**	**468.2453**	234.6263
A	**1368.6834**	684.8454	**381.2132**	191.1103
Y	1531.7468	766.3770	**310.1761**	155.5917
K	1659.8417	**830.4245**	**147.1128**	74.0600

Peptide sequence 5: IIEKPMHIGFLTMEPK



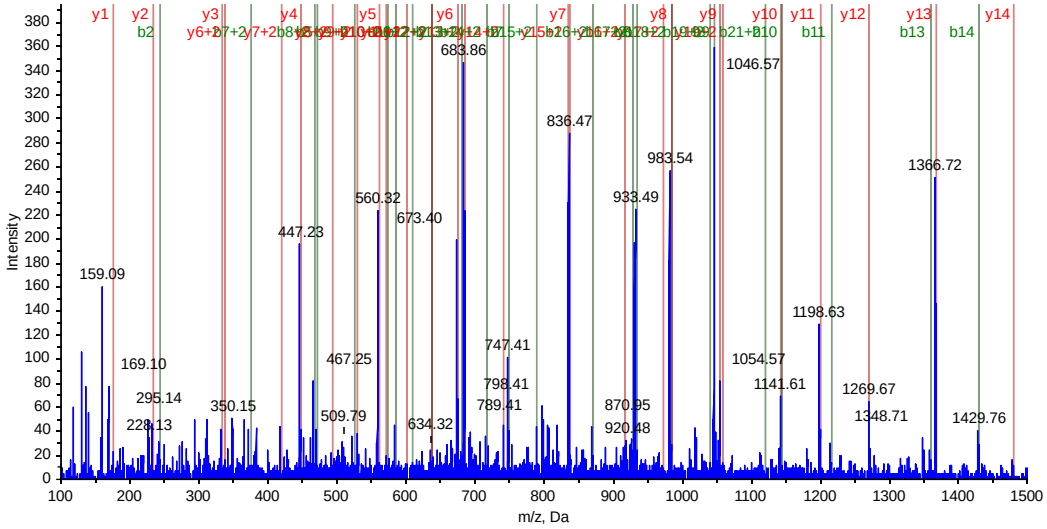
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1884.0122	942.5097
I	**227.1754**	114.0913	1770.9281	885.9677
E	**356.2180**	178.6126	1657.8440	**829.4257**
K	**484.3130**	242.6601	1528.8015	**764.9044**
P	581.3657	291.1865	1400.7065	**700.8569**
M	**712.4062**	356.7067	1303.6537	652.3305
H	**849.4651**	**425.2362**	**1172.6132**	**586.8103**
I	**962.5492**	**481.7782**	**1035.5543**	**518.2808**
G	**1019.5706**	**510.2890**	**922.4703**	**461.7388**
F	**1166.6391**	**583.8232**	**865.4488**	433.2280
L	**1279.7231**	**640.3652**	**718.3804**	**359.6938**
T	1380.7708	**690.8890**	**605.2963**	**303.1518**
M	1511.8113	**756.4093**	**504.2486**	**252.6280**
E	1640.8539	**820.9306**	**373.2082**	**187.1077**
P	1737.9066	869.4570	**244.1656**	122.5864
K	1866.0016	933.5044	**147.1128**	74.0600

Peptide sequence 6: KNDFENDYGWSK



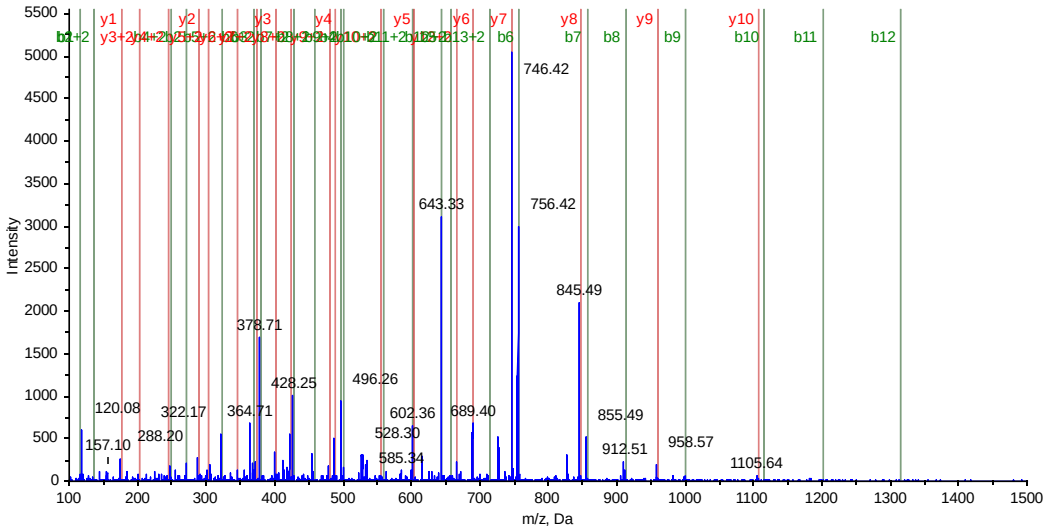
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	1502.6546	751.8310
N	**243.1452**	122.0762	1374.5597	687.7835
D	**358.1721**	179.5897	1260.5168	630.7620
F	**505.2405**	253.1239	1145.4898	573.2485
E	**634.2831**	**317.6452**	998.4214	**499.7143**
N	**748.3260**	**374.6667**	**869.3788**	**435.1930**
D	**863.3530**	**432.1801**	**755.3359**	**378.1716**
Y	**1026.4163**	513.7118	**640.3089**	**320.6581**
G	**1083.4378**	542.2225	**477.2456**	**239.1264**
W	1269.5171	**635.2622**	**420.2241**	210.6157
S	1356.5491	678.7782	**234.1448**	117.5761
K	1484.6441	742.8257	**147.1128**	74.0600

Peptide sequence 7: LKGGDIYWIPAGSAFYLLNTGR



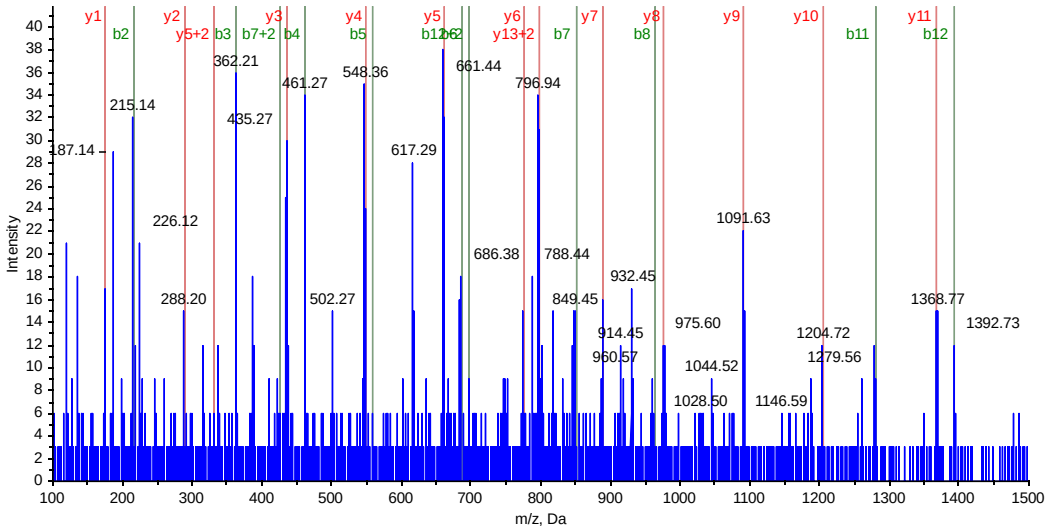
Residue	b	b+2	y	y+2
L	114.0913	57.5493	2412.2710	1206.6392
K	**242.1863**	121.5968	2299.1870	1150.0971
G	299.2078	150.1075	2171.0920	1086.0496
G	356.2292	178.6183	2114.0706	**1057.5389**
D	**471.2562**	236.1317	2057.0491	1029.0282
I	**584.3402**	292.6738	1942.0221	**971.5147**
Y	**747.4036**	**374.2054**	1828.9381	**914.9727**
W	**933.4829**	**467.2451**	1665.8748	**833.4410**
I	**1046.5669**	**523.7871**	**1479.7954**	**740.4014**
P	**1143.6197**	**572.3135**	**1366.7114**	**683.8593**
A	**1214.6568**	**607.8320**	**1269.6586**	**635.3329**
G	1271.6783	**636.3428**	**1198.6215**	**599.8144**
S	**1358.7103**	**679.8588**	**1141.6000**	**571.3037**
A	**1429.7474**	**715.3774**	**1054.5680**	**527.7876**
F	1576.8158	**788.9116**	**983.5309**	**492.2691**
Y	1739.8792	**870.4432**	**836.4625**	**418.7349**
L	1852.9632	**926.9853**	**673.3991**	**337.2032**
L	1966.0473	**983.5273**	**560.3151**	280.6612
N	2080.0902	**1040.5488**	**447.2310**	224.1191
T	2181.1379	1091.0726	**333.1881**	167.0977
G	2238.1594	**1119.5833**	**232.1404**	116.5738
R	2394.2605	1197.6339	**175.1190**	88.0631

Peptide sequence 8: NRPQFLVGSNSLLR



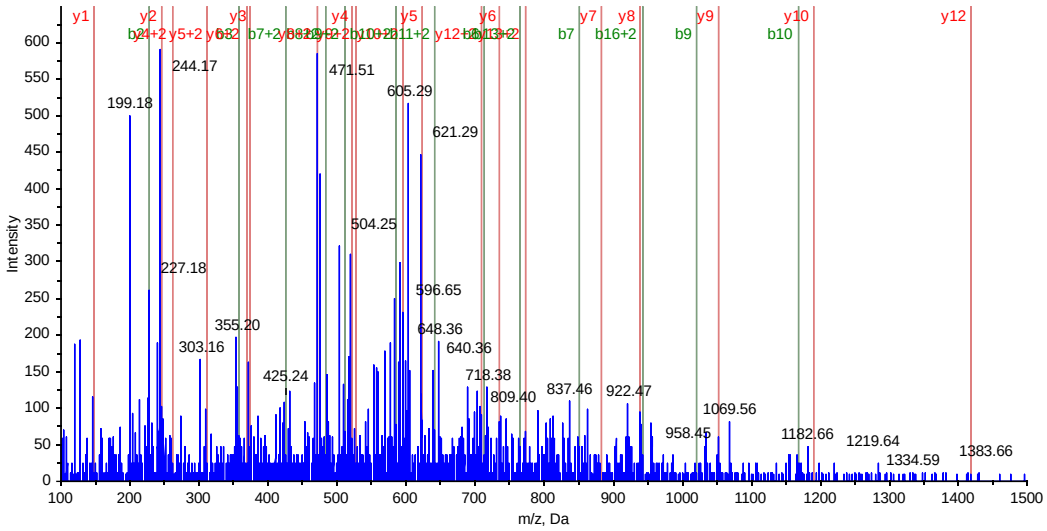
Residue	b	b+2	y	y+2
N	**115.0502**	58.0287	1600.8918	800.9495
R	**271.1513**	**136.0793**	1486.8489	743.9281
P	**368.2041**	184.6057	1330.7478	**665.8775**
Q	**496.2627**	**248.6350**	1233.6950	617.3511
F	**643.3311**	**322.1692**	**1105.6364**	**553.3218**
L	**756.4151**	**378.7112**	**958.5680**	**479.7876**
V	**855.4835**	**428.2454**	**845.4839**	**423.2456**
G	**912.5050**	**456.7561**	**746.4155**	**373.7114**
S	**999.5370**	**500.2722**	**689.3941**	**345.2007**
N	**1113.5800**	**557.2936**	**602.3620**	**301.6847**
S	**1200.6120**	**600.8096**	**488.3191**	**244.6632**
L	**1313.6961**	**657.3517**	**401.2871**	**201.1472**
L	1426.7801	**713.8937**	**288.2030**	144.6051
R	1582.8812	791.9443	**175.1190**	88.0631

Peptide sequence 9: TLFVPQYLDSNLLIFIR



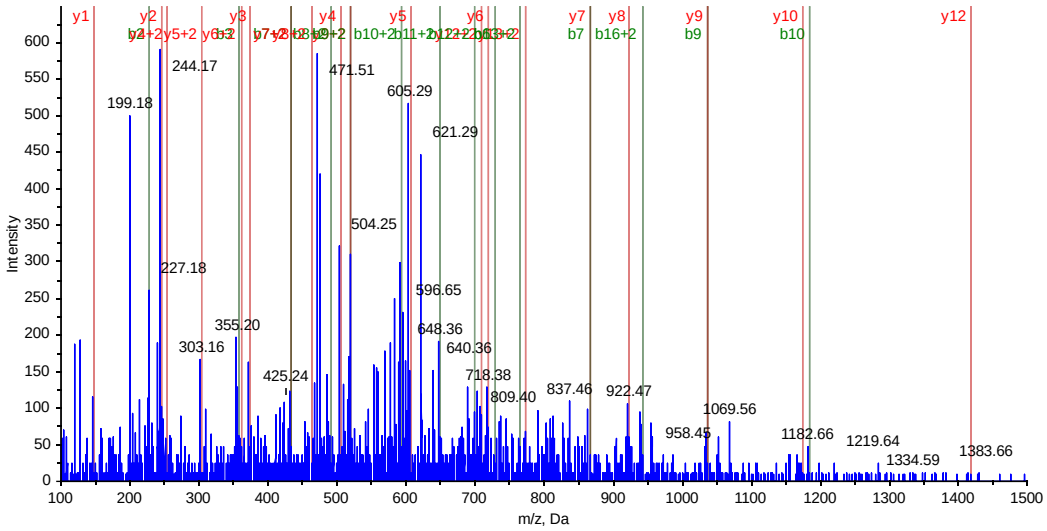
Residue	b	b+2	y	y+2
T	102.0550	51.5311	2052.1528	1026.5801
L	**215.1390**	108.0731	1951.1051	976.0562
F	**362.2074**	181.6074	1838.0211	919.5142
V	**461.2758**	231.1416	1690.9527	845.9800
P	**558.3286**	279.6679	1591.8843	**796.4458**
Q	**686.3872**	343.6972	1494.8315	747.9194
Y	**849.4505**	**425.2289**	**1366.7729**	683.8901
L	**962.5346**	481.7709	**1203.7096**	602.3584
D	1077.5615	539.2844	**1090.6255**	545.8164
S	1164.5936	582.8004	**975.5986**	488.3029
N	**1278.6365**	639.8219	**888.5665**	444.7869
L	**1391.7205**	**696.3639**	**774.5236**	387.7654
L	1504.8046	752.9059	**661.4396**	**331.2234**
I	1617.8887	809.4480	**548.3555**	274.6814
F	1764.9571	882.9822	**435.2714**	218.1394
I	1878.0411	939.5242	**288.2030**	144.6051
R	2034.1423	1017.5748	**175.1190**	88.0631

Peptide sequence 10: IIEKPMHIGFLTM[Oxi]EPK



Residue	b	b+2	y	y+2
I	114.0913	57.5493	1900.0071	950.5072
I	**227.1754**	114.0913	1786.9230	893.9652
E	**356.2180**	178.6126	1673.8390	837.4231
K	484.3130	242.6601	1544.7964	**772.9018**
P	581.3657	291.1865	**1416.7014**	**708.8543**
M	**712.4062**	356.7067	1319.6486	660.3280
H	**849.4651**	**425.2362**	**1188.6082**	**594.8077**
I	962.5492	**481.7782**	**1051.5492**	**526.2783**
G	**1019.5706**	**510.2890**	**938.4652**	**469.7362**
F	**1166.6391**	**583.8232**	**881.4437**	441.2255
L	1279.7231	**640.3652**	**734.3753**	**367.6913**
T	1380.7708	690.8890	**621.2912**	**311.1493**
M[Oxi]	1527.8062	**764.4067**	**520.2436**	**260.6254**
E	1656.8488	828.9280	**373.2082**	187.1077
P	1753.9016	877.4544	**244.1656**	122.5864
K	1881.9965	**941.5019**	**147.1128**	74.0600

Peptide sequence 11: IIEKPM[Oxi]HIGFLTMEPK



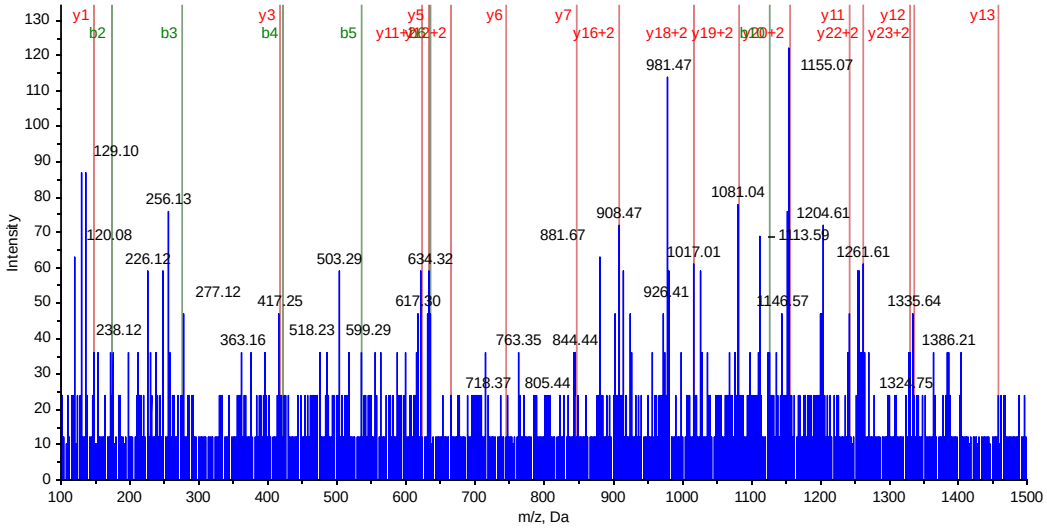
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1900.0071	950.5072
I	**227.1754**	114.0913	1786.9230	893.9652
E	**356.2180**	178.6126	1673.8390	837.4231
K	484.3130	242.6601	1544.7964	**772.9018**
P	581.3657	291.1865	**1416.7014**	**708.8543**
M[Oxi]	**728.4011**	364.7042	1319.6486	660.3280
H	**865.4600**	**433.2337**	**1172.6132**	586.8103
I	978.5441	**489.7757**	**1035.5543**	**518.2808**
G	**1035.5656**	**518.2864**	**922.4703**	**461.7388**
F	**1182.6340**	**591.8206**	**865.4488**	**433.2280**
L	1295.7180	**648.3627**	**718.3804**	**359.6938**
T	1396.7657	**698.8865**	**605.2963**	**303.1518**
M	1527.8062	**764.4067**	**504.2486**	**252.6280**
E	1656.8488	828.9280	**373.2082**	187.1077
P	1753.9016	877.4544	**244.1656**	122.5864
K	1881.9965	**941.5019**	**147.1128**	74.0600

Protein: B.rapa.Ro18.Candidate-2, 12 peptides (95%)

Protein sequence coverage

MIRFTVLSFFVVFVLLFACNESSAKTAKYDKSDESVENDDLAAVPSCCGFSSPLLIK**KDQWKPIFANK**F
GQISTVQIGDGCGGMGPYKIHSITLEPNALMLPLLLHSDMVFFVDSGSGILNWVEAQATSTEIRLGDVY
R**LRPGTVFYLQSKPVDIFLGTK**LKIYAIFSNSQECLHDPCFGAYSSVTDLLFGFDETILK**SAFGVPEEI**
IGLMRNRTQPPLIVHDMLTTPGEANTDTDTNTWPLQTRLLKLFSGDASADSVENKKVKKEKKEKKEKKK
KPK**KATTFNVFESEPDFQSPNGQTITINRK**DLKVLQGSMVGVSMVNLTQGSMMGPHWNPWACEISVVVR
GSGMVRVLRNSISRSSSECKNMR**FKVEKGDIFAVPR**LHPMAQMSFLNDSLVFVGFTTSAK**NNEPQFLAG**
KNSALWSLDREVLAASFNVSSFMIAGLLEAQKEAAVLGCPACAEGELEKLKEDEEKKESPPQQPPQPFQ
PQPPGEKPQQPPQPFQPQPPQGEPQKPPQGEPQKPPQGEPEGPQKPFQPQPGQGEPQEPQASMETKMRD
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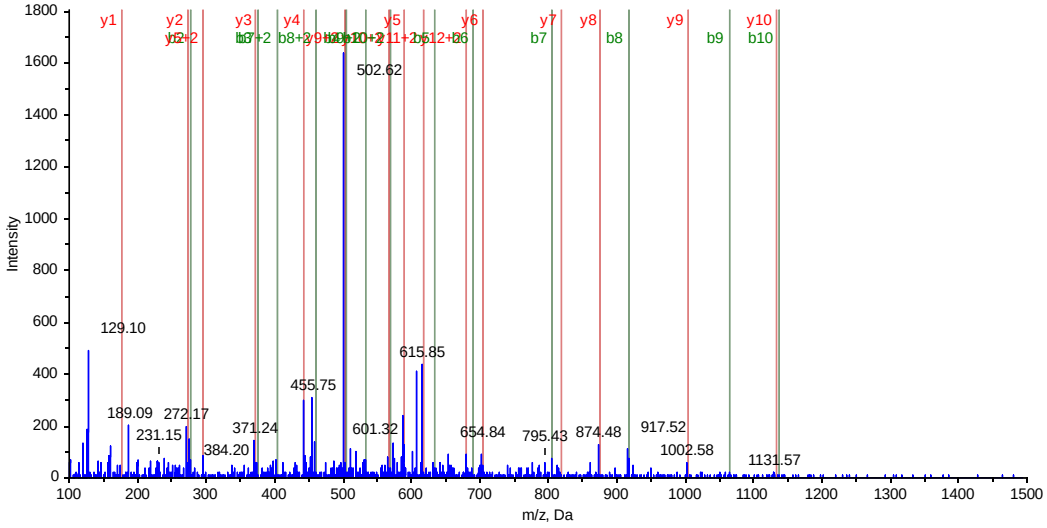
Peptide sequence 1: ATTFNVFESEPDFQSPNGQTITINRK



Residue	b	b+2	y	y+2
A	72.0444	36.5258	2941.4326	1471.2200
T	**173.0921**	87.0497	2870.3955	1435.7014
T	**274.1397**	137.5735	2769.3478	1385.1776
F	**421.2082**	211.1077	2668.3002	**1334.6537**
N	**535.2511**	268.1292	2521.2318	**1261.1195**
V	**634.3195**	317.6634	2407.1888	1204.0981
F	781.3879	391.1976	2308.1204	**1154.5638**
E	910.4305	455.7189	2161.0520	**1081.0296**
S	997.4625	499.2349	2032.0094	**1016.5083**
E	**1126.5051**	563.7562	1944.9774	972.9923
P	1223.5579	612.2826	1815.9348	**908.4710**
D	1338.5848	669.7961	1718.8820	859.9446
F	1485.6533	743.3303	1603.8551	802.4312
Q	1613.7118	807.3596	**1456.7867**	728.8970
S	1700.7439	850.8756	**1328.7281**	**664.8677**
P	1797.7966	899.4019	**1241.6961**	**621.3517**
N	1911.8395	956.4234	1144.6433	572.8253
G	1968.8610	984.9341	1030.6004	515.8038

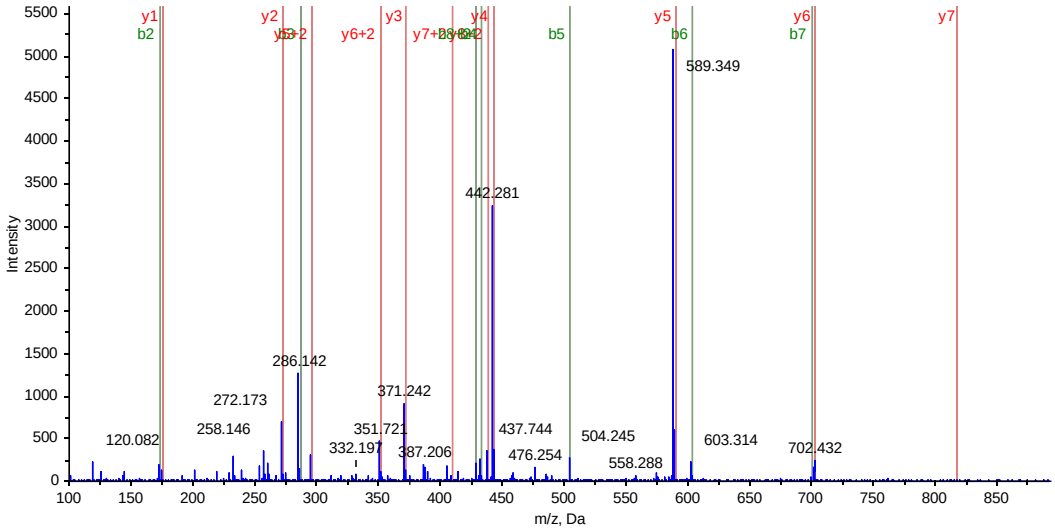
Q	2096.9196	1048.9634	973.5789	487.2931
T	2197.9673	1099.4873	**845.5203**	423.2638
I	2311.0513	1156.0293	**744.4726**	372.7400
T	2412.0990	1206.5531	**631.3886**	316.1979
I	2525.1831	1263.0952	530.3409	265.6741
N	2639.2260	1320.1166	**417.2568**	209.1321
R	2795.3271	1398.1672	303.2139	152.1106
K	2923.4221	1462.2147	**147.1128**	74.0600

Peptide sequence 2: FKVEKGDIFAVPR



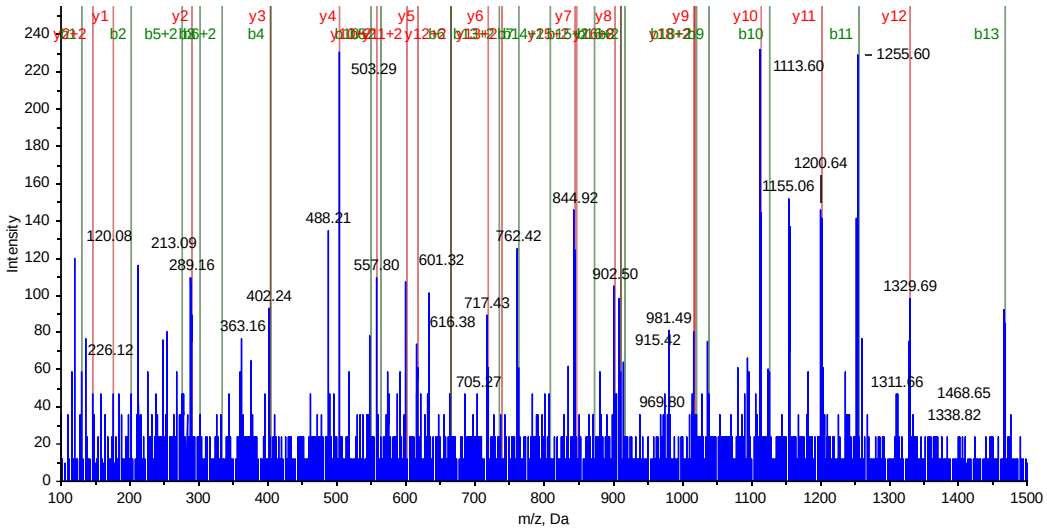
Residue	b	b+2	y	y+2
F	148.0757	74.5415	1505.8475	753.4274
K	**276.1707**	138.5890	1358.7791	**679.8932**
V	**375.2391**	188.1232	1230.6841	**615.8457**
E	**504.2817**	252.6445	**1131.6157**	**566.3115**
K	**632.3766**	316.6919	**1002.5731**	**501.7902**
G	**689.3981**	345.2027	**874.4781**	437.7427
D	**804.4250**	**402.7162**	**817.4567**	409.2320
I	**917.5091**	**459.2582**	**702.4297**	351.7185
F	**1064.5775**	**532.7924**	**589.3457**	**295.1765**
A	**1135.6146**	**568.3109**	**442.2772**	221.6423
V	1234.6830	617.8452	**371.2401**	186.1237
P	1331.7358	666.3715	**272.1717**	136.5895
R	1487.8369	744.4221	**175.1190**	88.0631

Peptide sequence 3: GDIFAVPR



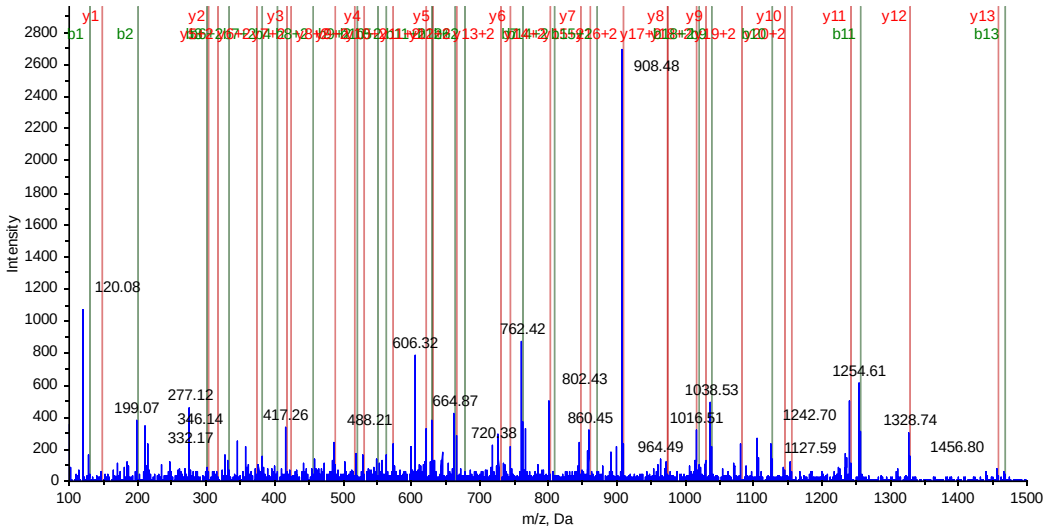
Residue	b	b+2	y	y+2
G	58.0287	29.5180	874.4781	**437.7427**
D	**173.0557**	87.0315	**817.4567**	**409.2320**
I	**286.1397**	143.5735	**702.4297**	**351.7185**
F	**433.2082**	217.1077	**589.3457**	**295.1765**
A	**504.2453**	252.6263	**442.2772**	221.6423
V	**603.3137**	302.1605	**371.2401**	186.1237
P	**700.3665**	350.6869	**272.1717**	136.5895
R	856.4676	**428.7374**	**175.1190**	88.0631

Peptide sequence 4: KATTFNVFESEPDFQSPNGQTITINR



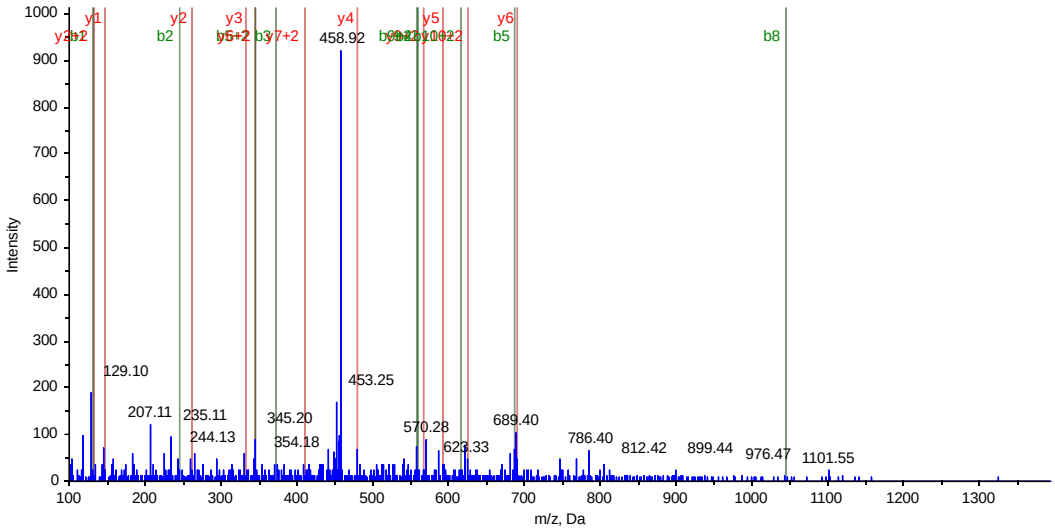
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	2941.4326	1471.2200
A	**200.1394**	100.5733	2813.3377	1407.1725
T	**301.1870**	151.0972	2742.3006	1371.6539
T	**402.2347**	201.6210	2641.2529	1321.1301
F	**549.3031**	**275.1552**	2540.2052	1270.6062
N	**663.3461**	**332.1767**	2393.1368	1197.0720
V	**762.4145**	381.7109	2279.0939	1140.0506
F	**909.4829**	455.2451	2180.0255	1090.5164
E	**1038.5255**	519.7664	2032.9570	**1016.9822**
S	**1125.5575**	**563.2824**	1903.9144	952.4609
E	**1254.6001**	627.8037	1816.8824	**908.9448**
P	1351.6529	676.3301	1687.8398	**844.4236**
D	**1466.6798**	**733.8435**	1590.7871	795.8972
F	1613.7482	**807.3777**	1475.7601	**738.3837**
Q	1741.8068	**871.4070**	**1328.6917**	**664.8495**
S	1828.8388	**914.9230**	**1200.6331**	**600.8202**
P	1925.8916	963.4494	**1113.6011**	**557.3042**
N	2039.9345	**1020.4709**	**1016.5483**	508.7778
G	2096.9560	1048.9816	**902.5054**	451.7563
Q	2225.0146	1113.0109	**845.4839**	423.2456
T	2326.0622	1163.5348	**717.4254**	359.2163
I	2439.1463	1220.0768	**616.3777**	308.6925
T	2540.1940	1270.6006	**503.2936**	252.1504
I	2653.2780	1327.1427	**402.2459**	201.6266
N	2767.3210	1384.1641	**289.1619**	**145.0846**
R	2923.4221	1462.2147	**175.1190**	88.0631

Peptide sequence 5: KATTFNVFESEPDFQSPNGQTITINRK



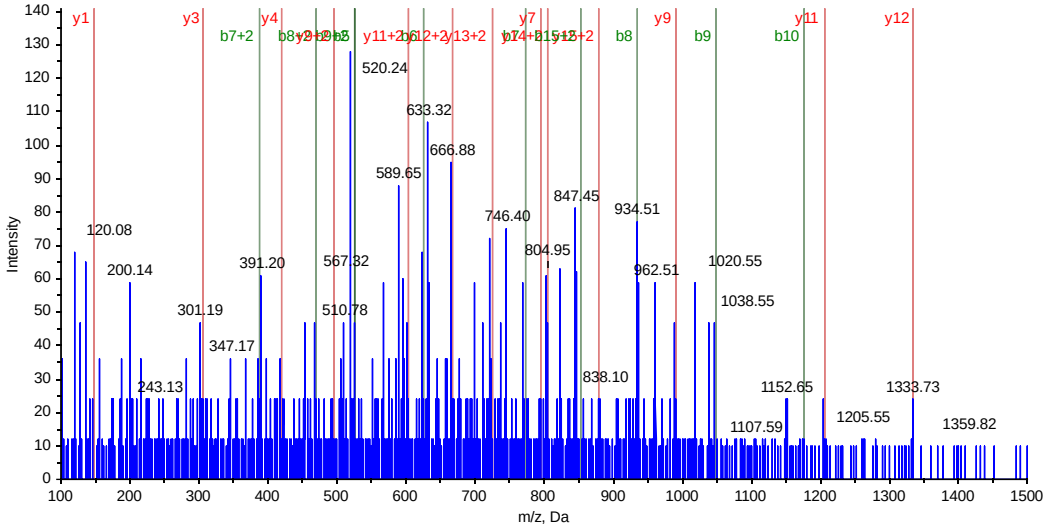
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	3069.5276	1535.2674
A	**200.1394**	100.5733	2941.4326	1471.2200
T	**301.1870**	151.0972	2870.3955	1435.7014
T	**402.2347**	201.6210	2769.3478	1385.1776
F	**549.3031**	275.1552	2668.3002	1334.6537
N	**663.3461**	**332.1767**	2521.2318	1261.1195
V	**762.4145**	**381.7109**	2407.1888	1204.0981
F	909.4829	**455.2451**	2308.1204	**1154.5638**
E	**1038.5255**	**519.7664**	2161.0520	**1081.0296**
S	**1125.5575**	**563.2824**	2032.0094	**1016.5083**
E	**1254.6001**	**627.8037**	1944.9774	**972.9923**
P	1351.6529	**676.3301**	1815.9348	**908.4710**
D	**1466.6798**	733.8435	1718.8820	**859.9446**
F	1613.7482	**807.3777**	1603.8551	**802.4312**
Q	1741.8068	**871.4070**	**1456.7867**	**728.8970**
S	1828.8388	914.9230	**1328.7281**	**664.8677**
P	1925.8916	963.4494	**1241.6961**	**621.3517**
N	2039.9345	**1020.4709**	**1144.6433**	**572.8253**
G	2096.9560	1048.9816	**1030.6004**	**515.8038**
Q	2225.0146	1113.0109	**973.5789**	**487.2931**
T	2326.0622	1163.5348	**845.5203**	**423.2638**
I	2439.1463	1220.0768	**744.4726**	**372.7400**
T	2540.1940	1270.6006	**631.3886**	**316.1979**
I	2653.2780	1327.1427	**530.3409**	265.6741
N	2767.3210	1384.1641	**417.2568**	209.1321
R	2923.4221	1462.2147	**303.2139**	152.1106
K	3051.5170	1526.2622	**147.1128**	74.0600

Peptide sequence 6: KDQWKPIFANK



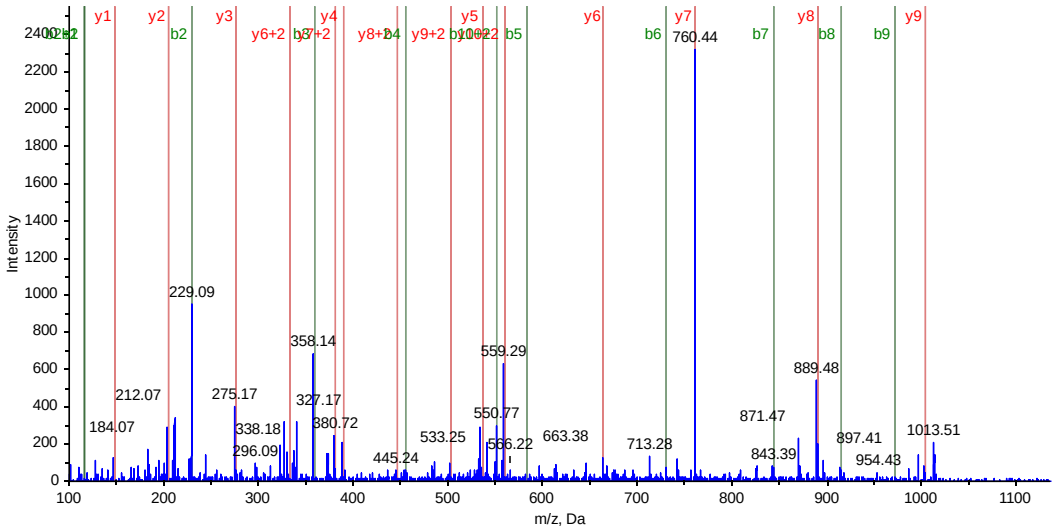
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	1374.7528	687.8801
D	**244.1292**	122.5682	1246.6579	**623.8326**
Q	**372.1878**	186.5975	1131.6309	**566.3191**
W	**558.2671**	279.6372	1003.5724	502.2898
K	**686.3620**	**343.6847**	817.4931	**409.2502**
P	783.4148	392.2110	**689.3981**	**345.2027**
I	896.4989	448.7531	**592.3453**	296.6763
F	**1043.5673**	522.2873	**479.2613**	240.1343
A	1114.6044	**557.8058**	**332.1928**	166.6001
N	1228.6473	**614.8273**	**261.1557**	**131.0815**
K	1356.7423	678.8748	**147.1128**	74.0600

Peptide sequence 7: LRPGTVFYLQSKPVDIFLGTK



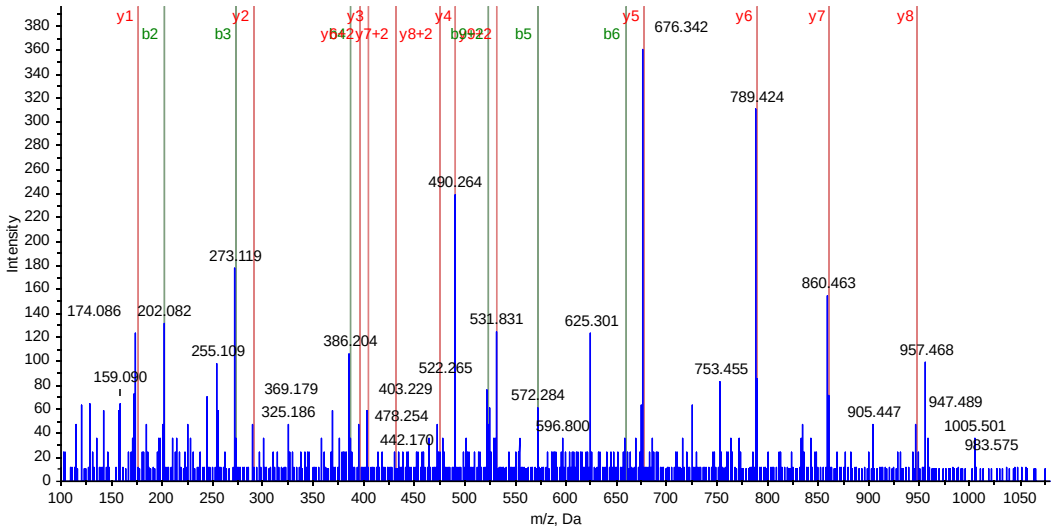
Residue	b	b+2	y	y+2
L	114.0913	57.5493	2379.3435	1190.1754
R	270.1925	135.5999	2266.2594	1133.6333
P	367.2452	184.1262	2110.1583	1055.5828
G	424.2667	212.6370	2013.1055	1007.0564
T	**525.3144**	263.1608	1956.0841	978.5457
V	**624.3828**	312.6950	1855.0364	928.0218
F	**771.4512**	**386.2292**	1755.9680	**878.4876**
Y	**934.5145**	**467.7609**	1608.8996	**804.9534**
L	**1047.5986**	**524.3029**	1445.8362	**723.4218**
Q	**1175.6572**	588.3322	**1332.7522**	**666.8797**
S	1262.6892	631.8482	**1204.6936**	**602.8504**
K	1390.7841	695.8957	1117.6616	559.3344
P	1487.8369	744.4221	**989.5666**	**495.2869**
V	1586.9053	793.9563	892.5138	446.7606
D	1701.9323	**851.4698**	**793.4454**	397.2264
I	1815.0163	908.0118	678.4185	339.7129
F	1962.0847	981.5460	565.3344	283.1709
L	2075.1688	1038.0880	**418.2660**	209.6366
G	2132.1903	1066.5988	**305.1819**	153.0946
T	2233.2380	1117.1226	248.1605	124.5839
K	2361.3329	1181.1701	**147.1128**	74.0600

Peptide sequence 8: NNEPQFLAGK



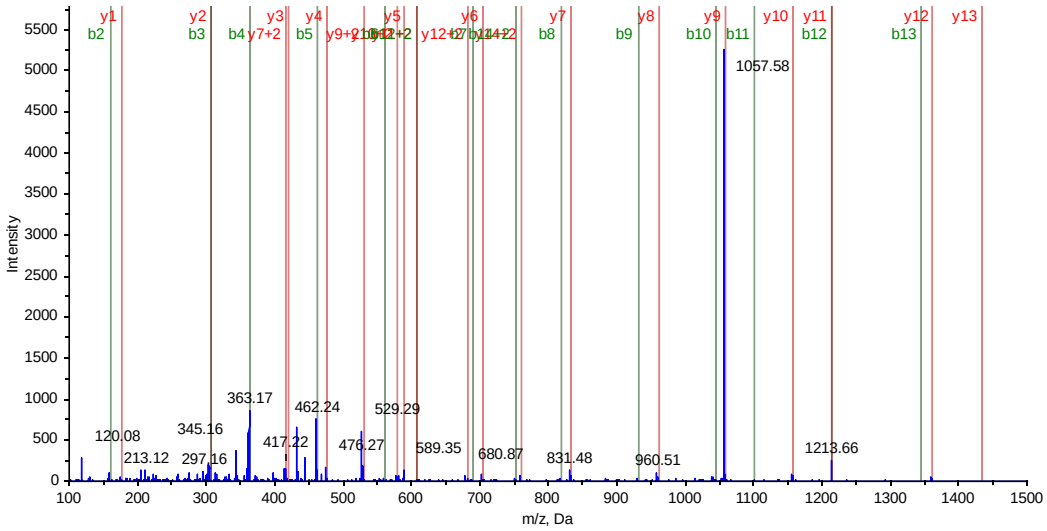
Residue	b	b+2	y	y+2
N	**115.0502**	58.0287	1117.5636	**559.2855**
N	**229.0931**	**115.0502**	**1003.5207**	**502.2640**
E	**358.1357**	179.5715	**889.4778**	**445.2425**
P	**455.1885**	228.0979	**760.4352**	**380.7212**
Q	**583.2471**	292.1272	**663.3824**	**332.1949**
F	**730.3155**	365.6614	**535.3239**	268.1656
L	**843.3995**	422.2034	**388.2554**	194.6314
A	**914.4367**	457.7220	**275.1714**	138.0893
G	**971.4581**	486.2327	**204.1343**	102.5708
K	1099.5531	**550.2802**	**147.1128**	74.0600

Peptide sequence 9: NSALWSLDR



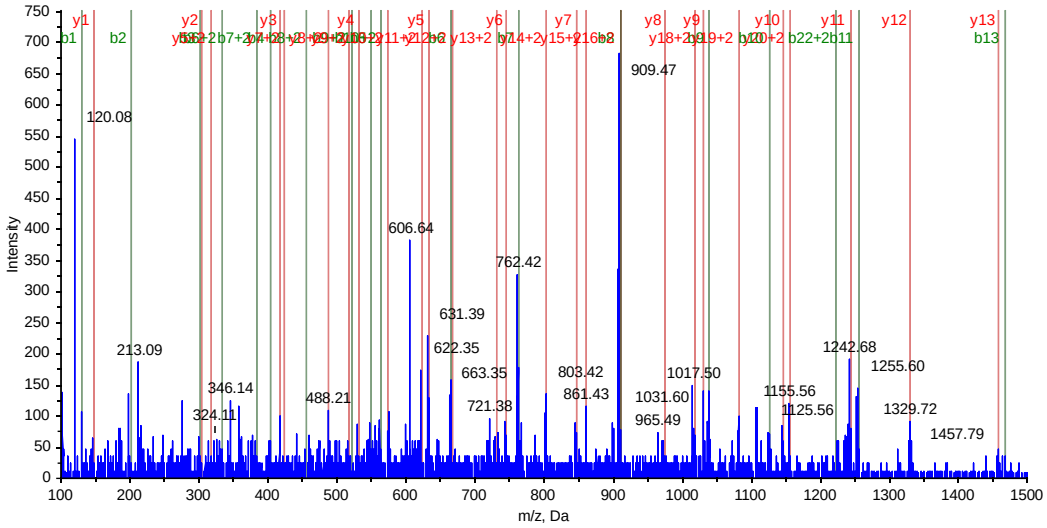
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1061.5374	**531.2724**
S	**202.0822**	101.5448	**947.4945**	**474.2509**
A	**273.1193**	137.0633	**860.4625**	**430.7349**
L	**386.2034**	193.6053	**789.4254**	**395.2163**
W	**572.2827**	286.6450	**676.3413**	338.6743
S	**659.3148**	330.1610	**490.2620**	245.6346
L	772.3988	386.7030	**403.2300**	202.1186
D	887.4258	444.2165	**290.1459**	145.5766
R	1043.5269	**522.2671**	**175.1190**	88.0631

Peptide sequence 10: SAFGVPEEIIGLMR



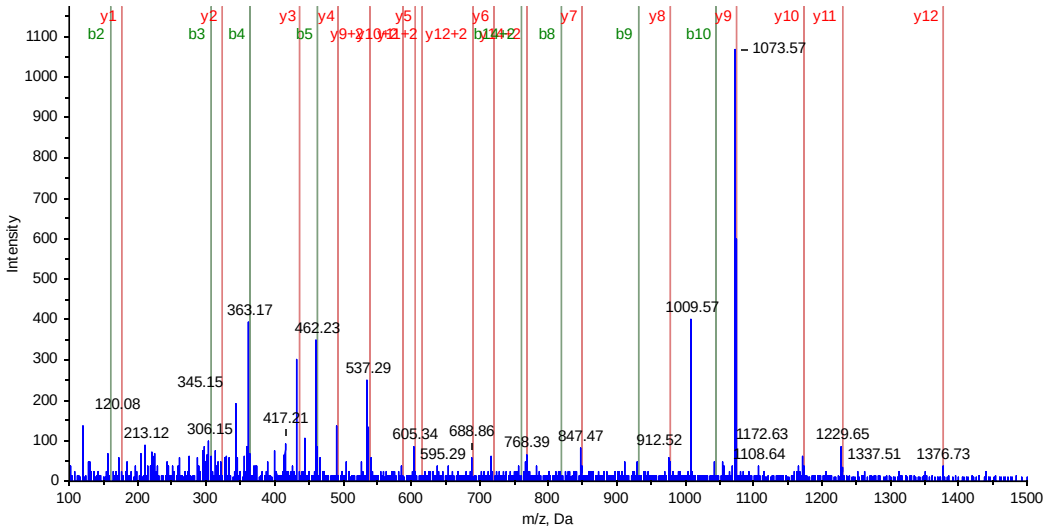
Residue	b	b+2	y	y+2
S	88.0393	44.5233	1518.7985	**759.9029**
A	**159.0764**	80.0418	**1431.7664**	716.3869
F	**306.1448**	153.5761	**1360.7293**	**680.8683**
G	**363.1663**	182.0868	**1213.6609**	**607.3341**
V	**462.2347**	231.6210	**1156.6395**	**578.8234**
P	**559.2875**	280.1474	**1057.5710**	**529.2892**
E	**688.3301**	344.6687	**960.5183**	480.7628
E	**817.3727**	409.1900	**831.4757**	**416.2415**
I	**930.4567**	465.7320	**702.4331**	351.7202
I	**1043.5408**	522.2740	**589.3490**	295.1782
G	**1100.5623**	550.7848	**476.2650**	238.6361
L	**1213.6463**	**607.3268**	**419.2435**	210.1254
M	**1344.6868**	672.8470	**306.1594**	153.5834
R	1500.7879	**750.8976**	**175.1190**	88.0631

Peptide sequence 11: KATTFNVFESEPDFQSPN[Dea]GQTITINRK



Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	3070.5116	1535.7594
A	**200.1394**	100.5733	2942.4167	1471.7120
T	**301.1870**	151.0972	2871.3795	1436.1934
T	**402.2347**	201.6210	2770.3319	1385.6696
F	**549.3031**	275.1552	2669.2842	1335.1457
N	**663.3461**	**332.1767**	2522.2158	1261.6115
V	**762.4145**	**381.7109**	2408.1728	1204.5901
F	**909.4829**	**455.2451**	2309.1044	**1155.0559**
E	**1038.5255**	**519.7664**	2162.0360	**1081.5216**
S	**1125.5575**	**563.2824**	2032.9934	**1017.0004**
E	**1254.6001**	627.8037	1945.9614	973.4843
P	1351.6529	676.3301	1816.9188	**908.9630**
D	**1466.6798**	733.8435	1719.8660	**860.4367**
F	1613.7482	807.3777	1604.8391	**802.9232**
Q	1741.8068	871.4070	**1457.7707**	**729.3890**
S	1828.8388	914.9230	**1329.7121**	**665.3597**
P	1925.8916	963.4494	**1242.6801**	**621.8437**
N[Dea]	2040.9185	1020.9629	**1145.6273**	**573.3173**
G	2097.9400	1049.4736	**1030.6004**	**515.8038**
Q	2225.9986	1113.5029	**973.5789**	**487.2931**
T	2327.0462	1164.0268	**845.5203**	**423.2638**
I	2440.1303	**1220.5688**	**744.4726**	372.7400
T	2541.1780	1271.0926	**631.3886**	**316.1979**
I	2654.2621	1327.6347	**530.3409**	265.6741
N	2768.3050	1384.6561	**417.2568**	209.1321
R	2924.4061	1462.7067	**303.2139**	152.1106
K	3052.5011	1526.7542	**147.1128**	74.0600

Peptide sequence 12: SAFGVPEEIIGLM[Oxi]R



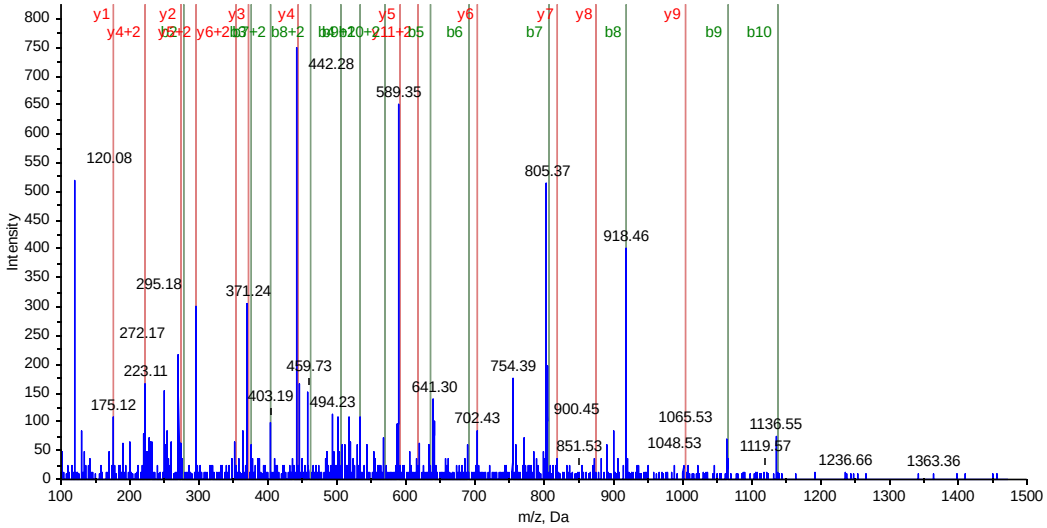
Residue	b	b+2	y	y+2
S	88.0393	44.5233	1534.7934	**767.9003**
A	**159.0764**	80.0418	1447.7614	724.3843
F	**306.1448**	153.5761	**1376.7242**	**688.8658**
G	**363.1663**	182.0868	**1229.6558**	**615.3316**
V	**462.2347**	231.6210	**1172.6344**	**586.8208**
P	559.2875	280.1474	**1073.5660**	**537.2866**
E	688.3301	344.6687	**976.5132**	488.7602
E	**817.3727**	409.1900	**847.4706**	424.2389
I	**930.4567**	465.7320	**718.4280**	359.7176
I	**1043.5408**	522.2740	**605.3439**	303.1756
G	1100.5623	550.7848	**492.2599**	246.6336
L	1213.6463	607.3268	**435.2384**	218.1228
M[Oxi]	1360.6817	680.8445	**322.1544**	161.5808
R	1516.7828	**758.8951**	**175.1190**	88.0631

Protein: B.rapa.Ro18.Candidate-3, 2 peptides (95%)

Protein sequence coverage

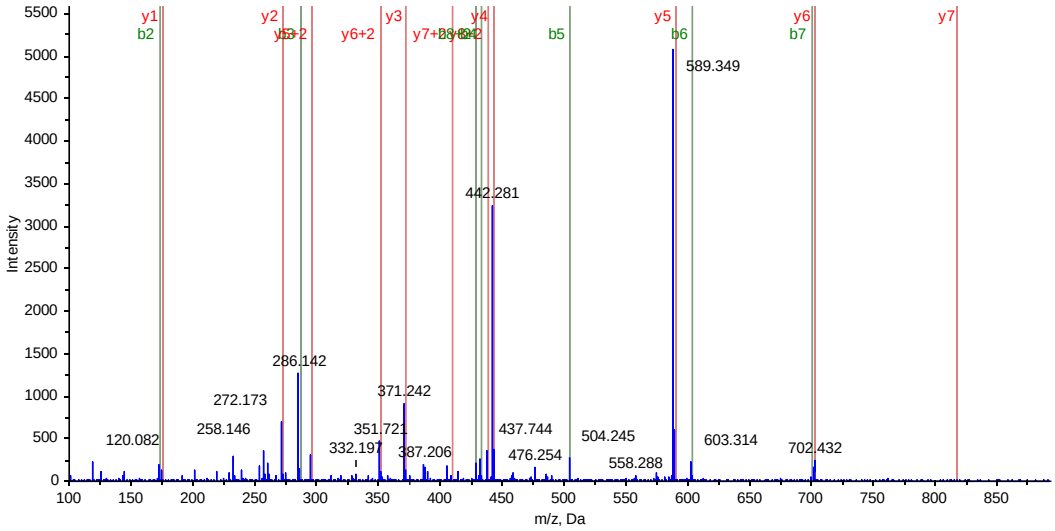
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LMTNRTQPPLIVHDMLSTPGEANTYTWQLQVQPRLLKLFAGYVSAAEKKKKEKKTKKAK**TFNVFESEPD**
FQSPSGRTITINRKDLEVLSGSMVGVSMVNLTQASMMGPHWNPWACEISIVLKGSGMVRVLRSSISSTS
SSSSSSECKNMR**FKVEEGDIFAVPR**LHPMAQMSFINESLVFIGFTTSAR**NNEPQFLAGQR**SALRLLDQE
VLAASLNVSSVMIEGLLGAQKDAVVLGCPYCAEGELEKLKVETEMKKRDDERKREEEEAKKEEEERRKR
EEEEEEEKQWPPLPQQPPE

Peptide sequence 1: FKVEEGDIFAVPR



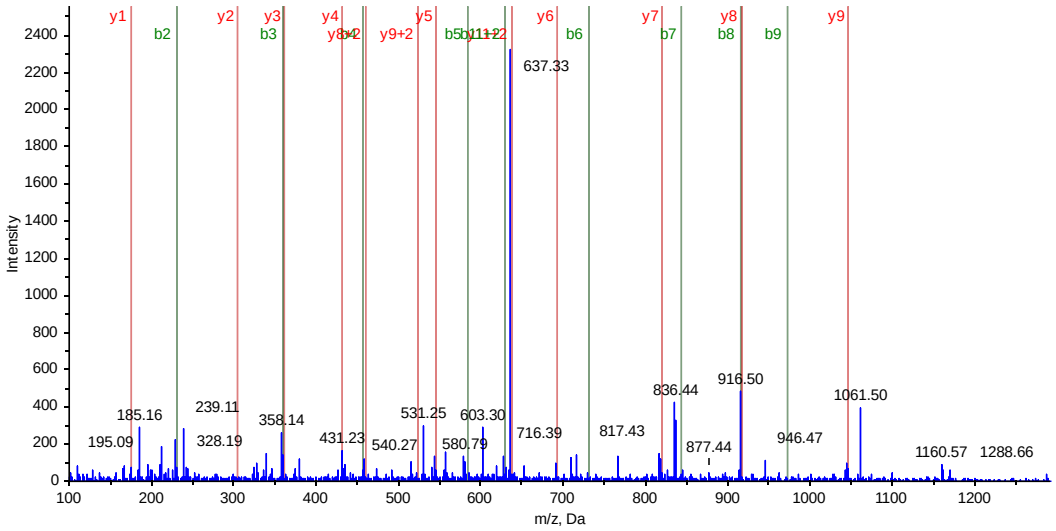
Residue	b	b+2	y	y+2
F	148.0757	74.5415	1506.7951	753.9012
K	**276.1707**	138.5890	1359.7267	680.3670
V	**375.2391**	188.1232	1231.6317	**616.3195**
E	**504.2817**	252.6445	1132.5633	566.7853
E	**633.3243**	317.1658	**1003.5207**	502.2640
G	**690.3457**	345.6765	**874.4781**	437.7427
D	**805.3727**	**403.1900**	**817.4567**	409.2320
I	**918.4567**	**459.7320**	**702.4297**	**351.7185**
F	**1065.5251**	**533.2662**	**589.3457**	**295.1765**
A	**1136.5623**	**568.7848**	**442.2772**	**221.6423**
V	1235.6307	618.3190	**371.2401**	186.1237
P	1332.6834	666.8454	**272.1717**	136.5895
R	1488.7845	744.8959	**175.1190**	88.0631

Peptide sequence 2: GDIFAVPR



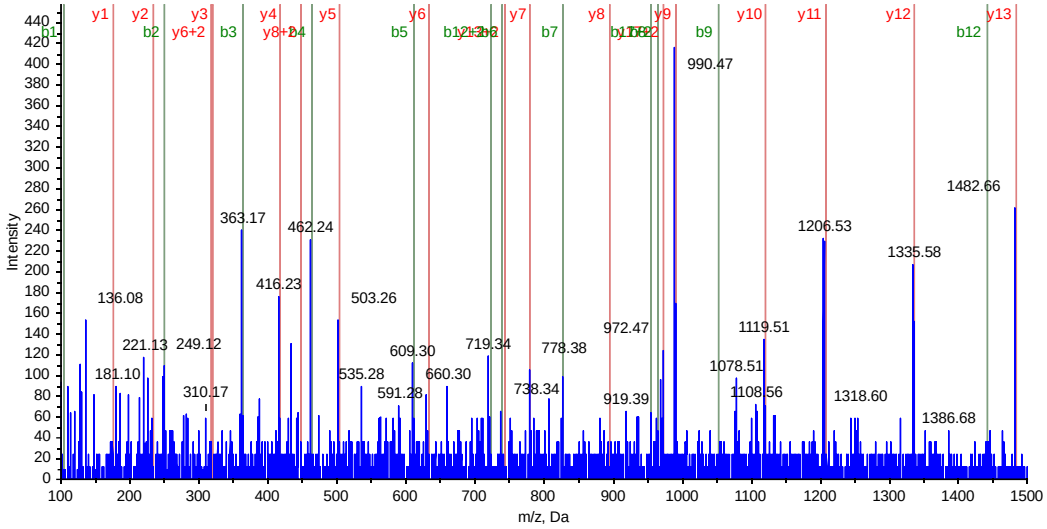
Residue	b	b+2	y	y+2
G	58.0287	29.5180	874.4781	**437.7427**
D	**173.0557**	87.0315	**817.4567**	**409.2320**
I	**286.1397**	143.5735	**702.4297**	**351.7185**
F	**433.2082**	217.1077	**589.3457**	**295.1765**
A	**504.2453**	252.6263	**442.2772**	221.6423
V	**603.3137**	302.1605	**371.2401**	186.1237
P	**700.3665**	350.6869	**272.1717**	136.5895
R	856.4676	**428.7374**	**175.1190**	88.0631

Peptide sequence 3: NNEPQFLAGQR



Residue	b	b+2	y	y+2
N	115.0502	58.0287	1273.6284	**637.3178**
N	**229.0931**	115.0502	1159.5854	580.2964
E	**358.1357**	179.5715	**1045.5425**	**523.2749**
P	**455.1885**	228.0979	**916.4999**	**458.7536**
Q	**583.2471**	292.1272	**819.4472**	410.2272
F	**730.3155**	365.6614	**691.3886**	346.1979
L	**843.3995**	422.2034	**544.3202**	272.6637
A	**914.4367**	457.7220	**431.2361**	216.1217
G	**971.4581**	486.2327	**360.1990**	180.6031
Q	1099.5167	550.2620	**303.1775**	152.0924
R	1255.6178	**628.3125**	**175.1190**	88.0631

Peptide sequence 4: TFNVFESEPDFQSPSGR



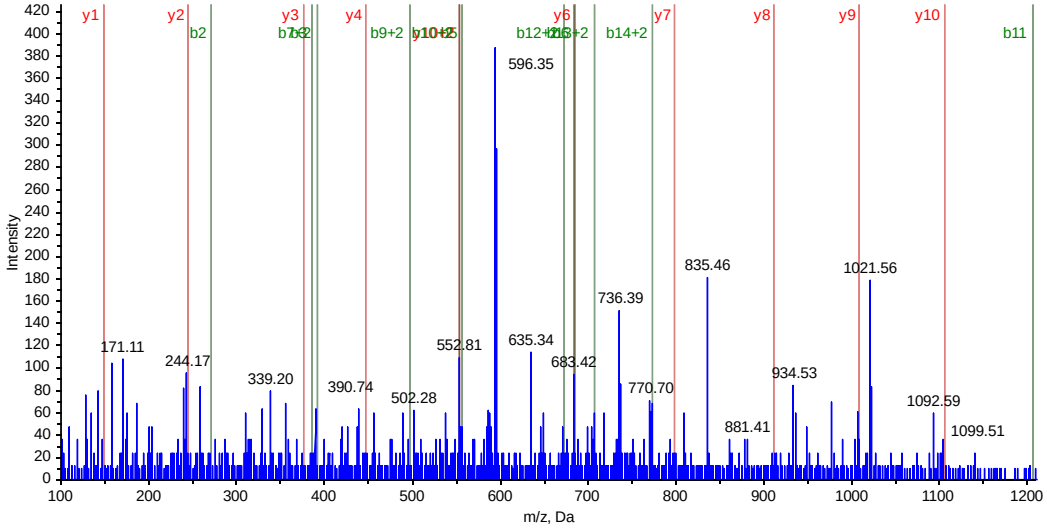
Residue	b	b+2	y	y+2
T	**102.0550**	51.5311	1943.8770	**972.4421**
F	**249.1234**	125.0653	1842.8293	921.9183
N	**363.1663**	182.0868	1695.7609	848.3841
V	**462.2347**	231.6210	1581.7180	791.3626
F	**609.3031**	305.1552	**1482.6496**	**741.8284**
E	**738.3457**	369.6765	**1335.5811**	668.2942
S	**825.3777**	413.1925	**1206.5386**	603.7729
E	**954.4203**	477.7138	**1119.5065**	560.2569
P	**1051.4731**	526.2402	**990.4639**	495.7356
D	1166.5000	583.7537	**893.4112**	**447.2092**
F	1313.5685	657.2879	**778.3842**	389.6958
Q	**1441.6270**	**721.3172**	**631.3158**	**316.1615**
S	1528.6591	764.8332	**503.2572**	252.1323
P	1625.7118	813.3596	**416.2252**	208.6162
S	1712.7439	856.8756	**319.1724**	160.0899
G	1769.7653	885.3863	**232.1404**	116.5738
R	1925.8664	**963.4369**	**175.1190**	88.0631

Protein: B.rapa.Ro18.Candidate-4, 3 peptides (95%)

Protein sequence coverage

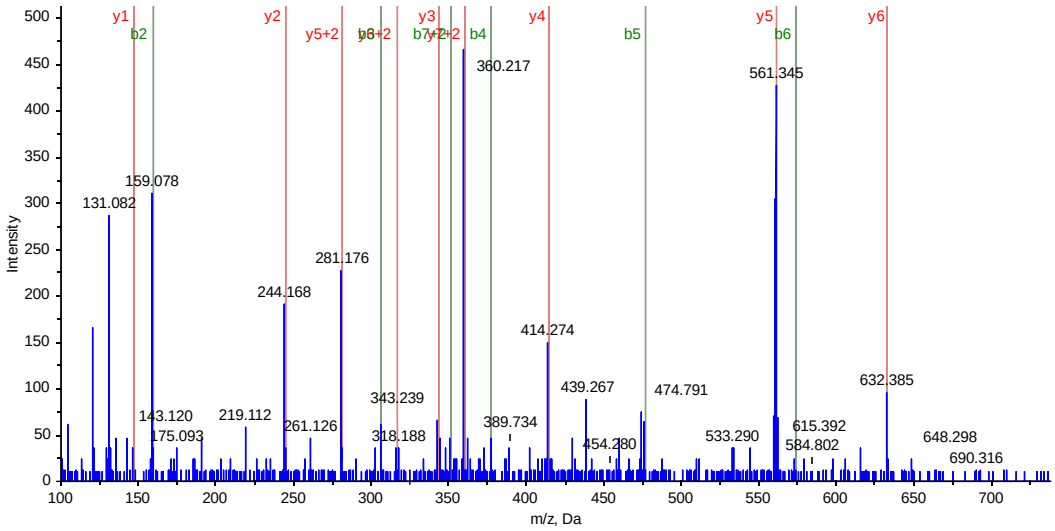
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VYAIFDVGKCLSDQCLGAYSSIRDLLWGFDEKTLR**SAFAVPK**DVFGR**LRDAVKPPLITHAMPK**NRTQGS
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FNRDVLATSFNMRYATVERLLGAQKDGLLLECVSCAEVELSRLMREIEERRRREEEEIERRKREEEEAK
RQEEERRRREEEEAERKKKAEEEARKREKERE REEEAAKRREEERRRREEEEAERKRKEEEEARKREEE
RKREEEAAKKREEERRKREKEEEEARKREEARE REEEEAKKREEERRKREEEEAERKRRAEEEARE REE
EEAKKREEEKEAARRREEERE KEEEMAKRREEERQRKERE DVERKKREEEEERKRREEEAMRREEERKR
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Peptide sequence 1: LRDAVKPPLITHAMPK



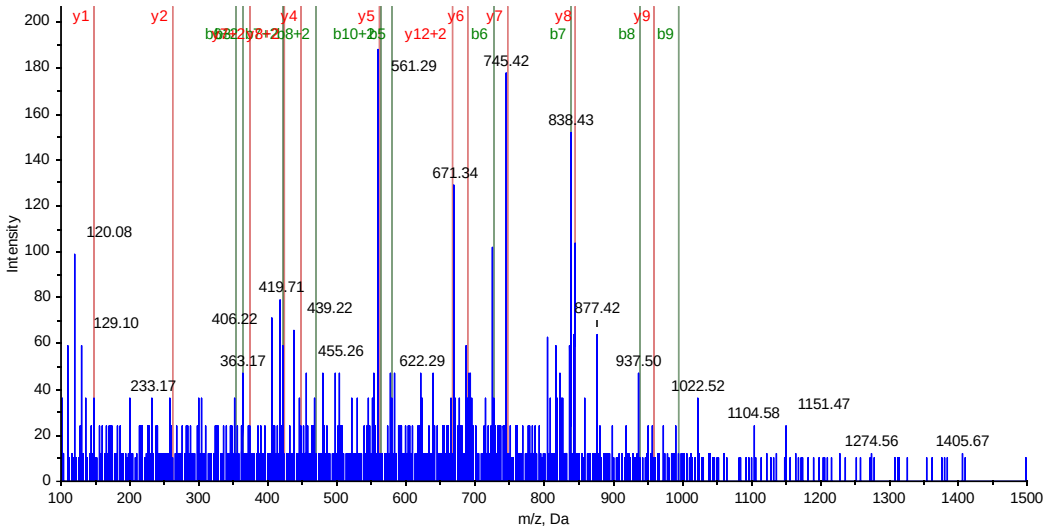
Residue	b	b+2	y	y+2
L	114.0913	57.5493	1787.0360	894.0216
R	**270.1925**	135.5999	1673.9520	837.4796
D	**385.2194**	193.1133	1517.8508	759.4291
A	456.2565	228.6319	1402.8239	701.9156
V	**555.3249**	278.1661	1331.7868	666.3970
K	**683.4199**	342.2136	1232.7184	616.8628
P	780.4726	**390.7400**	**1104.6234**	**552.8153**
P	877.5254	439.2663	**1007.5706**	504.2890
L	990.6095	**495.8084**	**910.5179**	455.7626
I	1103.6935	**552.3504**	**797.4338**	399.2205
T	**1204.7412**	602.8742	**684.3498**	342.6785
H	1341.8001	**671.4037**	583.3021	292.1547
A	1412.8372	**706.9223**	**446.2432**	223.6252
M	1543.8777	**772.4425**	**375.2061**	188.1067
P	1640.9305	820.9689	**244.1656**	122.5864
K	1769.0255	885.0164	**147.1128**	74.0600

Peptide sequence 2: SAFAVPK



Residue	b	b+2	y	y+2
S	88.0393	44.5233	719.4087	**360.2080**
A	**159.0764**	80.0418	**632.3766**	**316.6919**
F	**306.1448**	153.5761	**561.3395**	**281.1734**
A	**377.1819**	189.0946	**414.2711**	207.6392
V	**476.2504**	238.6288	**343.2340**	172.1206
P	**573.3031**	287.1552	**244.1656**	122.5864
K	701.3981	**351.2027**	**147.1128**	74.0600

Peptide sequence 3: TNHPQFLVGQNSVLK



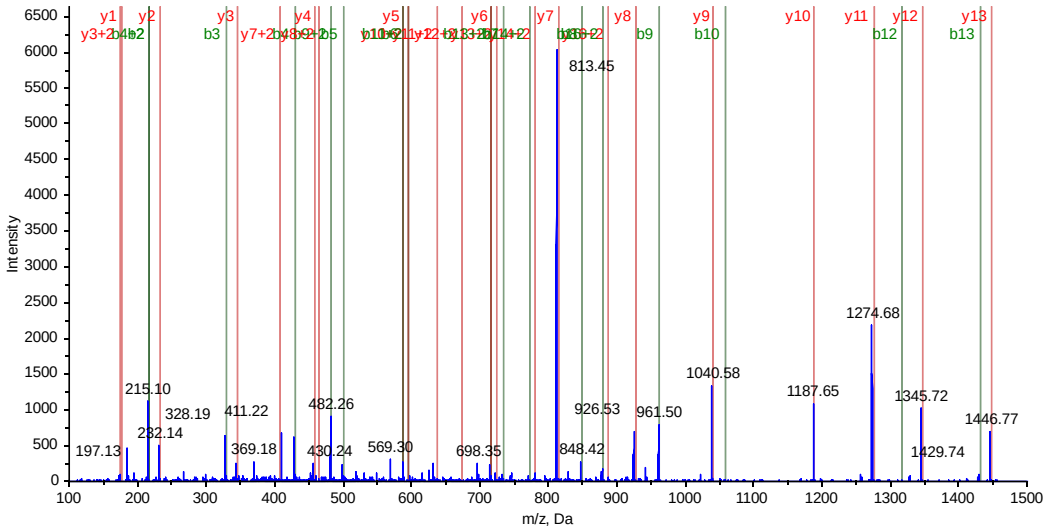
Residue	b	b+2	y	y+2
T	102.0550	51.5311	1681.9020	841.4547
N	216.0979	108.5526	1580.8544	790.9308
H	**353.1568**	177.0820	1466.8114	733.9094
P	450.2096	225.6084	1329.7525	**665.3799**
Q	**578.2681**	289.6377	1232.6997	616.8535
F	**725.3365**	**363.1719**	1104.6412	552.8242
L	**838.4206**	**419.7139**	**957.5728**	479.2900
V	**937.4890**	**469.2482**	**844.4887**	**422.7480**
G	**994.5105**	497.7589	**745.4203**	**373.2138**
Q	1122.5691	**561.7882**	**688.3988**	344.7030
N	1236.6120	618.8096	**560.3402**	280.6738
S	1323.6440	662.3257	**446.2973**	223.6523
V	1422.7124	711.8599	359.2653	180.1363
L	1535.7965	768.4019	**260.1969**	130.6021
K	1663.8915	832.4494	**147.1128**	74.0600

Protein: B.rapa.Ro18.Candidate-5, 18 peptides (95%)

Protein sequence coverage

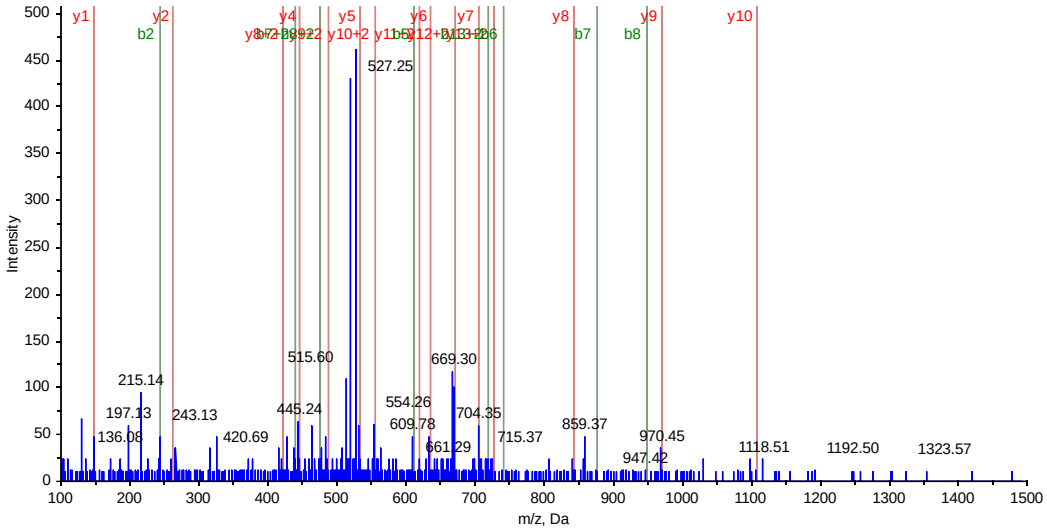
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ESFQITKGDVVR**VPSSVTHFFANTNGTVPLR**LAK**IAVPANVPGHFQVFFPAHSGFHQSYFNGFSKDVLT**
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SPYTFQGEQQQPWFGPGQEEEVEEEMSGQVHKIVSRVCKGEVFILPAGHPFAILSQDENFVAVGFGIHA
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VGF

Peptide sequence 1: DVLTASFNIPEELLGR



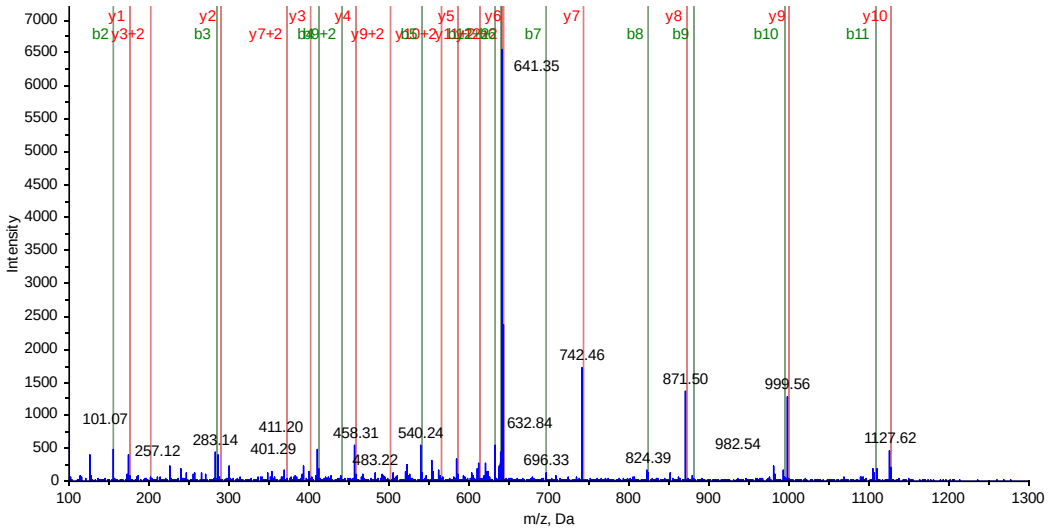
Residue	b	b+2	y	y+2
D	116.0342	58.5207	1773.9381	**887.4727**
V	**215.1026**	108.0550	1658.9112	829.9592
L	**328.1867**	164.5970	1559.8428	**780.4250**
T	**429.2344**	**215.1208**	**1446.7587**	**723.8830**
A	**500.2715**	250.6394	**1345.7110**	**673.3592**
S	**587.3035**	294.1554	**1274.6739**	**637.8406**
F	**734.3719**	367.6896	**1187.6419**	**594.3246**
N	**848.4149**	424.7111	**1040.5735**	520.7904
I	**961.4989**	**481.2531**	**926.5306**	**463.7689**
P	**1058.5517**	529.7795	**813.4465**	**407.2269**
E	1187.5943	**594.3008**	**716.3937**	358.7005
E	**1316.6369**	658.8221	**587.3511**	294.1792
L	**1429.7209**	**715.3641**	**458.3085**	229.6579
L	1542.8050	**771.9061**	**345.2245**	**173.1159**
G	1599.8265	800.4169	**232.1404**	116.5738
R	1755.9276	**878.4674**	**175.1190**	88.0631

Peptide sequence 2: ELTEHEHATSPSNK



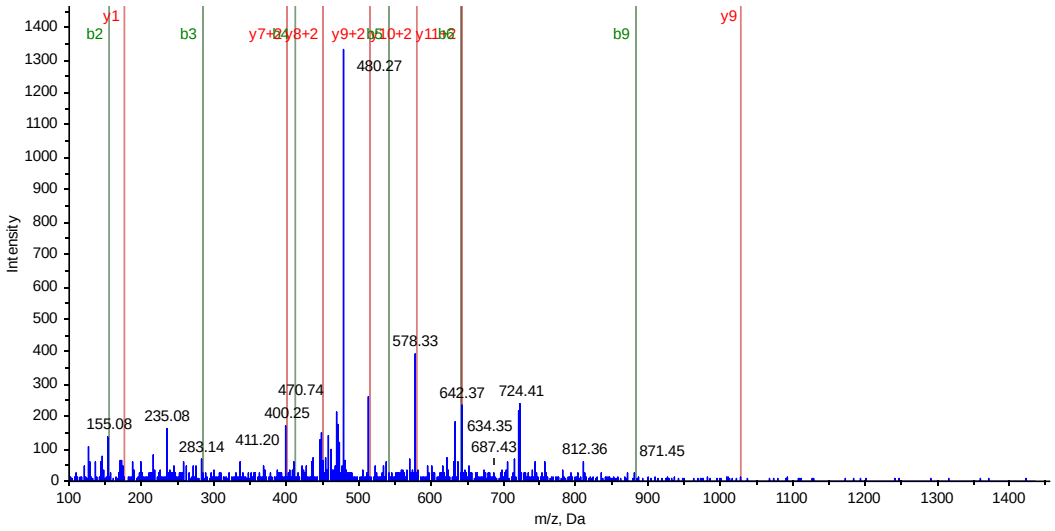
Residue	b	b+2	y	y+2
E	130.0499	65.5286	1579.7347	790.3710
L	**243.1339**	122.0706	1450.6921	**725.8497**
T	344.1816	172.5944	1337.6080	**669.3077**
E	473.2242	237.1157	1236.5604	**618.7838**
H	**610.2831**	305.6452	**1107.5178**	**554.2625**
E	**739.3257**	370.1665	**970.4588**	**485.7331**
H	**876.3846**	**438.6959**	**841.4163**	**421.2118**
A	**947.4217**	**474.2145**	**704.3573**	352.6823
T	1048.4694	524.7383	**633.3202**	317.1638
S	1135.5014	568.2544	**532.2726**	266.6399
P	1232.5542	616.7807	**445.2405**	223.1239
S	1319.5862	660.2968	348.1878	174.5975
N	1433.6292	**717.3182**	**261.1557**	131.0815
K	1561.7241	781.3657	**147.1128**	74.0600

Peptide sequence 3: GPQQEVGQGIIR



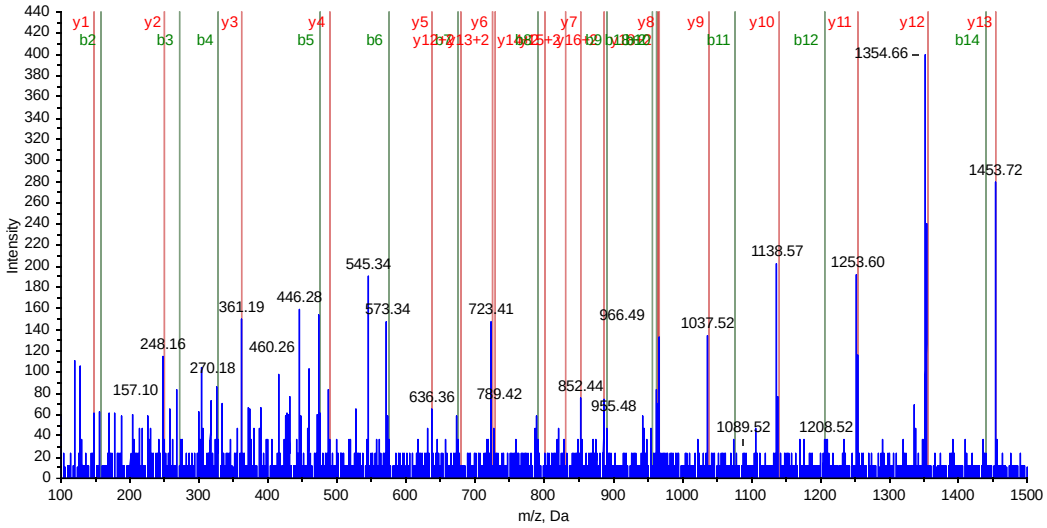
Residue	b	b+2	y	y+2
G	58.0287	29.5180	1281.6910	**641.3491**
P	**155.0815**	78.0444	1224.6695	**612.8384**
Q	**283.1401**	142.0737	**1127.6167**	**564.3120**
Q	**411.1987**	206.1030	**999.5582**	**500.2827**
E	**540.2413**	270.6243	**871.4996**	436.2534
V	**639.3097**	320.1585	**742.4570**	**371.7321**
G	**696.3311**	348.6692	**643.3886**	322.1979
Q	**824.3897**	412.6985	**586.3671**	293.6872
G	**881.4112**	**441.2092**	**458.3085**	229.6579
I	**994.4952**	497.7513	**401.2871**	**201.1472**
I	**1107.5793**	554.2933	**288.2030**	144.6051
R	1263.6804	**632.3438**	**175.1190**	88.0631

Peptide sequence 4: GPQQEVGQGIIRR



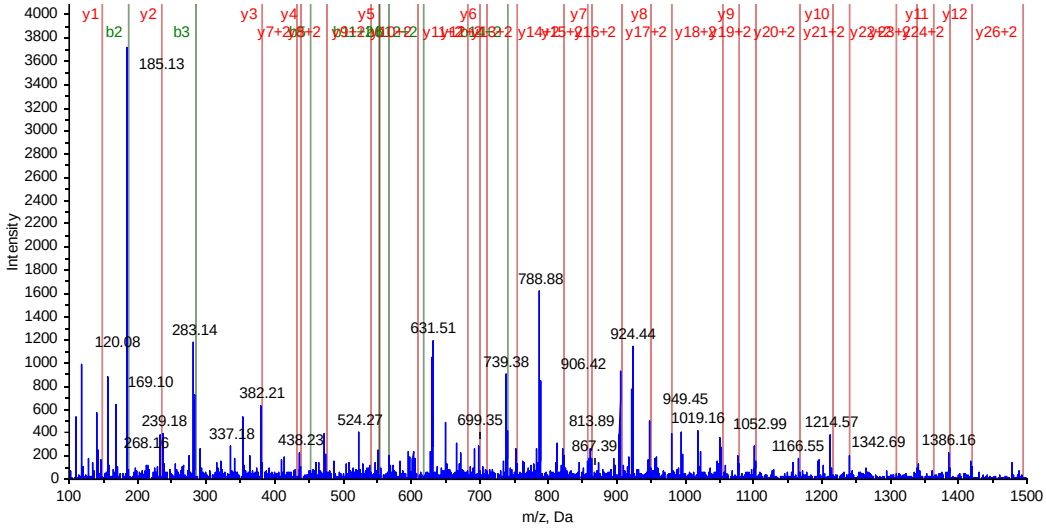
Residue	b	b+2	y	y+2
G	58.0287	29.5180	1437.7921	719.3997
P	**155.0815**	78.0444	1380.7706	690.8889
Q	**283.1401**	142.0737	1283.7179	**642.3626**
Q	**411.1987**	206.1030	1155.6593	**578.3333**
E	**540.2413**	270.6243	**1027.6007**	**514.3040**
V	**639.3097**	320.1585	898.5581	**449.7827**
G	696.3311	348.6692	799.4897	**400.2485**
Q	824.3897	412.6985	742.4682	371.7378
G	**881.4112**	441.2092	614.4097	307.7085
I	994.4952	497.7513	557.3882	279.1977
I	1107.5793	554.2933	444.3041	222.6557
R	1263.6804	632.3438	331.2201	166.1137
R	1419.7815	710.3944	**175.1190**	88.0631

Peptide sequence 5: GVIGFVTDTANESFQITK



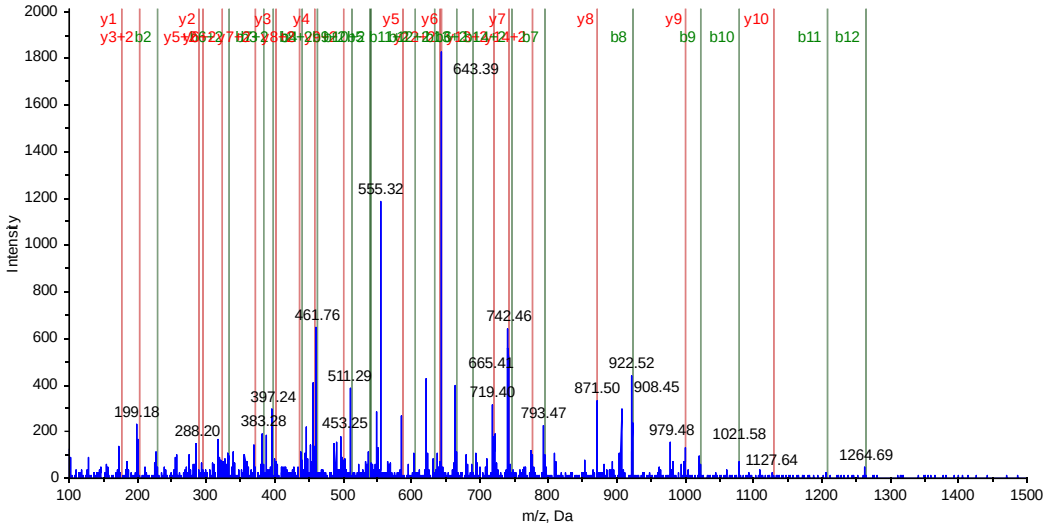
Residue	b	b+2	y	y+2
G	58.0287	29.5180	1926.9807	**963.9940**
V	**157.0972**	79.0522	1869.9593	935.4833
I	**270.1812**	135.5942	1770.8909	**885.9491**
G	**327.2027**	164.1050	1657.8068	**829.4070**
F	**474.2711**	237.6392	1600.7853	**800.8963**
V	**573.3395**	287.1734	**1453.7169**	**727.3621**
T	**674.3872**	337.6972	**1354.6485**	**677.8279**
D	**789.4141**	395.2107	**1253.6008**	627.3040
T	**890.4618**	445.7345	**1138.5739**	569.7906
A	**961.4989**	481.2531	**1037.5262**	519.2667
N	**1075.5419**	538.2746	**966.4891**	483.7482
E	**1204.5844**	602.7959	**852.4462**	426.7267
S	1291.6165	646.3119	**723.4036**	362.2054
F	**1438.6849**	719.8461	**636.3715**	318.6894
Q	1566.7435	783.8754	**489.3031**	245.1552
I	1679.8275	840.4174	**361.2445**	181.1259
T	1780.8752	890.9412	**248.1605**	124.5839
K	1908.9702	**954.9887**	**147.1128**	74.0600

Peptide sequence 6: IAVPANVPGHFQVFFPAHSGFHQSYFNGFSK



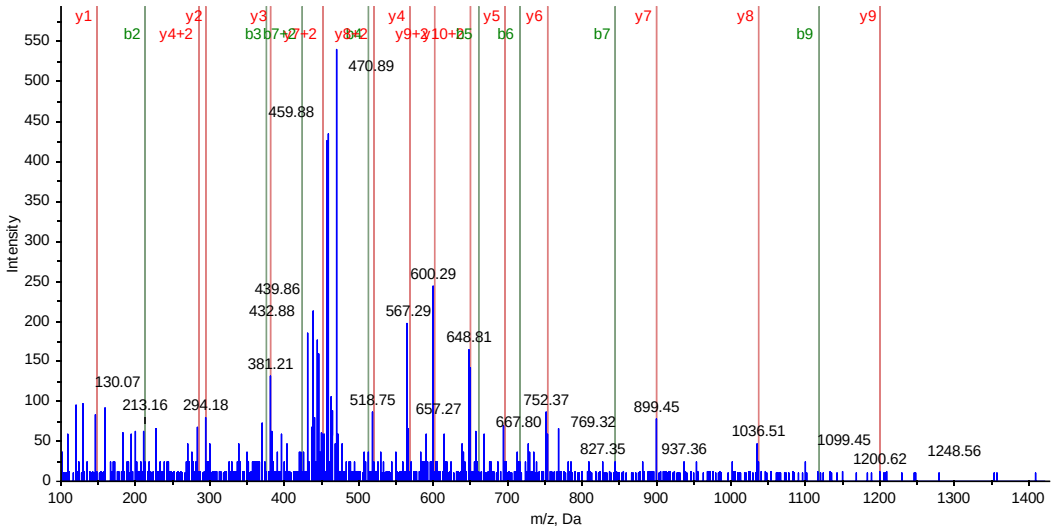
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3434.6858	1717.8465
A	**185.1285**	93.0679	3321.6017	1661.3045
V	**284.1969**	142.6021	3250.5646	1625.7859
P	381.2496	191.1285	3151.4962	1576.2517
A	**452.2867**	226.6470	3054.4434	1527.7253
N	**566.3297**	283.6685	2983.4063	**1492.2068**
V	665.3981	333.2027	2869.3634	1435.1853
P	762.4509	381.7291	2770.2950	**1385.6511**
G	819.4723	410.2398	2673.2422	**1337.1247**
H	956.5312	478.7693	2616.2207	**1308.6140**
F	1103.5996	**552.3035**	2479.1618	**1240.0846**
Q	1231.6582	**616.3327**	2332.0934	**1166.5503**
V	1330.7266	665.8670	2204.0348	**1102.5211**
F	1477.7950	**739.4012**	2104.9664	**1052.9868**
F	1624.8635	812.9354	1957.8980	**979.4526**
P	1721.9162	861.4618	1810.8296	**905.9184**
A	1792.9533	896.9803	1713.7768	**857.3921**
H	1930.0122	965.5098	1642.7397	**821.8735**
S	2017.0443	1009.0258	1505.6808	**753.3440**
G	2074.0657	1037.5365	**1418.6488**	**709.8280**
F	2221.1342	1111.0707	**1361.6273**	**681.3173**
H	2358.1931	1179.6002	**1214.5589**	**607.7831**
Q	2486.2516	1243.6295	**1077.5000**	**539.2536**
S	2573.2837	1287.1455	**949.4414**	**475.2243**
Y	2736.3470	1368.6771	**862.4094**	**431.7083**
F	2883.4154	1442.2113	**699.3461**	350.1767
N	2997.4583	1499.2328	**552.2776**	276.6425
G	3054.4798	1527.7435	**438.2347**	219.6210
F	3201.5482	1601.2777	**381.2132**	191.1103
S	3288.5802	1644.7938	**234.1448**	117.5761
K	3416.6752	1708.8412	**147.1128**	74.0600

Peptide sequence 7: LIRGPQQEVGQGIIR



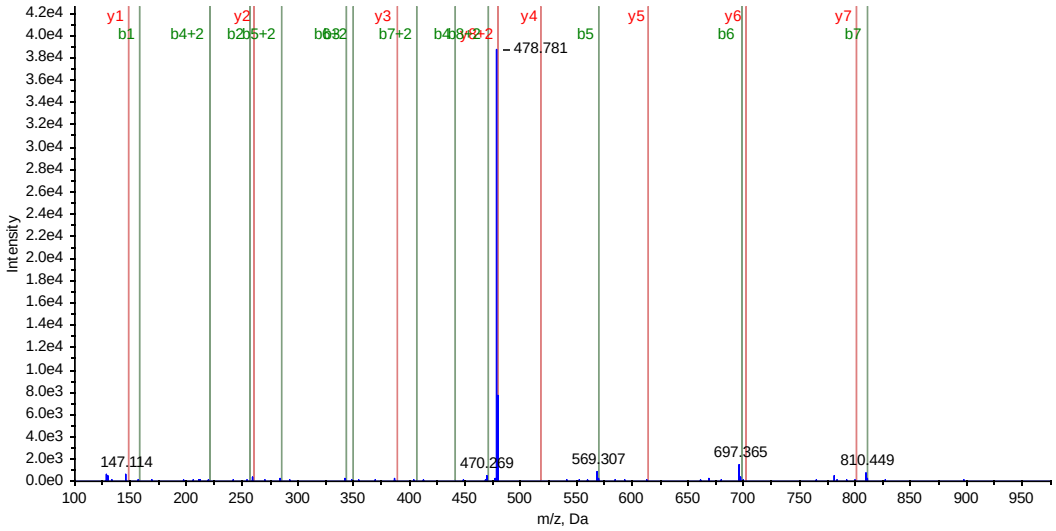
Residue	b	b+2	y	y+2
L	114.0913	57.5493	1663.9602	832.4837
I	**227.1754**	114.0913	1550.8761	**775.9417**
R	**383.2765**	192.1419	1437.7921	**719.3997**
G	**440.2980**	220.6526	1281.6910	**641.3491**
P	**537.3507**	269.1790	1224.6695	612.8384
Q	**665.4093**	**333.2083**	**1127.6167**	564.3120
Q	**793.4679**	**397.2376**	**999.5582**	**500.2827**
E	**922.5105**	**461.7589**	**871.4996**	**436.2534**
V	**1021.5789**	**511.2931**	**742.4570**	**371.7321**
G	**1078.6004**	**539.8038**	**643.3886**	**322.1979**
Q	**1206.6589**	**603.8331**	**586.3671**	**293.6872**
G	**1263.6804**	**632.3438**	**458.3085**	229.6579
I	1376.7645	**688.8859**	**401.2871**	**201.1472**
I	1489.8485	**745.4279**	**288.2030**	144.6051
R	1645.9496	823.4785	**175.1190**	88.0631

Peptide sequence 8: NPYHFGQWSFK



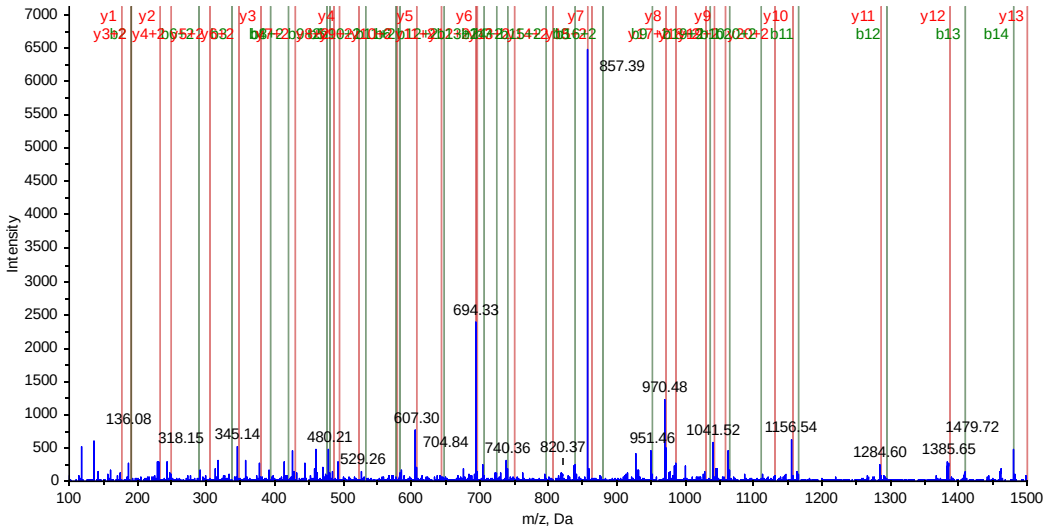
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1410.6589	705.8331
P	**212.1030**	106.5551	1296.6160	**648.8116**
Y	**375.1663**	188.0868	**1199.5633**	**600.2853**
H	**512.2252**	256.6162	**1036.4999**	**518.7536**
F	**659.2936**	330.1504	**899.4410**	**450.2241**
G	**716.3151**	358.6612	**752.3726**	376.6899
Q	**844.3737**	**422.6905**	**695.3511**	348.1792
W	1030.4530	515.7301	**567.2926**	**284.1499**
S	**1117.4850**	559.2461	**381.2132**	191.1103
F	1264.5534	632.7803	**294.1812**	147.5942
K	1392.6484	696.8278	**147.1128**	74.0600

Peptide sequence 9: RVSPEQIK



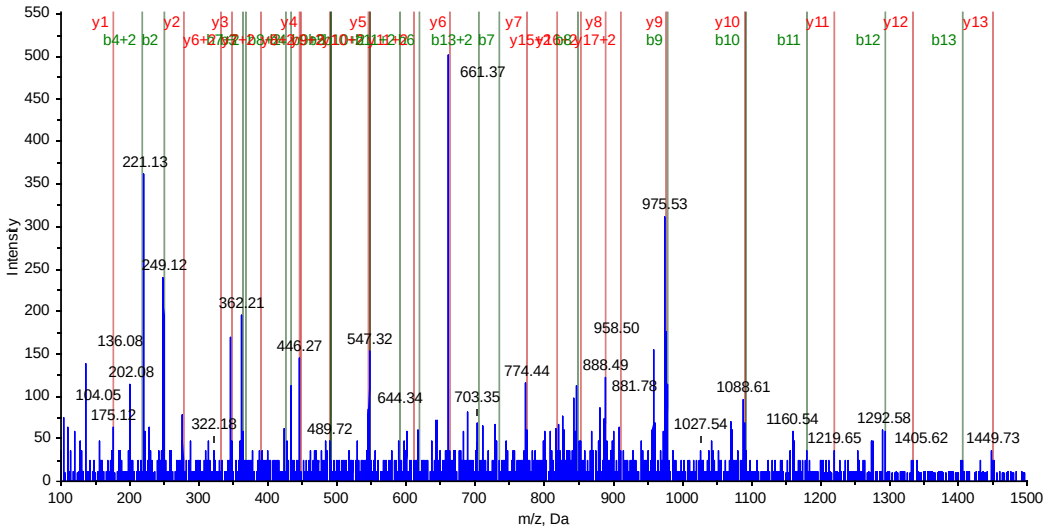
Residue	b	b+2	y	y+2
R	**157.1084**	79.0578	956.5524	**478.7798**
V	**256.1768**	128.5920	**800.4512**	400.7293
S	**343.2088**	172.1081	**701.3828**	351.1951
P	**440.2616**	**220.6344**	**614.3508**	307.6790
E	**569.3042**	**285.1557**	**517.2980**	259.1527
Q	**697.3628**	**349.1850**	**388.2554**	194.6314
I	**810.4468**	**405.7271**	**260.1969**	130.6021
K	938.5418	**469.7745**	**147.1128**	74.0600

Peptide sequence 10: STFGSPFNLLTQDAIYSNNFGR



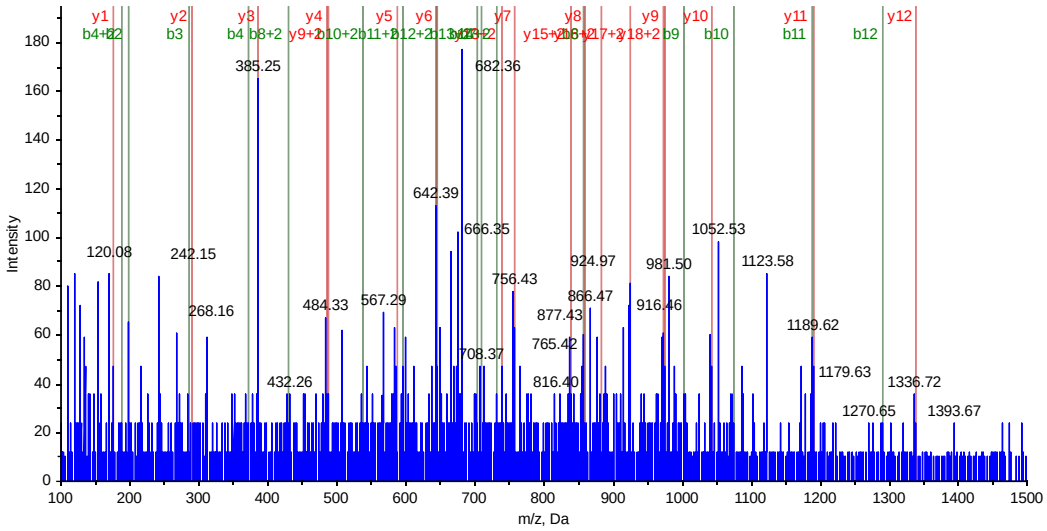
Residue	b	b+2	y	y+2
S	88.0393	44.5233	2449.1783	1225.0928
T	**189.0870**	95.0471	2362.1462	1181.5768
F	**336.1554**	168.5813	2261.0986	**1131.0529**
G	**393.1769**	197.0921	2114.0301	**1057.5187**
S	**480.2089**	240.6081	2057.0087	**1029.0080**
P	**577.2617**	**289.1345**	1969.9767	**985.4920**
F	**724.3301**	362.6687	1872.9239	936.9656
N	**838.3730**	**419.6901**	1725.8555	**863.4314**
L	**951.4571**	**476.2322**	1611.8125	**806.4099**
L	**1064.5411**	**532.7742**	**1498.7285**	**749.8679**
T	**1165.5888**	**583.2980**	**1385.6444**	**693.3258**
Q	**1293.6474**	**647.3273**	**1284.5967**	**642.8020**
D	**1408.6743**	**704.8408**	**1156.5382**	**578.7727**
A	**1479.7114**	**740.3594**	**1041.5112**	**521.2592**
I	1592.7955	**796.9014**	**970.4741**	**485.7407**
Y	1755.8588	**878.4331**	**857.3900**	**429.1987**
S	1842.8909	921.9491	**694.3267**	**347.6670**
N	1956.9338	978.9705	**607.2947**	**304.1510**
N	2070.9767	**1035.9920**	**493.2518**	**247.1295**
F	2218.0451	**1109.5262**	**379.2088**	**190.1081**
G	2275.0666	1138.0369	**232.1404**	116.5738
R	2431.1677	1216.0875	**175.1190**	88.0631

Peptide sequence 11: TFLAGQDNMLSNINTVATR



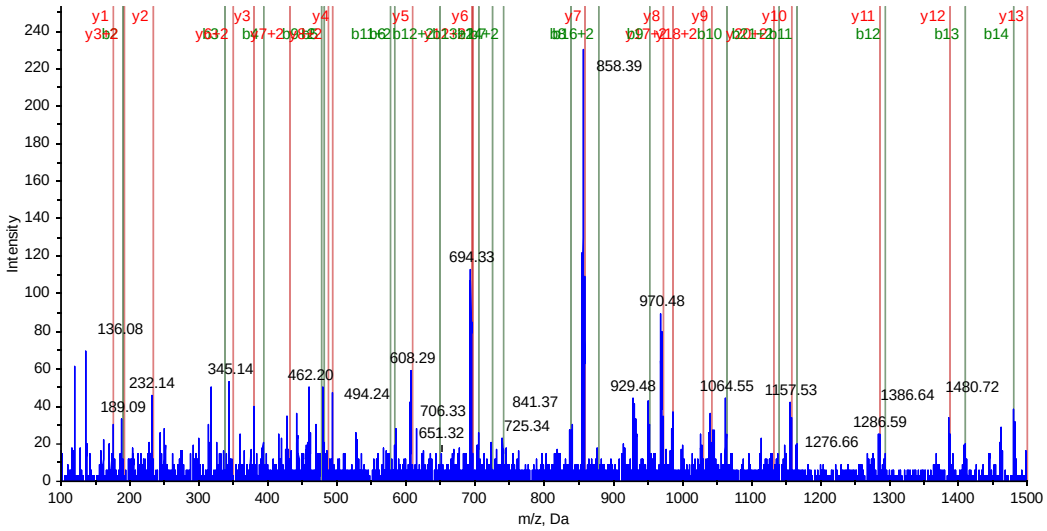
Residue	b	b+2	y	y+2
T	102.0550	51.5311	2066.0335	1033.5204
F	**249.1234**	125.0653	1964.9858	982.9966
L	**362.2074**	181.6074	1817.9174	**909.4623**
A	**433.2445**	**217.1259**	1704.8334	**852.9203**
G	**490.2660**	245.6366	1633.7962	**817.4018**
Q	**618.3246**	309.6659	1576.7748	788.8910
D	**733.3515**	**367.1794**	**1448.7162**	724.8617
N	**847.3945**	**424.2009**	**1333.6893**	667.3483
M	**978.4349**	**489.7211**	**1219.6463**	**610.3268**
L	**1091.5190**	**546.2631**	**1088.6058**	**544.8066**
S	**1178.5510**	**589.7792**	**975.5218**	**488.2645**
N	**1292.5940**	646.8006	**888.4898**	**444.7485**
I	**1405.6780**	**703.3427**	**774.4468**	**387.7271**
N	1519.7210	760.3641	**661.3628**	**331.1850**
T	1620.7686	810.8880	**547.3198**	274.1636
V	1719.8370	860.4222	**446.2722**	223.6397
A	1790.8742	895.9407	**347.2037**	174.1055
T	1891.9218	946.4646	**276.1666**	138.5870
R	2048.0229	1024.5151	**175.1190**	88.0631

Peptide sequence 12: VPSSVTHFFANTNGTVPLR



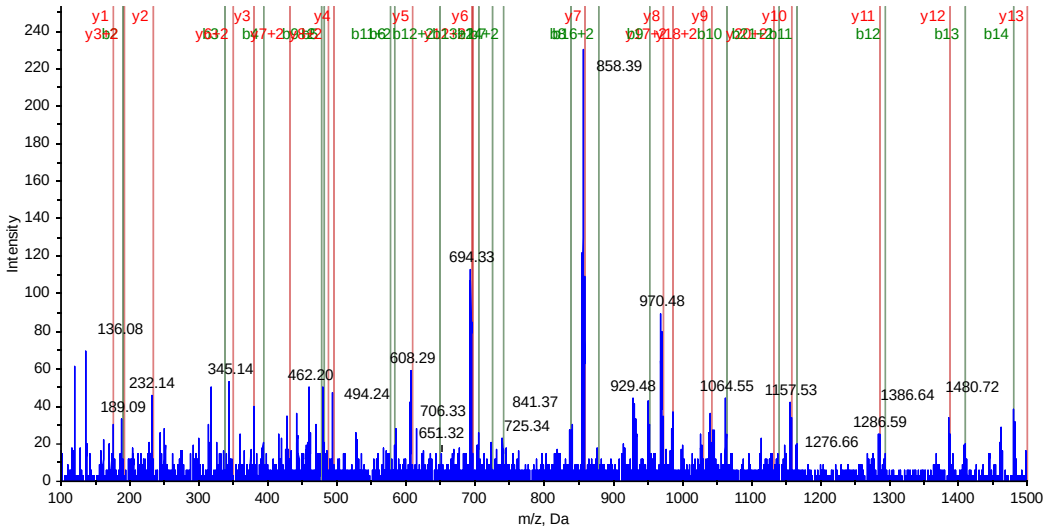
Residue	b	b+2	y	y+2
V	100.0757	50.5415	2044.0610	1022.5342
P	**197.1285**	99.0679	1944.9926	**973.0000**
S	**284.1605**	142.5839	1847.9399	**924.4736**
S	**371.1925**	**186.0999**	1760.9078	**880.9576**
V	470.2609	235.6341	1673.8758	**837.4415**
T	571.3086	286.1579	1574.8074	787.9073
H	**708.3675**	354.6874	1473.7597	**737.3835**
F	**855.4359**	**428.2216**	**1336.7008**	668.8540
F	**1002.5043**	501.7558	**1189.6324**	595.3198
A	**1073.5415**	**537.2744**	**1042.5640**	521.7856
N	**1187.5844**	**594.2958**	**971.5269**	**486.2671**
T	**1288.6321**	**644.8197**	**857.4839**	429.2456
N	1402.6750	**701.8411**	**756.4363**	378.7218
G	1459.6965	**730.3519**	**642.3933**	321.7003
T	1560.7441	780.8757	**585.3719**	293.1896
V	1659.8125	830.4099	**484.3242**	242.6657
P	1756.8653	878.9363	**385.2558**	193.1315
L	1869.9494	935.4783	**288.2030**	144.6051
R	2026.0505	1013.5289	**175.1190**	88.0631

Peptide sequence 13: STFGSPFNLLTQDAIYSN[Dea]NFGR



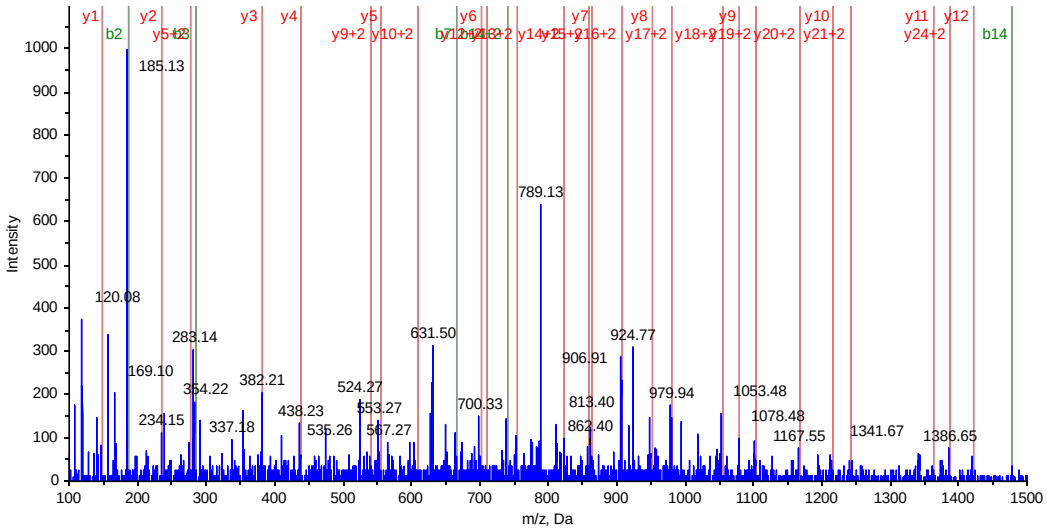
Residue	b	b+2	y	y+2
S	88.0393	44.5233	2450.1623	1225.5848
T	**189.0870**	95.0471	2363.1303	1182.0688
F	**336.1554**	168.5813	2262.0826	**1131.5449**
G	**393.1769**	197.0921	2115.0142	1058.0107
S	**480.2089**	240.6081	2057.9927	**1029.5000**
P	**577.2617**	289.1345	1970.9607	**985.9840**
F	**724.3301**	362.6687	1873.9079	937.4576
N	**838.3730**	419.6901	1726.8395	863.9234
L	**951.4571**	**476.2322**	1612.7966	806.9019
L	**1064.5411**	532.7742	**1499.7125**	750.3599
T	**1165.5888**	**583.2980**	**1386.6284**	**693.8179**
Q	**1293.6474**	**647.3273**	**1285.5808**	643.2940
D	**1408.6743**	**704.8408**	**1157.5222**	579.2647
A	**1479.7114**	**740.3594**	**1042.4952**	521.7513
I	1592.7955	796.9014	**971.4581**	**486.2327**
Y	1755.8588	**878.4331**	**858.3741**	**429.6907**
S	1842.8909	921.9491	**695.3107**	**348.1590**
N[Dea]	1957.9178	979.4625	**608.2787**	304.6430
N	2071.9607	1036.4840	**493.2518**	247.1295
F	2219.0291	1110.0182	**379.2088**	**190.1081**
G	2276.0506	**1138.5289**	**232.1404**	116.5738
R	2432.1517	1216.5795	**175.1190**	88.0631

Peptide sequence 14: STFGSPFNLLTQDAIYSNN[Dea]FGR



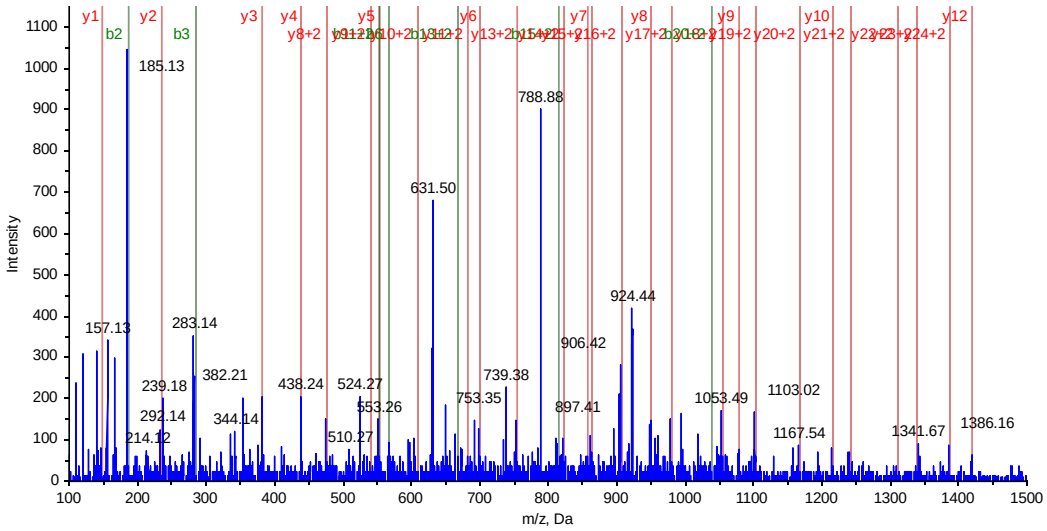
Residue	b	b+2	y	y+2
S	88.0393	44.5233	2450.1623	1225.5848
T	**189.0870**	95.0471	2363.1303	1182.0688
F	**336.1554**	168.5813	2262.0826	**1131.5449**
G	**393.1769**	197.0921	2115.0142	1058.0107
S	**480.2089**	240.6081	2057.9927	**1029.5000**
P	**577.2617**	289.1345	1970.9607	**985.9840**
F	**724.3301**	362.6687	1873.9079	937.4576
N	**838.3730**	419.6901	1726.8395	863.9234
L	**951.4571**	**476.2322**	1612.7966	806.9019
L	**1064.5411**	532.7742	**1499.7125**	750.3599
T	**1165.5888**	**583.2980**	**1386.6284**	**693.8179**
Q	**1293.6474**	**647.3273**	**1285.5808**	643.2940
D	**1408.6743**	**704.8408**	**1157.5222**	579.2647
A	**1479.7114**	**740.3594**	**1042.4952**	521.7513
I	1592.7955	796.9014	**971.4581**	**486.2327**
Y	1755.8588	**878.4331**	**858.3741**	**429.6907**
S	1842.8909	921.9491	**695.3107**	**348.1590**
N	1956.9338	978.9705	**608.2787**	304.6430
N[Dea]	2071.9607	1036.4840	**494.2358**	247.6215
F	2219.0291	1110.0182	**379.2088**	**190.1081**
G	2276.0506	**1138.5289**	**232.1404**	116.5738
R	2432.1517	1216.5795	**175.1190**	88.0631

Peptide sequence 15: IAVPANVPGHFQVFFPAHSGFHQSYFN[Dea]GFSK



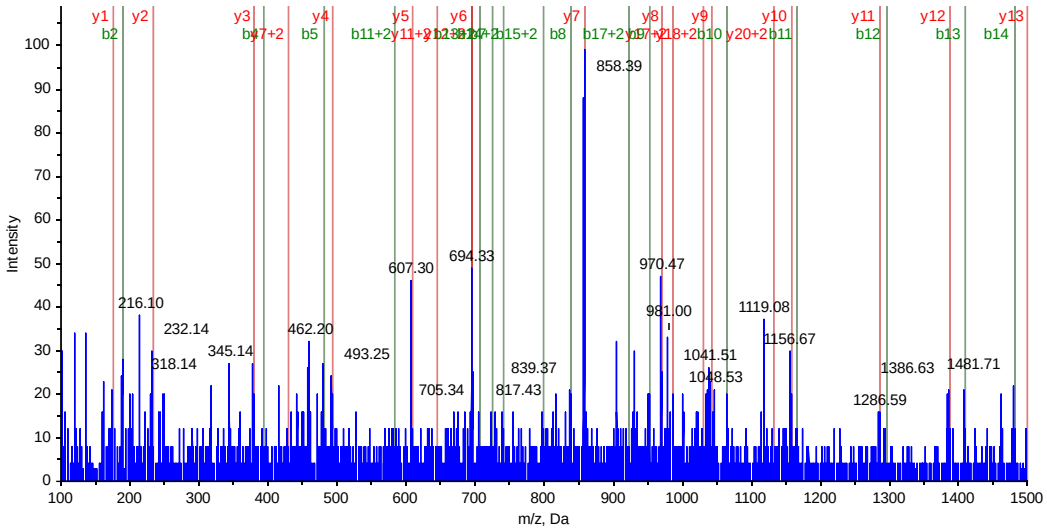
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3435.6698	1718.3385
A	**185.1285**	93.0679	3322.5857	1661.7965
V	**284.1969**	142.6021	3251.5486	1626.2779
P	381.2496	191.1285	3152.4802	1576.7437
A	452.2867	226.6470	3055.4274	1528.2174
N	566.3297	283.6685	2984.3903	1492.6988
V	**665.3981**	333.2027	2870.3474	1435.6773
P	762.4509	381.7291	2771.2790	**1386.1431**
G	819.4723	410.2398	2674.2262	1337.6167
H	956.5312	478.7693	2617.2048	1309.1060
F	1103.5996	552.3035	2480.1458	**1240.5766**
Q	1231.6582	616.3327	2333.0774	**1167.0424**
V	1330.7266	665.8670	2205.0189	**1103.0131**
F	**1477.7950**	**739.4012**	2105.9504	**1053.4789**
F	1624.8635	812.9354	1958.8820	**979.9446**
P	1721.9162	861.4618	1811.8136	**906.4104**
A	1792.9533	896.9803	1714.7608	**857.8841**
H	1930.0122	965.5098	1643.7237	**822.3655**
S	2017.0443	1009.0258	1506.6648	**753.8360**
G	2074.0657	1037.5365	**1419.6328**	**710.3200**
F	2221.1342	1111.0707	**1362.6113**	681.8093
H	2358.1931	1179.6002	**1215.5429**	**608.2751**
Q	2486.2516	1243.6295	**1078.4840**	**539.7456**
S	2573.2837	1287.1455	**950.4254**	475.7164
Y	2736.3470	1368.6771	**863.3934**	432.2003
F	2883.4154	1442.2113	**700.3301**	350.6687
N[Dea]	2998.4424	1499.7248	**553.2617**	**277.1345**
G	3055.4638	1528.2355	**438.2347**	219.6210
F	3202.5322	1601.7698	**381.2132**	191.1103
S	3289.5643	1645.2858	**234.1448**	117.5761
K	3417.6592	1709.3333	**147.1128**	74.0600

Peptide sequence 16: IAVPANVPGHFQ[Dea]VFFPAHSGFHQSYFNGFSK



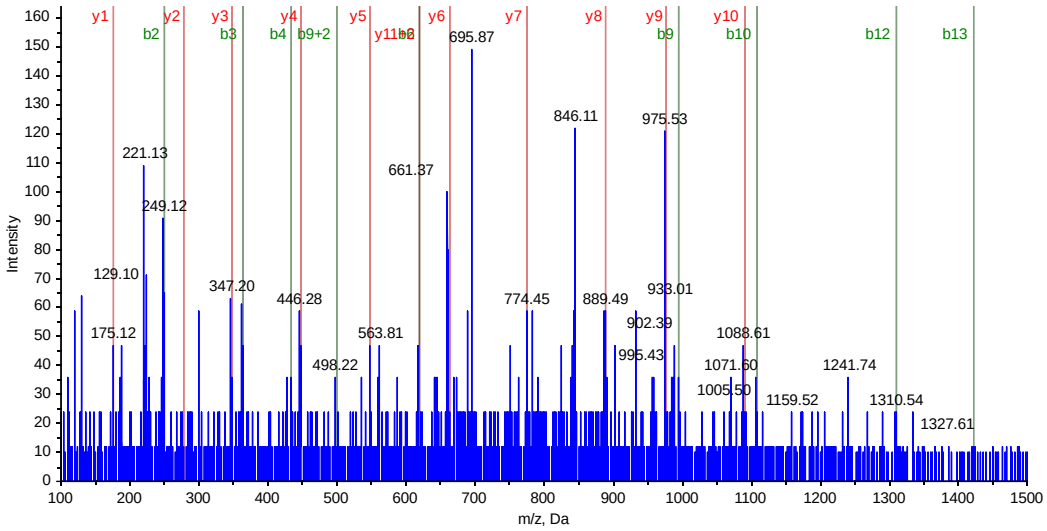
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3435.6698	1718.3385
A	**185.1285**	93.0679	3322.5857	1661.7965
V	**284.1969**	142.6021	3251.5486	1626.2779
P	381.2496	191.1285	3152.4802	1576.7437
A	452.2867	226.6470	3055.4274	1528.2174
N	**566.3297**	283.6685	2984.3903	1492.6988
V	665.3981	333.2027	2870.3474	1435.6773
P	762.4509	381.7291	2771.2790	**1386.1431**
G	819.4723	410.2398	2674.2262	**1337.6167**
H	956.5312	478.7693	2617.2048	**1309.1060**
F	1103.5996	**552.3035**	2480.1458	**1240.5766**
Q[Dea]	1232.6422	616.8248	2333.0774	**1167.0424**
V	1331.7106	**666.3590**	2204.0348	**1102.5211**
F	1478.7791	739.8932	2104.9664	**1052.9868**
F	1625.8475	**813.4274**	1957.8980	**979.4526**
P	1722.9002	861.9538	1810.8296	**905.9184**
A	1793.9374	897.4723	1713.7768	**857.3921**
H	1930.9963	966.0018	1642.7397	**821.8735**
S	2018.0283	1009.5178	1505.6808	**753.3440**
G	2075.0498	**1038.0285**	**1418.6488**	709.8280
F	2222.1182	1111.5627	1361.6273	**681.3173**
H	2359.1771	1180.0922	**1214.5589**	**607.7831**
Q	2487.2357	1244.1215	**1077.5000**	**539.2536**
S	2574.2677	1287.6375	**949.4414**	**475.2243**
Y	2737.3310	1369.1691	**862.4094**	431.7083
F	2884.3994	1442.7034	**699.3461**	350.1767
N	2998.4424	1499.7248	**552.2776**	276.6425
G	3055.4638	1528.2355	**438.2347**	219.6210
F	3202.5322	1601.7698	**381.2132**	191.1103
S	3289.5643	1645.2858	**234.1448**	117.5761
K	3417.6592	1709.3333	**147.1128**	74.0600

Peptide sequence 17: STFGSPFNLLTQ[Dea]DAIYSNNFGR



Residue	b	b+2	y	y+2
S	88.0393	44.5233	2450.1623	1225.5848
T	**189.0870**	95.0471	2363.1303	1182.0688
F	336.1554	168.5813	2262.0826	**1131.5449**
G	**393.1769**	197.0921	2115.0142	1058.0107
S	**480.2089**	240.6081	2057.9927	**1029.5000**
P	577.2617	289.1345	1970.9607	**985.9840**
F	**724.3301**	362.6687	1873.9079	937.4576
N	**838.3730**	419.6901	1726.8395	863.9234
L	**951.4571**	476.2322	1612.7966	806.9019
L	**1064.5411**	532.7742	**1499.7125**	750.3599
T	**1165.5888**	**583.2980**	**1386.6284**	**693.8179**
Q[Dea]	**1294.6314**	647.8193	**1285.5808**	**643.2940**
D	**1409.6583**	**705.3328**	**1156.5382**	578.7727
A	**1480.6955**	**740.8514**	**1041.5112**	521.2592
I	1593.7795	**797.3934**	**970.4741**	485.7407
Y	1756.8428	878.9251	**857.3900**	**429.1987**
S	1843.8749	**922.4411**	**694.3267**	347.6670
N	1957.9178	979.4625	**607.2947**	304.1510
N	2071.9607	1036.4840	**493.2518**	247.1295
F	2219.0291	1110.0182	**379.2088**	190.1081
G	2276.0506	1138.5289	**232.1404**	116.5738
R	2432.1517	1216.5795	**175.1190**	88.0631

Peptide sequence 18: TFLAGQDNM[Oxi]LSNINTVATR



Residue	b	b+2	y	y+2
T	102.0550	51.5311	2082.0284	1041.5179
F	**249.1234**	125.0653	1980.9808	990.9940
L	**362.2074**	181.6074	1833.9123	917.4598
A	**433.2445**	217.1259	1720.8283	860.9178
G	490.2660	245.6366	1649.7912	825.3992
Q	**618.3246**	309.6659	1592.7697	796.8885
D	733.3515	367.1794	1464.7111	732.8592
N	847.3945	424.2009	1349.6842	675.3457
M[Oxi]	**994.4299**	**497.7186**	1235.6412	**618.3243**
L	**1107.5139**	554.2606	**1088.6058**	544.8066
S	1194.5459	597.7766	**975.5218**	488.2645
N	**1308.5889**	654.7981	**888.4898**	444.7485
I	**1421.6729**	711.3401	**774.4468**	387.7271
N	1535.7159	768.3616	**661.3628**	331.1850
T	1636.7635	818.8854	**547.3198**	274.1636
V	1735.8320	868.4196	**446.2722**	223.6397
A	1806.8691	903.9382	**347.2037**	174.1055
T	1907.9168	954.4620	**276.1666**	138.5870
R	2064.0179	1032.5126	**175.1190**	88.0631

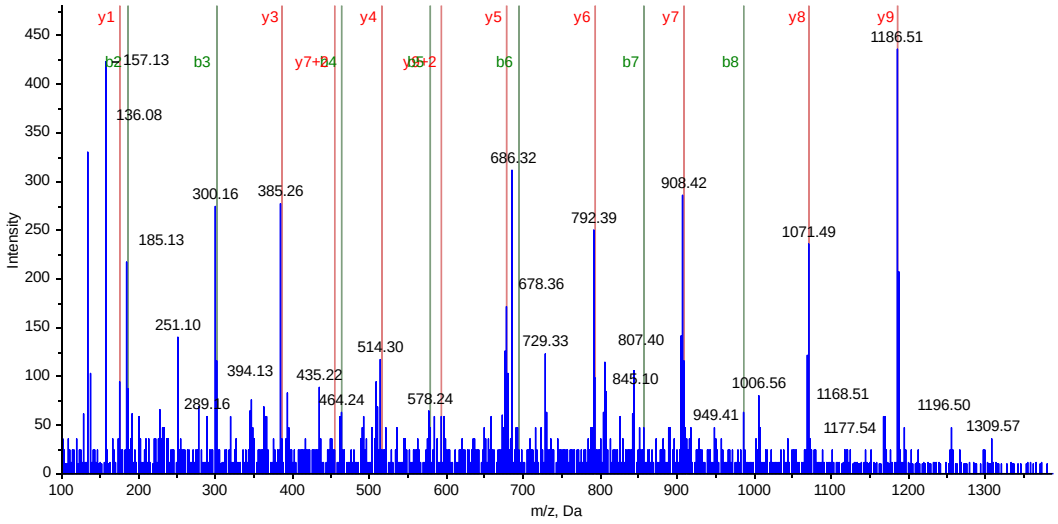
Sample Pool 3

Protein: B.rapa.Ro18.Candidate-1, 17 peptides (95%)

Protein sequence coverage

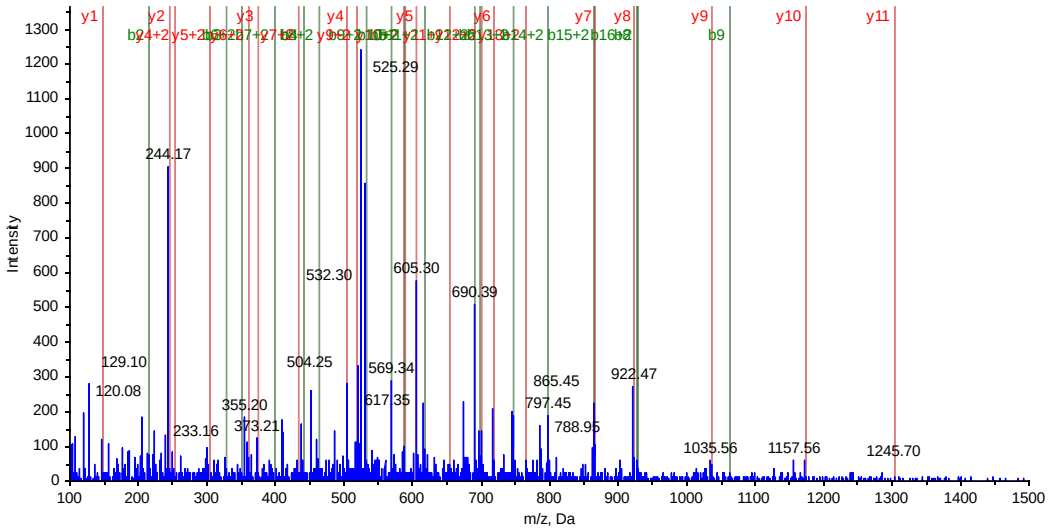
MEKNKRIFTFLLVIVFFHGVMMMRSIGYEGEEEQGGGGRERGGFMMKESR**QVIKSEGGEMR**VVISPR**GR**
IIEKPMHIGFLTMEPKTLFVPQYLDSNLLIFIRQGEATLGVICKDEFGEKR**LKGGDIYWIPAGSAFYLL**
NTGRGQRLHVICSIDPSQSLGFETFQPFYIGGGPSSVLAGFDPDTITSALNVSRPEVQQLMTSQVRGPI
VHITEHAPTMWTDFLGLRGEEKHKHLKKLLELKQGTSQEQEDNPWWSWKNIVSSILDVTGEKNRGSGSS
KCEDSYNIYDR**KNDFENDYGWSKALDYDDYEPLR**YSGVGVYLVNLTAGSMMAPHMNPTATEYGIVLSGS
GEIQVVLPNGTSAMNMR**VSPGDVFWIPR**YFAFCQIASR**IAPFEFVGFTTSAYKNRPQFLVGSNSLLR**SL
NLTSLAMAFGVDEGTMKR**FVEAQR**EAVILPTASAAPPHEGEPERFGSDHIFT

Peptide sequence 1: ALDYDDYEPLR



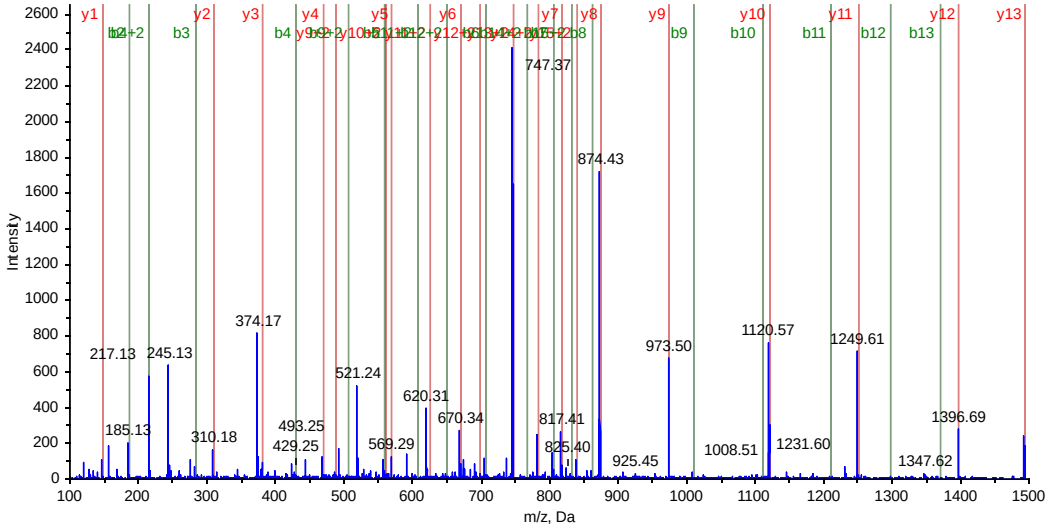
Residue	b	b+2	y	y+2
A	72.0444	36.5258	1369.6270	685.3172
L	**185.1285**	93.0679	1298.5899	649.7986
D	**300.1554**	150.5813	**1185.5059**	**593.2566**
Y	**463.2187**	232.1130	**1070.4789**	535.7431
D	**578.2457**	289.6265	**907.4156**	**454.2114**
D	**693.2726**	347.1399	**792.3886**	396.6980
Y	**856.3359**	428.6716	**677.3617**	339.1845
E	**985.3785**	493.1929	**514.2984**	257.6528
P	1082.4313	541.7193	**385.2558**	193.1315
L	1195.5154	598.2613	288.2030	144.6051
R	1351.6165	676.3119	**175.1190**	88.0631

Peptide sequence 2: GRIIEKPMHIGFLTMEPK



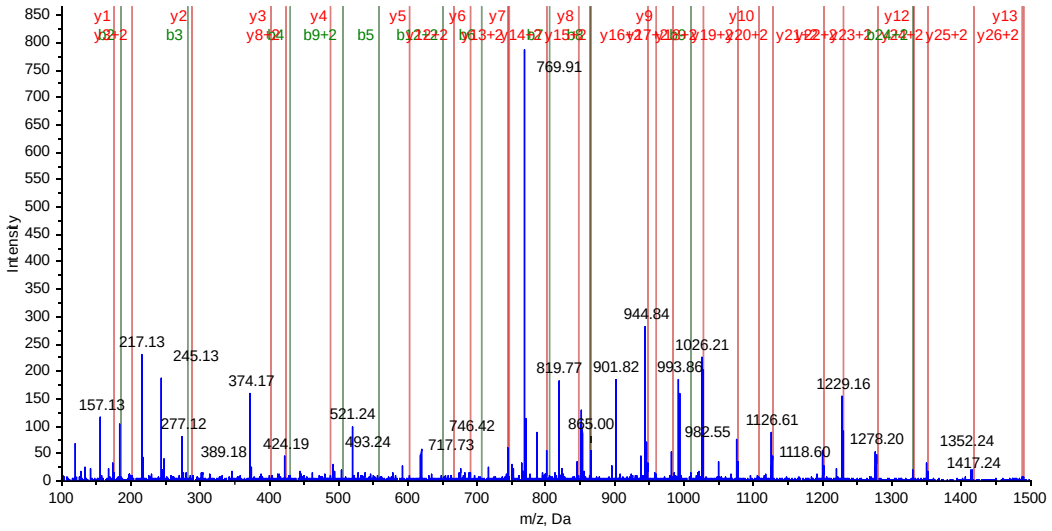
Residue	b	b+2	y	y+2
G	58.0287	29.5180	2097.1347	1049.0710
R	**214.1299**	107.5686	2040.1133	1020.5603
I	**327.2139**	164.1106	1884.0122	942.5097
I	**440.2980**	220.6526	1770.9281	885.9677
E	**569.3406**	285.1739	1657.8440	829.4257
K	**697.4355**	**349.2214**	1528.8015	**764.9044**
P	794.4883	**397.7478**	1400.7065	**700.8569**
M	**925.5288**	**463.2680**	**1303.6537**	**652.3305**
H	**1062.5877**	**531.7975**	**1172.6132**	**586.8103**
I	1175.6718	**588.3395**	**1035.5543**	**518.2808**
G	1232.6932	**616.8502**	**922.4703**	461.7388
F	1379.7616	**690.3845**	**865.4488**	**433.2280**
L	1492.8457	**746.9265**	**718.3804**	**359.6938**
T	1593.8934	**797.4503**	**605.2963**	**303.1518**
M	1724.9339	**862.9706**	**504.2486**	**252.6280**
E	1853.9765	**927.4919**	**373.2082**	187.1077
P	1951.0292	976.0182	**244.1656**	122.5864
K	2079.1242	1040.0657	**147.1128**	74.0600

Peptide sequence 3: IAPFEFVGFTTSAYK



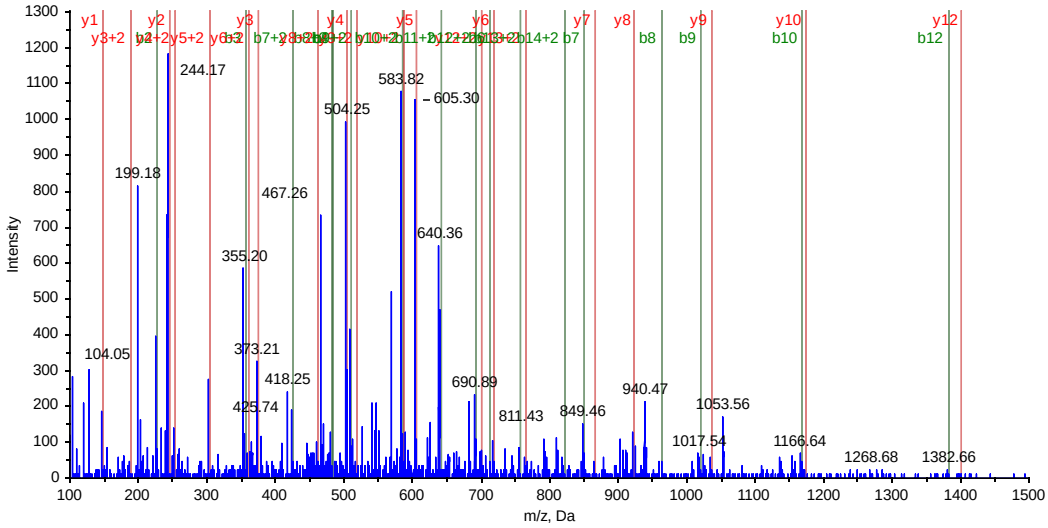
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1677.8523	**839.4298**
A	**185.1285**	93.0679	1564.7682	**782.8877**
P	**282.1812**	141.5942	**1493.7311**	**747.3692**
F	**429.2496**	**215.1285**	**1396.6783**	**698.8428**
E	**558.2922**	279.6498	**1249.6099**	**625.3086**
F	**705.3606**	353.1840	**1120.5673**	**560.7873**
V	**804.4291**	402.7182	**973.4989**	**487.2531**
G	**861.4505**	431.2289	**874.4305**	437.7189
F	**1008.5189**	**504.7631**	**817.4090**	409.2082
T	**1109.5666**	555.2869	**670.3406**	335.6740
T	**1210.6143**	**605.8108**	**569.2930**	285.1501
S	**1297.6463**	**649.3268**	**468.2453**	234.6263
A	**1368.6834**	684.8454	**381.2132**	191.1103
Y	1531.7468	**766.3770**	**310.1761**	155.5917
K	1659.8417	**830.4245**	**147.1128**	74.0600

Peptide sequence 4: IAPFEFVGFTTSAYKNRPQFLVGSNSLLR



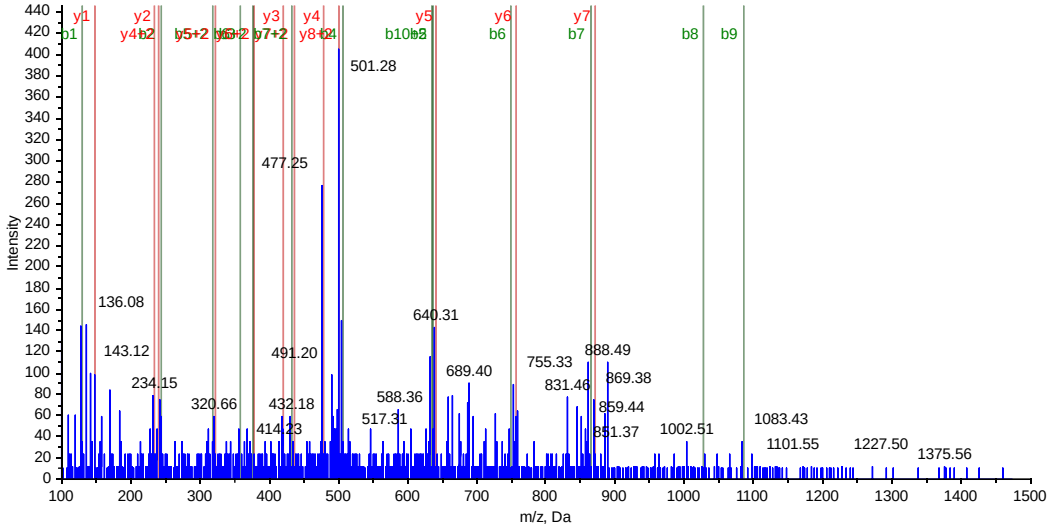
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3259.7262	1630.3668
A	**185.1285**	93.0679	3146.6422	1573.8247
P	**282.1812**	141.5942	3075.6051	1538.3062
F	**429.2496**	215.1285	2978.5523	**1489.7798**
E	**558.2922**	279.6498	2831.4839	**1416.2456**
F	**705.3606**	353.1840	2702.4413	**1351.7243**
V	**804.4291**	402.7182	2555.3729	**1278.1901**
G	**861.4505**	431.2289	2456.3045	**1228.6559**
F	**1008.5189**	**504.7631**	2399.2830	**1200.1451**
T	1109.5666	555.2869	2252.2146	**1126.6109**
T	1210.6143	605.8108	2151.1669	**1076.0871**
S	1297.6463	**649.3268**	2050.1192	**1025.5633**
A	1368.6834	684.8454	1963.0872	**982.0472**
Y	1531.7468	766.3770	1892.0501	**946.5287**
K	1659.8417	830.4245	1728.9868	**864.9970**
N	1773.8846	887.4460	1600.8918	**800.9495**
R	1929.9858	965.4965	**1486.8489**	**743.9281**
P	2027.0385	1014.0229	**1330.7478**	**665.8775**
Q	2155.0971	1078.0522	1233.6950	617.3511
F	2302.1655	1151.5864	**1105.6364**	553.3218
L	2415.2496	1208.1284	**958.5680**	479.7876
V	2514.3180	1257.6626	**845.4839**	**423.2456**
G	2571.3395	1286.1734	**746.4155**	373.7114
S	2658.3715	**1329.6894**	**689.3941**	345.2007
N	2772.4144	1386.7108	**602.3620**	301.6847
S	2859.4464	1430.2269	**488.3191**	244.6632
L	2972.5305	1486.7689	**401.2871**	**201.1472**
L	3085.6146	1543.3109	**288.2030**	144.6051
R	3241.7157	1621.3615	**175.1190**	88.0631

Peptide sequence 5: IIEKPMHIGFLTMEPK



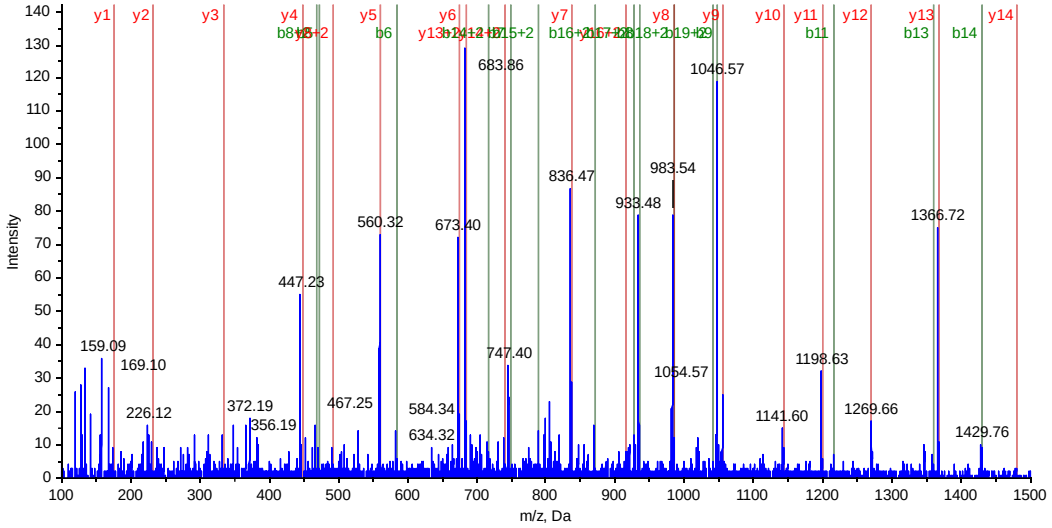
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1884.0122	942.5097
I	**227.1754**	114.0913	1770.9281	885.9677
E	**356.2180**	178.6126	1657.8440	829.4257
K	**484.3130**	242.6601	1528.8015	**764.9044**
P	581.3657	291.1865	**1400.7065**	**700.8569**
M	**712.4062**	356.7067	1303.6537	652.3305
H	**849.4651**	**425.2362**	**1172.6132**	**586.8103**
I	**962.5492**	**481.7782**	**1035.5543**	**518.2808**
G	**1019.5706**	**510.2890**	**922.4703**	**461.7388**
F	**1166.6391**	**583.8232**	**865.4488**	433.2280
L	1279.7231	**640.3652**	**718.3804**	**359.6938**
T	**1380.7708**	**690.8890**	**605.2963**	**303.1518**
M	1511.8113	**756.4093**	**504.2486**	**252.6280**
E	1640.8539	**820.9306**	**373.2082**	**187.1077**
P	1737.9066	869.4570	**244.1656**	122.5864
K	1866.0016	933.5044	**147.1128**	74.0600

Peptide sequence 6: KNDFENDYGWSK



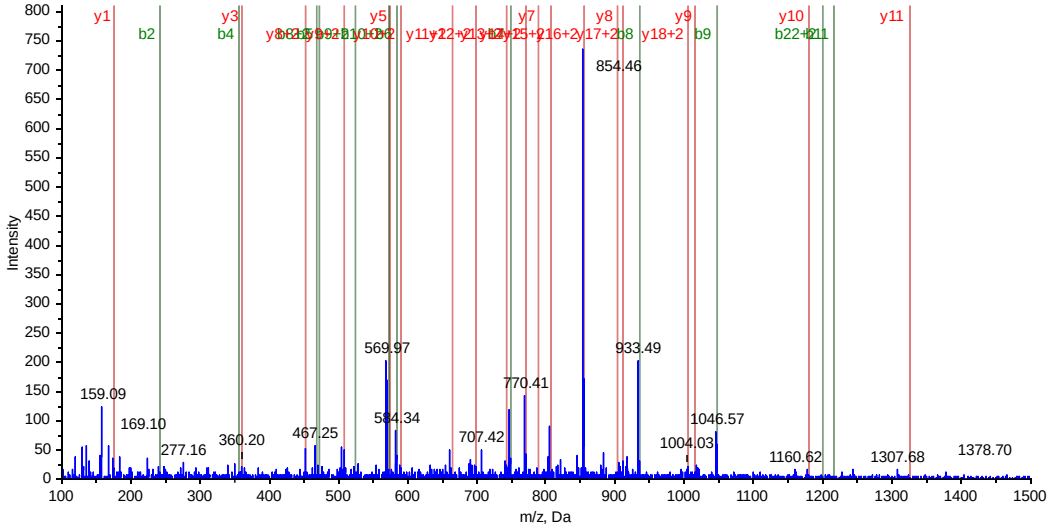
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	1502.6546	751.8310
N	**243.1452**	122.0762	1374.5597	687.7835
D	**358.1721**	179.5897	1260.5168	630.7620
F	**505.2405**	253.1239	1145.4898	573.2485
E	**634.2831**	**317.6452**	998.4214	**499.7143**
N	**748.3260**	**374.6667**	**869.3788**	**435.1930**
D	**863.3530**	**432.1801**	**755.3359**	**378.1716**
Y	**1026.4163**	513.7118	**640.3089**	**320.6581**
G	**1083.4378**	542.2225	**477.2456**	**239.1264**
W	1269.5171	**635.2622**	**420.2241**	210.6157
S	1356.5491	678.7782	**234.1448**	117.5761
K	1484.6441	742.8257	**147.1128**	74.0600

Peptide sequence 7: LKGGDIYWIPAGSAFYLLNTGR



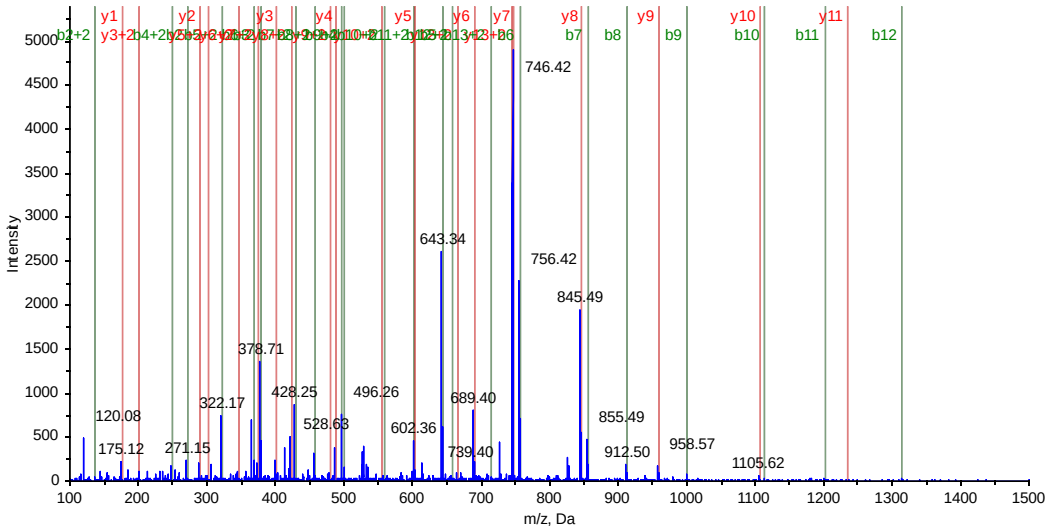
Residue	b	b+2	y	y+2
L	114.0913	57.5493	2412.2710	1206.6392
K	242.1863	121.5968	2299.1870	1150.0971
G	299.2078	150.1075	2171.0920	1086.0496
G	356.2292	178.6183	2114.0706	1057.5389
D	**471.2562**	236.1317	2057.0491	1029.0282
I	**584.3402**	292.6738	1942.0221	971.5147
Y	**747.4036**	374.2054	1828.9381	**914.9727**
W	**933.4829**	**467.2451**	1665.8748	833.4410
I	**1046.5669**	523.7871	**1479.7954**	**740.4014**
P	1143.6197	572.3135	**1366.7114**	**683.8593**
A	**1214.6568**	607.8320	**1269.6586**	635.3329
G	1271.6783	636.3428	**1198.6215**	599.8144
S	**1358.7103**	679.8588	**1141.6000**	571.3037
A	**1429.7474**	**715.3774**	**1054.5680**	527.7876
F	1576.8158	**788.9116**	**983.5309**	**492.2691**
Y	1739.8792	**870.4432**	**836.4625**	418.7349
L	1852.9632	**926.9853**	**673.3991**	337.2032
L	1966.0473	**983.5273**	**560.3151**	280.6612
N	2080.0902	**1040.5488**	**447.2310**	224.1191
T	2181.1379	1091.0726	**333.1881**	167.0977
G	2238.1594	1119.5833	**232.1404**	116.5738
R	2394.2605	1197.6339	**175.1190**	88.0631

Peptide sequence 8: LKGGDIYWIPAGSAFYLLNTGRGQR



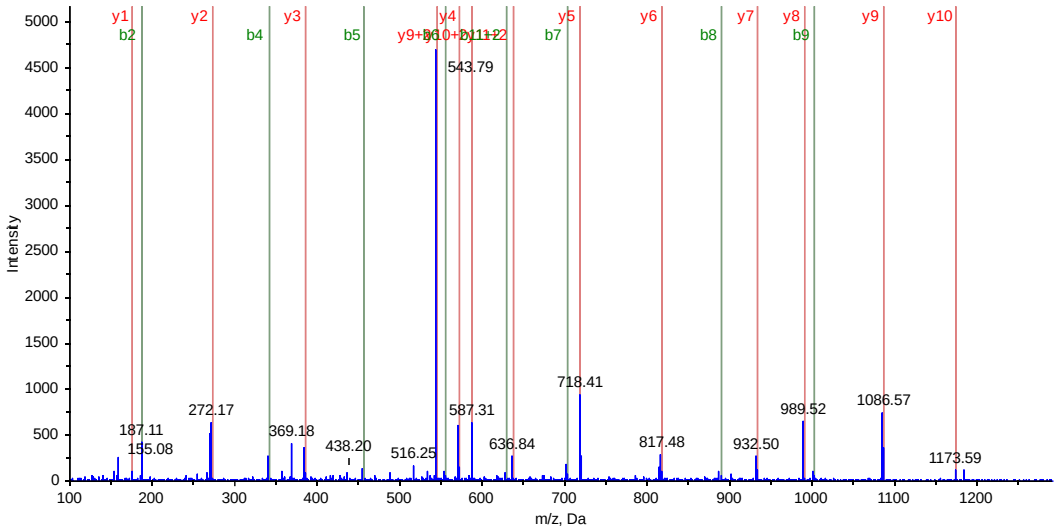
Residue	b	b+2	y	y+2
L	114.0913	57.5493	2753.4522	1377.2297
K	**242.1863**	121.5968	2640.3681	1320.6877
G	299.2078	150.1075	2512.2732	1256.6402
G	**356.2292**	178.6183	2455.2517	1228.1295
D	**471.2562**	236.1317	2398.2302	1199.6188
I	**584.3402**	292.6738	2283.2033	1142.1053
Y	**747.4036**	374.2054	2170.1192	1085.5633
W	**933.4829**	**467.2451**	2007.0559	**1004.0316**
I	**1046.5669**	**523.7871**	1820.9766	**910.9919**
P	1143.6197	**572.3135**	1707.8925	**854.4499**
A	**1214.6568**	607.8320	1610.8398	**805.9235**
G	1271.6783	636.3428	1539.8027	**770.4050**
S	1358.7103	679.8588	1482.7812	**741.8942**
A	1429.7474	715.3774	1395.7492	**698.3782**
F	1576.8158	788.9116	**1324.7120**	**662.8597**
Y	1739.8792	870.4432	**1177.6436**	**589.3255**
L	1852.9632	926.9853	**1014.5803**	**507.7938**
L	1966.0473	983.5273	**901.4962**	**451.2518**
N	2080.0902	1040.5488	**788.4122**	394.7097
T	2181.1379	1091.0726	674.3692	337.6883
G	2238.1594	1119.5833	**573.3216**	287.1644
R	2394.2605	**1197.6339**	516.3001	258.6537
G	2451.2819	1226.1446	**360.1990**	180.6031
Q	2579.3405	1290.1739	303.1775	152.0924
R	2735.4416	1368.2245	**175.1190**	88.0631

Peptide sequence 9: NRPQFLVGSNSLLR



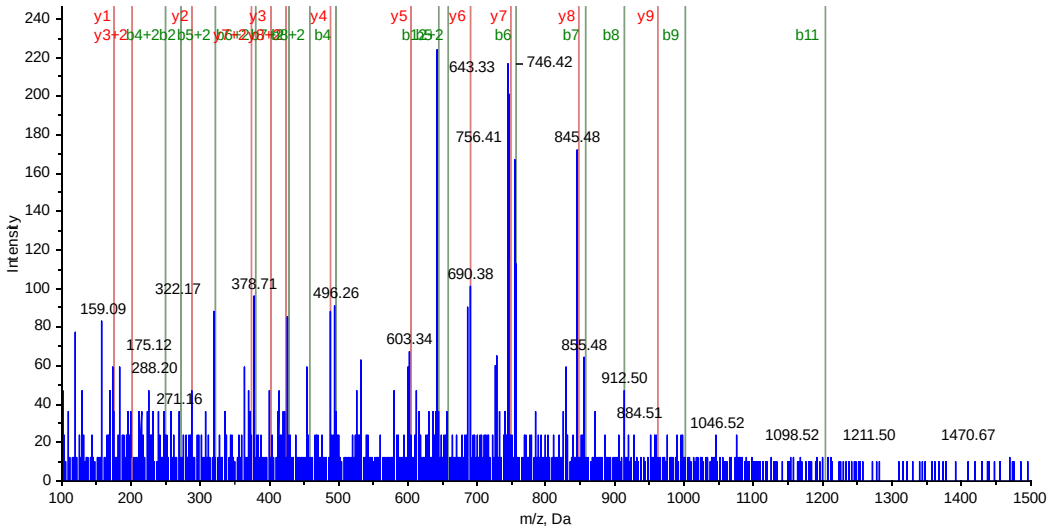
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1600.8918	800.9495
R	**271.1513**	**136.0793**	1486.8489	**743.9281**
P	**368.2041**	184.6057	1330.7478	**665.8775**
Q	**496.2627**	**248.6350**	**1233.6950**	617.3511
F	**643.3311**	**322.1692**	**1105.6364**	**553.3218**
L	**756.4151**	**378.7112**	**958.5680**	**479.7876**
V	**855.4835**	**428.2454**	**845.4839**	**423.2456**
G	**912.5050**	**456.7561**	**746.4155**	**373.7114**
S	**999.5370**	**500.2722**	**689.3941**	**345.2007**
N	**1113.5800**	**557.2936**	**602.3620**	**301.6847**
S	**1200.6120**	**600.8096**	**488.3191**	244.6632
L	**1313.6961**	**657.3517**	**401.2871**	**201.1472**
L	1426.7801	**713.8937**	**288.2030**	144.6051
R	1582.8812	791.9443	**175.1190**	88.0631

Peptide sequence 10: VSPGDVFWIPR



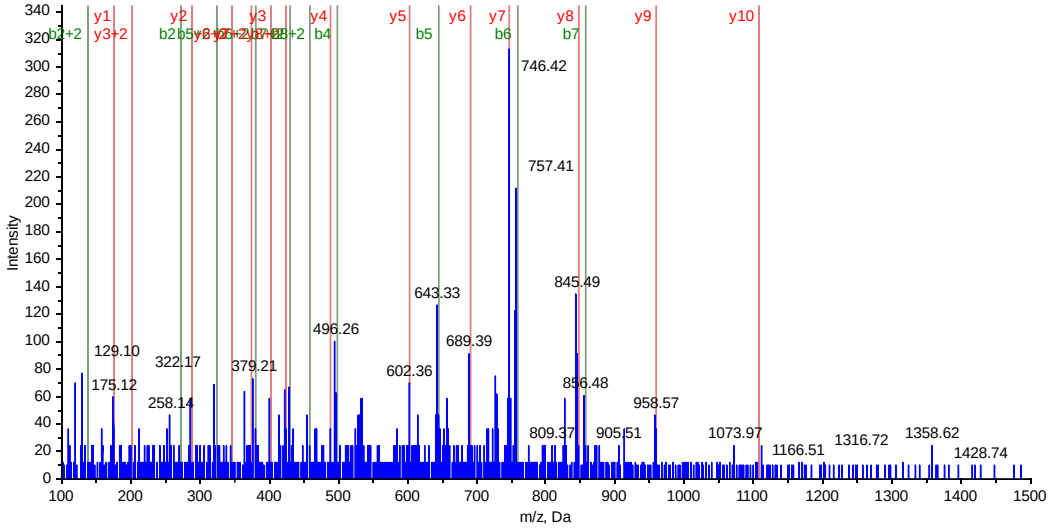
Residue	b	b+2	y	y+2
V	100.0757	50.5415	1272.6735	**636.8404**
S	**187.1077**	94.0575	**1173.6051**	**587.3062**
P	284.1605	142.5839	**1086.5731**	**543.7902**
G	**341.1819**	171.0946	**989.5203**	495.2638
D	**456.2089**	228.6081	**932.4989**	466.7531
V	**555.2773**	278.1423	**817.4719**	409.2396
F	**702.3457**	351.6765	**718.4035**	359.7054
W	**888.4250**	444.7162	**571.3351**	286.1712
I	**1001.5091**	501.2582	**385.2558**	193.1315
P	1098.5619	549.7846	**272.1717**	136.5895
R	1254.6630	**627.8351**	**175.1190**	88.0631

Peptide sequence 11: NRPQFLVGSN[Dea]SLLR



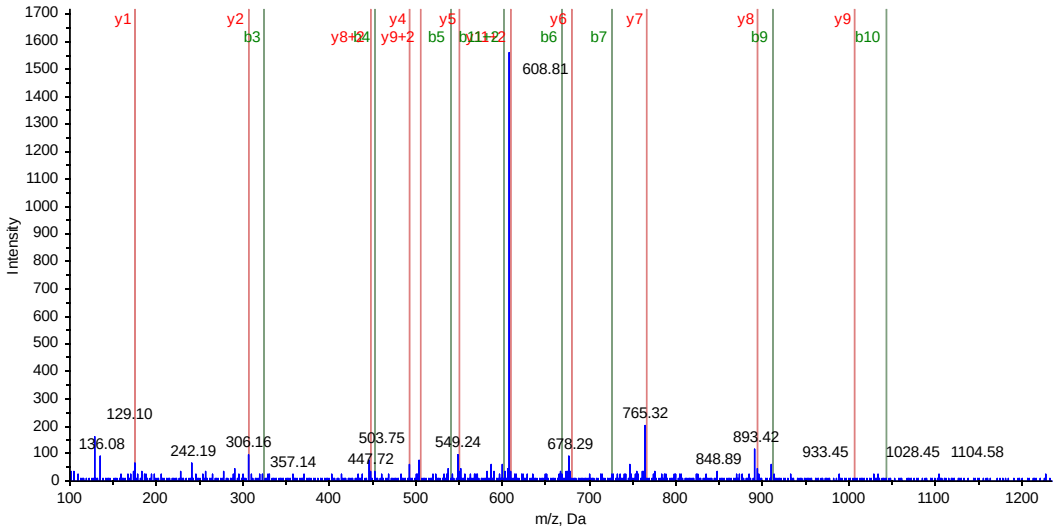
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1601.8758	801.4415
R	**271.1513**	136.0793	1487.8329	744.4201
P	368.2041	184.6057	1331.7318	666.3695
Q	**496.2627**	**248.6350**	1234.6790	617.8431
F	**643.3311**	**322.1692**	1106.6204	553.8139
L	**756.4151**	**378.7112**	**959.5520**	480.2796
V	**855.4835**	**428.2454**	**846.4680**	**423.7376**
G	**912.5050**	**456.7561**	**747.3995**	**374.2034**
S	**999.5370**	500.2722	**690.3781**	345.6927
N[Dea]	1114.5640	557.7856	**603.3461**	302.1767
S	**1201.5960**	601.3016	**488.3191**	244.6632
L	1314.6801	**657.8437**	**401.2871**	**201.1472**
L	1427.7641	714.3857	**288.2030**	144.6051
R	1583.8653	792.4363	**175.1190**	88.0631

Peptide sequence 12: NRPQ[Dea]FLVGSNSLLR



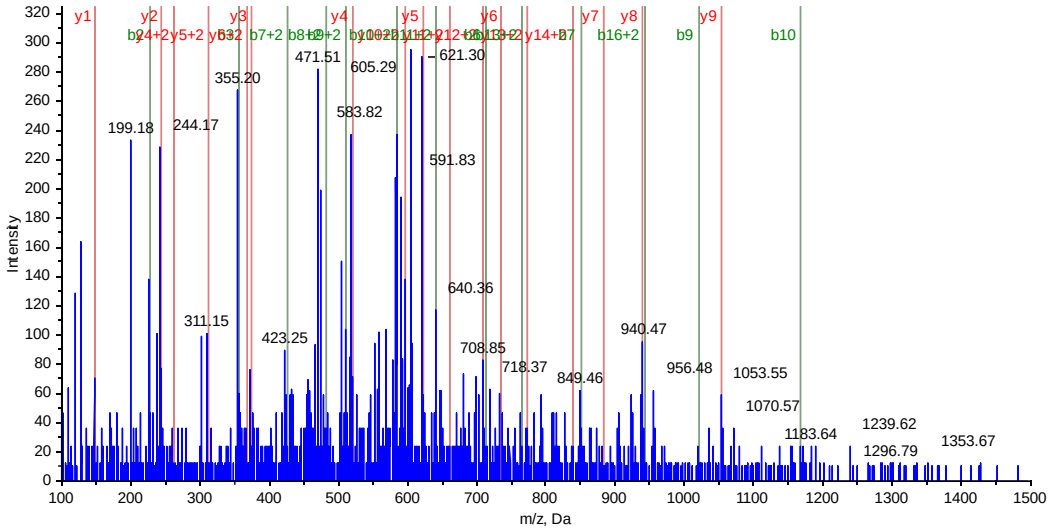
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1601.8758	801.4415
R	**271.1513**	**136.0793**	1487.8329	744.4201
P	368.2041	184.6057	1331.7318	666.3695
Q[Dea]	**497.2467**	249.1270	1234.6790	617.8431
F	**644.3151**	**322.6612**	**1105.6364**	553.3218
L	**757.3991**	**379.2032**	**958.5680**	479.7876
V	**856.4676**	**428.7374**	**845.4839**	**423.2456**
G	913.4890	**457.2482**	**746.4155**	**373.7114**
S	1000.5211	500.7642	**689.3941**	**345.2007**
N	1114.5640	557.7856	**602.3620**	301.6847
S	1201.5960	601.3016	**488.3191**	244.6632
L	1314.6801	657.8437	**401.2871**	**201.1472**
L	1427.7641	714.3857	**288.2030**	144.6051
R	1583.8653	792.4363	**175.1190**	88.0631

Peptide sequence 13: QVIKSEGGEMR



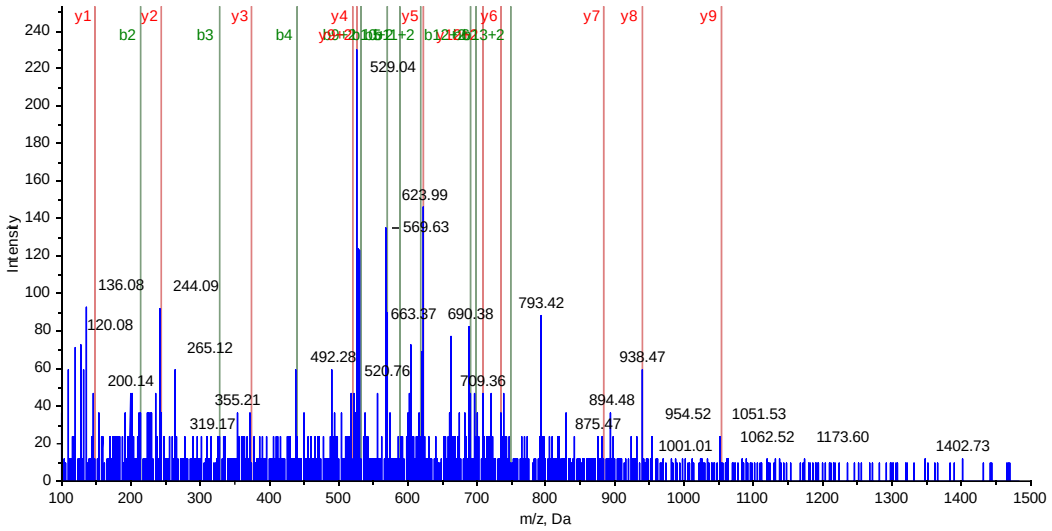
Residue	b	b+2	y	y+2
Q	112.0393	56.5233	1216.5990	**608.8032**
V	211.1077	106.0575	1105.5670	553.2871
I	**324.1918**	162.5995	**1006.4986**	**503.7529**
K	**452.2867**	226.6470	**893.4145**	**447.2109**
S	**539.3188**	270.1630	**765.3196**	383.1634
E	**668.3614**	334.6843	**678.2876**	339.6474
G	**725.3828**	363.1951	**549.2450**	275.1261
G	782.4043	391.7058	**492.2235**	246.6154
E	**911.4469**	456.2271	435.2020	218.1047
M	**1042.4874**	521.7473	**306.1594**	153.5834
R	1198.5885	**599.7979**	**175.1190**	88.0631

Peptide sequence 14: IIEKPMHIGFLTM[Oxi]EPK



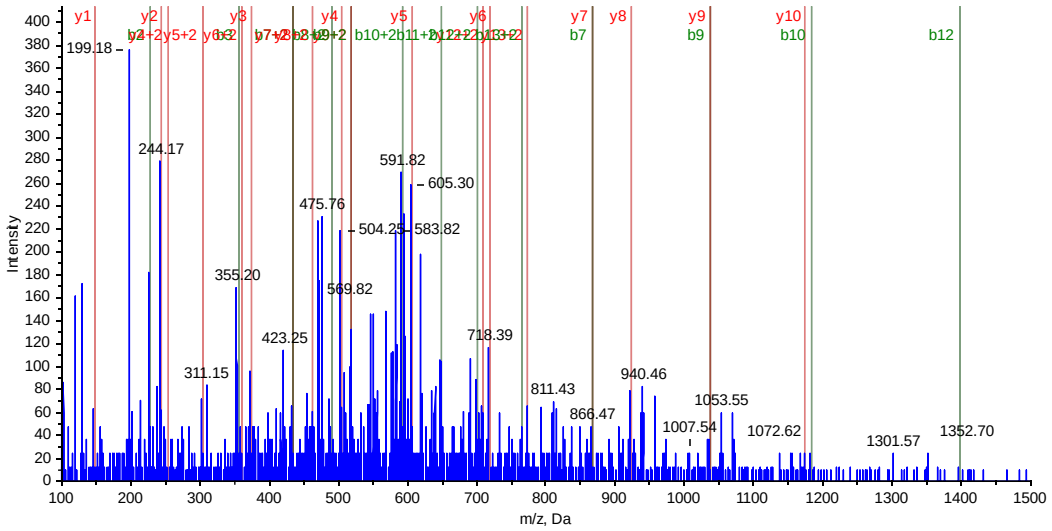
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1900.0071	950.5072
I	**227.1754**	114.0913	1786.9230	893.9652
E	**356.2180**	178.6126	1673.8390	**837.4231**
K	484.3130	242.6601	1544.7964	**772.9018**
P	581.3657	291.1865	1416.7014	**708.8543**
M	**712.4062**	356.7067	1319.6486	**660.3280**
H	**849.4651**	**425.2362**	1188.6082	**594.8077**
I	962.5492	**481.7782**	**1051.5492**	526.2783
G	**1019.5706**	**510.2890**	**938.4652**	469.7362
F	**1166.6391**	**583.8232**	**881.4437**	441.2255
L	1279.7231	**640.3652**	**734.3753**	**367.6913**
T	1380.7708	690.8890	**621.2912**	**311.1493**
M[Oxi]	1527.8062	**764.4067**	**520.2436**	**260.6254**
E	1656.8488	828.9280	**373.2082**	187.1077
P	1753.9016	877.4544	**244.1656**	122.5864
K	1881.9965	**941.5019**	**147.1128**	74.0600

Peptide sequence 15: GRIIEKPMHIGFLTM[Oxi]EPK



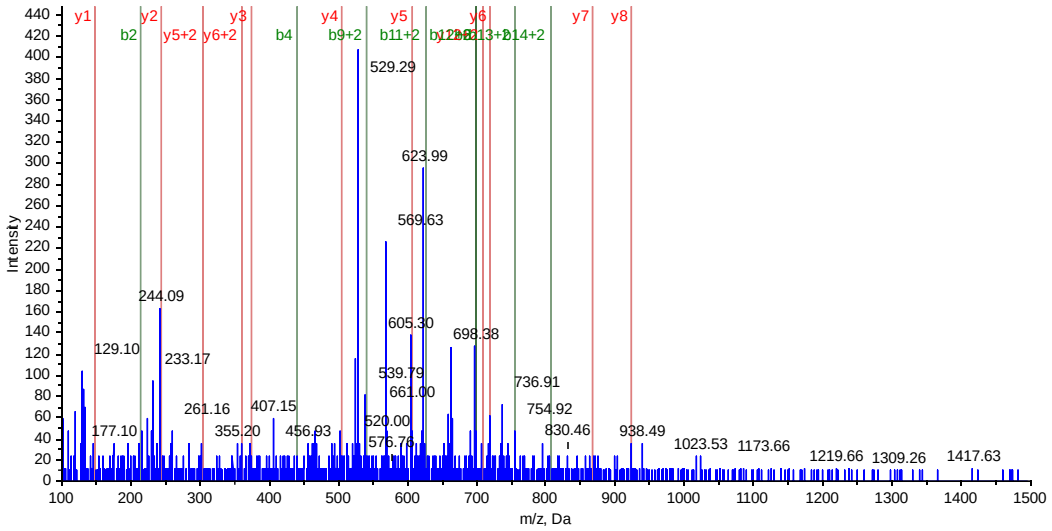
Residue	b	b+2	y	y+2
G	58.0287	29.5180	2113.1297	1057.0685
R	**214.1299**	107.5686	2056.1082	1028.5577
I	**327.2139**	164.1106	1900.0071	950.5072
I	**440.2980**	220.6526	1786.9230	893.9652
E	**569.3406**	285.1739	1673.8390	837.4231
K	**697.4355**	349.2214	1544.7964	772.9018
P	794.4883	397.7478	1416.7014	**708.8543**
M	925.5288	463.2680	1319.6486	660.3280
H	1062.5877	**531.7975**	1188.6082	594.8077
I	1175.6718	**588.3395**	**1051.5492**	**526.2783**
G	1232.6932	**616.8502**	**938.4652**	469.7362
F	1379.7616	**690.3845**	**881.4437**	441.2255
L	1492.8457	**746.9265**	**734.3753**	367.6913
T	1593.8934	797.4503	**621.2912**	311.1493
M[Oxi]	1740.9288	870.9680	**520.2436**	260.6254
E	1869.9714	935.4893	**373.2082**	187.1077
P	1967.0241	984.0157	**244.1656**	122.5864
K	2095.1191	1048.0632	**147.1128**	74.0600

Peptide sequence 16: IIEKPM[Oxi]HIGFLTMEPK



Residue	b	b+2	y	y+2
I	114.0913	57.5493	1900.0071	950.5072
I	**227.1754**	114.0913	1786.9230	893.9652
E	**356.2180**	178.6126	1673.8390	837.4231
K	484.3130	242.6601	1544.7964	**772.9018**
P	581.3657	291.1865	1416.7014	**708.8543**
M[Oxi]	728.4011	364.7042	1319.6486	660.3280
H	**865.4600**	**433.2337**	**1172.6132**	586.8103
I	978.5441	**489.7757**	**1035.5543**	**518.2808**
G	**1035.5656**	**518.2864**	**922.4703**	**461.7388**
F	**1182.6340**	**591.8206**	**865.4488**	**433.2280**
L	1295.7180	**648.3627**	**718.3804**	**359.6938**
T	**1396.7657**	**698.8865**	**605.2963**	**303.1518**
M	1527.8062	**764.4067**	**504.2486**	**252.6280**
E	1656.8488	828.9280	**373.2082**	187.1077
P	1753.9016	877.4544	**244.1656**	122.5864
K	1881.9965	941.5019	**147.1128**	74.0600

Peptide sequence 17: GRIIEKPM[Oxi]HIGFLTMEPK



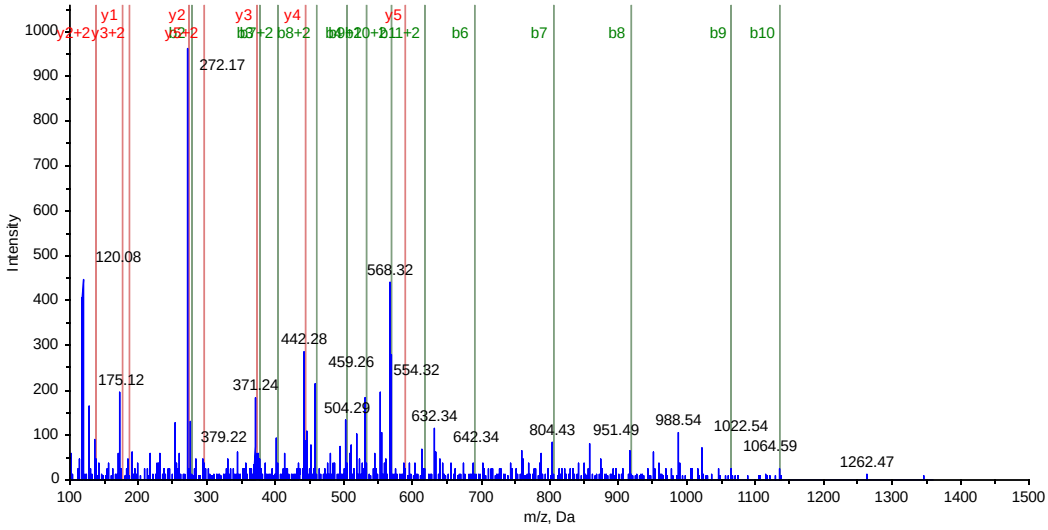
Residue	b	b+2	y	y+2
G	58.0287	29.5180	2113.1297	1057.0685
R	**214.1299**	107.5686	2056.1082	1028.5577
I	327.2139	164.1106	1900.0071	950.5072
I	**440.2980**	220.6526	1786.9230	893.9652
E	569.3406	285.1739	1673.8390	837.4231
K	**697.4355**	349.2214	1544.7964	772.9018
P	794.4883	397.7478	1416.7014	**708.8543**
M[Oxi]	941.5237	471.2655	1319.6486	660.3280
H	1078.5826	**539.7949**	1172.6132	586.8103
I	1191.6667	596.3370	1035.5543	518.2808
G	1248.6881	**624.8477**	**922.4703**	461.7388
F	1395.7566	**698.3819**	**865.4488**	433.2280
L	1508.8406	**754.9239**	**718.3804**	**359.6938**
T	1609.8883	**805.4478**	**605.2963**	**303.1518**
M	1740.9288	870.9680	**504.2486**	252.6280
E	1869.9714	935.4893	**373.2082**	187.1077
P	1967.0241	984.0157	**244.1656**	122.5864
K	2095.1191	1048.0632	**147.1128**	74.0600

Protein: B.rapa.Ro18.Candidate-2, 4 peptides (95%)

Protein sequence coverage

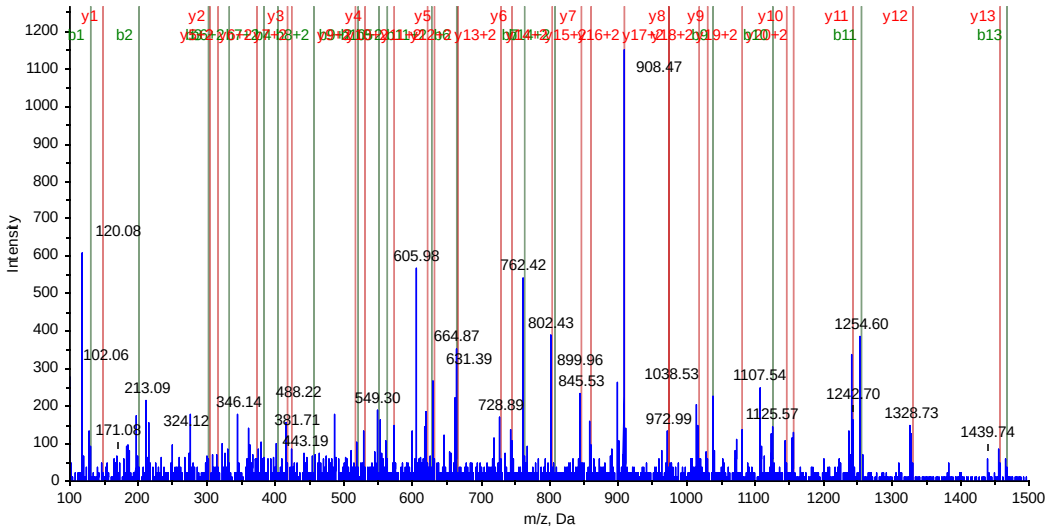
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IGLMRNRTQPPLIVHDMLTTPGEANTDTDTNTWPLQTRLLKLFSGDASADSVENKKVKKEKKEKKEKKK
KPK**KATTFNVFESEPDFQSPNGQTITINRK**DLKVLQGSMVGVSMVNLTQGSMMGPHWNPWACEISVVVR
GSGMVRVLRNSISRSSSECKNMR**FKVEKGDIFAVPR**LHPMAQMSFLNDSLVFVGFTTSAK**NNEPQFLAG**
KNSALWSLDREVLAASFNVSSFMIAGLLEAQKEAAVLGCPACAEGELEKLKEDEEKKESPPQQPPQPFQ
PQPPGEKPQQPPQPFQPQPPQGEPQKPPQGEPQKPPQGEPEGPQKPFQPQPGQGEPQEPQASMETKMRD
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Peptide sequence 1: FKVEKGDIFAVPR



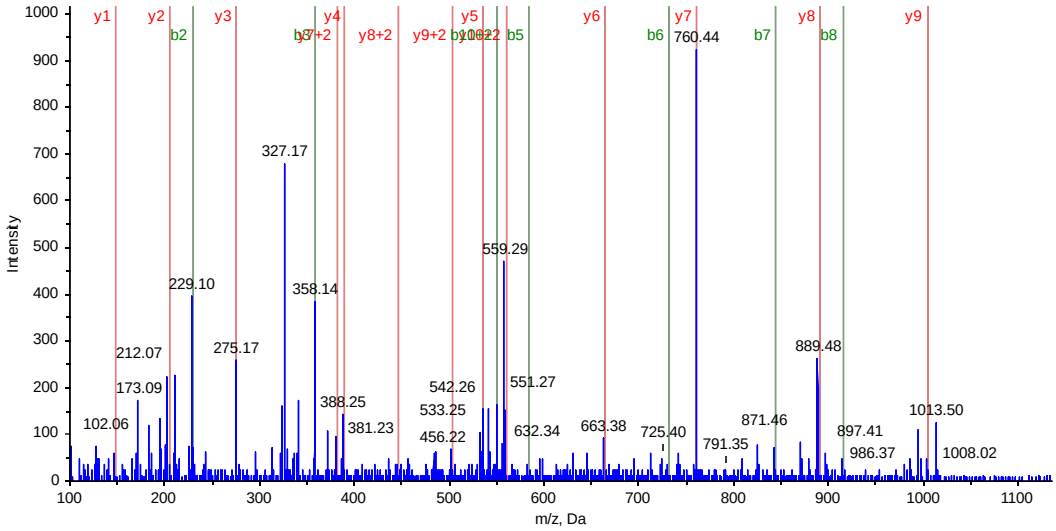
Residue	b	b+2	y	y+2
F	148.0757	74.5415	1505.8475	753.4274
K	**276.1707**	138.5890	1358.7791	679.8932
V	**375.2391**	188.1232	1230.6841	615.8457
E	**504.2817**	252.6445	1131.6157	566.3115
K	632.3766	316.6919	1002.5731	501.7902
G	**689.3981**	345.2027	874.4781	437.7427
D	**804.4250**	**402.7162**	817.4567	409.2320
I	**917.5091**	**459.2582**	702.4297	351.7185
F	**1064.5775**	**532.7924**	**589.3457**	**295.1765**
A	**1135.6146**	**568.3109**	**442.2772**	221.6423
V	1234.6830	**617.8452**	**371.2401**	**186.1237**
P	1331.7358	666.3715	**272.1717**	**136.5895**
R	1487.8369	744.4221	**175.1190**	88.0631

Peptide sequence 2: KATTFNVFESEPDFQSPNGQTITINRK



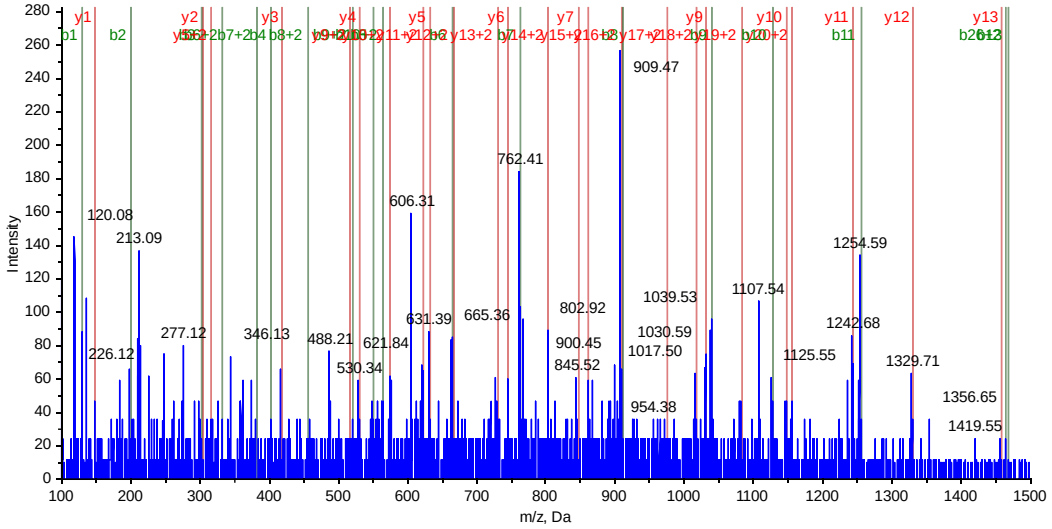
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	3069.5276	1535.2674
A	**200.1394**	100.5733	2941.4326	1471.2200
T	**301.1870**	151.0972	2870.3955	1435.7014
T	**402.2347**	201.6210	2769.3478	1385.1776
F	**549.3031**	275.1552	2668.3002	1334.6537
N	**663.3461**	**332.1767**	2521.2318	1261.1195
V	**762.4145**	**381.7109**	2407.1888	1204.0981
F	909.4829	**455.2451**	2308.1204	**1154.5638**
E	**1038.5255**	**519.7664**	2161.0520	**1081.0296**
S	**1125.5575**	**563.2824**	2032.0094	**1016.5083**
E	**1254.6001**	**627.8037**	1944.9774	**972.9923**
P	1351.6529	676.3301	1815.9348	**908.4710**
D	**1466.6798**	733.8435	1718.8820	**859.9446**
F	1613.7482	**807.3777**	1603.8551	**802.4312**
Q	1741.8068	871.4070	**1456.7867**	**728.8970**
S	1828.8388	914.9230	**1328.7281**	**664.8677**
P	1925.8916	963.4494	**1241.6961**	**621.3517**
N	2039.9345	1020.4709	**1144.6433**	**572.8253**
G	2096.9560	1048.9816	**1030.6004**	**515.8038**
Q	2225.0146	1113.0109	**973.5789**	487.2931
T	2326.0622	1163.5348	**845.5203**	**423.2638**
I	2439.1463	1220.0768	**744.4726**	**372.7400**
T	2540.1940	1270.6006	**631.3886**	**316.1979**
I	2653.2780	1327.1427	**530.3409**	265.6741
N	2767.3210	1384.1641	**417.2568**	209.1321
R	2923.4221	1462.2147	**303.2139**	152.1106
K	3051.5170	1526.2622	**147.1128**	74.0600

Peptide sequence 3: NNEPQFLAGK



Residue	b	b+2	y	y+2
N	115.0502	58.0287	1117.5636	**559.2855**
N	**229.0931**	115.0502	**1003.5207**	**502.2640**
E	**358.1357**	179.5715	**889.4778**	**445.2425**
P	455.1885	228.0979	**760.4352**	**380.7212**
Q	**583.2471**	292.1272	**663.3824**	332.1949
F	**730.3155**	365.6614	**535.3239**	268.1656
L	**843.3995**	422.2034	**388.2554**	194.6314
A	**914.4367**	457.7220	**275.1714**	138.0893
G	971.4581	486.2327	**204.1343**	102.5708
K	1099.5531	**550.2802**	**147.1128**	74.0600

Peptide sequence 4: KATTFNVFESEPDFQSPN[Dea]GQTITINRK



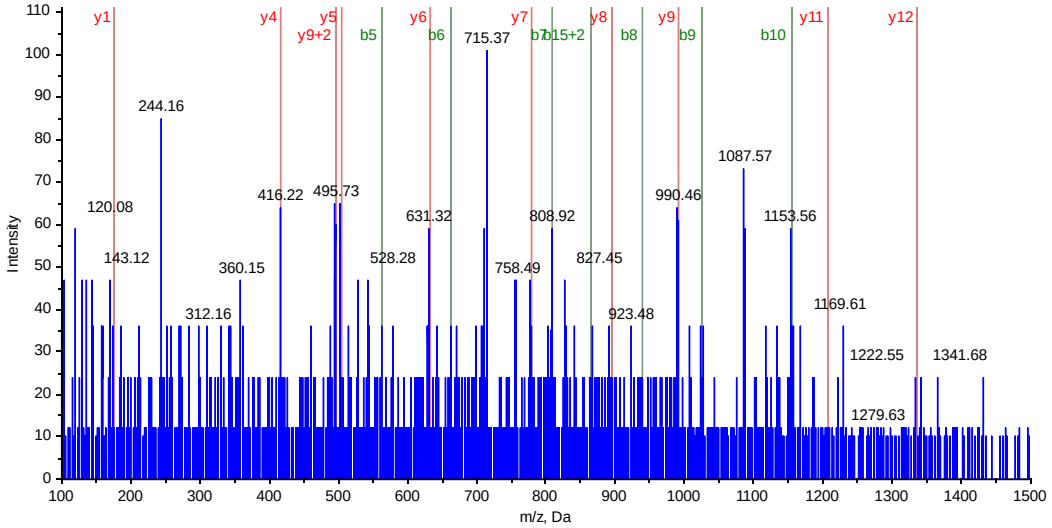
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	3070.5116	1535.7594
A	**200.1394**	100.5733	2942.4167	1471.7120
T	**301.1870**	151.0972	2871.3795	1436.1934
T	**402.2347**	201.6210	2770.3319	1385.6696
F	**549.3031**	275.1552	2669.2842	1335.1457
N	**663.3461**	**332.1767**	2522.2158	1261.6115
V	**762.4145**	**381.7109**	2408.1728	1204.5901
F	**909.4829**	**455.2451**	2309.1044	**1155.0559**
E	**1038.5255**	**519.7664**	2162.0360	**1081.5216**
S	**1125.5575**	**563.2824**	2032.9934	**1017.0004**
E	**1254.6001**	627.8037	1945.9614	**973.4843**
P	1351.6529	676.3301	1816.9188	**908.9630**
D	**1466.6798**	733.8435	1719.8660	**860.4367**
F	1613.7482	807.3777	1604.8391	**802.9232**
Q	1741.8068	871.4070	**1457.7707**	**729.3890**
S	1828.8388	914.9230	**1329.7121**	**665.3597**
P	1925.8916	963.4494	**1242.6801**	**621.8437**
N[Dea]	2040.9185	1020.9629	**1145.6273**	**573.3173**
G	2097.9400	1049.4736	**1030.6004**	**515.8038**
Q	2225.9986	1113.5029	973.5789	487.2931
T	2327.0462	1164.0268	**845.5203**	423.2638
I	2440.1303	1220.5688	**744.4726**	372.7400
T	2541.1780	1271.0926	**631.3886**	**316.1979**
I	2654.2621	1327.6347	**530.3409**	265.6741
N	2768.3050	1384.6561	**417.2568**	209.1321
R	2924.4061	**1462.7067**	**303.2139**	152.1106
K	3052.5011	1526.7542	**147.1128**	74.0600

Protein: B.rapa.Ro18.Candidate-3, 2 peptides (95%)

Protein sequence coverage

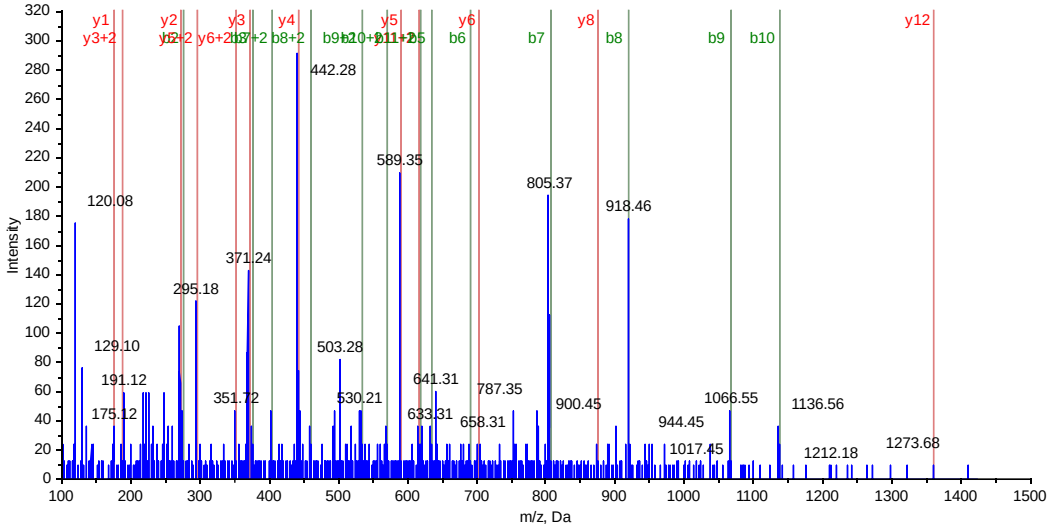
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RPGTVFYLQSKPIDIFLGTKLRVYAIFSNTEECLHDPCFGAYSSITDLLFGFDEAILQSAFGVPEEIIG
LMTNRTQPPLIVHDMLSTPGEANTYTWQLQVQPRLLKLFAGYVSAAEKKKKEKKTKK**AKTFNVFESEPD**
FQSPSGRTITINRKDLEVLSGSMVGVSMVNLTQASMMGPHWNPWACEISIVLKGSGMVRVLRSSISSTS
SSSSSSECKNMR**FKVEEGDIFAVPR**LHPMAQMSFINESLVFIGFTTSARNNEPQFLAGQRSALRLLDQE
VLAASLNVSSVMIEGLLGAQKDAVVLGCPYCAEGELEKLKVETEMKKRDDERKREEEEAKKEEEERRKR
EEEEEEEKQWPPLPQQPPE

Peptide sequence 1: AKTFNVFESEPDFQSPSGR



Residue	b	b+2	y	y+2
A	72.0444	36.5258	2143.0091	1072.0082
K	200.1394	100.5733	2071.9720	1036.4896
T	301.1870	151.0972	1943.8770	972.4421
F	448.2554	224.6314	1842.8293	921.9183
N	**562.2984**	281.6528	1695.7609	848.3841
V	**661.3668**	331.1870	1581.7180	791.3626
F	**808.4352**	404.7212	1482.6496	741.8284
E	**937.4778**	469.2425	**1335.5811**	668.2942
S	**1024.5098**	512.7585	**1206.5386**	603.7729
E	**1153.5524**	577.2798	1119.5065	560.2569
P	1250.6052	625.8062	**990.4639**	**495.7356**
D	1365.6321	683.3197	**893.4112**	447.2092
F	1512.7005	756.8539	**778.3842**	389.6958
Q	1640.7591	820.8832	**631.3158**	316.1615
S	1727.7911	**864.3992**	**503.2572**	252.1323
P	1824.8439	912.9256	**416.2252**	208.6162
S	1911.8759	956.4416	319.1724	160.0899
G	1968.8974	984.9523	232.1404	116.5738
R	2124.9985	1063.0029	**175.1190**	88.0631

Peptide sequence 2: FKVEEGDIFAVPR



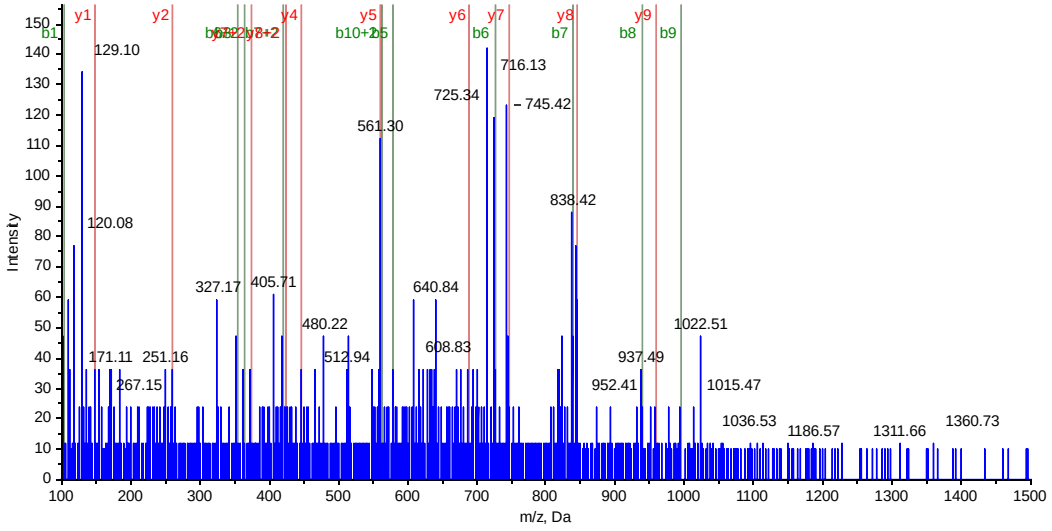
Residue	b	b+2	y	y+2
F	148.0757	74.5415	1506.7951	753.9012
K	**276.1707**	138.5890	**1359.7267**	680.3670
V	**375.2391**	188.1232	1231.6317	**616.3195**
E	504.2817	252.6445	1132.5633	566.7853
E	**633.3243**	317.1658	1003.5207	502.2640
G	**690.3457**	345.6765	**874.4781**	437.7427
D	**805.3727**	**403.1900**	817.4567	409.2320
I	**918.4567**	**459.7320**	**702.4297**	**351.7185**
F	**1065.5251**	**533.2662**	**589.3457**	**295.1765**
A	**1136.5623**	**568.7848**	**442.2772**	221.6423
V	1235.6307	**618.3190**	**371.2401**	**186.1237**
P	1332.6834	666.8454	**272.1717**	136.5895
R	1488.7845	744.8959	**175.1190**	88.0631

Protein: B.rapa.Ro18.Candidate-4, 1 peptides (95%)

Protein sequence coverage

MSKFTIIPLCLLTLFLCTNSFSDQNDGVPSSQSPLLVKRHQRTQLVATEFGEISAVHIGEEYTIQFITL
EPNALLLPLLLHSDMVFFVHTGSGVLNWVDEEKERTLELKRGDVFRLRYGTVFYLHCNLERDEVPEKLR
VYAIFDVGKCLSDQCLGAYSSIRDLLWGFDEKTLRSAFAVPKDVFGRLRDAVKPPLITHAMPKNRTQGS
EEETWGSRLAKLFVRVEDSIVVDEKDMDALKGSSFGVYMVNLTKGSMMGPHWNPNACEISIVLQGEGMI
RVVNHPSYQSKNESERFMVEDGDVFVVPQFYPMAQLSFVNSSFMFMGFSTSAK**TNHPQFLVGQNSVLK**I
FNRDVLATSFNMRYATVERLLGAQKDGLLLECVSCAEVELSRLMREIEERRRREEEEIERRKREEEEAK
RQEEERRRREEEEAERKKKAEEEARKREKERE REEEAAKRREEERRRREEEEAERKRKEEEEARKREEE
RKREEEAAKKREEERRKREKEEEEARKREEARE REEEEAKKREEERRKREEEEAERKRRAEEEARE REE
EEAKKREEEKEAARRREEERE KEEEMAKRREEERQRKERE DVERKKREEEEERKRREEEAMRREEERKR
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Peptide sequence 1: TNHPQFLVGQNSVLK



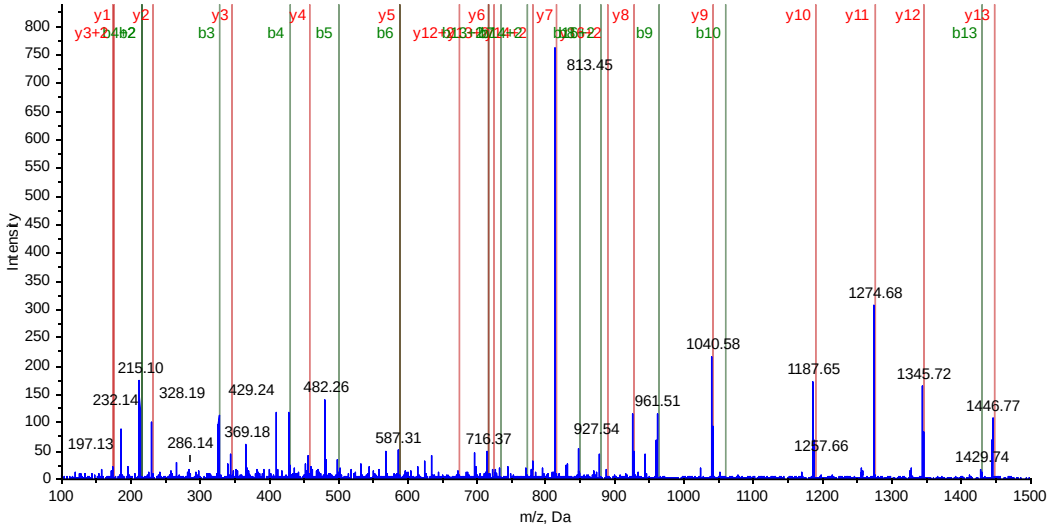
Residue	b	b+2	y	y+2
T	**102.0550**	51.5311	1681.9020	841.4547
N	216.0979	108.5526	1580.8544	790.9308
H	**353.1568**	177.0820	1466.8114	733.9094
P	450.2096	225.6084	1329.7525	665.3799
Q	**578.2681**	289.6377	1232.6997	616.8535
F	**725.3365**	**363.1719**	1104.6412	552.8242
L	**838.4206**	**419.7139**	**957.5728**	479.2900
V	**937.4890**	469.2482	**844.4887**	**422.7480**
G	**994.5105**	497.7589	**745.4203**	**373.2138**
Q	1122.5691	**561.7882**	**688.3988**	344.7030
N	1236.6120	618.8096	**560.3402**	280.6738
S	1323.6440	662.3257	**446.2973**	223.6523
V	1422.7124	711.8599	359.2653	180.1363
L	1535.7965	768.4019	**260.1969**	130.6021
K	1663.8915	832.4494	**147.1128**	74.0600

Protein: B.rapa.Ro18.Candidate-5, 20 peptides (95%)

Protein sequence coverage

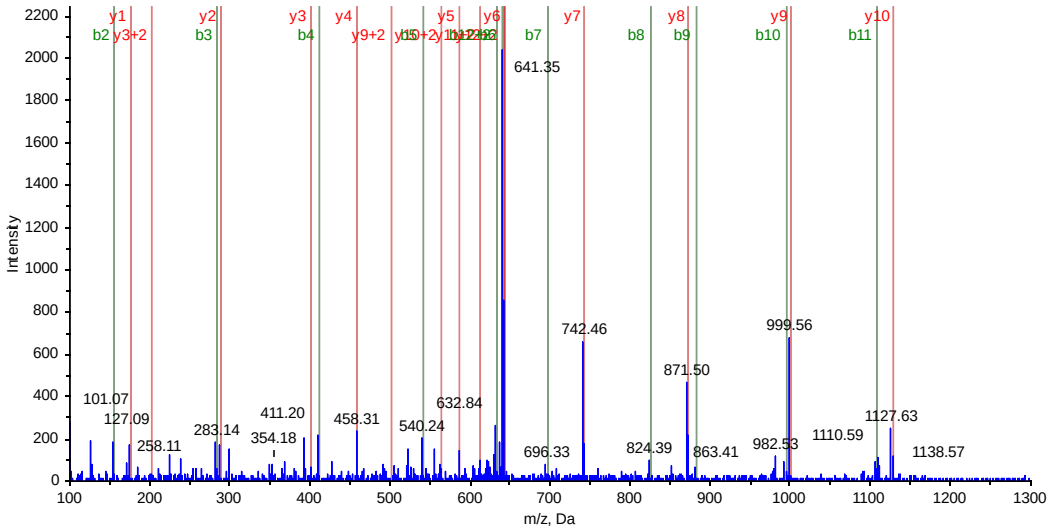
MAINKLTITLFLLISLAVFHCLAFRVEVQEFEPPRQEGQEGPGGGSGEGWDEEATKNPYHFGQWSFKNF
FQSKDGFVKMLPKFTKR**SSTLFR**GIENYRFLFQEMQPNTFLVPHHLDADYVFLVVQGK**GVIGFVTDTAN**
ESFQITKGDVVRVPSSVTHFFANTNGTVPLRLAK**IAVPANVPGHFQVFFPAHSGFHQSYFNGFSKDVLT**
ASFNIPEELLGRLIRGPQQEVGQGIIRRVSPEQIKELTEHEHATSPSNKHKDKKDKHKDKDR**STFGSPF**
NLLTQDAIYSNNFGRYHEAHPKRFSQLQDLDIAVGWVNMTQGSLFLPQYNSETTFVTFVENGCARYEMA
SPYTFQGEQQQPWFGPGQEEEVEEEMSGQVHKIVSRVCKGEVFILPAGHPFAILSQDENFVAVGFGIHA
SNSTR**TFLAGQDNMLSNINTVATR**LSFGLGSKMAEKLFTSQNYSHFAPTTPSHQFPEKPKPSFQSVFNL
VGF

Peptide sequence 1: DVLTASFNIPEELLGR



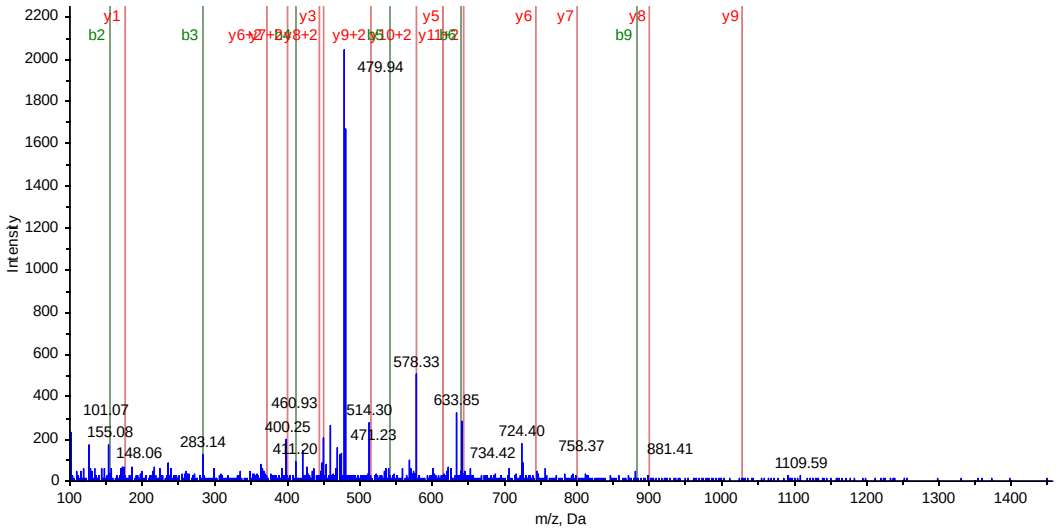
Residue	b	b+2	y	y+2
D	116.0342	58.5207	1773.9381	**887.4727**
V	**215.1026**	108.0550	1658.9112	829.9592
L	**328.1867**	164.5970	1559.8428	**780.4250**
T	**429.2344**	**215.1208**	**1446.7587**	**723.8830**
A	**500.2715**	250.6394	**1345.7110**	**673.3592**
S	**587.3035**	294.1554	**1274.6739**	637.8406
F	**734.3719**	367.6896	**1187.6419**	594.3246
N	**848.4149**	424.7111	**1040.5735**	520.7904
I	**961.4989**	481.2531	**926.5306**	463.7689
P	**1058.5517**	529.7795	**813.4465**	407.2269
E	1187.5943	594.3008	**716.3937**	358.7005
E	1316.6369	658.8221	**587.3511**	294.1792
L	**1429.7209**	**715.3641**	**458.3085**	229.6579
L	1542.8050	**771.9061**	**345.2245**	**173.1159**
G	1599.8265	800.4169	**232.1404**	116.5738
R	1755.9276	**878.4674**	**175.1190**	88.0631

Peptide sequence 2: GPQQEVGQGIIR



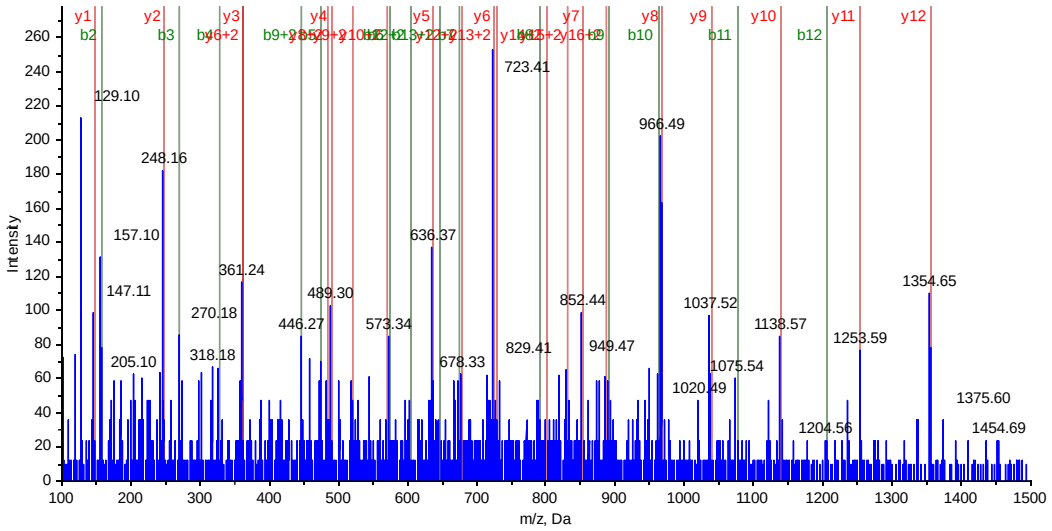
Residue	b	b+2	y	y+2
G	58.0287	29.5180	1281.6910	**641.3491**
P	**155.0815**	78.0444	1224.6695	**612.8384**
Q	**283.1401**	142.0737	**1127.6167**	**564.3120**
Q	**411.1987**	206.1030	**999.5582**	**500.2827**
E	**540.2413**	270.6243	**871.4996**	436.2534
V	**639.3097**	320.1585	**742.4570**	371.7321
G	**696.3311**	348.6692	**643.3886**	322.1979
Q	**824.3897**	412.6985	**586.3671**	293.6872
G	**881.4112**	441.2092	**458.3085**	229.6579
I	**994.4952**	497.7513	**401.2871**	**201.1472**
I	**1107.5793**	554.2933	**288.2030**	144.6051
R	1263.6804	**632.3438**	**175.1190**	88.0631

Peptide sequence 3: GPQQEVGQGIIRR



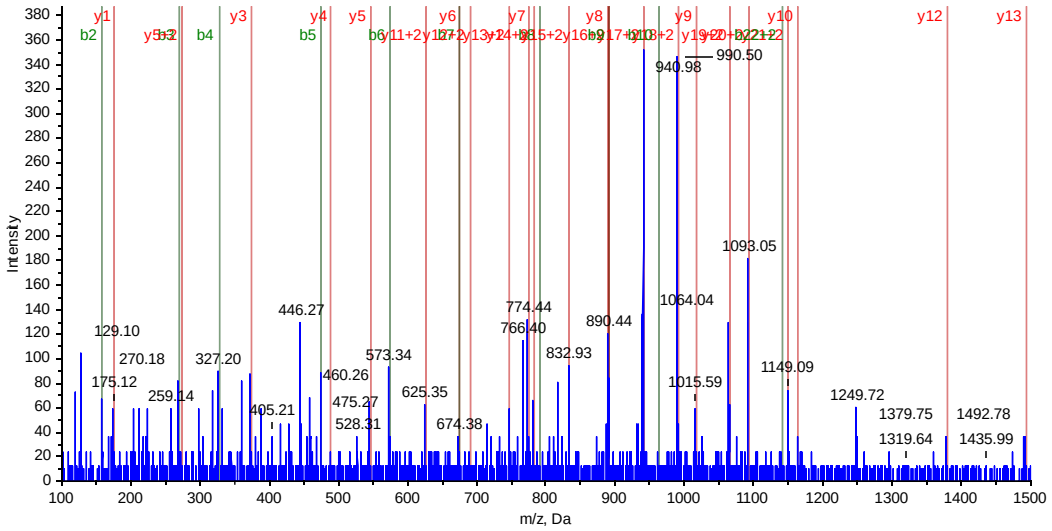
Residue	b	b+2	y	y+2
G	58.0287	29.5180	1437.7921	719.3997
P	**155.0815**	78.0444	1380.7706	690.8889
Q	**283.1401**	142.0737	1283.7179	**642.3626**
Q	**411.1987**	206.1030	1155.6593	**578.3333**
E	**540.2413**	270.6243	**1027.6007**	**514.3040**
V	**639.3097**	320.1585	**898.5581**	**449.7827**
G	696.3311	348.6692	**799.4897**	**400.2485**
Q	824.3897	412.6985	**742.4682**	**371.7378**
G	**881.4112**	441.2092	**614.4097**	307.7085
I	994.4952	497.7513	557.3882	279.1977
I	1107.5793	554.2933	**444.3041**	222.6557
R	1263.6804	632.3438	331.2201	166.1137
R	1419.7815	710.3944	**175.1190**	88.0631

Peptide sequence 4: GVIGFVTDTANESFQITK



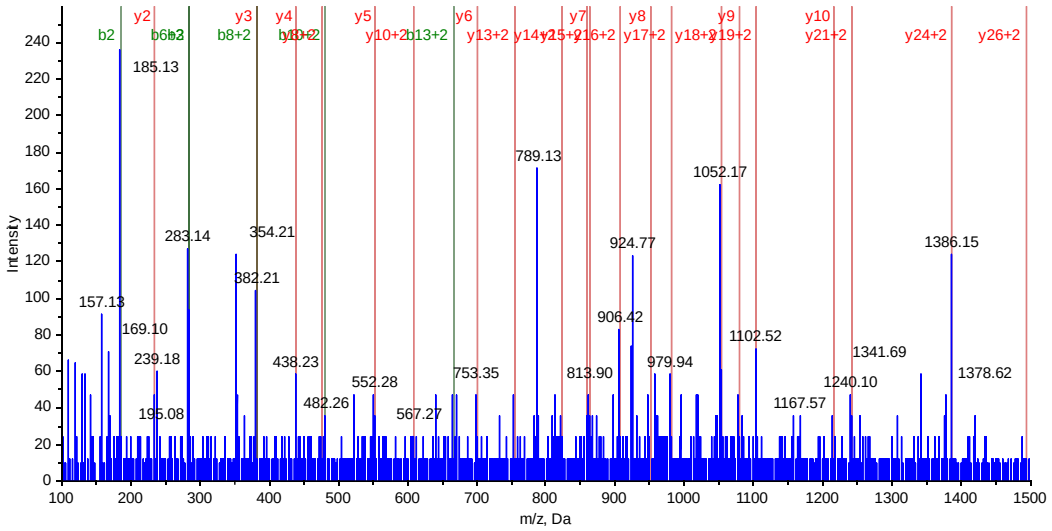
Residue	b	b+2	y	y+2
G	58.0287	29.5180	1926.9807	963.9940
V	**157.0972**	79.0522	1869.9593	935.4833
I	**270.1812**	135.5942	1770.8909	**885.9491**
G	**327.2027**	164.1050	1657.8068	**829.4070**
F	**474.2711**	237.6392	1600.7853	**800.8963**
V	**573.3395**	287.1734	1453.7169	**727.3621**
T	**674.3872**	337.6972	**1354.6485**	**677.8279**
D	**789.4141**	395.2107	**1253.6008**	627.3040
T	**890.4618**	**445.7345**	**1138.5739**	**569.7906**
A	**961.4989**	481.2531	**1037.5262**	**519.2667**
N	**1075.5419**	538.2746	**966.4891**	**483.7482**
E	**1204.5844**	**602.7959**	**852.4462**	426.7267
S	1291.6165	**646.3119**	**723.4036**	**362.2054**
F	1438.6849	719.8461	**636.3715**	318.6894
Q	1566.7435	783.8754	**489.3031**	245.1552
I	1679.8275	840.4174	**361.2445**	181.1259
T	1780.8752	890.9412	**248.1605**	124.5839
K	1908.9702	954.9887	**147.1128**	74.0600

Peptide sequence 5: GVIGFVTDTANESFQITKGDVVR



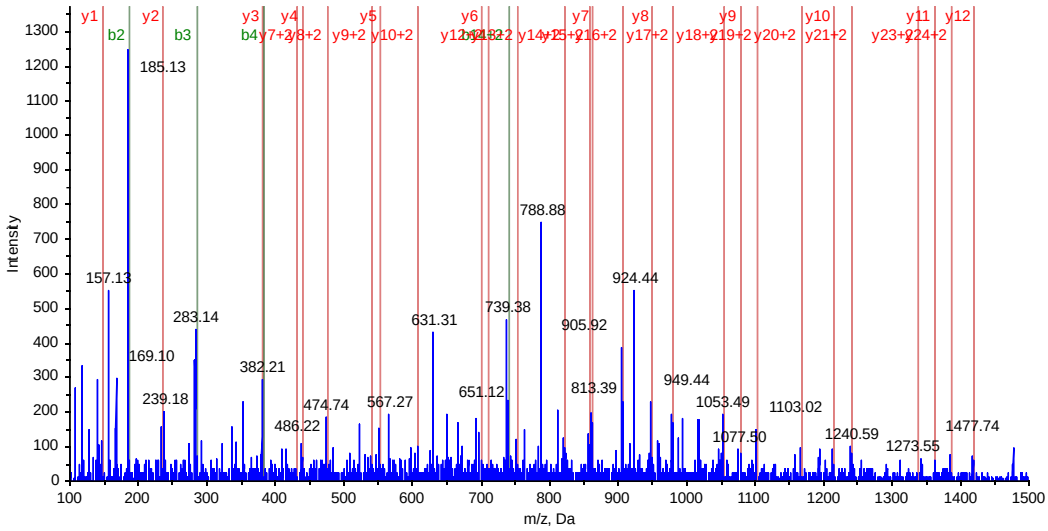
Residue	b	b+2	y	y+2
G	58.0287	29.5180	2453.2671	1227.1372
V	**157.0972**	79.0522	2396.2456	1198.6264
I	**270.1812**	135.5942	2297.1772	**1149.0922**
G	**327.2027**	164.1050	2184.0931	**1092.5502**
F	**474.2711**	237.6392	2127.0717	**1064.0395**
V	**573.3395**	287.1734	1980.0033	**990.5053**
T	**674.3872**	337.6972	1880.9348	**940.9711**
D	**789.4141**	395.2107	1779.8872	**890.4472**
T	**890.4618**	445.7345	1664.8602	**832.9338**
A	**961.4989**	481.2531	1563.8125	**782.4099**
N	1075.5419	538.2746	**1492.7754**	**746.8914**
E	1204.5844	602.7959	**1378.7325**	**689.8699**
S	1291.6165	646.3119	1249.6899	**625.3486**
F	1438.6849	719.8461	**1162.6579**	581.8326
Q	1566.7435	783.8754	**1015.5895**	508.2984
I	1679.8275	840.4174	**887.5309**	444.2691
T	1780.8752	890.9412	**774.4468**	387.7271
K	1908.9702	954.9887	**673.3991**	337.2032
G	1965.9916	983.4995	**545.3042**	**273.1557**
D	2081.0186	1041.0129	**488.2827**	244.6450
V	2180.0870	1090.5471	**373.2558**	187.1315
V	2279.1554	**1140.0813**	274.1874	137.5973
R	2435.2565	1218.1319	**175.1190**	88.0631

Peptide sequence 6: IAVPAN[Dea]VPGHFQVFFPAHSGFHQSYFNGFSK



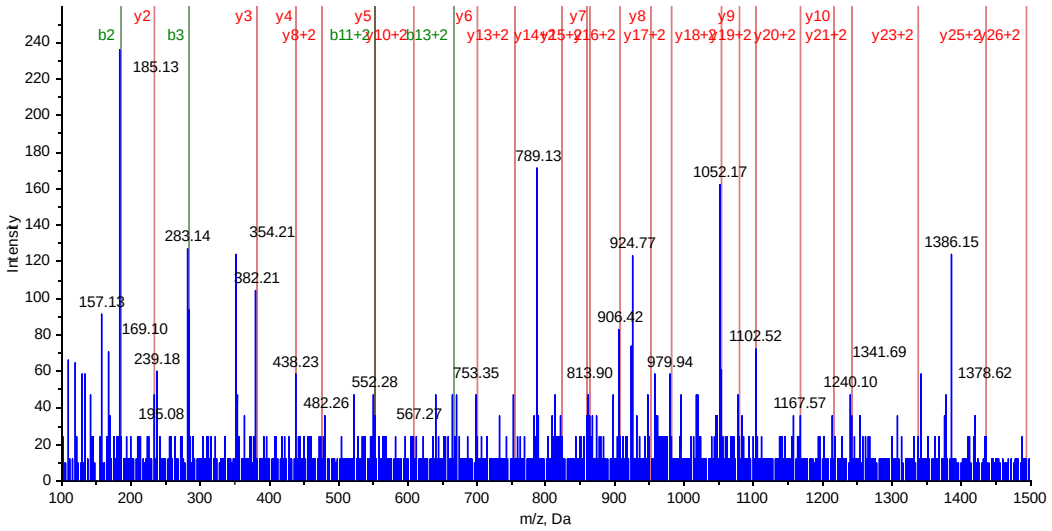
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3435.6698	1718.3385
A	**185.1285**	93.0679	3322.5857	1661.7965
V	**284.1969**	142.6021	3251.5486	1626.2779
P	381.2496	191.1285	3152.4802	1576.7437
A	452.2867	226.6470	3055.4274	1528.2174
N[Dea]	567.3137	**284.1605**	2984.3903	**1492.6988**
V	666.3821	333.6947	2869.3634	1435.1853
P	763.4349	**382.2211**	2770.2950	**1385.6511**
G	820.4563	410.7318	2673.2422	1337.1247
H	957.5152	**479.2613**	2616.2207	1308.6140
F	1104.5837	552.7955	2479.1618	**1240.0846**
Q	1232.6422	616.8248	2332.0934	1166.5503
V	1331.7106	**666.3590**	2204.0348	**1102.5211**
F	1478.7791	739.8932	2104.9664	**1052.9868**
F	1625.8475	813.4274	1957.8980	**979.4526**
P	1722.9002	861.9538	1810.8296	**905.9184**
A	1793.9374	897.4723	1713.7768	**857.3921**
H	1930.9963	966.0018	1642.7397	**821.8735**
S	2018.0283	1009.5178	1505.6808	**753.3440**
G	2075.0498	1038.0285	1418.6488	709.8280
F	2222.1182	1111.5627	1361.6273	681.3173
H	2359.1771	1180.0922	**1214.5589**	**607.7831**
Q	2487.2357	1244.1215	**1077.5000**	539.2536
S	2574.2677	1287.6375	**949.4414**	**475.2243**
Y	2737.3310	1369.1691	**862.4094**	431.7083
F	2884.3994	1442.7034	**699.3461**	350.1767
N	2998.4424	1499.7248	**552.2776**	276.6425
G	3055.4638	1528.2355	**438.2347**	219.6210
F	3202.5322	1601.7698	**381.2132**	191.1103
S	3289.5643	1645.2858	**234.1448**	117.5761
K	3417.6592	1709.3333	147.1128	74.0600

Peptide sequence 7: IAVPANVPGHFQVFFPAHSGFHQSYFNGFSK



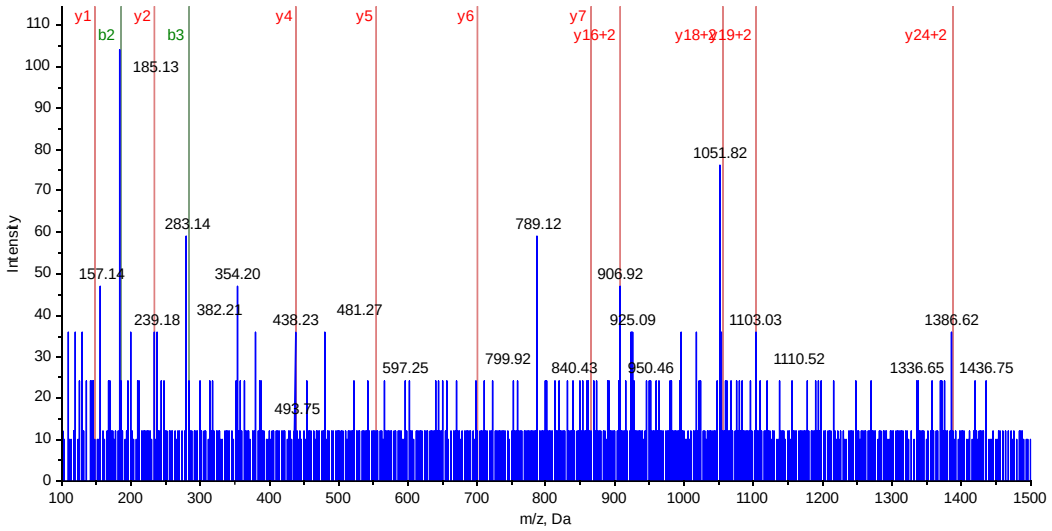
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3434.6858	1717.8465
A	**185.1285**	93.0679	3321.6017	1661.3045
V	**284.1969**	142.6021	3250.5646	1625.7859
P	**381.2496**	191.1285	3151.4962	1576.2517
A	452.2867	226.6470	3054.4434	1527.7253
N	566.3297	283.6685	2983.4063	1492.2068
V	665.3981	333.2027	2869.3634	1435.1853
P	762.4509	381.7291	2770.2950	**1385.6511**
G	819.4723	410.2398	2673.2422	**1337.1247**
H	956.5312	478.7693	2616.2207	1308.6140
F	1103.5996	552.3035	2479.1618	**1240.0846**
Q	1231.6582	616.3327	2332.0934	**1166.5503**
V	1330.7266	665.8670	2204.0348	**1102.5211**
F	1477.7950	**739.4012**	2104.9664	**1052.9868**
F	1624.8635	812.9354	1957.8980	**979.4526**
P	1721.9162	861.4618	1810.8296	**905.9184**
A	1792.9533	896.9803	1713.7768	**857.3921**
H	1930.0122	965.5098	1642.7397	**821.8735**
S	2017.0443	1009.0258	1505.6808	**753.3440**
G	2074.0657	1037.5365	**1418.6488**	**709.8280**
F	2221.1342	1111.0707	**1361.6273**	681.3173
H	2358.1931	1179.6002	**1214.5589**	**607.7831**
Q	2486.2516	1243.6295	**1077.5000**	**539.2536**
S	2573.2837	1287.1455	**949.4414**	**475.2243**
Y	2736.3470	1368.6771	**862.4094**	**431.7083**
F	2883.4154	1442.2113	**699.3461**	350.1767
N	2997.4583	1499.2328	**552.2776**	276.6425
G	3054.4798	1527.7435	**438.2347**	219.6210
F	3201.5482	1601.2777	**381.2132**	191.1103
S	3288.5802	1644.7938	**234.1448**	117.5761
K	3416.6752	1708.8412	**147.1128**	74.0600

Peptide sequence 8: IAVPANVPGHFQ[Dea]VFFPAHSGFHQSYFNGFSK



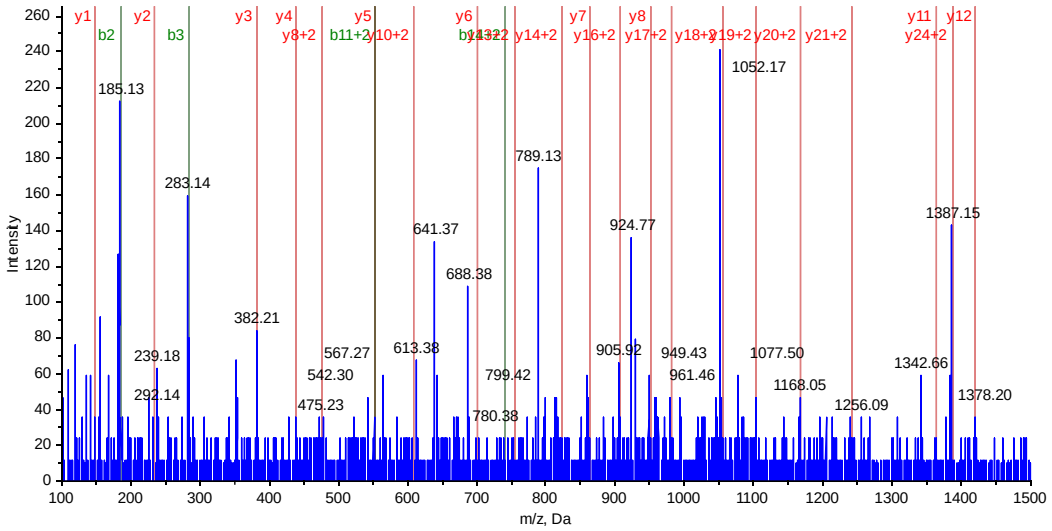
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3435.6698	1718.3385
A	**185.1285**	93.0679	3322.5857	1661.7965
V	**284.1969**	142.6021	3251.5486	1626.2779
P	381.2496	191.1285	3152.4802	1576.7437
A	452.2867	226.6470	3055.4274	1528.2174
N	566.3297	283.6685	2984.3903	**1492.6988**
V	665.3981	333.2027	2870.3474	**1435.6773**
P	762.4509	381.7291	2771.2790	1386.1431
G	819.4723	410.2398	2674.2262	**1337.6167**
H	956.5312	478.7693	2617.2048	1309.1060
F	1103.5996	**552.3035**	2480.1458	**1240.5766**
Q[Dea]	1232.6422	616.8248	2333.0774	**1167.0424**
V	1331.7106	**666.3590**	2204.0348	**1102.5211**
F	1478.7791	739.8932	2104.9664	**1052.9868**
F	1625.8475	813.4274	1957.8980	**979.4526**
P	1722.9002	861.9538	1810.8296	**905.9184**
A	1793.9374	897.4723	1713.7768	**857.3921**
H	1930.9963	966.0018	1642.7397	**821.8735**
S	2018.0283	1009.5178	1505.6808	**753.3440**
G	2075.0498	1038.0285	1418.6488	709.8280
F	2222.1182	1111.5627	1361.6273	681.3173
H	2359.1771	1180.0922	**1214.5589**	**607.7831**
Q	2487.2357	1244.1215	**1077.5000**	539.2536
S	2574.2677	1287.6375	**949.4414**	**475.2243**
Y	2737.3310	1369.1691	**862.4094**	431.7083
F	2884.3994	1442.7034	**699.3461**	350.1767
N	2998.4424	1499.7248	**552.2776**	276.6425
G	3055.4638	1528.2355	**438.2347**	219.6210
F	3202.5322	1601.7698	**381.2132**	191.1103
S	3289.5643	1645.2858	**234.1448**	117.5761
K	3417.6592	1709.3333	147.1128	74.0600

Peptide sequence 9: IAVPANVPGHFQVFFPAHSGFHQSYFN[Dea]GFSK



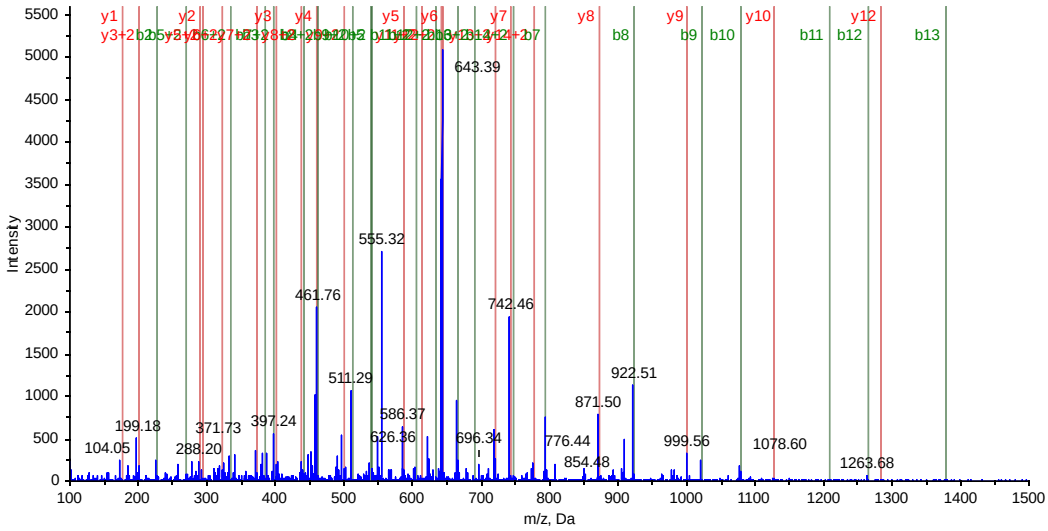
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3435.6698	1718.3385
A	**185.1285**	93.0679	3322.5857	1661.7965
V	**284.1969**	142.6021	3251.5486	1626.2779
P	381.2496	191.1285	3152.4802	1576.7437
A	452.2867	226.6470	3055.4274	1528.2174
N	566.3297	283.6685	2984.3903	1492.6988
V	665.3981	333.2027	2870.3474	1435.6773
P	762.4509	381.7291	2771.2790	**1386.1431**
G	819.4723	410.2398	2674.2262	1337.6167
H	956.5312	478.7693	2617.2048	1309.1060
F	1103.5996	552.3035	2480.1458	1240.5766
Q	1231.6582	616.3327	2333.0774	1167.0424
V	1330.7266	665.8670	2205.0189	**1103.0131**
F	1477.7950	739.4012	2105.9504	**1053.4789**
F	1624.8635	812.9354	1958.8820	979.9446
P	1721.9162	861.4618	1811.8136	**906.4104**
A	1792.9533	896.9803	1714.7608	857.8841
H	1930.0122	965.5098	1643.7237	822.3655
S	2017.0443	1009.0258	1506.6648	753.8360
G	2074.0657	1037.5365	1419.6328	710.3200
F	2221.1342	1111.0707	1362.6113	681.8093
H	2358.1931	1179.6002	1215.5429	608.2751
Q	2486.2516	1243.6295	1078.4840	539.7456
S	2573.2837	1287.1455	950.4254	475.7164
Y	2736.3470	1368.6771	**863.3934**	432.2003
F	2883.4154	1442.2113	**700.3301**	350.6687
N[Dea]	2998.4424	1499.7248	**553.2617**	277.1345
G	3055.4638	1528.2355	**438.2347**	219.6210
F	3202.5322	1601.7698	381.2132	191.1103
S	3289.5643	1645.2858	**234.1448**	117.5761
K	3417.6592	1709.3333	**147.1128**	74.0600

Peptide sequence 10: IAVPANVPGHFQVFFPAHSGFHQ[Dea]SYFNGFSK



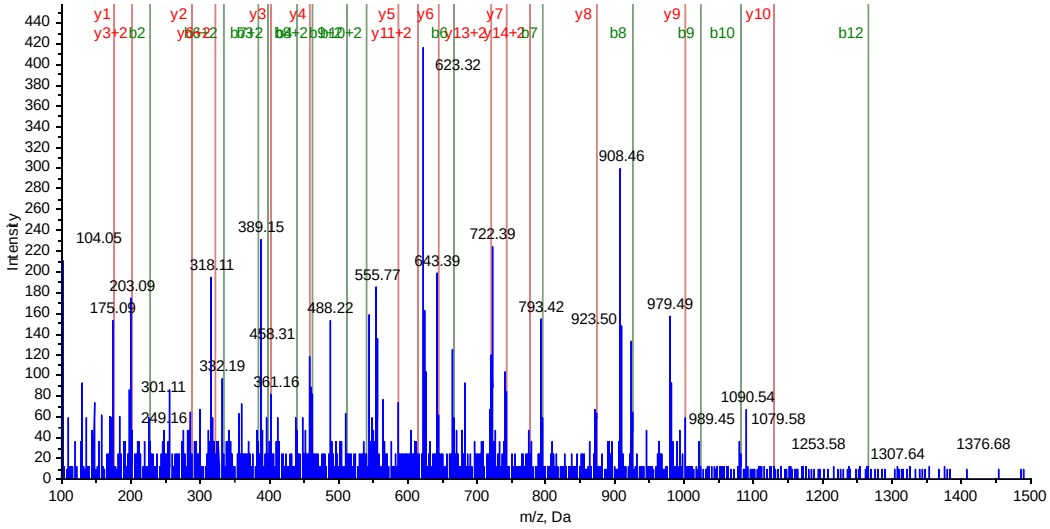
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3435.6698	1718.3385
A	**185.1285**	93.0679	3322.5857	1661.7965
V	**284.1969**	142.6021	3251.5486	1626.2779
P	381.2496	191.1285	3152.4802	1576.7437
A	452.2867	226.6470	3055.4274	1528.2174
N	566.3297	283.6685	2984.3903	1492.6988
V	665.3981	333.2027	2870.3474	1435.6773
P	762.4509	381.7291	2771.2790	1386.1431
G	819.4723	410.2398	2674.2262	1337.6167
H	956.5312	478.7693	2617.2048	1309.1060
F	1103.5996	**552.3035**	2480.1458	**1240.5766**
Q	1231.6582	616.3327	2333.0774	**1167.0424**
V	1330.7266	665.8670	2205.0189	**1103.0131**
F	1477.7950	**739.4012**	2105.9504	**1053.4789**
F	1624.8635	812.9354	1958.8820	**979.9446**
P	1721.9162	861.4618	1811.8136	**906.4104**
A	1792.9533	896.9803	1714.7608	857.8841
H	1930.0122	965.5098	1643.7237	**822.3655**
S	2017.0443	1009.0258	1506.6648	**753.8360**
G	2074.0657	1037.5365	**1419.6328**	710.3200
F	2221.1342	1111.0707	**1362.6113**	681.8093
H	2358.1931	1179.6002	1215.5429	**608.2751**
Q[Dea]	2487.2357	1244.1215	1078.4840	539.7456
S	2574.2677	1287.6375	**949.4414**	**475.2243**
Y	2737.3310	1369.1691	**862.4094**	431.7083
F	2884.3994	1442.7034	**699.3461**	350.1767
N	2998.4424	1499.7248	**552.2776**	276.6425
G	3055.4638	1528.2355	**438.2347**	219.6210
F	3202.5322	1601.7698	**381.2132**	191.1103
S	3289.5643	1645.2858	**234.1448**	117.5761
K	3417.6592	1709.3333	**147.1128**	74.0600

Peptide sequence 11: LIRGPQQEVGQGIIR



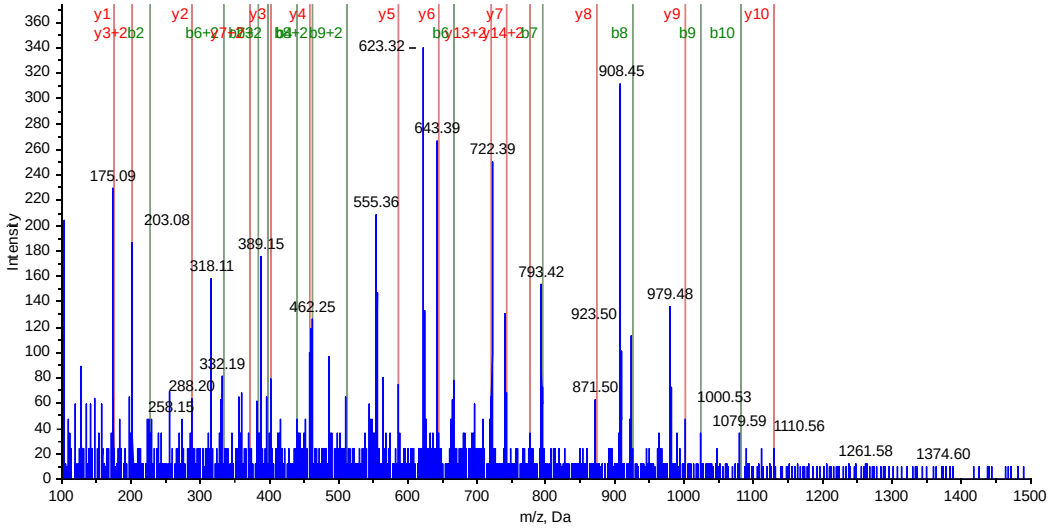
Residue	b	b+2	y	y+2
L	114.0913	57.5493	1663.9602	832.4837
I	**227.1754**	114.0913	1550.8761	**775.9417**
R	**383.2765**	192.1419	1437.7921	**719.3997**
G	**440.2980**	220.6526	**1281.6910**	**641.3491**
P	**537.3507**	**269.1790**	1224.6695	**612.8384**
Q	**665.4093**	**333.2083**	**1127.6167**	564.3120
Q	**793.4679**	**397.2376**	**999.5582**	**500.2827**
E	**922.5105**	**461.7589**	**871.4996**	**436.2534**
V	**1021.5789**	**511.2931**	**742.4570**	**371.7321**
G	**1078.6004**	**539.8038**	**643.3886**	**322.1979**
Q	**1206.6589**	**603.8331**	**586.3671**	**293.6872**
G	**1263.6804**	**632.3438**	**458.3085**	229.6579
I	**1376.7645**	**688.8859**	**401.2871**	**201.1472**
I	1489.8485	**745.4279**	**288.2030**	144.6051
R	1645.9496	823.4785	**175.1190**	88.0631

Peptide sequence 12: LIRGPQQ[Dea]EVGQGIIR



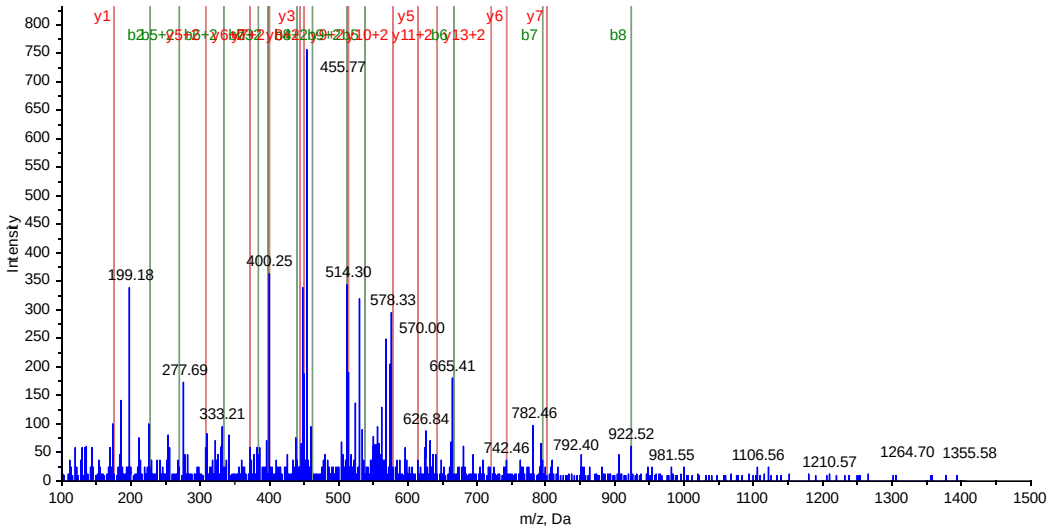
Residue	b	b+2	y	y+2
L	114.0913	57.5493	1664.9442	832.9758
I	**227.1754**	114.0913	1551.8602	**776.4337**
R	**383.2765**	192.1419	1438.7761	**719.8917**
G	**440.2980**	220.6526	1282.6750	641.8411
P	537.3507	269.1790	1225.6535	**613.3304**
Q	**665.4093**	**333.2083**	**1128.6008**	564.8040
Q[Dea]	**794.4519**	**397.7296**	**1000.5422**	500.7747
E	**923.4945**	**462.2509**	**871.4996**	436.2534
V	**1022.5629**	**511.7851**	**742.4570**	371.7321
G	**1079.5844**	**540.2958**	**643.3886**	**322.1979**
Q	1207.6430	604.3251	**586.3671**	293.6872
G	**1264.6644**	632.8359	**458.3085**	229.6579
I	1377.7485	689.3779	**401.2871**	**201.1472**
I	1490.8326	745.9199	**288.2030**	144.6051
R	1646.9337	823.9705	**175.1190**	88.0631

Peptide sequence 13: LIRGPQ[Dea]QEVGQGIIR



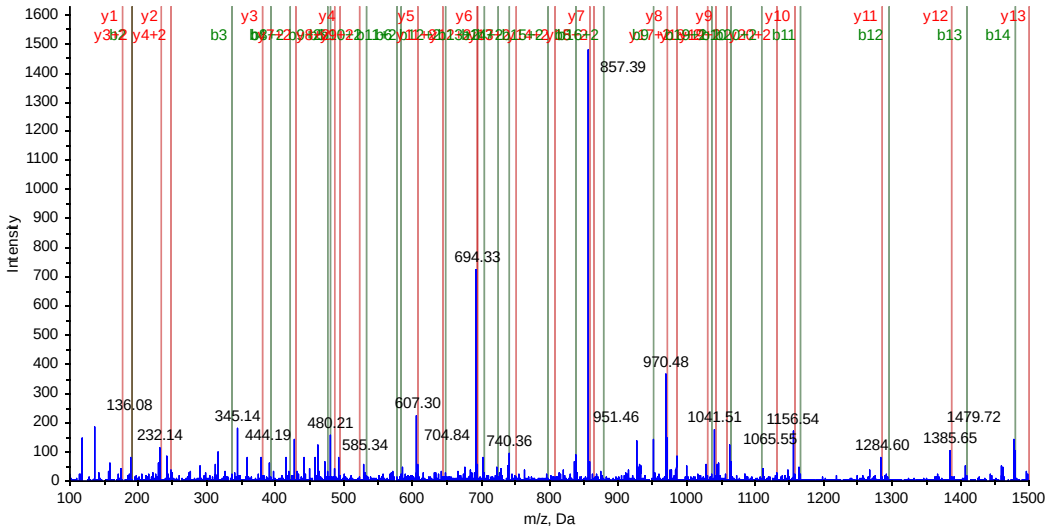
Residue	b	b+2	y	y+2
L	114.0913	57.5493	1664.9442	832.9758
I	**227.1754**	114.0913	1551.8602	**776.4337**
R	**383.2765**	192.1419	1438.7761	**719.8917**
G	**440.2980**	220.6526	1282.6750	641.8411
P	537.3507	269.1790	1225.6535	613.3304
Q[Dea]	**666.3933**	**333.7003**	**1128.6008**	564.8040
Q	**794.4519**	**397.7296**	**999.5582**	500.2827
E	**923.4945**	**462.2509**	**871.4996**	436.2534
V	**1022.5629**	511.7851	**742.4570**	**371.7321**
G	**1079.5844**	540.2958	**643.3886**	322.1979
Q	1207.6430	604.3251	**586.3671**	293.6872
G	1264.6644	632.8359	**458.3085**	229.6579
I	1377.7485	689.3779	**401.2871**	**201.1472**
I	1490.8326	745.9199	**288.2030**	144.6051
R	1646.9337	823.9705	**175.1190**	88.0631

Peptide sequence 14: LIRGPQQEVGQGIIRR



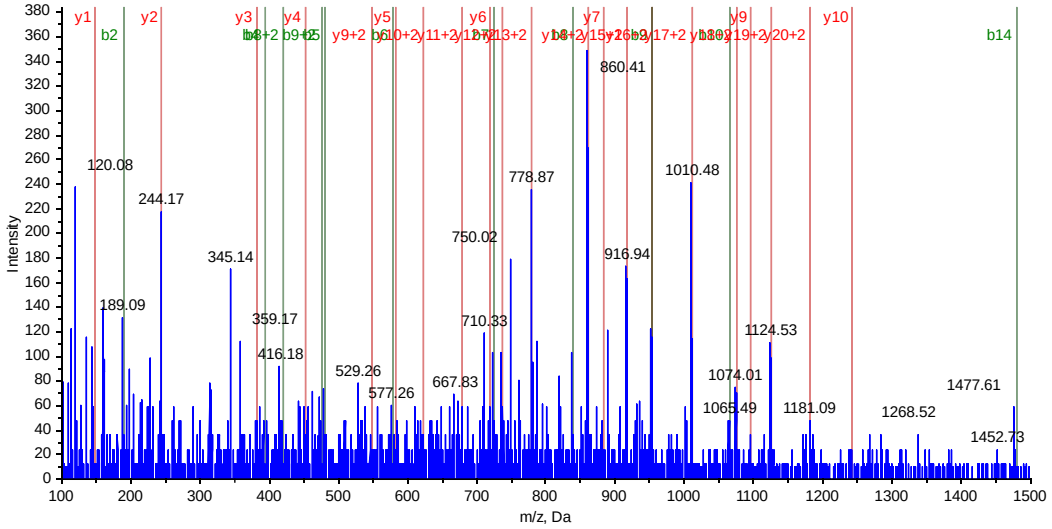
Residue	b	b+2	y	y+2
L	114.0913	57.5493	1820.0613	910.5343
I	**227.1754**	114.0913	1706.9773	853.9923
R	**383.2765**	192.1419	1593.8932	797.4502
G	**440.2980**	220.6526	1437.7921	**719.3997**
P	**537.3507**	**269.1790**	1380.7706	690.8889
Q	**665.4093**	**333.2083**	1283.7179	**642.3626**
Q	**793.4679**	**397.2376**	1155.6593	**578.3333**
E	**922.5105**	**461.7589**	1027.6007	**514.3040**
V	1021.5789	**511.2931**	898.5581	**449.7827**
G	1078.6004	539.8038	**799.4897**	**400.2485**
Q	1206.6589	603.8331	**742.4682**	**371.7378**
G	1263.6804	632.3438	**614.4097**	**307.7085**
I	1376.7645	688.8859	557.3882	279.1977
I	1489.8485	745.4279	**444.3041**	222.6557
R	1645.9496	823.4785	331.2201	166.1137
R	1802.0508	901.5290	**175.1190**	88.0631

Peptide sequence 15: STFGSPFNLLTQDAIYSNNFGR



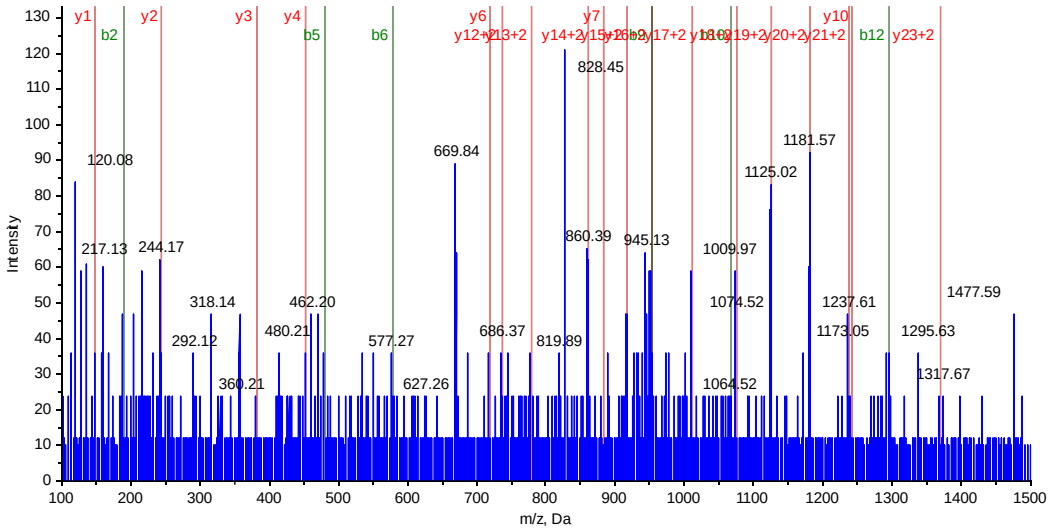
Residue	b	b+2	y	y+2
S	88.0393	44.5233	2449.1783	1225.0928
T	**189.0870**	95.0471	2362.1462	1181.5768
F	**336.1554**	168.5813	2261.0986	**1131.0529**
G	**393.1769**	197.0921	2114.0301	**1057.5187**
S	**480.2089**	240.6081	2057.0087	**1029.0080**
P	**577.2617**	289.1345	1969.9767	**985.4920**
F	**724.3301**	362.6687	1872.9239	936.9656
N	**838.3730**	**419.6901**	1725.8555	**863.4314**
L	**951.4571**	**476.2322**	1611.8125	**806.4099**
L	**1064.5411**	**532.7742**	**1498.7285**	**749.8679**
T	**1165.5888**	**583.2980**	**1385.6444**	**693.3258**
Q	**1293.6474**	**647.3273**	**1284.5967**	**642.8020**
D	**1408.6743**	**704.8408**	**1156.5382**	578.7727
A	**1479.7114**	**740.3594**	**1041.5112**	**521.2592**
I	1592.7955	**796.9014**	**970.4741**	**485.7407**
Y	1755.8588	**878.4331**	**857.3900**	**429.1987**
S	1842.8909	921.9491	**694.3267**	347.6670
N	1956.9338	978.9705	**607.2947**	304.1510
N	2070.9767	**1035.9920**	**493.2518**	**247.1295**
F	2218.0451	**1109.5262**	**379.2088**	**190.1081**
G	2275.0666	1138.0369	**232.1404**	116.5738
R	2431.1677	1216.0875	**175.1190**	88.0631

Peptide sequence 16: STFGSPFNLLTQDAIYSNNFGRYHEAHPK



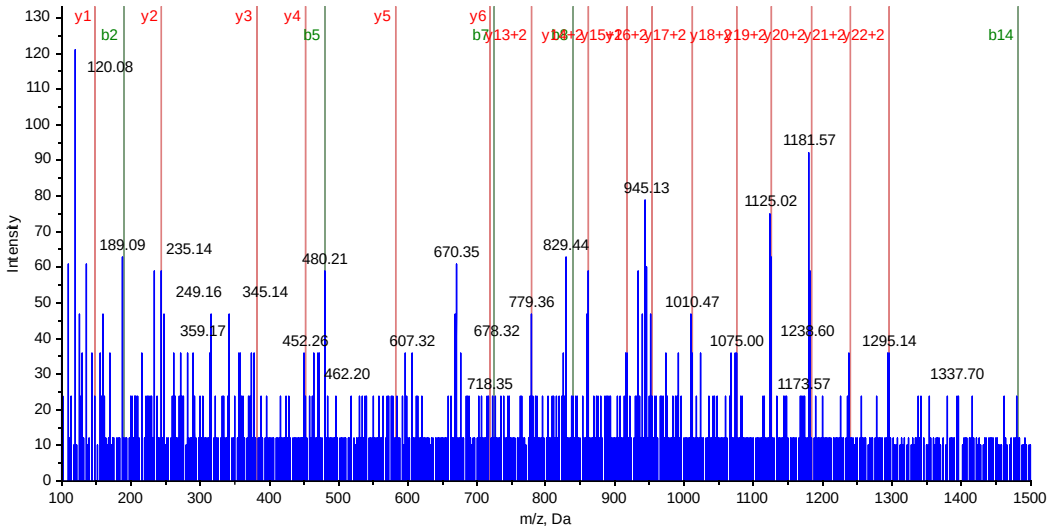
Residue	b	b+2	y	y+2
S	88.0393	44.5233	3311.5869	1656.2971
T	189.0870	95.0471	3224.5548	1612.7810
F	**336.1554**	168.5813	3123.5071	1562.2572
G	**393.1769**	197.0921	2976.4387	1488.7230
S	**480.2089**	240.6081	2919.4173	1460.2123
P	**577.2617**	289.1345	2832.3852	1416.6963
F	**724.3301**	362.6687	2735.3325	1368.1699
N	**838.3730**	**419.6901**	2588.2641	1294.6357
L	**951.4571**	**476.2322**	2474.2211	1237.6142
L	**1064.5411**	532.7742	2361.1371	**1181.0722**
T	1165.5888	583.2980	2248.0530	**1124.5301**
Q	1293.6474	647.3273	2147.0053	**1074.0063**
D	1408.6743	704.8408	2018.9467	**1009.9770**
A	**1479.7114**	740.3594	1903.9198	**952.4635**
I	1592.7955	796.9014	1832.8827	**916.9450**
Y	1755.8588	878.4331	1719.7986	**860.4030**
S	1842.8909	921.9491	1556.7353	**778.8713**
N	1956.9338	978.9705	1469.7033	**735.3553**
N	2070.9767	1035.9920	1355.6603	**678.3338**
F	2218.0451	1109.5262	**1241.6174**	**621.3123**
G	2275.0666	1138.0369	**1094.5490**	**547.7781**
R	2431.1677	1216.0875	1037.5275	519.2674
Y	2594.2310	1297.6192	**881.4264**	441.2169
H	2731.2899	1366.1486	**718.3631**	359.6852
E	2860.3325	1430.6699	**581.3042**	291.1557
A	2931.3696	1466.1885	**452.2616**	226.6344
H	3068.4286	1534.7179	**381.2245**	191.1159
P	3165.4813	1583.2443	**244.1656**	122.5864
K	3293.5763	1647.2918	**147.1128**	74.0600

Peptide sequence 17: STFGSPFN[Dea]LLTQDAIYSNNFGRYHEAHPK



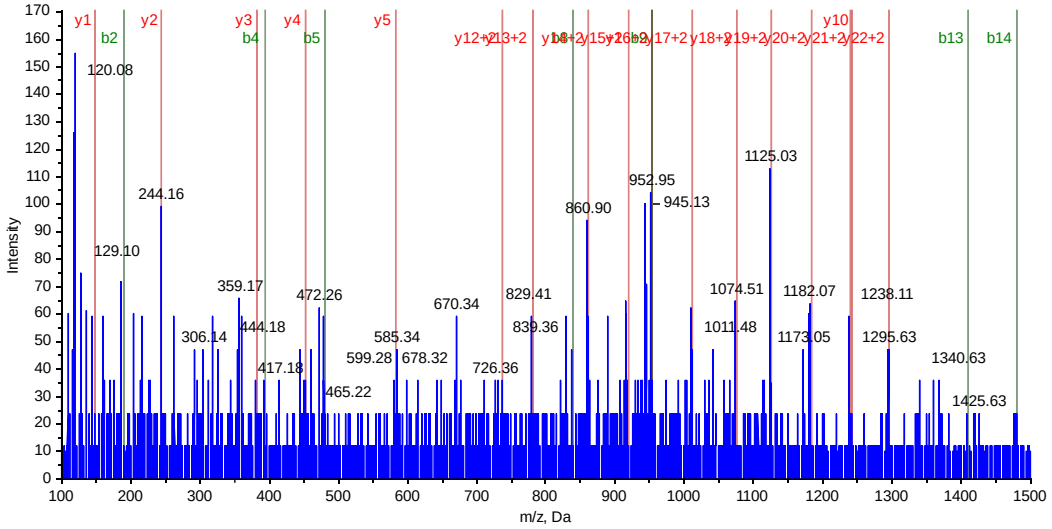
Residue	b	b+2	y	y+2
S	88.0393	44.5233	3312.5709	1656.7891
T	**189.0870**	95.0471	3225.5388	1613.2731
F	336.1554	168.5813	3124.4912	1562.7492
G	393.1769	197.0921	2977.4227	1489.2150
S	**480.2089**	240.6081	2920.4013	1460.7043
P	**577.2617**	289.1345	2833.3693	1417.1883
F	724.3301	362.6687	2736.3165	**1368.6619**
N[Dea]	839.3570	420.1821	2589.2481	1295.1277
L	**952.4411**	476.7242	2474.2211	**1237.6142**
L	**1065.5251**	533.2662	2361.1371	**1181.0722**
T	1166.5728	583.7900	2248.0530	**1124.5301**
Q	**1294.6314**	647.8193	2147.0053	**1074.0063**
D	1409.6583	705.3328	2018.9467	**1009.9770**
A	1480.6955	740.8514	1903.9198	**952.4635**
I	1593.7795	797.3934	1832.8827	**916.9450**
Y	1756.8428	878.9251	1719.7986	**860.4030**
S	1843.8749	922.4411	1556.7353	**778.8713**
N	1957.9178	979.4625	1469.7033	**735.3553**
N	2071.9607	1036.4840	1355.6603	678.3338
F	2219.0291	1110.0182	**1241.6174**	621.3123
G	2276.0506	1138.5289	1094.5490	547.7781
R	2432.1517	1216.5795	1037.5275	519.2674
Y	2595.2150	1298.1112	**881.4264**	441.2169
H	2732.2740	1366.6406	**718.3631**	359.6852
E	2861.3165	1431.1619	581.3042	291.1557
A	2932.3537	1466.6805	**452.2616**	226.6344
H	3069.4126	1535.2099	**381.2245**	191.1159
P	3166.4653	1583.7363	**244.1656**	122.5864
K	3294.5603	1647.7838	**147.1128**	74.0600

Peptide sequence 18: STFGSPFNLLTQ[Dea]DAIYSNNFGRYHEAHPK



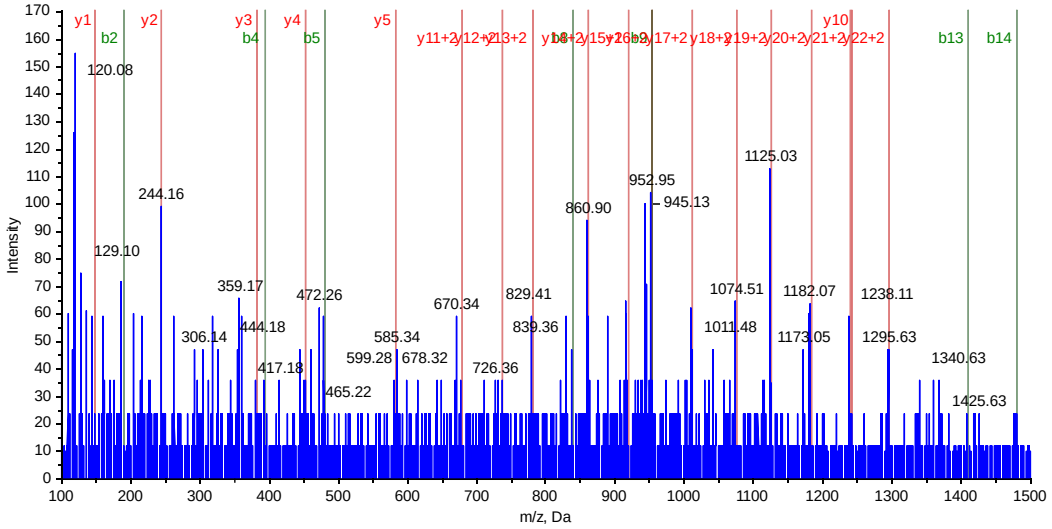
Residue	b	b+2	y	y+2
S	88.0393	44.5233	3312.5709	1656.7891
T	**189.0870**	95.0471	3225.5388	1613.2731
F	336.1554	168.5813	3124.4912	1562.7492
G	393.1769	197.0921	2977.4227	1489.2150
S	**480.2089**	240.6081	2920.4013	1460.7043
P	577.2617	289.1345	2833.3693	1417.1883
F	**724.3301**	362.6687	2736.3165	1368.6619
N	**838.3730**	419.6901	2589.2481	**1295.1277**
L	951.4571	476.2322	2475.2051	**1238.1062**
L	1064.5411	532.7742	2362.1211	**1181.5642**
T	1165.5888	583.2980	2249.0370	**1125.0221**
Q[Dea]	1294.6314	647.8193	2147.9893	**1074.4983**
D	**1409.6583**	705.3328	2018.9467	**1009.9770**
A	1480.6955	740.8514	1903.9198	**952.4635**
I	1593.7795	797.3934	1832.8827	**916.9450**
Y	1756.8428	878.9251	1719.7986	**860.4030**
S	1843.8749	922.4411	1556.7353	**778.8713**
N	1957.9178	979.4625	1469.7033	735.3553
N	2071.9607	1036.4840	1355.6603	678.3338
F	2219.0291	1110.0182	1241.6174	621.3123
G	2276.0506	1138.5289	1094.5490	547.7781
R	2432.1517	1216.5795	1037.5275	519.2674
Y	2595.2150	1298.1112	881.4264	441.2169
H	2732.2740	1366.6406	**718.3631**	359.6852
E	2861.3165	1431.1619	**581.3042**	291.1557
A	2932.3537	1466.6805	**452.2616**	226.6344
H	3069.4126	1535.2099	**381.2245**	191.1159
P	3166.4653	1583.7363	**244.1656**	122.5864
K	3294.5603	1647.7838	**147.1128**	74.0600

Peptide sequence 19: STFGSPFNLLTQDAIYSNN[Dea]FGRYHEAHPK



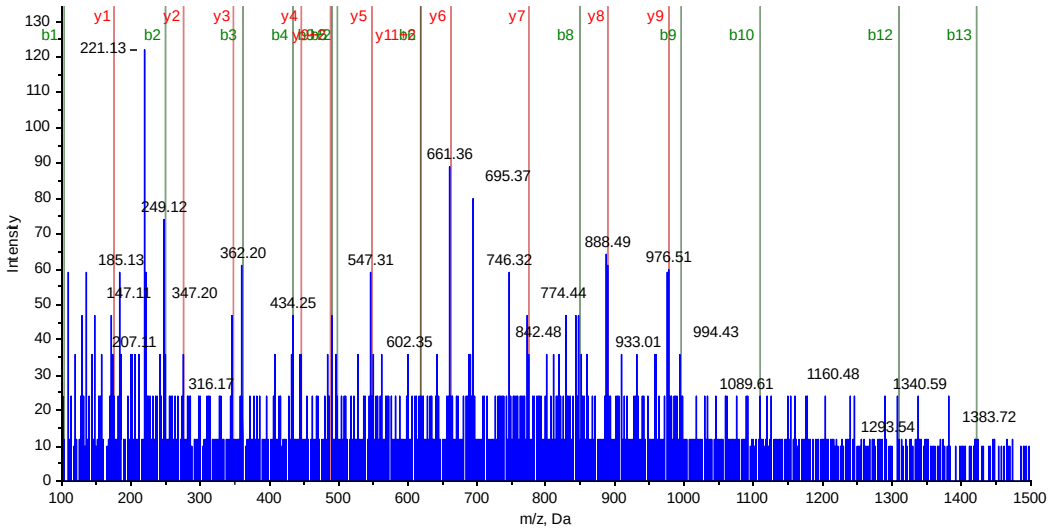
Residue	b	b+2	y	y+2
S	88.0393	44.5233	3312.5709	1656.7891
T	**189.0870**	95.0471	3225.5388	1613.2731
F	336.1554	168.5813	3124.4912	1562.7492
G	**393.1769**	197.0921	2977.4227	1489.2150
S	**480.2089**	240.6081	2920.4013	1460.7043
P	577.2617	289.1345	2833.3693	1417.1883
F	724.3301	362.6687	2736.3165	1368.6619
N	**838.3730**	419.6901	2589.2481	**1295.1277**
L	**951.4571**	476.2322	2475.2051	**1238.1062**
L	1064.5411	532.7742	2362.1211	**1181.5642**
T	1165.5888	583.2980	2249.0370	**1125.0221**
Q	1293.6474	647.3273	2147.9893	**1074.4983**
D	**1408.6743**	704.8408	2019.9308	**1010.4690**
A	**1479.7114**	740.3594	1904.9038	**952.9555**
I	1592.7955	796.9014	1833.8667	**917.4370**
Y	1755.8588	878.4331	1720.7826	**860.8950**
S	1842.8909	921.9491	1557.7193	**779.3633**
N	1956.9338	978.9705	1470.6873	**735.8473**
N[Dea]	2071.9607	1036.4840	1356.6444	678.8258
F	2219.0291	1110.0182	**1241.6174**	621.3123
G	2276.0506	1138.5289	1094.5490	547.7781
R	2432.1517	1216.5795	1037.5275	519.2674
Y	2595.2150	1298.1112	881.4264	441.2169
H	2732.2740	1366.6406	718.3631	359.6852
E	2861.3165	1431.1619	**581.3042**	291.1557
A	2932.3537	1466.6805	**452.2616**	226.6344
H	3069.4126	1535.2099	**381.2245**	191.1159
P	3166.4653	1583.7363	**244.1656**	122.5864
K	3294.5603	1647.7838	**147.1128**	74.0600

Peptide sequence 20: STFGSPFNLLTQDAIYSN[Dea]NFGRYHEAHPK



Residue	b	b+2	y	y+2
S	88.0393	44.5233	3312.5709	1656.7891
T	**189.0870**	95.0471	3225.5388	1613.2731
F	336.1554	168.5813	3124.4912	1562.7492
G	**393.1769**	197.0921	2977.4227	1489.2150
S	**480.2089**	240.6081	2920.4013	1460.7043
P	577.2617	289.1345	2833.3693	1417.1883
F	724.3301	362.6687	2736.3165	1368.6619
N	**838.3730**	419.6901	2589.2481	**1295.1277**
L	**951.4571**	476.2322	2475.2051	**1238.1062**
L	1064.5411	532.7742	2362.1211	**1181.5642**
T	1165.5888	583.2980	2249.0370	**1125.0221**
Q	1293.6474	647.3273	2147.9893	**1074.4983**
D	**1408.6743**	704.8408	2019.9308	**1010.4690**
A	**1479.7114**	740.3594	1904.9038	**952.9555**
I	1592.7955	796.9014	1833.8667	**917.4370**
Y	1755.8588	878.4331	1720.7826	**860.8950**
S	1842.8909	921.9491	1557.7193	**779.3633**
N[Dea]	1957.9178	979.4625	1470.6873	**735.8473**
N	2071.9607	1036.4840	1355.6603	**678.3338**
F	2219.0291	1110.0182	**1241.6174**	621.3123
G	2276.0506	1138.5289	1094.5490	547.7781
R	2432.1517	1216.5795	1037.5275	519.2674
Y	2595.2150	1298.1112	881.4264	441.2169
H	2732.2740	1366.6406	718.3631	359.6852
E	2861.3165	1431.1619	**581.3042**	291.1557
A	2932.3537	1466.6805	**452.2616**	226.6344
H	3069.4126	1535.2099	**381.2245**	191.1159
P	3166.4653	1583.7363	**244.1656**	122.5864
K	3294.5603	1647.7838	**147.1128**	74.0600

Peptide sequence 21: TFLAGQDNM[Oxi]LSNINTVATR



Residue	b	b+2	y	y+2
T	**102.0550**	51.5311	2082.0284	1041.5179
F	**249.1234**	125.0653	1980.9808	990.9940
L	**362.2074**	181.6074	1833.9123	917.4598
A	**433.2445**	217.1259	1720.8283	860.9178
G	**490.2660**	245.6366	1649.7912	825.3992
Q	**618.3246**	309.6659	1592.7697	796.8885
D	733.3515	367.1794	1464.7111	732.8592
N	**847.3945**	424.2009	1349.6842	675.3457
M[Oxi]	**994.4299**	**497.7186**	1235.6412	**618.3243**
L	**1107.5139**	554.2606	1088.6058	544.8066
S	1194.5459	597.7766	**975.5218**	**488.2645**
N	**1308.5889**	654.7981	**888.4898**	444.7485
I	**1421.6729**	711.3401	**774.4468**	387.7271
N	1535.7159	768.3616	**661.3628**	331.1850
T	1636.7635	818.8854	**547.3198**	274.1636
V	1735.8320	868.4196	**446.2722**	223.6397
A	1806.8691	903.9382	**347.2037**	174.1055
T	1907.9168	954.4620	**276.1666**	138.5870
R	2064.0179	1032.5126	**175.1190**	88.0631

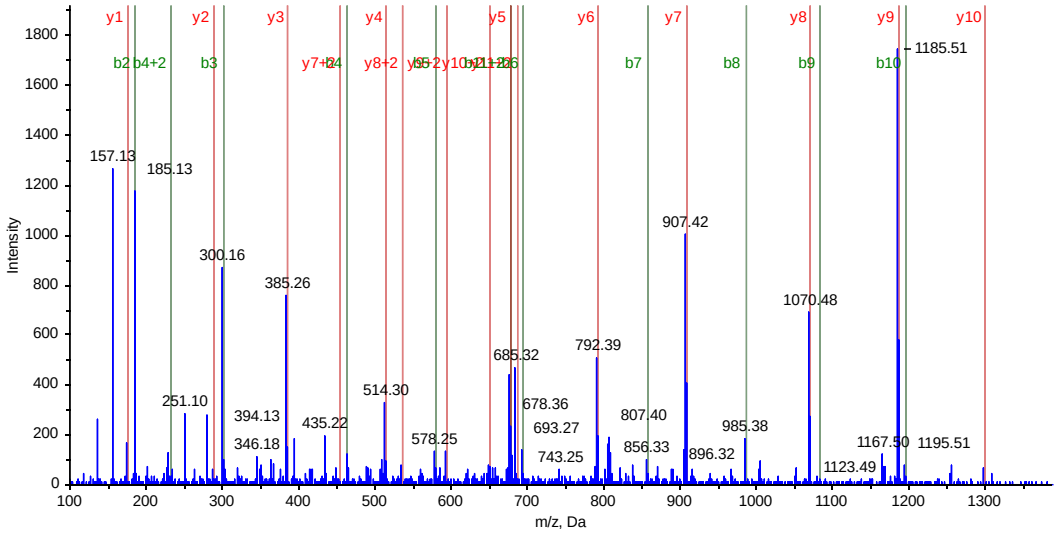
Sample Pool 4

Protein: B.rapa.Ro18.Candidate-1, 11 peptides (95%)

Protein sequence coverage

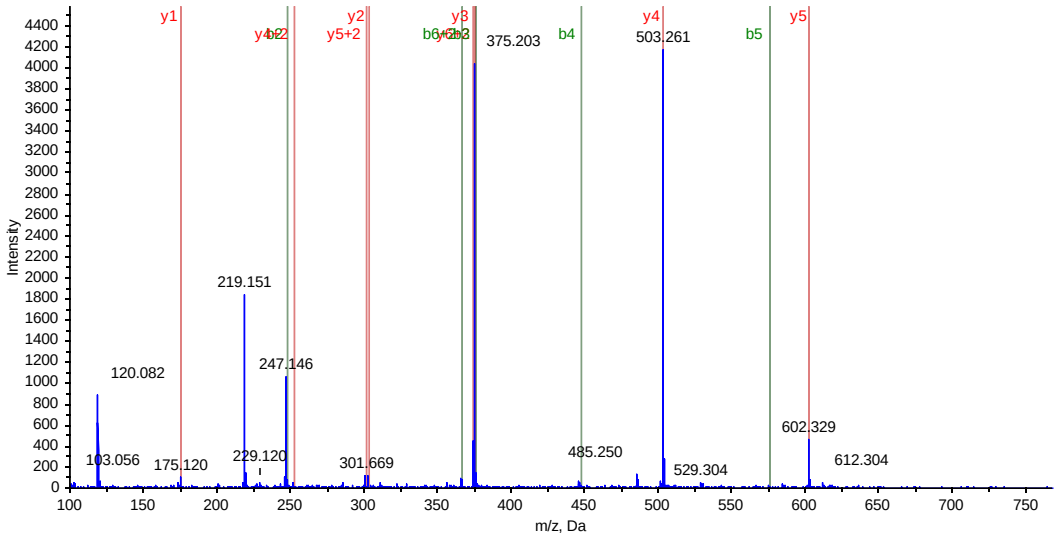
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IIEKPMHIGFLTMEPKTLFVPQYLDSNLLIFIRQGEATLGVICKDEFGEKRLKGGDIYWIPAGSAFYLL
NTGRGQRLHVICSIDPSQSLGFETFQPFYIGGGPSSVLAGFDPDTITSALNVSRPEVQQLMTSQVRGPI
VHITEHAPTMWTDFLGLRGEEKHKHLKKLLELKQGTSQEQEDNPWWSWKNIVSSILDVTGEKNRGSGSS
KCEDSYNIYDR**KNDFENDYGWSKALDYDDYEPLR**YSGVGVYLVNLTAGSMMAPHMNPTATEYGIVLSGS
GEIQVVLPNGTSAMNMR**VSPGDVFWIPR**YFAFCQIASR**IAPFEFVGFTTSAYKNRPQFLVGSNSLLR**SL
NLTSLAMAFGVDEGTMKR**FVEAQR**EAVILPTASAAPPHEGEPERFGSDHIFT

Peptide sequence 1: ALDYDDYEPLR



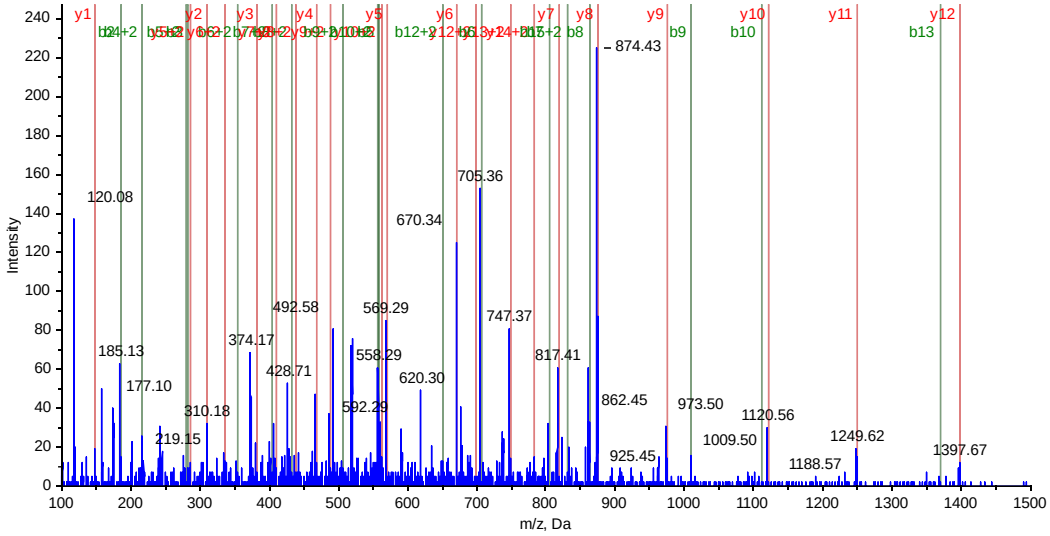
Residue	b	b+2	y	y+2
A	72.0444	36.5258	1369.6270	**685.3172**
L	185.1285	93.0679	**1298.5899**	**649.7986**
D	300.1554	150.5813	**1185.5059**	**593.2566**
Y	463.2187	**232.1130**	**1070.4789**	**535.7431**
D	578.2457	289.6265	**907.4156**	**454.2114**
D	693.2726	347.1399	**792.3886**	396.6980
Y	856.3359	428.6716	**677.3617**	339.1845
E	985.3785	493.1929	**514.2984**	257.6528
P	1082.4313	541.7193	**385.2558**	193.1315
L	1195.5154	598.2613	**288.2030**	144.6051
R	1351.6165	**676.3119**	**175.1190**	88.0631

Peptide sequence 2: FVEAQR



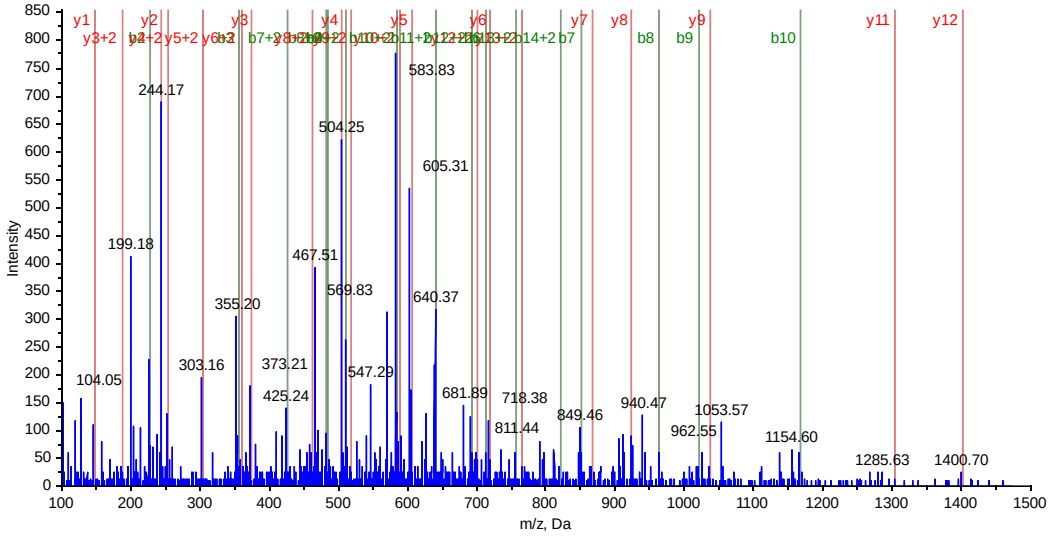
Residue	b	b+2	y	y+2
F	148.0757	74.5415	749.3941	**375.2007**
V	**247.1441**	124.0757	**602.3257**	**301.6665**
E	**376.1867**	188.5970	**503.2572**	**252.1323**
A	**447.2238**	224.1155	**374.2146**	187.6110
Q	**575.2824**	288.1448	**303.1775**	152.0924
R	731.3835	**366.1954**	**175.1190**	88.0631

Peptide sequence 3: IAPFEFVGFTTSAYK



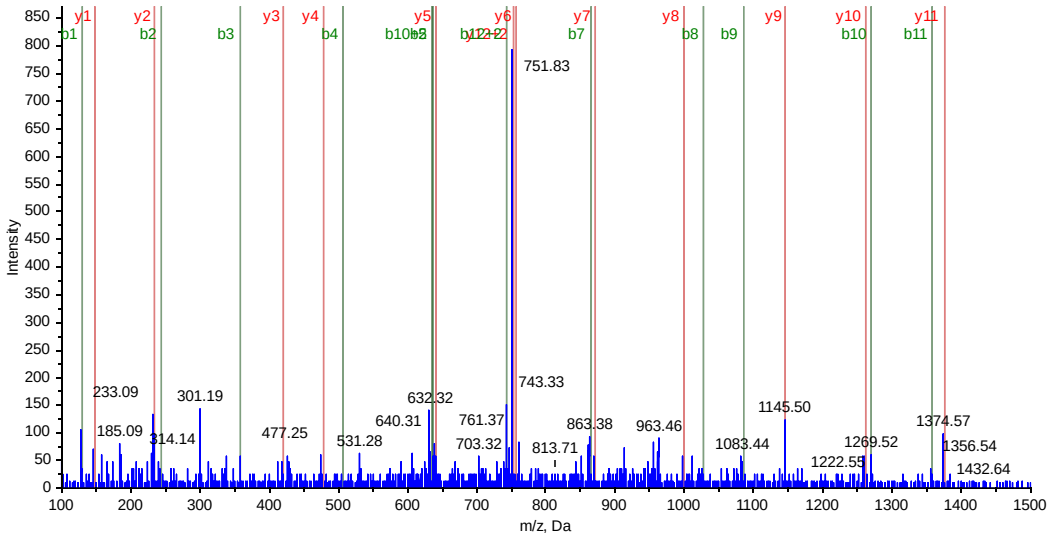
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1677.8523	839.4298
A	**185.1285**	93.0679	1564.7682	**782.8877**
P	**282.1812**	141.5942	1493.7311	**747.3692**
F	429.2496	**215.1285**	**1396.6783**	**698.8428**
E	**558.2922**	**279.6498**	**1249.6099**	625.3086
F	**705.3606**	**353.1840**	**1120.5673**	**560.7873**
V	**804.4291**	**402.7182**	**973.4989**	**487.2531**
G	**861.4505**	**431.2289**	**874.4305**	**437.7189**
F	**1008.5189**	**504.7631**	**817.4090**	**409.2082**
T	**1109.5666**	**555.2869**	**670.3406**	**335.6740**
T	1210.6143	605.8108	**569.2930**	**285.1501**
S	1297.6463	**649.3268**	**468.2453**	234.6263
A	**1368.6834**	684.8454	**381.2132**	191.1103
Y	1531.7468	766.3770	**310.1761**	155.5917
K	1659.8417	**830.4245**	**147.1128**	74.0600

Peptide sequence 4: IIEKPMHIGFLTMEPK



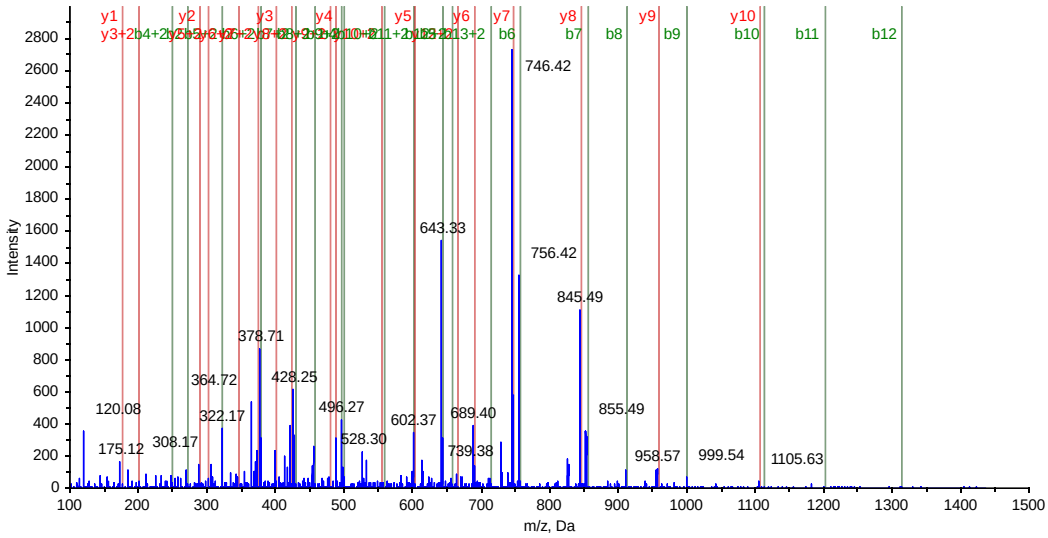
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1884.0122	942.5097
I	**227.1754**	114.0913	1770.9281	885.9677
E	**356.2180**	178.6126	1657.8440	829.4257
K	**484.3130**	242.6601	1528.8015	**764.9044**
P	581.3657	291.1865	**1400.7065**	**700.8569**
M	**712.4062**	356.7067	**1303.6537**	652.3305
H	**849.4651**	**425.2362**	1172.6132	**586.8103**
I	**962.5492**	**481.7782**	**1035.5543**	**518.2808**
G	**1019.5706**	**510.2890**	**922.4703**	**461.7388**
F	**1166.6391**	**583.8232**	**865.4488**	433.2280
L	1279.7231	**640.3652**	**718.3804**	**359.6938**
T	1380.7708	**690.8890**	**605.2963**	**303.1518**
M	1511.8113	**756.4093**	**504.2486**	**252.6280**
E	1640.8539	**820.9306**	**373.2082**	**187.1077**
P	1737.9066	869.4570	**244.1656**	122.5864
K	1866.0016	933.5044	**147.1128**	74.0600

Peptide sequence 5: KNDFENDYGWSK



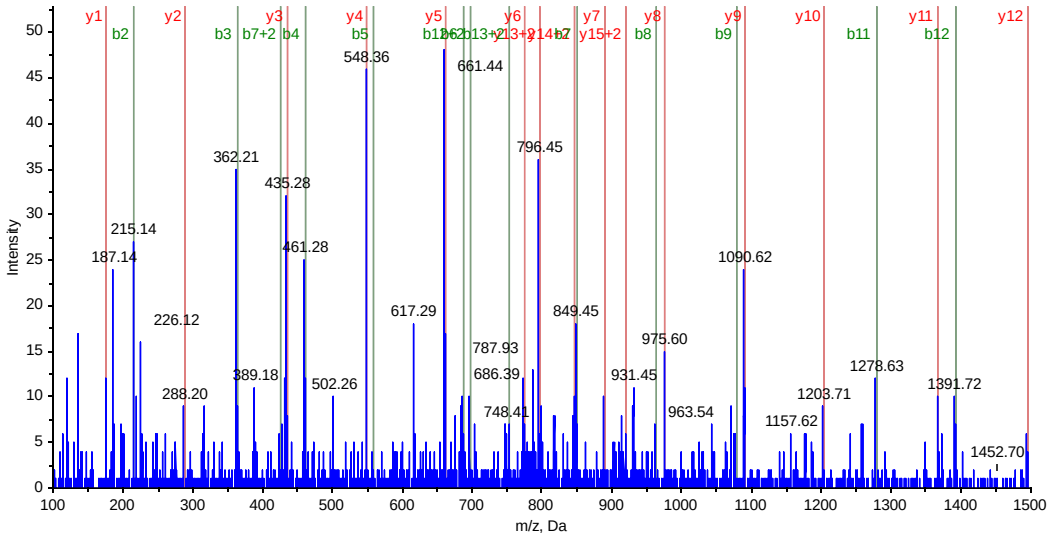
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	1502.6546	**751.8310**
N	**243.1452**	122.0762	**1374.5597**	687.7835
D	**358.1721**	179.5897	**1260.5168**	630.7620
F	**505.2405**	253.1239	**1145.4898**	573.2485
E	**634.2831**	317.6452	**998.4214**	499.7143
N	748.3260	374.6667	**869.3788**	435.1930
D	**863.3530**	432.1801	**755.3359**	378.1716
Y	**1026.4163**	513.7118	**640.3089**	320.6581
G	**1083.4378**	542.2225	**477.2456**	239.1264
W	**1269.5171**	**635.2622**	**420.2241**	210.6157
S	**1356.5491**	678.7782	**234.1448**	117.5761
K	1484.6441	**742.8257**	**147.1128**	74.0600

Peptide sequence 6: NRPQFLVGSNSLLR



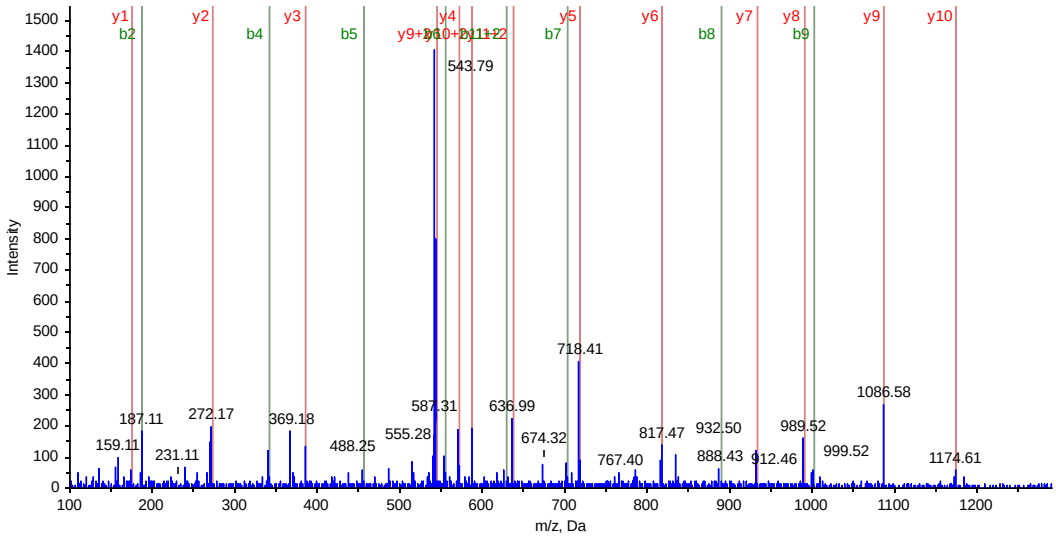
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1600.8918	800.9495
R	**271.1513**	136.0793	1486.8489	743.9281
P	368.2041	184.6057	1330.7478	**665.8775**
Q	**496.2627**	**248.6350**	1233.6950	617.3511
F	**643.3311**	**322.1692**	**1105.6364**	**553.3218**
L	**756.4151**	**378.7112**	**958.5680**	**479.7876**
V	**855.4835**	**428.2454**	**845.4839**	**423.2456**
G	**912.5050**	**456.7561**	**746.4155**	**373.7114**
S	**999.5370**	**500.2722**	**689.3941**	**345.2007**
N	**1113.5800**	**557.2936**	**602.3620**	**301.6847**
S	**1200.6120**	**600.8096**	**488.3191**	244.6632
L	**1313.6961**	**657.3517**	**401.2871**	**201.1472**
L	1426.7801	**713.8937**	**288.2030**	144.6051
R	1582.8812	791.9443	**175.1190**	88.0631

Peptide sequence 7: TLFVPQYLDSNLLIFIR



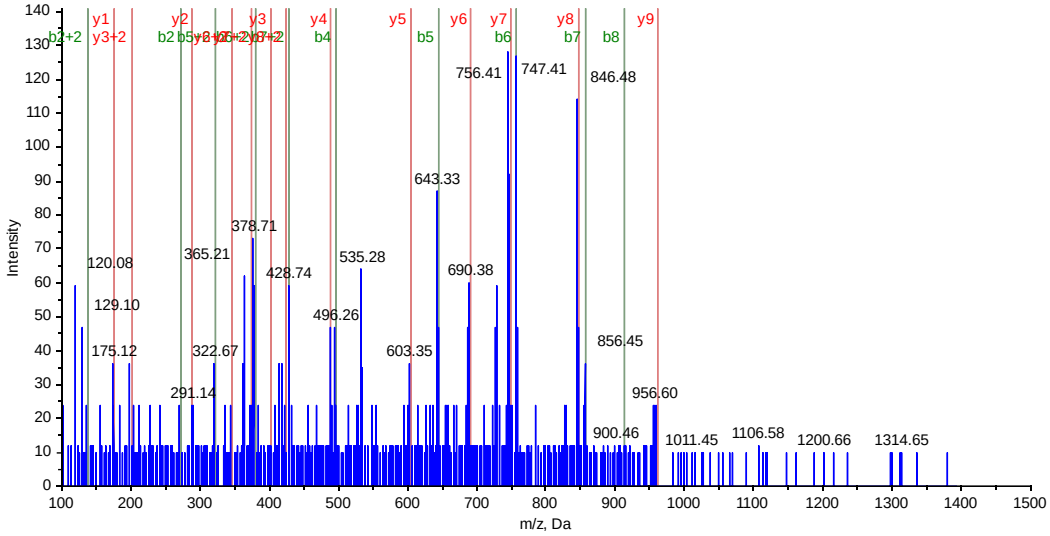
Residue	b	b+2	y	y+2
T	102.0550	51.5311	2052.1528	1026.5801
L	**215.1390**	108.0731	1951.1051	976.0562
F	**362.2074**	181.6074	1838.0211	**919.5142**
V	**461.2758**	231.1416	1690.9527	**845.9800**
P	**558.3286**	279.6679	1591.8843	**796.4458**
Q	**686.3872**	343.6972	**1494.8315**	747.9194
Y	**849.4505**	**425.2289**	**1366.7729**	683.8901
L	**962.5346**	481.7709	**1203.7096**	602.3584
D	**1077.5615**	539.2844	**1090.6255**	545.8164
S	1164.5936	582.8004	**975.5986**	488.3029
N	**1278.6365**	639.8219	**888.5665**	444.7869
L	**1391.7205**	**696.3639**	**774.5236**	387.7654
L	1504.8046	**752.9059**	**661.4396**	331.2234
I	1617.8887	809.4480	**548.3555**	274.6814
F	1764.9571	882.9822	**435.2714**	218.1394
I	1878.0411	939.5242	**288.2030**	144.6051
R	2034.1423	1017.5748	**175.1190**	88.0631

Peptide sequence 8: VSPGDVFWIPR



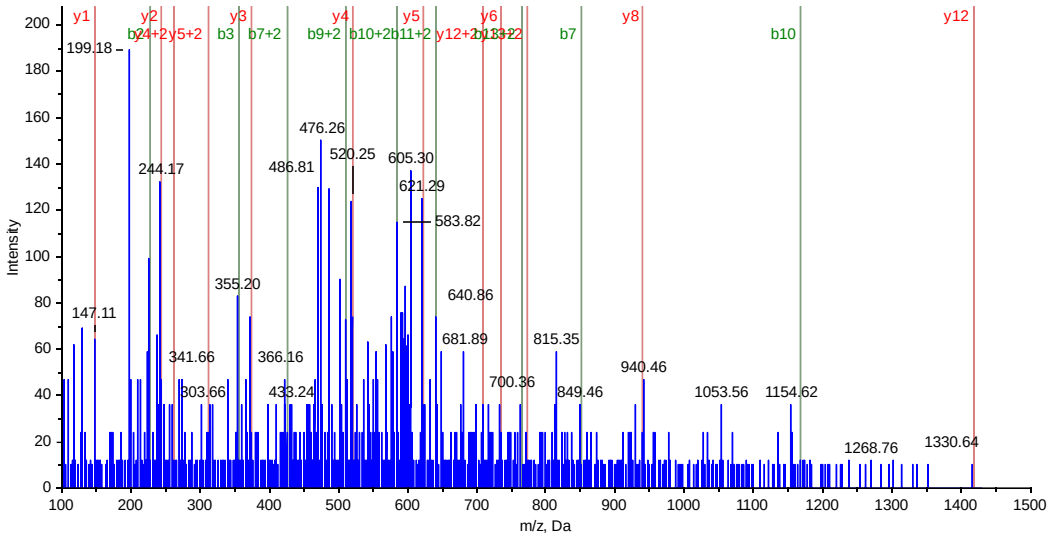
Residue	b	b+2	y	y+2
V	100.0757	50.5415	1272.6735	**636.8404**
S	**187.1077**	94.0575	**1173.6051**	**587.3062**
P	284.1605	142.5839	**1086.5731**	**543.7902**
G	**341.1819**	171.0946	**989.5203**	495.2638
D	**456.2089**	228.6081	**932.4989**	466.7531
V	**555.2773**	278.1423	**817.4719**	409.2396
F	**702.3457**	351.6765	**718.4035**	359.7054
W	**888.4250**	444.7162	**571.3351**	286.1712
I	**1001.5091**	501.2582	**385.2558**	193.1315
P	1098.5619	549.7846	**272.1717**	136.5895
R	1254.6630	**627.8351**	**175.1190**	88.0631

Peptide sequence 9: NRPQFLVGSN[Dea]SLLR



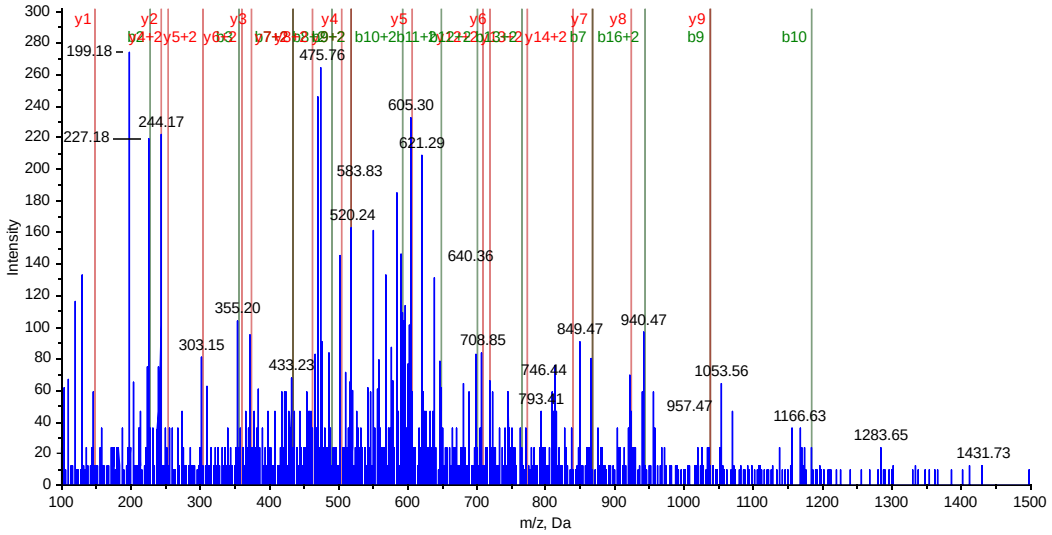
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1601.8758	801.4415
R	**271.1513**	**136.0793**	1487.8329	744.4201
P	368.2041	184.6057	1331.7318	666.3695
Q	**496.2627**	248.6350	1234.6790	617.8431
F	**643.3311**	**322.1692**	1106.6204	553.8139
L	**756.4151**	**378.7112**	**959.5520**	480.2796
V	**855.4835**	**428.2454**	**846.4680**	**423.7376**
G	**912.5050**	456.7561	**747.3995**	**374.2034**
S	999.5370	500.2722	**690.3781**	**345.6927**
N[Dea]	1114.5640	557.7856	**603.3461**	302.1767
S	1201.5960	601.3016	**488.3191**	244.6632
L	1314.6801	657.8437	**401.2871**	**201.1472**
L	1427.7641	714.3857	**288.2030**	144.6051
R	1583.8653	792.4363	**175.1190**	88.0631

Peptide sequence 10: IIEKPMHIGFLTM[Oxi]EPK



Residue	b	b+2	y	y+2
I	114.0913	57.5493	1900.0071	950.5072
I	**227.1754**	114.0913	1786.9230	893.9652
E	**356.2180**	178.6126	1673.8390	837.4231
K	484.3130	242.6601	1544.7964	**772.9018**
P	581.3657	291.1865	**1416.7014**	**708.8543**
M	712.4062	356.7067	1319.6486	660.3280
H	**849.4651**	**425.2362**	1188.6082	594.8077
I	962.5492	481.7782	1051.5492	526.2783
G	1019.5706	**510.2890**	**938.4652**	469.7362
F	**1166.6391**	**583.8232**	881.4437	441.2255
L	1279.7231	**640.3652**	**734.3753**	367.6913
T	1380.7708	690.8890	**621.2912**	**311.1493**
M[Oxi]	1527.8062	**764.4067**	**520.2436**	**260.6254**
E	1656.8488	828.9280	**373.2082**	187.1077
P	1753.9016	877.4544	**244.1656**	122.5864
K	1881.9965	941.5019	**147.1128**	74.0600

Peptide sequence 11: IIEKPM[Oxi]HIGFLTMEPK



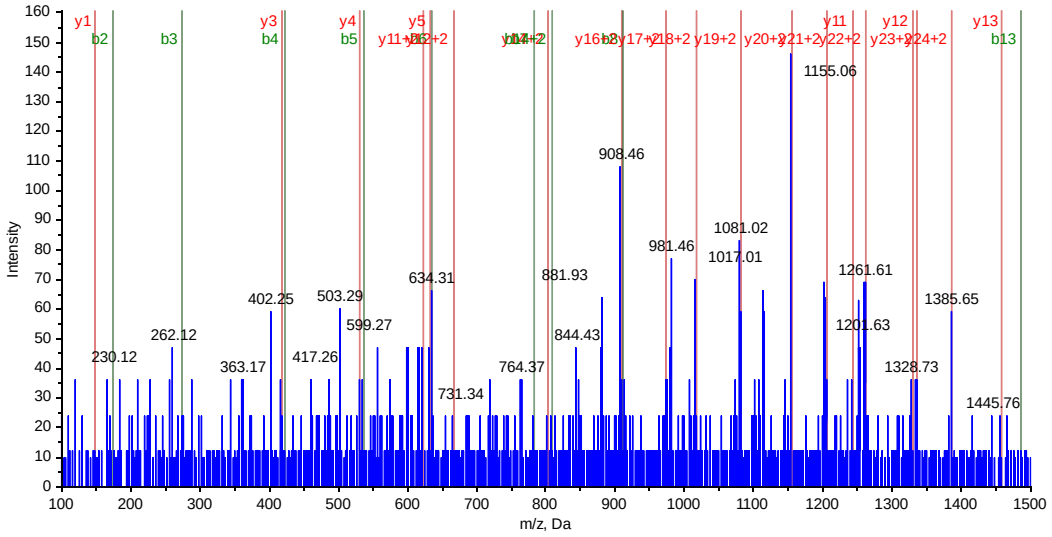
Residue	b	b+2	y	y+2
I	114.0913	57.5493	1900.0071	950.5072
I	**227.1754**	114.0913	1786.9230	893.9652
E	**356.2180**	178.6126	1673.8390	**837.4231**
K	484.3130	242.6601	1544.7964	**772.9018**
P	581.3657	291.1865	1416.7014	**708.8543**
M[Oxi]	728.4011	364.7042	1319.6486	660.3280
H	**865.4600**	**433.2337**	1172.6132	586.8103
I	978.5441	**489.7757**	**1035.5543**	**518.2808**
G	**1035.5656**	**518.2864**	**922.4703**	**461.7388**
F	**1182.6340**	**591.8206**	**865.4488**	**433.2280**
L	1295.7180	**648.3627**	**718.3804**	**359.6938**
T	1396.7657	**698.8865**	**605.2963**	**303.1518**
M	1527.8062	**764.4067**	**504.2486**	**252.6280**
E	1656.8488	828.9280	**373.2082**	187.1077
P	1753.9016	877.4544	**244.1656**	122.5864
K	1881.9965	**941.5019**	**147.1128**	74.0600

Protein: B.rapa.Ro18.Candidate-2, 10 peptides (95%)

Protein sequence coverage

MIRFTVLSFFVVFVLLFACNESSAKTAKYDKSDESVENDDLAAVPSCCGFSSPLLIKKDQWKPIFANKF
GQISTVQIGDGCGGMGPYKIHSITLEPNALMLPLLLHSDMVFFVDSGSGILNWVEAQATSTEIRLGDVY
RLRPGTVFYLQSKPVDIFLGTKLKIYAIFSNSQECLHDPCFGAYSSVTDLLFGFDETILK**SAFGVPEEI**
IGLMRNRTQPPLIVHDMLTTPGEANTDTDTNTWPLQTRLLKLFSGDASADSVENKKVKKEKKEKKEKKK
KPK**KATTFNVFESEPDFQSPNGQTITINRK**DLKVLQGSMVGVSMVNLTQGSMMGPHWNPWACEISVVVR
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K**NSALWSLDR**EVLAASFNVSSFMIAGLLEAQKEAAVLGCPACAEGELEKLKEDEEKKESPPQQPPQPFQ
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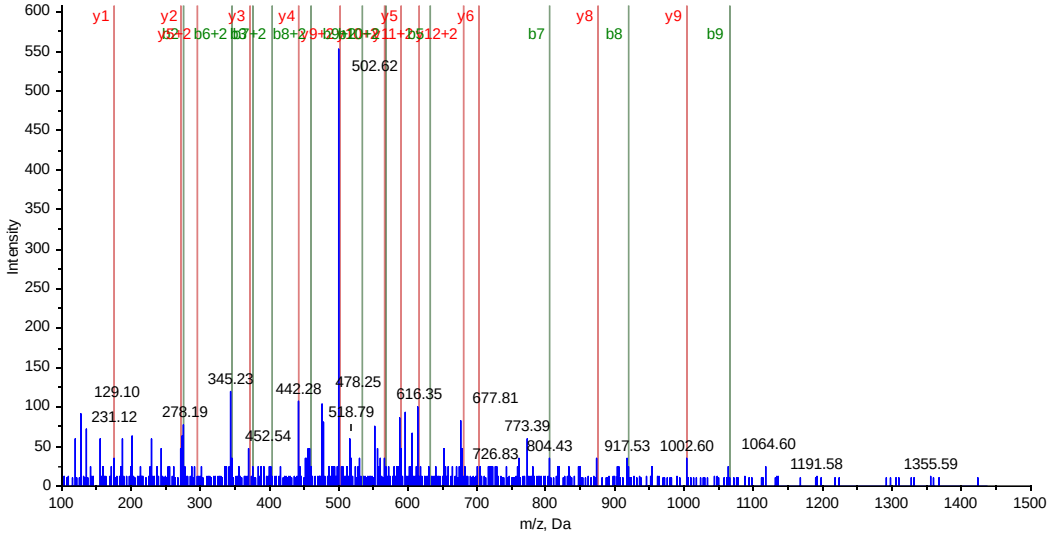
Peptide sequence 1: ATTFNVFESEPDFQSPNGQTITINRK



Residue	b	b+2	y	y+2
A	72.0444	36.5258	2941.4326	1471.2200
T	**173.0921**	87.0497	2870.3955	1435.7014
T	**274.1397**	137.5735	2769.3478	**1385.1776**
F	**421.2082**	211.1077	2668.3002	**1334.6537**
N	**535.2511**	268.1292	2521.2318	**1261.1195**
V	**634.3195**	317.6634	2407.1888	**1204.0981**
F	**781.3879**	391.1976	2308.1204	**1154.5638**
E	**910.4305**	455.7189	2161.0520	**1081.0296**
S	997.4625	499.2349	2032.0094	**1016.5083**
E	1126.5051	563.7562	1944.9774	**972.9923**
P	1223.5579	612.2826	1815.9348	**908.4710**
D	1338.5848	669.7961	1718.8820	859.9446
F	**1485.6533**	743.3303	1603.8551	**802.4312**
Q	1613.7118	**807.3596**	**1456.7867**	728.8970
S	1700.7439	850.8756	**1328.7281**	**664.8677**
P	1797.7966	899.4019	**1241.6961**	**621.3517**
N	1911.8395	956.4234	1144.6433	572.8253
G	1968.8610	984.9341	1030.6004	515.8038

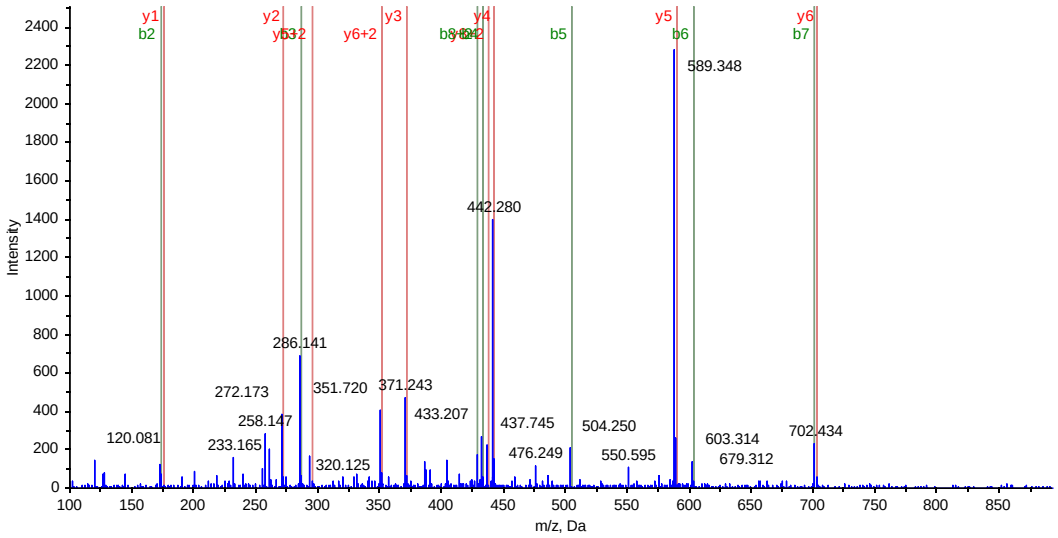
Q	2096.9196	1048.9634	973.5789	487.2931
T	2197.9673	1099.4873	845.5203	423.2638
I	2311.0513	1156.0293	744.4726	372.7400
T	2412.0990	1206.5531	**631.3886**	316.1979
I	2525.1831	1263.0952	**530.3409**	265.6741
N	2639.2260	1320.1166	**417.2568**	209.1321
R	2795.3271	1398.1672	303.2139	152.1106
K	2923.4221	1462.2147	**147.1128**	74.0600

Peptide sequence 2: FKVEKGDIFAVPR



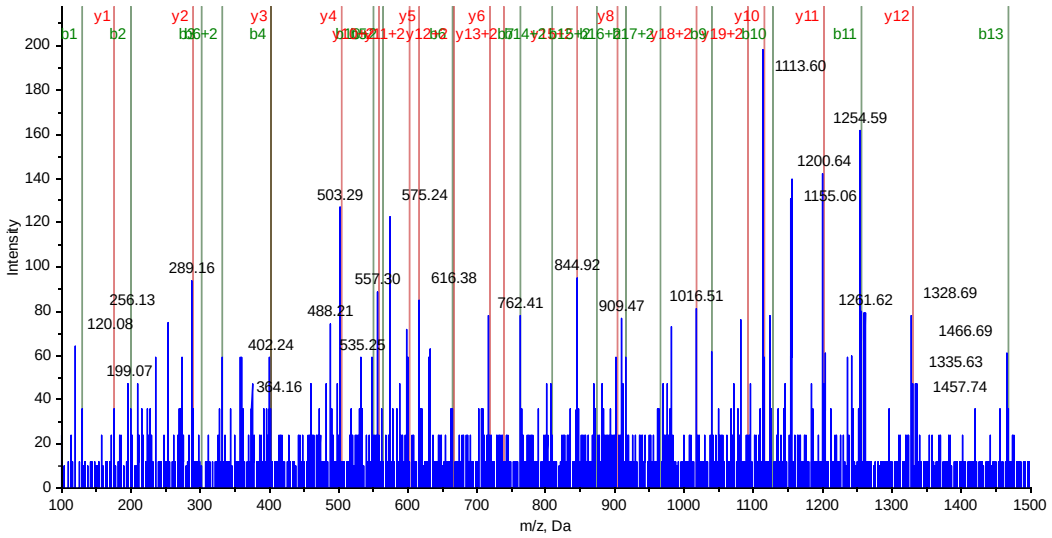
Residue	b	b+2	y	y+2
F	148.0757	74.5415	1505.8475	753.4274
K	**276.1707**	138.5890	1358.7791	**679.8932**
V	375.2391	188.1232	1230.6841	**615.8457**
E	504.2817	252.6445	1131.6157	**566.3115**
K	**632.3766**	316.6919	**1002.5731**	**501.7902**
G	689.3981	**345.2027**	**874.4781**	437.7427
D	**804.4250**	**402.7162**	817.4567	409.2320
I	**917.5091**	**459.2582**	**702.4297**	351.7185
F	**1064.5775**	**532.7924**	**589.3457**	**295.1765**
A	1135.6146	**568.3109**	**442.2772**	221.6423
V	1234.6830	617.8452	**371.2401**	186.1237
P	1331.7358	666.3715	**272.1717**	136.5895
R	1487.8369	744.4221	**175.1190**	88.0631

Peptide sequence 3: GDIFAVPR



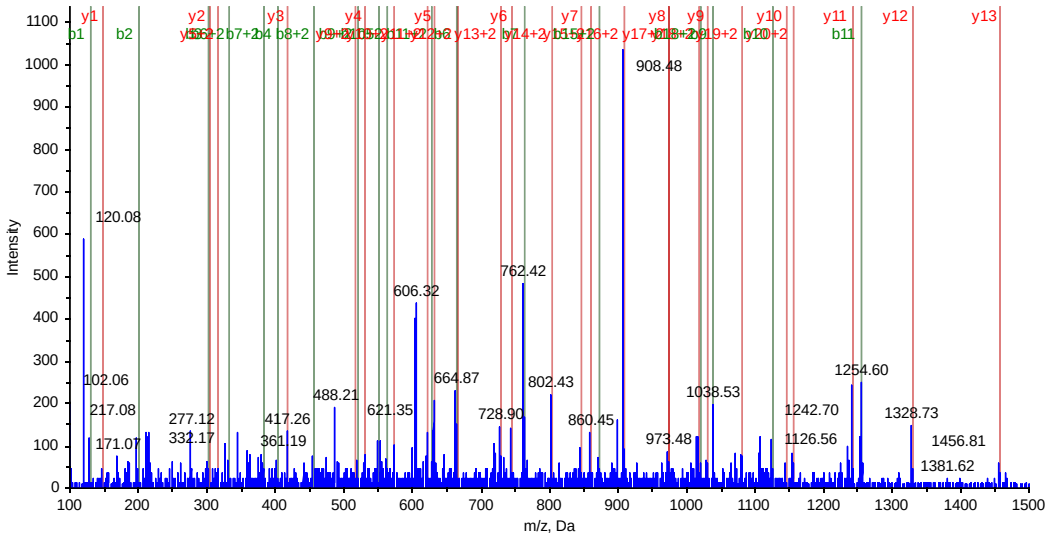
Residue	b	b+2	y	y+2
G	58.0287	29.5180	874.4781	**437.7427**
D	**173.0557**	87.0315	817.4567	409.2320
I	**286.1397**	143.5735	**702.4297**	**351.7185**
F	**433.2082**	217.1077	**589.3457**	**295.1765**
A	**504.2453**	252.6263	**442.2772**	221.6423
V	**603.3137**	302.1605	**371.2401**	186.1237
P	**700.3665**	350.6869	**272.1717**	136.5895
R	856.4676	**428.7374**	**175.1190**	88.0631

Peptide sequence 4: KATTFNVFESEPDFQSPNGQTITINR



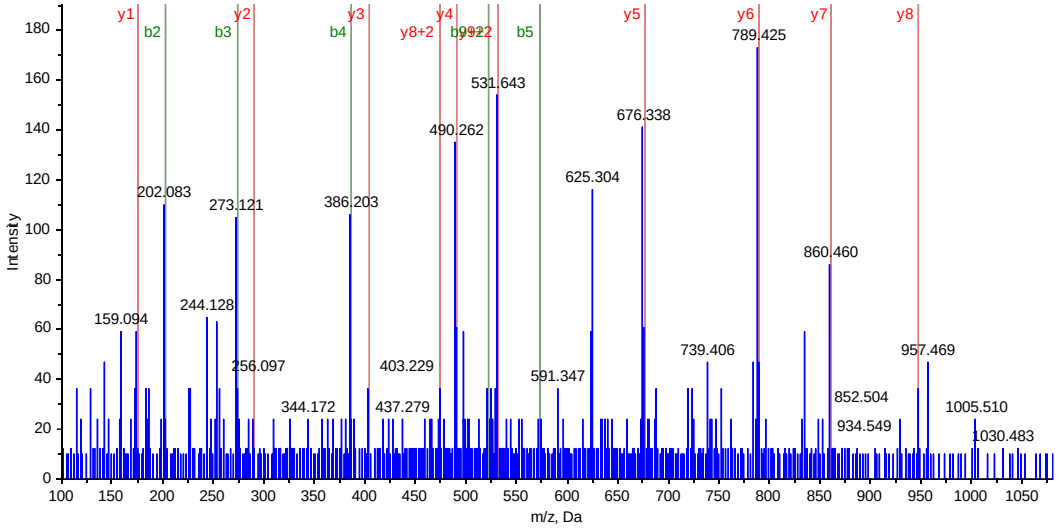
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	2941.4326	1471.2200
A	**200.1394**	100.5733	2813.3377	1407.1725
T	**301.1870**	151.0972	2742.3006	1371.6539
T	**402.2347**	201.6210	2641.2529	1321.1301
F	**549.3031**	275.1552	2540.2052	1270.6062
N	**663.3461**	**332.1767**	2393.1368	1197.0720
V	**762.4145**	381.7109	2279.0939	1140.0506
F	909.4829	455.2451	2180.0255	**1090.5164**
E	**1038.5255**	519.7664	2032.9570	**1016.9822**
S	**1125.5575**	**563.2824**	1903.9144	952.4609
E	**1254.6001**	627.8037	1816.8824	908.9448
P	1351.6529	676.3301	1687.8398	**844.4236**
D	**1466.6798**	733.8435	1590.7871	795.8972
F	1613.7482	**807.3777**	1475.7601	**738.3837**
Q	1741.8068	**871.4070**	**1328.6917**	**664.8495**
S	1828.8388	**914.9230**	**1200.6331**	**600.8202**
P	1925.8916	**963.4494**	**1113.6011**	**557.3042**
N	2039.9345	1020.4709	1016.5483	508.7778
G	2096.9560	1048.9816	**902.5054**	451.7563
Q	2225.0146	1113.0109	845.4839	423.2456
T	2326.0622	1163.5348	**717.4254**	359.2163
I	2439.1463	1220.0768	**616.3777**	308.6925
T	2540.1940	1270.6006	**503.2936**	252.1504
I	2653.2780	1327.1427	**402.2459**	201.6266
N	2767.3210	1384.1641	**289.1619**	145.0846
R	2923.4221	1462.2147	**175.1190**	88.0631

Peptide sequence 5: KATTFNVFESEPDFQSPNGQTITINRK



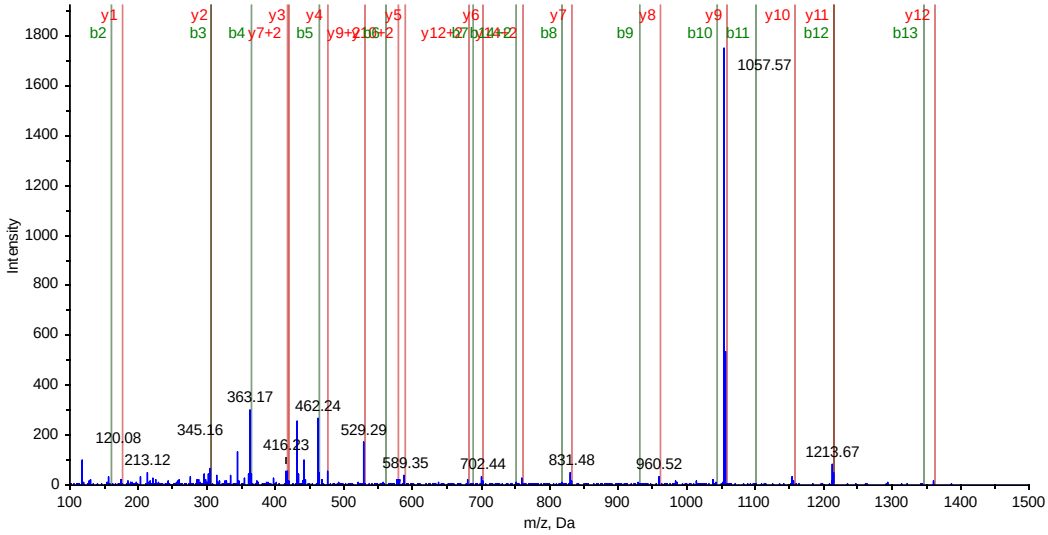
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	3069.5276	1535.2674
A	**200.1394**	100.5733	2941.4326	1471.2200
T	**301.1870**	151.0972	2870.3955	1435.7014
T	**402.2347**	201.6210	2769.3478	1385.1776
F	**549.3031**	275.1552	2668.3002	1334.6537
N	**663.3461**	**332.1767**	2521.2318	1261.1195
V	**762.4145**	**381.7109**	2407.1888	1204.0981
F	909.4829	**455.2451**	2308.1204	**1154.5638**
E	**1038.5255**	**519.7664**	2161.0520	**1081.0296**
S	**1125.5575**	**563.2824**	2032.0094	**1016.5083**
E	**1254.6001**	**627.8037**	1944.9774	**972.9923**
P	1351.6529	676.3301	1815.9348	**908.4710**
D	1466.6798	733.8435	1718.8820	**859.9446**
F	1613.7482	807.3777	1603.8551	**802.4312**
Q	1741.8068	**871.4070**	**1456.7867**	**728.8970**
S	1828.8388	914.9230	**1328.7281**	**664.8677**
P	1925.8916	963.4494	**1241.6961**	**621.3517**
N	2039.9345	**1020.4709**	**1144.6433**	**572.8253**
G	2096.9560	1048.9816	**1030.6004**	**515.8038**
Q	2225.0146	1113.0109	**973.5789**	487.2931
T	2326.0622	1163.5348	**845.5203**	423.2638
I	2439.1463	1220.0768	**744.4726**	372.7400
T	2540.1940	1270.6006	**631.3886**	**316.1979**
I	2653.2780	1327.1427	**530.3409**	265.6741
N	2767.3210	1384.1641	**417.2568**	209.1321
R	2923.4221	1462.2147	**303.2139**	152.1106
K	3051.5170	1526.2622	**147.1128**	74.0600

Peptide sequence 6: NSALWSLDR



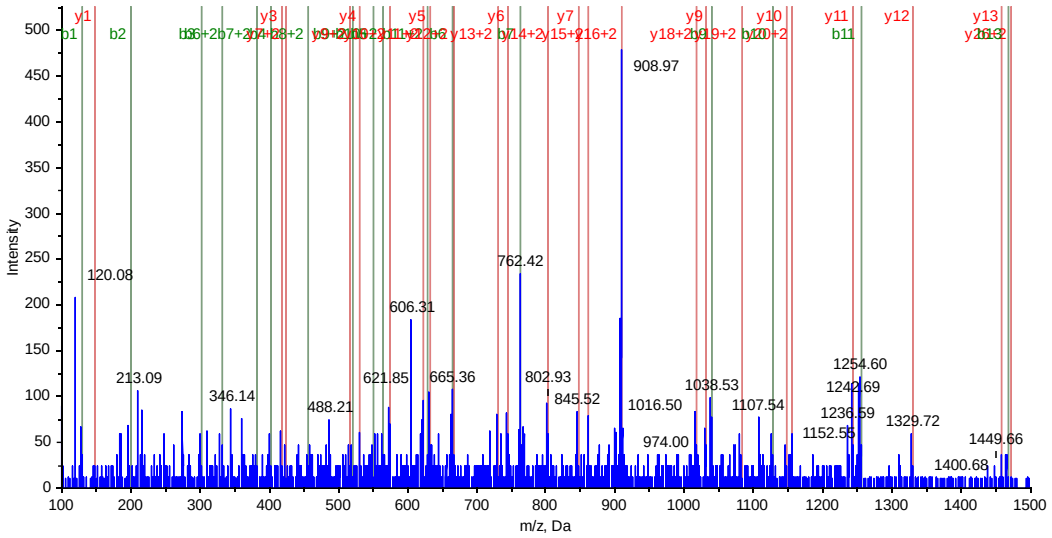
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1061.5374	**531.2724**
S	**202.0822**	101.5448	**947.4945**	**474.2509**
A	**273.1193**	137.0633	**860.4625**	430.7349
L	**386.2034**	193.6053	**789.4254**	395.2163
W	**572.2827**	286.6450	**676.3413**	338.6743
S	659.3148	330.1610	**490.2620**	245.6346
L	772.3988	386.7030	**403.2300**	202.1186
D	887.4258	444.2165	**290.1459**	145.5766
R	1043.5269	**522.2671**	**175.1190**	88.0631

Peptide sequence 7: SAFGVPEEIIGLMR



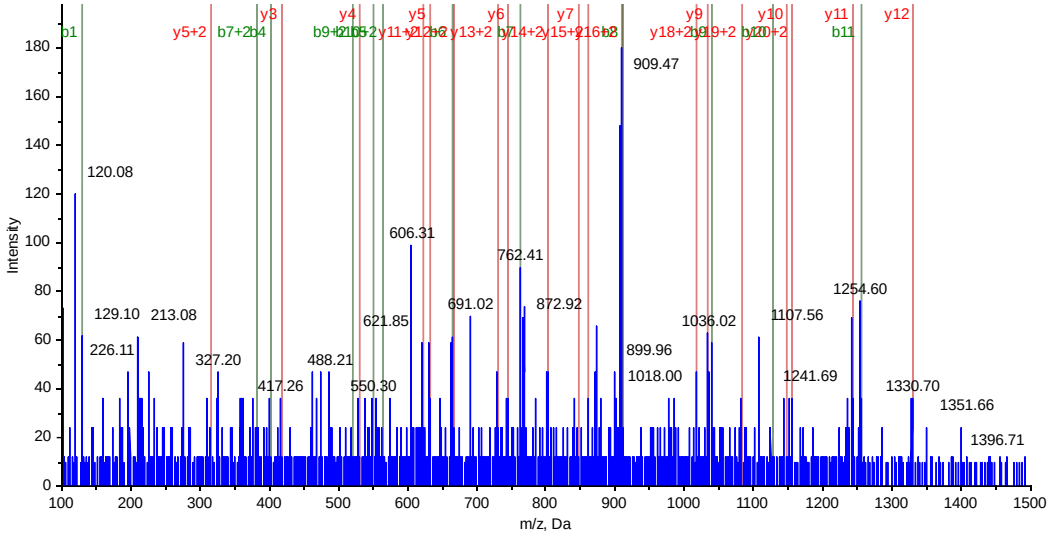
Residue	b	b+2	y	y+2
S	88.0393	44.5233	1518.7985	**759.9029**
A	**159.0764**	80.0418	1431.7664	716.3869
F	**306.1448**	153.5761	**1360.7293**	**680.8683**
G	**363.1663**	182.0868	**1213.6609**	607.3341
V	**462.2347**	231.6210	**1156.6395**	**578.8234**
P	**559.2875**	280.1474	**1057.5710**	**529.2892**
E	**688.3301**	344.6687	**960.5183**	480.7628
E	**817.3727**	409.1900	**831.4757**	**416.2415**
I	**930.4567**	465.7320	**702.4331**	351.7202
I	**1043.5408**	522.2740	**589.3490**	295.1782
G	**1100.5623**	550.7848	**476.2650**	238.6361
L	**1213.6463**	607.3268	**419.2435**	210.1254
M	**1344.6868**	672.8470	**306.1594**	153.5834
R	1500.7879	**750.8976**	**175.1190**	88.0631

Peptide sequence 8: KATTFNVFESEPDFQSPN[Dea]GQTITINRK



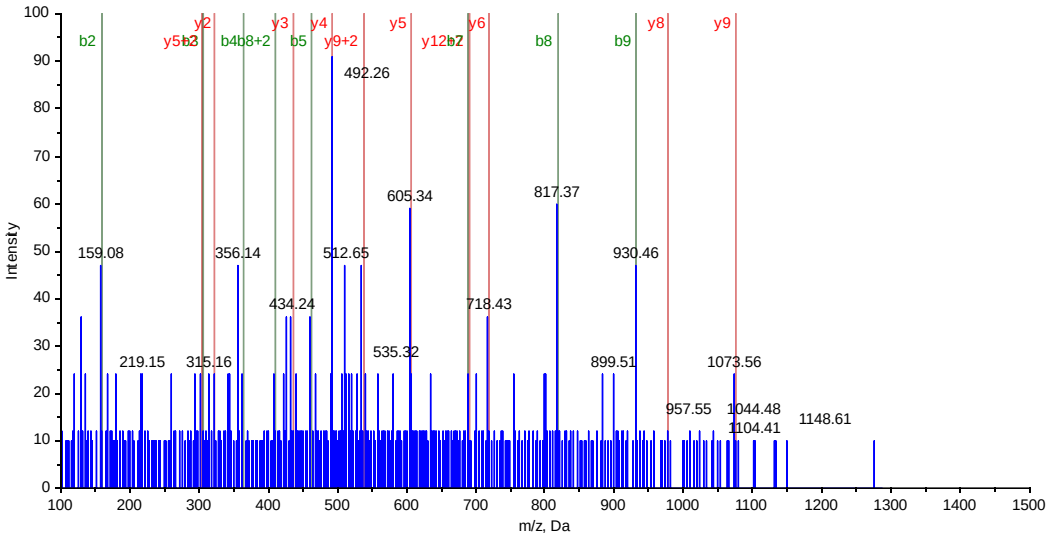
Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	3070.5116	1535.7594
A	**200.1394**	100.5733	2942.4167	**1471.7120**
T	**301.1870**	151.0972	2871.3795	1436.1934
T	**402.2347**	201.6210	2770.3319	1385.6696
F	**549.3031**	275.1552	2669.2842	1335.1457
N	**663.3461**	**332.1767**	2522.2158	1261.6115
V	**762.4145**	**381.7109**	2408.1728	1204.5901
F	909.4829	**455.2451**	2309.1044	**1155.0559**
E	**1038.5255**	**519.7664**	2162.0360	**1081.5216**
S	**1125.5575**	**563.2824**	2032.9934	**1017.0004**
E	**1254.6001**	**627.8037**	1945.9614	973.4843
P	1351.6529	676.3301	1816.9188	**908.9630**
D	**1466.6798**	733.8435	1719.8660	**860.4367**
F	1613.7482	807.3777	1604.8391	**802.9232**
Q	1741.8068	871.4070	**1457.7707**	**729.3890**
S	1828.8388	914.9230	**1329.7121**	**665.3597**
P	1925.8916	963.4494	**1242.6801**	**621.8437**
N[Dea]	2040.9185	1020.9629	**1145.6273**	**573.3173**
G	2097.9400	1049.4736	**1030.6004**	**515.8038**
Q	2225.9986	1113.5029	973.5789	487.2931
T	2327.0462	1164.0268	**845.5203**	**423.2638**
I	2440.1303	1220.5688	**744.4726**	372.7400
T	2541.1780	1271.0926	**631.3886**	316.1979
I	2654.2621	1327.6347	**530.3409**	265.6741
N	2768.3050	1384.6561	**417.2568**	209.1321
R	2924.4061	1462.7067	303.2139	152.1106
K	3052.5011	1526.7542	**147.1128**	74.0600

Peptide sequence 9: KATTFNVFESEPDFQSPNGQ[Dea]TITINRK



Residue	b	b+2	y	y+2
K	**129.1022**	65.0548	3070.5116	1535.7594
A	200.1394	100.5733	2942.4167	1471.7120
T	301.1870	151.0972	2871.3795	1436.1934
T	**402.2347**	201.6210	2770.3319	1385.6696
F	**549.3031**	275.1552	2669.2842	1335.1457
N	**663.3461**	332.1767	2522.2158	1261.6115
V	**762.4145**	**381.7109**	2408.1728	1204.5901
F	**909.4829**	455.2451	2309.1044	**1155.0559**
E	**1038.5255**	**519.7664**	2162.0360	**1081.5216**
S	**1125.5575**	**563.2824**	2032.9934	**1017.0004**
E	**1254.6001**	627.8037	1945.9614	973.4843
P	1351.6529	676.3301	1816.9188	**908.9630**
D	1466.6798	733.8435	1719.8660	**860.4367**
F	1613.7482	807.3777	1604.8391	**802.9232**
Q	1741.8068	871.4070	1457.7707	**729.3890**
S	1828.8388	914.9230	**1329.7121**	**665.3597**
P	1925.8916	963.4494	**1242.6801**	**621.8437**
N	2039.9345	1020.4709	**1145.6273**	573.3173
G	2096.9560	1048.9816	**1031.5844**	516.2958
Q[Dea]	2225.9986	1113.5029	974.5629	487.7851
T	2327.0462	1164.0268	**845.5203**	423.2638
I	2440.1303	1220.5688	**744.4726**	372.7400
T	2541.1780	1271.0926	**631.3886**	**316.1979**
I	2654.2621	1327.6347	**530.3409**	265.6741
N	2768.3050	1384.6561	**417.2568**	209.1321
R	2924.4061	1462.7067	303.2139	152.1106
K	3052.5011	1526.7542	147.1128	74.0600

Peptide sequence 10: SAFGVPEEIIGLM[Oxi]R



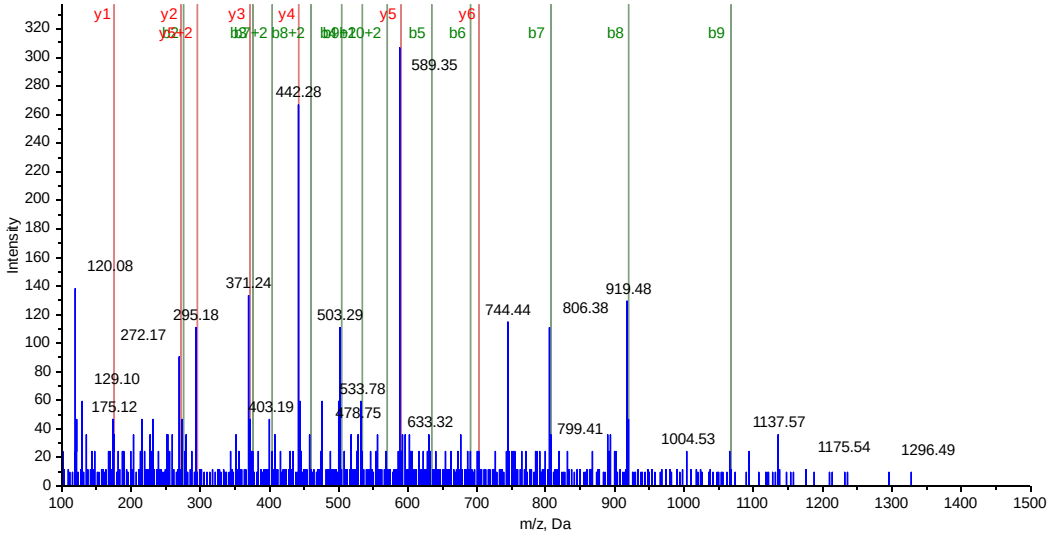
Residue	b	b+2	y	y+2
S	88.0393	44.5233	1534.7934	767.9003
A	**159.0764**	80.0418	1447.7614	724.3843
F	**306.1448**	153.5761	1376.7242	**688.8658**
G	**363.1663**	182.0868	1229.6558	615.3316
V	**462.2347**	231.6210	1172.6344	586.8208
P	559.2875	280.1474	**1073.5660**	**537.2866**
E	**688.3301**	344.6687	**976.5132**	488.7602
E	**817.3727**	**409.1900**	847.4706	424.2389
I	**930.4567**	465.7320	**718.4280**	359.7176
I	1043.5408	522.2740	**605.3439**	**303.1756**
G	1100.5623	550.7848	**492.2599**	246.6336
L	1213.6463	607.3268	**435.2384**	218.1228
M[Oxi]	1360.6817	680.8445	**322.1544**	161.5808
R	1516.7828	758.8951	175.1190	88.0631

Protein: B.rapa.Ro18.Candidate-3, 3 peptides (95%)

Protein sequence coverage

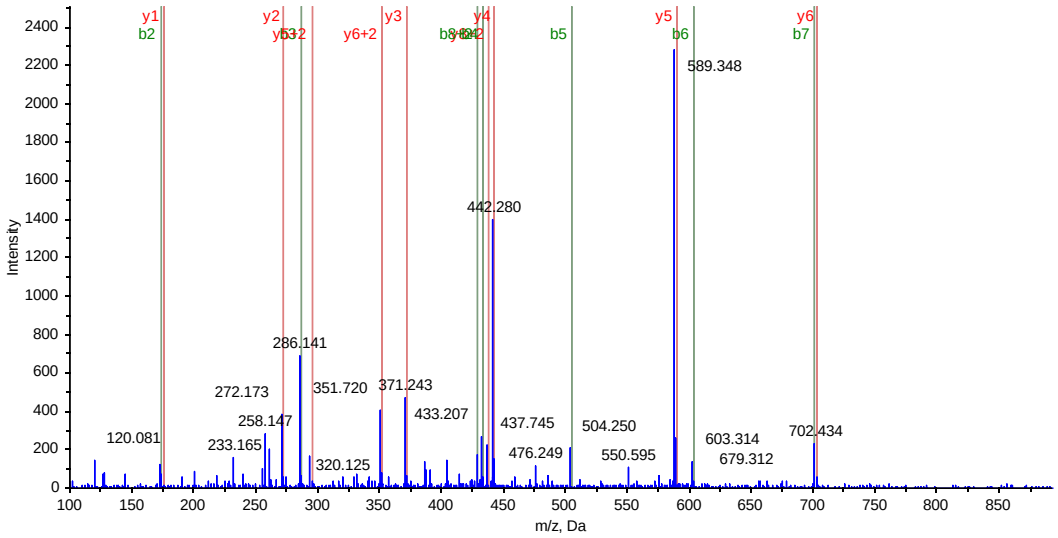
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FQSPSGRTITINRKDLEVLSGSMVGVSMVNLTQASMMGPHWNPWACEISIVLKGSGMVRVLRSSISSTS
SSSSSSECKNMR**FKVEEGDIFAVPR**LHPMAQMSFINESLVFIGFTTSARNNEPQFLAGQRSALRLLDQE
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EEEEEEEKQWPPLPQQPPE

Peptide sequence 1: FKVEEGDIFAVPR



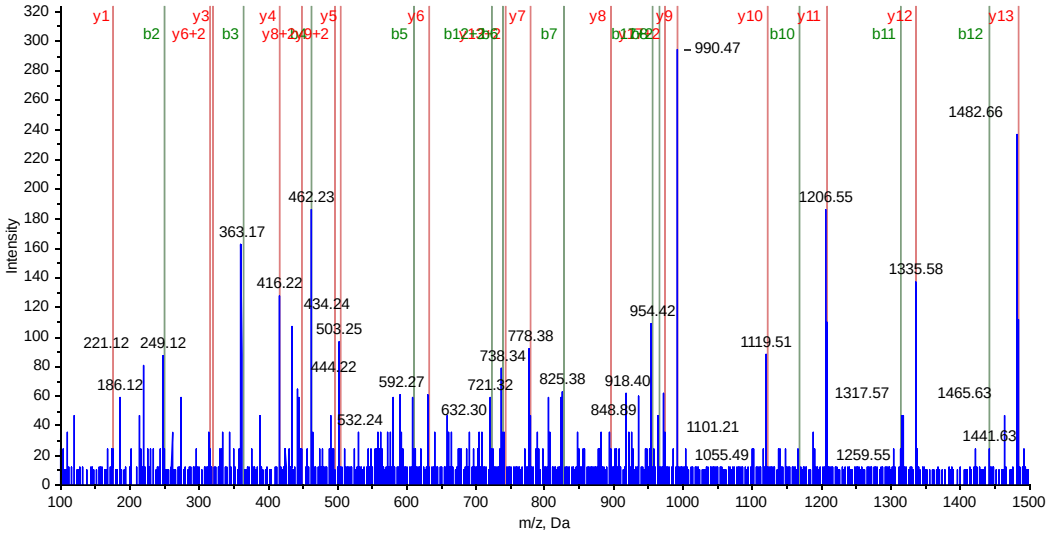
Residue	b	b+2	y	y+2
F	148.0757	74.5415	1506.7951	753.9012
K	**276.1707**	138.5890	1359.7267	680.3670
V	**375.2391**	188.1232	1231.6317	616.3195
E	**504.2817**	252.6445	1132.5633	566.7853
E	**633.3243**	317.1658	1003.5207	502.2640
G	**690.3457**	345.6765	874.4781	437.7427
D	**805.3727**	**403.1900**	817.4567	409.2320
I	**918.4567**	**459.7320**	**702.4297**	351.7185
F	**1065.5251**	**533.2662**	**589.3457**	**295.1765**
A	1136.5623	**568.7848**	**442.2772**	221.6423
V	1235.6307	618.3190	**371.2401**	186.1237
P	1332.6834	666.8454	**272.1717**	136.5895
R	1488.7845	744.8959	**175.1190**	88.0631

Peptide sequence 2: GDIFAVPR



Residue	b	b+2	y	y+2
G	58.0287	29.5180	874.4781	**437.7427**
D	**173.0557**	87.0315	817.4567	409.2320
I	**286.1397**	143.5735	**702.4297**	**351.7185**
F	**433.2082**	217.1077	**589.3457**	**295.1765**
A	**504.2453**	252.6263	**442.2772**	221.6423
V	**603.3137**	302.1605	**371.2401**	186.1237
P	**700.3665**	350.6869	**272.1717**	136.5895
R	856.4676	**428.7374**	**175.1190**	88.0631

Peptide sequence 3: TFNVFESEPDFQSPSGR



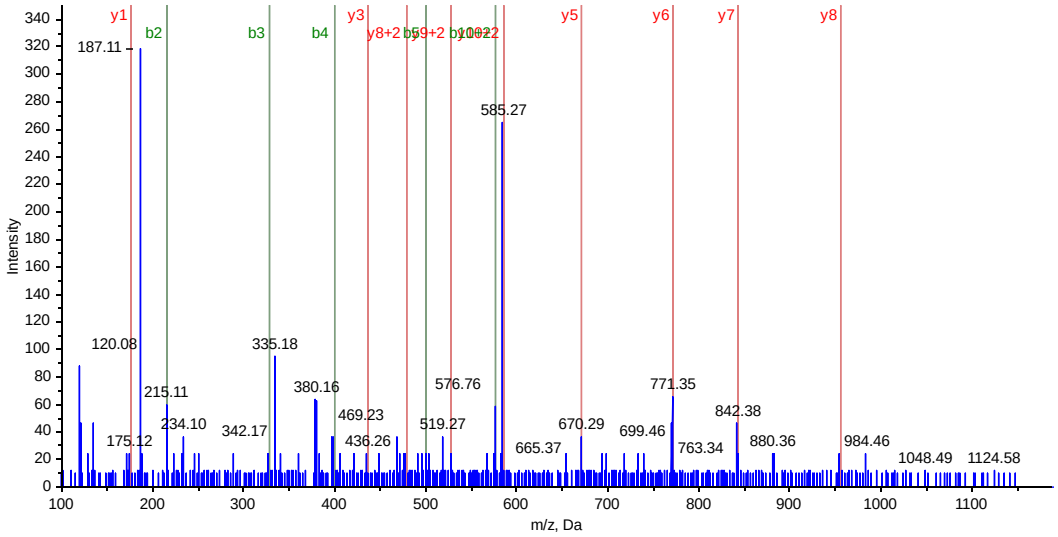
Residue	b	b+2	y	y+2
T	102.0550	51.5311	1943.8770	**972.4421**
F	**249.1234**	125.0653	1842.8293	921.9183
N	**363.1663**	182.0868	1695.7609	848.3841
V	**462.2347**	231.6210	1581.7180	791.3626
F	**609.3031**	305.1552	**1482.6496**	**741.8284**
E	**738.3457**	369.6765	**1335.5811**	668.2942
S	**825.3777**	413.1925	**1206.5386**	603.7729
E	**954.4203**	477.7138	**1119.5065**	560.2569
P	1051.4731	526.2402	**990.4639**	**495.7356**
D	**1166.5000**	583.7537	**893.4112**	**447.2092**
F	**1313.5685**	657.2879	**778.3842**	389.6958
Q	**1441.6270**	**721.3172**	**631.3158**	**316.1615**
S	1528.6591	764.8332	**503.2572**	252.1323
P	1625.7118	813.3596	**416.2252**	208.6162
S	1712.7439	856.8756	**319.1724**	160.0899
G	1769.7653	885.3863	232.1404	116.5738
R	1925.8664	**963.4369**	**175.1190**	88.0631

Protein: B.rapa.Ro18.Candidate-4, 2 peptides (95%)

Protein sequence coverage

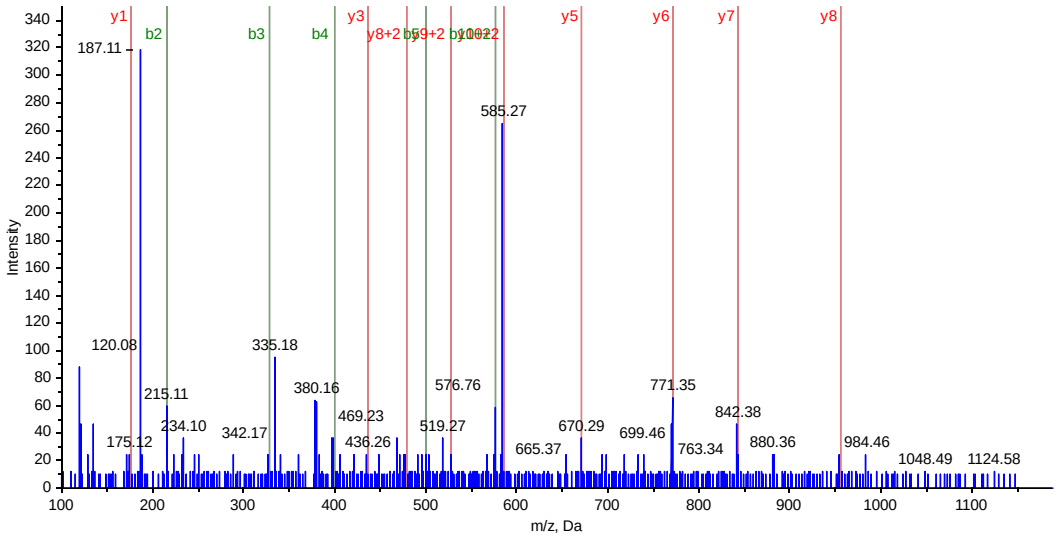
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EPNALLLPLLLHSDMVFFVHTGSGVLNWVDEEKERTLELKRGDVFRLRYGTVFYLHCNLERDEVPEKLR
VYAIFDVGKCLSDQCLGAYSSIRDLLWGFDEKTLRSAFAVPKDVFGRLRDAVKPPLITHAMPKNRTQGS
EEETWGSRLAKLFVRVEDVTDHLEMKPVVNKKKKKKKKSSAYNVFESDPDFENDNGQSIVVDEKDMDA
LKGSSFGVYMVNLTKGSMMGPHWNPNACEISIVLQGEGMIRVVNHPSYQSKNESERFMVEDGDVFVVPQ
FYPMAQLSFVNSSFMFMGFSTSAK**TNHPQFLVGQNSVLK**IFNR**DVLATSFNMR**YATVERLLGAQKDGLL
LECVSCAEVELSRLMREIEERRRREEEEIERRKREEEEAKRQEEERRRREEEEAERKKKAEEEARKREK
ERE REEEAAKRREEERRRREEEEAERKRKEEEEARKREEERKREEEAAKKREEERRKREKEEEEARKRE
EARE REEEEAKKREEERRKREEEEAERKRRAEEEARE REEEEAKKREEEKEAARRREEERE KEEEMAKR
REEERQRKERE DVERKKREEEEERKRREEEAMRREEERKREEEAAKRAEEERRKREEEAEHKKRPPPQG
PQPPIHH

Peptide sequence 1: TNHPQFLVGQNSVLK



Residue	b	b+2	y	y+2
T	102.0550	51.5311	1681.9020	841.4547
N	216.0979	108.5526	1580.8544	790.9308
H	353.1568	177.0820	1466.8114	733.9094
P	**450.2096**	225.6084	1329.7525	665.3799
Q	578.2681	289.6377	1232.6997	616.8535
F	**725.3365**	**363.1719**	1104.6412	552.8242
L	**838.4206**	**419.7139**	957.5728	479.2900
V	**937.4890**	**469.2482**	**844.4887**	**422.7480**
G	994.5105	**497.7589**	**745.4203**	373.2138
Q	1122.5691	**561.7882**	**688.3988**	344.7030
N	1236.6120	618.8096	560.3402	280.6738
S	1323.6440	**662.3257**	446.2973	223.6523
V	1422.7124	711.8599	359.2653	180.1363
L	1535.7965	768.4019	260.1969	130.6021
K	1663.8915	832.4494	**147.1128**	74.0600

Peptide sequence 1: DVLATSFNM[Oxi]R



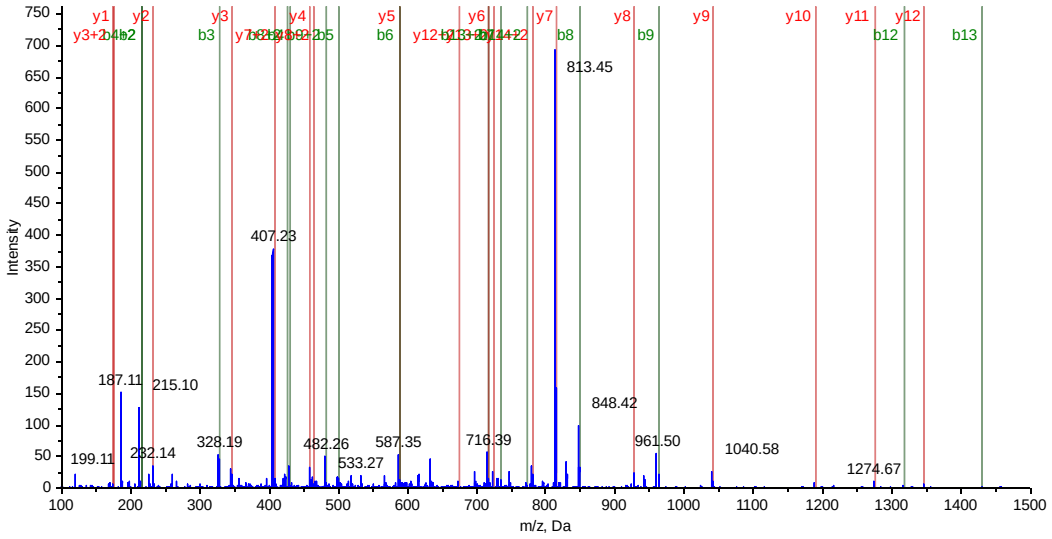
Residue	b	b+2	y	y+2
D	116.0342	58.5207	1169.5619	**585.2846**
V	**215.1026**	108.0550	1054.5350	**527.7711**
L	**328.1867**	164.5970	**955.4666**	**478.2369**
A	**399.2238**	200.1155	**842.3825**	421.6949
T	**500.2715**	250.6394	**771.3454**	386.1763
S	587.3035	294.1554	**670.2977**	335.6525
F	734.3719	367.6896	583.2657	292.1365
N	848.4149	424.7111	**436.1973**	218.6023
M[Oxi]	995.4503	498.2288	322.1544	161.5808
R	1151.5514	**576.2793**	**175.1190**	88.0631

Protein: B.rapa.Ro18.Candidate-5, 21 peptides (95%)

Protein sequence coverage

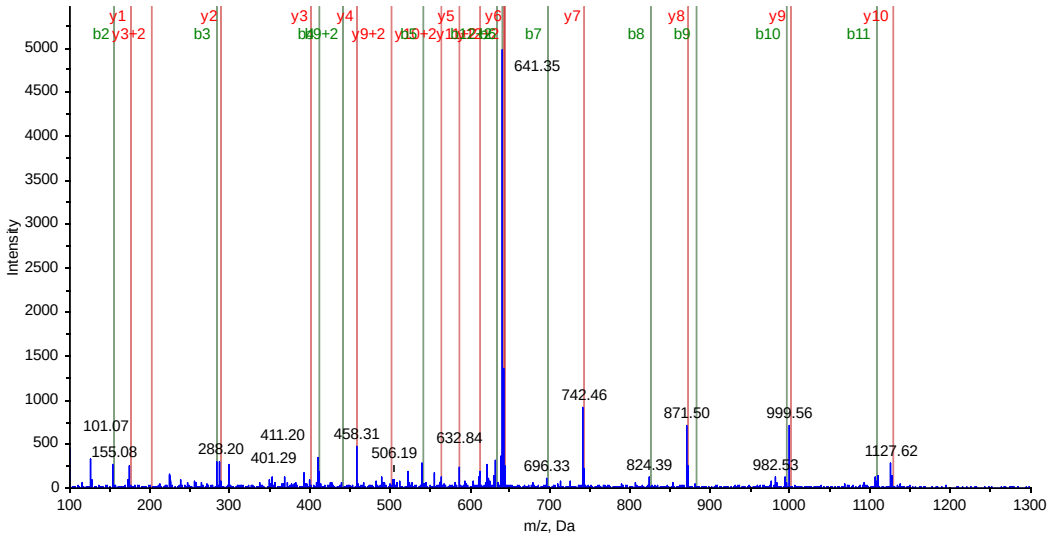
MAINKLTITLFLLISLAVFHCLAFRVEVQEFEPPRQEGQEGPGGGSGEGWDEEATK**NPYHFGQWSFKNF**
FQSKDGFVKMLPKFTKR**SSTLFR**GIENYRFLFQEMQPNTFLVPHHLDADYVFLVVQGK**GVIGFVTDTAN**
ESFQITKGDVVR**VPSSVTHFFANTNGTVPLR**LAK**IAVPANVPGHFQVFFPAHSGFHQSYFNGFSKDVLT**
ASFNIPEELLGRLIRGPQQEVGQGIIRRVSPEQIKELTEHEHATSPSNKHKDKKDKHKDKDR**STFGSPF**
NLLTQDAIYSNNFGRYHEAHPKRFSQLQDLDIAVGWVNMTQGSLFLPQYNSETTFVTFVENGCARYEMA
SPYTFQGEQQQPWFGPGQEEEVEEEMSGQVHKIVSRVCKGEVFILPAGHPFAILSQDENFVAVGFGIHA
SNSTR**TFLAGQDNMLSNINTVATRLSFGLGSK**MAEKLFTSQNYSHFAPTTPSHQFPEKPKPSFQSVFNL
VGF

Peptide sequence 1: DVLTASFNIPEELLGR



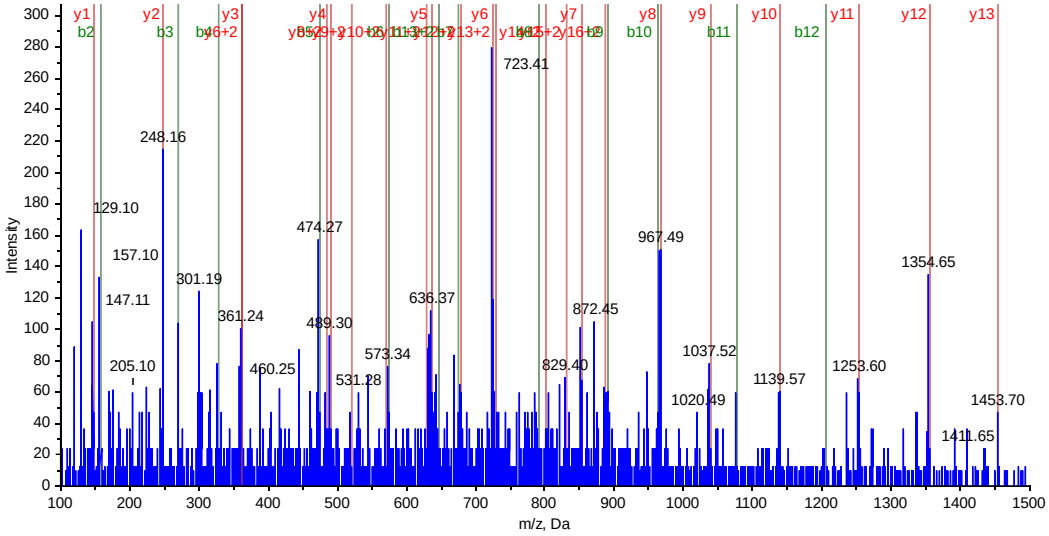
Residue	b	b+2	y	y+2
D	116.0342	58.5207	1773.9381	887.4727
V	**215.1026**	108.0550	1658.9112	829.9592
L	**328.1867**	164.5970	1559.8428	**780.4250**
T	**429.2344**	**215.1208**	1446.7587	**723.8830**
A	**500.2715**	250.6394	**1345.7110**	**673.3592**
S	**587.3035**	294.1554	**1274.6739**	637.8406
F	**734.3719**	367.6896	**1187.6419**	594.3246
N	**848.4149**	**424.7111**	**1040.5735**	520.7904
I	**961.4989**	**481.2531**	**926.5306**	**463.7689**
P	1058.5517	529.7795	**813.4465**	**407.2269**
E	1187.5943	594.3008	**716.3937**	358.7005
E	**1316.6369**	658.8221	**587.3511**	294.1792
L	**1429.7209**	**715.3641**	**458.3085**	229.6579
L	1542.8050	**771.9061**	**345.2245**	**173.1159**
G	1599.8265	800.4169	**232.1404**	116.5738
R	1755.9276	878.4674	**175.1190**	88.0631

Peptide sequence 2: GPQQEVGQGIIR



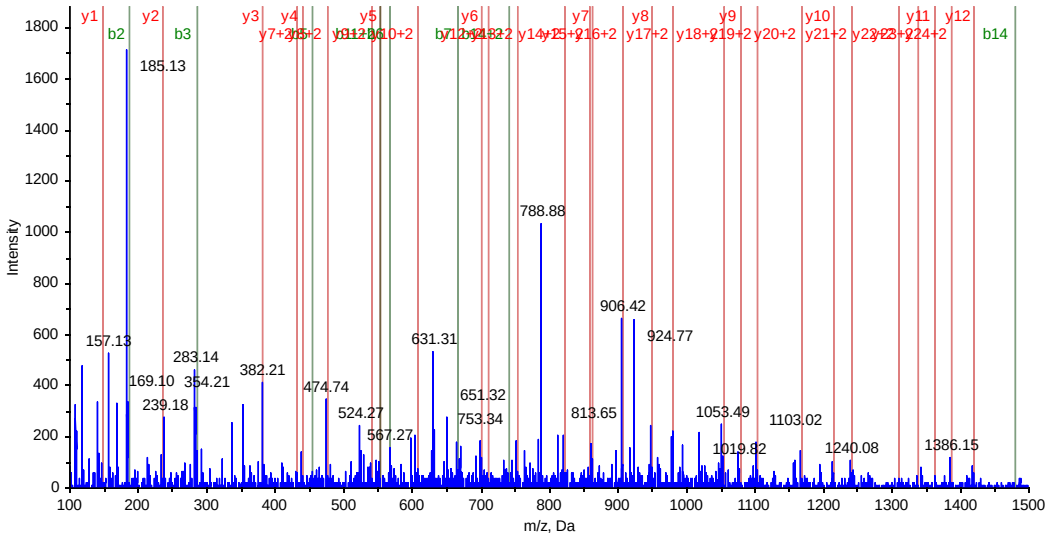
Residue	b	b+2	y	y+2
G	58.0287	29.5180	1281.6910	**641.3491**
P	**155.0815**	78.0444	1224.6695	**612.8384**
Q	**283.1401**	142.0737	**1127.6167**	**564.3120**
Q	**411.1987**	206.1030	**999.5582**	**500.2827**
E	**540.2413**	270.6243	**871.4996**	436.2534
V	**639.3097**	320.1585	**742.4570**	371.7321
G	**696.3311**	348.6692	**643.3886**	322.1979
Q	**824.3897**	412.6985	**586.3671**	293.6872
G	**881.4112**	**441.2092**	**458.3085**	229.6579
I	**994.4952**	497.7513	**401.2871**	**201.1472**
I	**1107.5793**	554.2933	**288.2030**	144.6051
R	1263.6804	**632.3438**	**175.1190**	88.0631

Peptide sequence 3: GVIGFVTDTANESFQITK



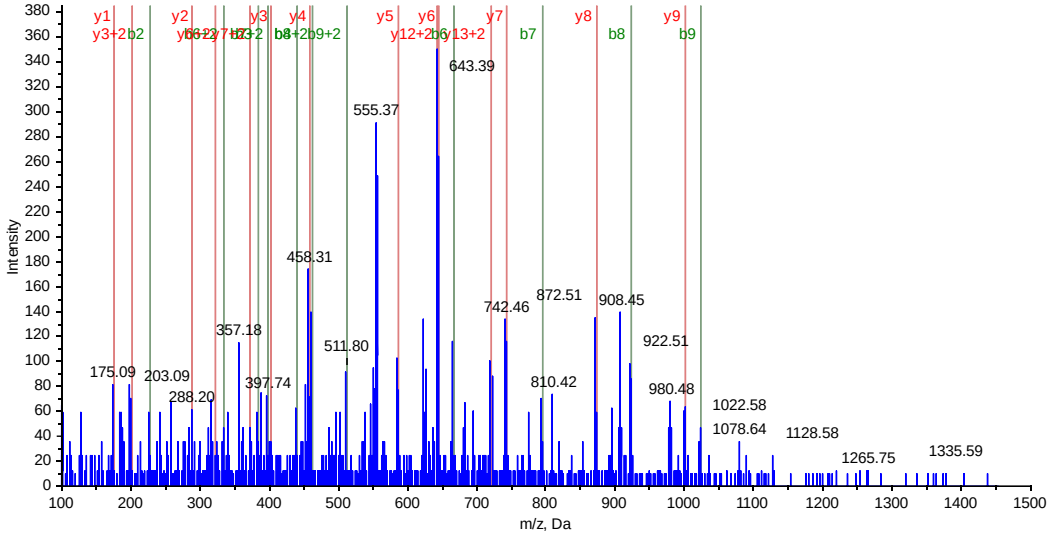
Residue	b	b+2	y	y+2
G	58.0287	29.5180	1926.9807	963.9940
V	**157.0972**	79.0522	1869.9593	935.4833
I	**270.1812**	135.5942	1770.8909	**885.9491**
G	**327.2027**	164.1050	1657.8068	**829.4070**
F	**474.2711**	237.6392	1600.7853	**800.8963**
V	**573.3395**	287.1734	**1453.7169**	**727.3621**
T	**674.3872**	337.6972	**1354.6485**	**677.8279**
D	**789.4141**	395.2107	**1253.6008**	**627.3040**
T	**890.4618**	445.7345	**1138.5739**	**569.7906**
A	**961.4989**	481.2531	**1037.5262**	**519.2667**
N	**1075.5419**	538.2746	**966.4891**	**483.7482**
E	**1204.5844**	602.7959	**852.4462**	426.7267
S	1291.6165	**646.3119**	**723.4036**	**362.2054**
F	1438.6849	719.8461	**636.3715**	318.6894
Q	1566.7435	783.8754	**489.3031**	245.1552
I	1679.8275	840.4174	**361.2445**	181.1259
T	1780.8752	890.9412	**248.1605**	124.5839
K	1908.9702	954.9887	**147.1128**	74.0600

Peptide sequence 4: IAVPANVPGHFQVFFPAHSGFHQSYFNGFSK



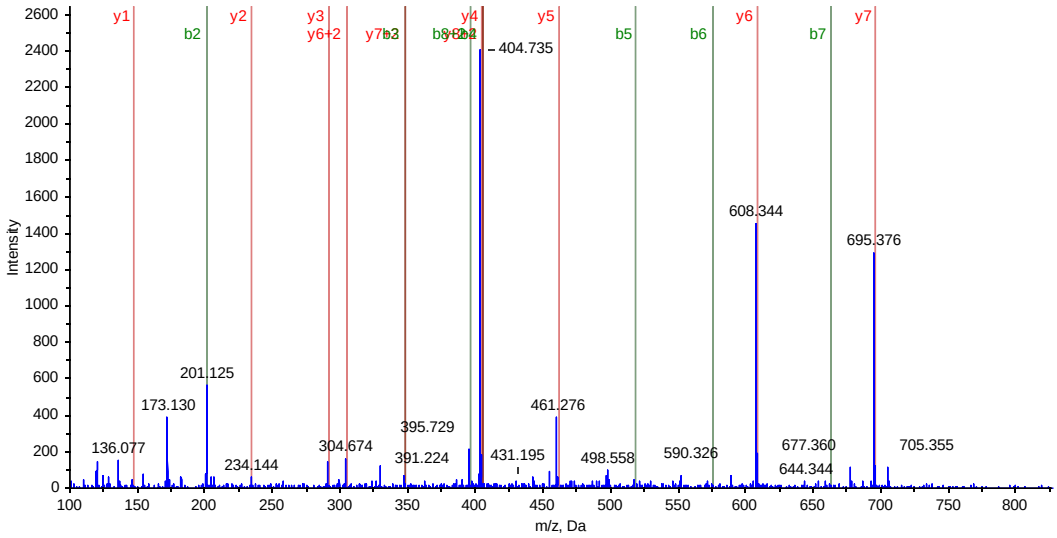
Residue	b	b+2	y	y+2
I	114.0913	57.5493	3434.6858	1717.8465
A	**185.1285**	93.0679	3321.6017	1661.3045
V	**284.1969**	142.6021	3250.5646	1625.7859
P	381.2496	191.1285	3151.4962	1576.2517
A	**452.2867**	226.6470	3054.4434	1527.7253
N	**566.3297**	283.6685	2983.4063	1492.2068
V	**665.3981**	333.2027	2869.3634	1435.1853
P	762.4509	381.7291	2770.2950	**1385.6511**
G	819.4723	410.2398	2673.2422	**1337.1247**
H	956.5312	478.7693	2616.2207	**1308.6140**
F	1103.5996	**552.3035**	2479.1618	**1240.0846**
Q	1231.6582	616.3327	2332.0934	**1166.5503**
V	1330.7266	665.8670	2204.0348	**1102.5211**
F	**1477.7950**	**739.4012**	2104.9664	**1052.9868**
F	1624.8635	812.9354	1957.8980	**979.4526**
P	1721.9162	861.4618	1810.8296	**905.9184**
A	1792.9533	896.9803	1713.7768	**857.3921**
H	1930.0122	965.5098	1642.7397	**821.8735**
S	2017.0443	1009.0258	1505.6808	**753.3440**
G	2074.0657	1037.5365	**1418.6488**	**709.8280**
F	2221.1342	1111.0707	**1361.6273**	681.3173
H	2358.1931	1179.6002	**1214.5589**	**607.7831**
Q	2486.2516	1243.6295	**1077.5000**	**539.2536**
S	2573.2837	1287.1455	**949.4414**	**475.2243**
Y	2736.3470	1368.6771	**862.4094**	**431.7083**
F	2883.4154	1442.2113	**699.3461**	350.1767
N	2997.4583	1499.2328	**552.2776**	276.6425
G	3054.4798	1527.7435	**438.2347**	219.6210
F	3201.5482	1601.2777	**381.2132**	191.1103
S	3288.5802	1644.7938	**234.1448**	117.5761
K	3416.6752	1708.8412	**147.1128**	74.0600

Peptide sequence 5: LIRGPQQEVGQGIIR



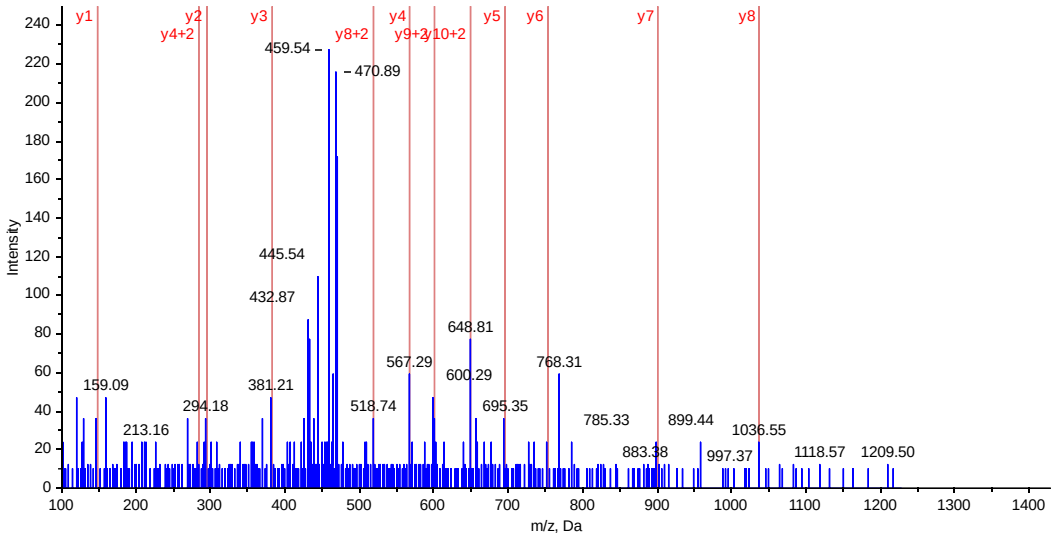
Residue	b	b+2	y	y+2
L	114.0913	57.5493	1663.9602	832.4837
I	**227.1754**	114.0913	1550.8761	775.9417
R	**383.2765**	192.1419	1437.7921	**719.3997**
G	**440.2980**	220.6526	1281.6910	**641.3491**
P	537.3507	269.1790	1224.6695	612.8384
Q	**665.4093**	**333.2083**	1127.6167	564.3120
Q	**793.4679**	**397.2376**	**999.5582**	500.2827
E	**922.5105**	**461.7589**	**871.4996**	436.2534
V	**1021.5789**	**511.2931**	**742.4570**	**371.7321**
G	1078.6004	539.8038	**643.3886**	**322.1979**
Q	1206.6589	603.8331	**586.3671**	293.6872
G	1263.6804	632.3438	**458.3085**	229.6579
I	1376.7645	688.8859	**401.2871**	**201.1472**
I	1489.8485	745.4279	**288.2030**	144.6051
R	1645.9496	823.4785	**175.1190**	88.0631

Peptide sequence 6: LSFGLGSK



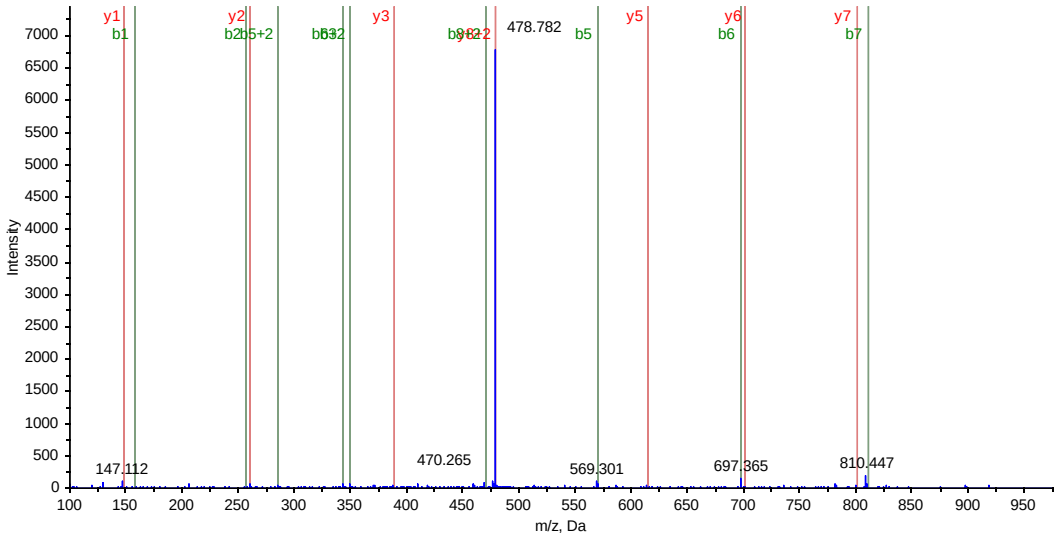
Residue	b	b+2	y	y+2
L	114.0913	57.5493	808.4563	**404.7318**
S	**201.1234**	101.0653	**695.3723**	**348.1898**
F	**348.1918**	174.5995	**608.3402**	**304.6738**
G	**405.2132**	203.1103	**461.2718**	231.1396
L	**518.2973**	259.6523	**404.2504**	202.6288
G	**575.3188**	288.1630	**291.1663**	146.0868
S	**662.3508**	331.6790	**234.1448**	117.5761
K	790.4458	**395.7265**	**147.1128**	74.0600

Peptide sequence 7: NPYHFGQWSFK



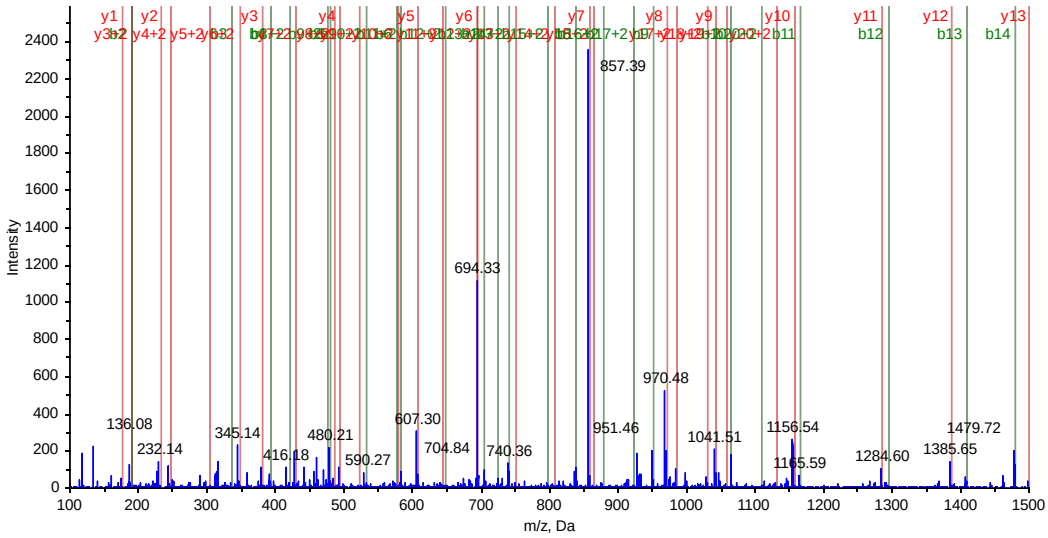
Residue	b	b+2	y	y+2
N	115.0502	58.0287	1410.6589	705.8331
P	212.1030	106.5551	1296.6160	**648.8116**
Y	375.1663	188.0868	1199.5633	**600.2853**
H	512.2252	256.6162	**1036.4999**	**518.7536**
F	659.2936	330.1504	**899.4410**	450.2241
G	716.3151	358.6612	**752.3726**	376.6899
Q	844.3737	422.6905	**695.3511**	348.1792
W	1030.4530	515.7301	**567.2926**	**284.1499**
S	1117.4850	559.2461	**381.2132**	191.1103
F	1264.5534	632.7803	**294.1812**	147.5942
K	1392.6484	696.8278	**147.1128**	74.0600

Peptide sequence 8: RVSPEQIK



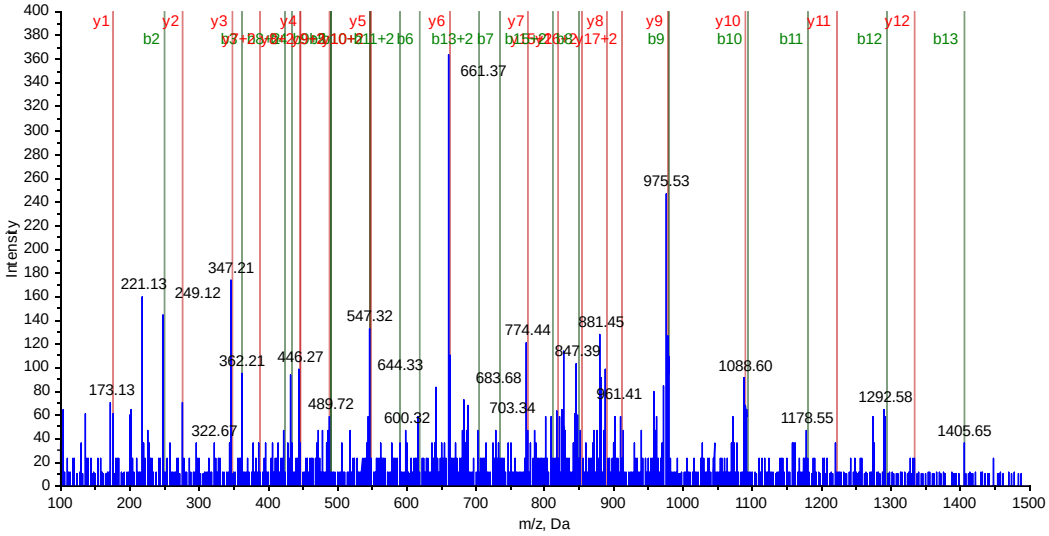
Residue	b	b+2	y	y+2
R	**157.1084**	79.0578	956.5524	**478.7798**
V	**256.1768**	128.5920	**800.4512**	400.7293
S	**343.2088**	172.1081	**701.3828**	351.1951
P	440.2616	220.6344	**614.3508**	307.6790
E	**569.3042**	**285.1557**	517.2980	259.1527
Q	**697.3628**	**349.1850**	**388.2554**	194.6314
I	**810.4468**	405.7271	**260.1969**	130.6021
K	938.5418	**469.7745**	**147.1128**	74.0600

Peptide sequence 9: STFGSPFNLLTQDAIYSNNFGR



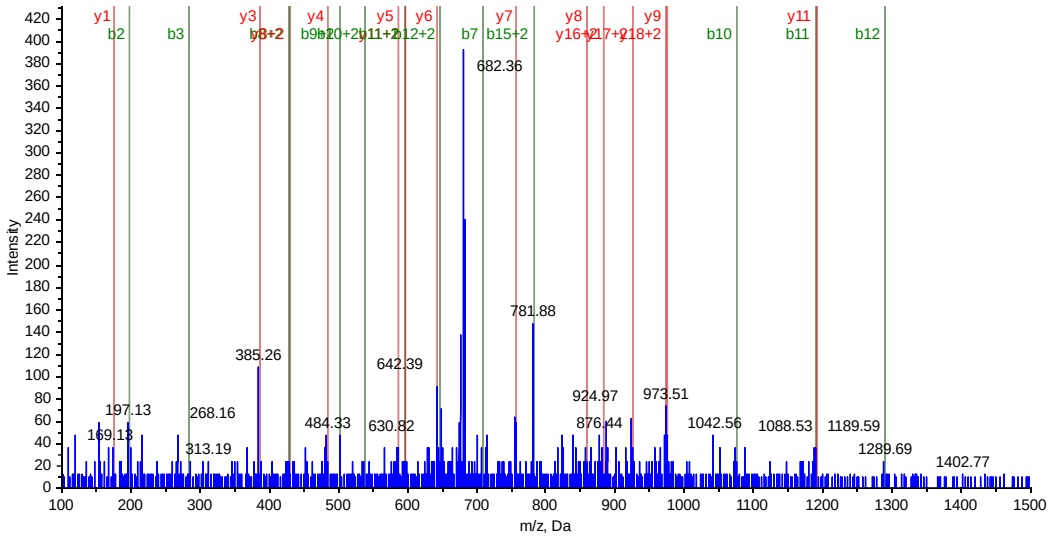
Residue	b	b+2	y	y+2
S	88.0393	44.5233	2449.1783	1225.0928
T	**189.0870**	95.0471	2362.1462	1181.5768
F	**336.1554**	168.5813	2261.0986	**1131.0529**
G	**393.1769**	197.0921	2114.0301	**1057.5187**
S	**480.2089**	240.6081	2057.0087	**1029.0080**
P	**577.2617**	289.1345	1969.9767	**985.4920**
F	**724.3301**	362.6687	1872.9239	936.9656
N	**838.3730**	**419.6901**	1725.8555	**863.4314**
L	**951.4571**	**476.2322**	1611.8125	**806.4099**
L	**1064.5411**	**532.7742**	**1498.7285**	**749.8679**
T	**1165.5888**	**583.2980**	**1385.6444**	**693.3258**
Q	**1293.6474**	**647.3273**	**1284.5967**	**642.8020**
D	**1408.6743**	**704.8408**	**1156.5382**	**578.7727**
A	**1479.7114**	**740.3594**	**1041.5112**	**521.2592**
I	1592.7955	**796.9014**	**970.4741**	**485.7407**
Y	1755.8588	**878.4331**	**857.3900**	**429.1987**
S	1842.8909	**921.9491**	**694.3267**	**347.6670**
N	1956.9338	978.9705	**607.2947**	**304.1510**
N	2070.9767	1035.9920	**493.2518**	**247.1295**
F	2218.0451	**1109.5262**	**379.2088**	**190.1081**
G	2275.0666	1138.0369	**232.1404**	116.5738
R	2431.1677	1216.0875	**175.1190**	88.0631

Peptide sequence 10: TFLAGQDNMLSNINTVATR



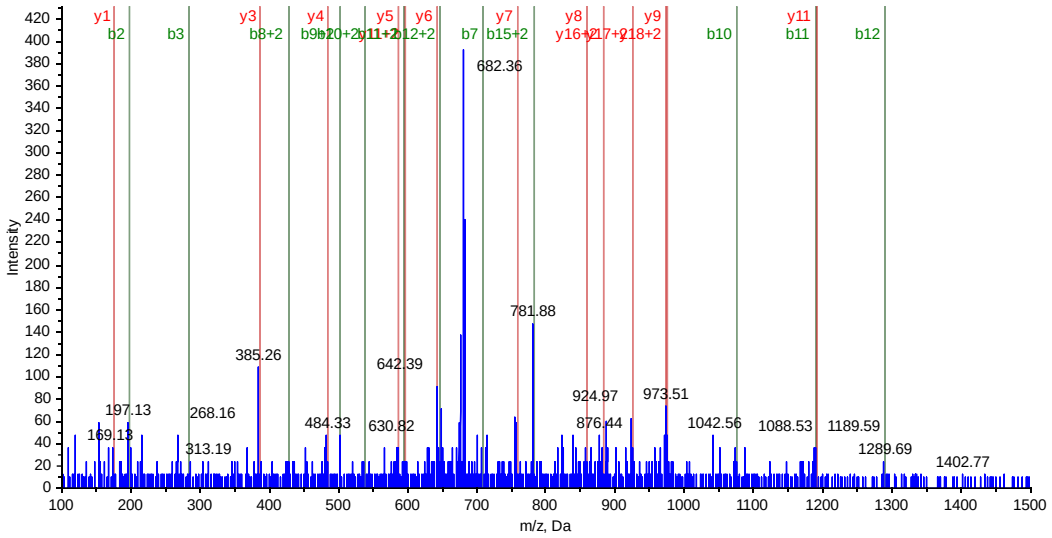
Residue	b	b+2	y	y+2
T	102.0550	51.5311	2066.0335	1033.5204
F	**249.1234**	125.0653	1964.9858	982.9966
L	**362.2074**	181.6074	1817.9174	**909.4623**
A	**433.2445**	217.1259	1704.8334	**852.9203**
G	**490.2660**	245.6366	1633.7962	**817.4018**
Q	**618.3246**	309.6659	1576.7748	788.8910
D	**733.3515**	367.1794	1448.7162	724.8617
N	**847.3945**	**424.2009**	**1333.6893**	667.3483
M	**978.4349**	**489.7211**	**1219.6463**	610.3268
L	**1091.5190**	**546.2631**	**1088.6058**	**544.8066**
S	**1178.5510**	**589.7792**	**975.5218**	**488.2645**
N	**1292.5940**	646.8006	**888.4898**	**444.7485**
I	**1405.6780**	**703.3427**	**774.4468**	**387.7271**
N	1519.7210	760.3641	**661.3628**	331.1850
T	1620.7686	**810.8880**	**547.3198**	274.1636
V	1719.8370	860.4222	**446.2722**	223.6397
A	1790.8742	895.9407	**347.2037**	174.1055
T	1891.9218	946.4646	**276.1666**	138.5870
R	2048.0229	1024.5151	**175.1190**	88.0631

Peptide sequence 11: VPSSVTHFFAN[Dea]TNGTVPLR



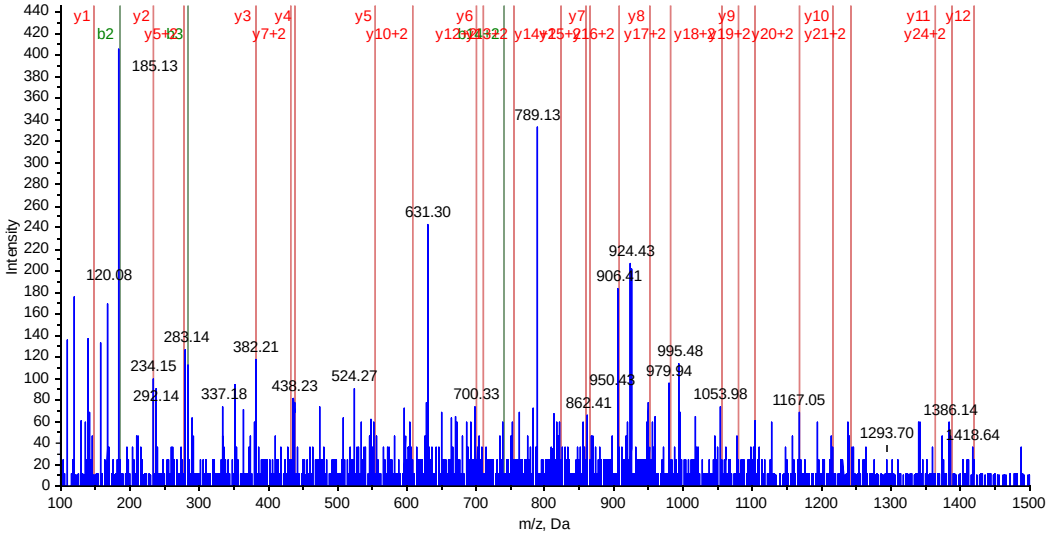
Residue	b	b+2	y	y+2
V	100.0757	50.5415	2045.0451	1023.0262
P	**197.1285**	99.0679	1945.9767	**973.4920**
S	**284.1605**	142.5839	1848.9239	**924.9656**
S	371.1925	186.0999	1761.8919	**881.4496**
V	470.2609	235.6341	1674.8598	837.9336
T	571.3086	286.1579	1575.7914	788.3993
H	**708.3675**	354.6874	1474.7437	737.8755
F	855.4359	**428.2216**	1337.6848	669.3461
F	1002.5043	**501.7558**	**1190.6164**	**595.8118**
A	**1073.5415**	**537.2744**	1043.5480	522.2776
N[Dea]	**1188.5684**	**594.7878**	**972.5109**	486.7591
T	**1289.6161**	**645.3117**	**857.4839**	429.2456
N	1403.6590	702.3331	**756.4363**	378.7218
G	1460.6805	730.8439	**642.3933**	321.7003
T	1561.7281	**781.3677**	**585.3719**	293.1896
V	1660.7966	830.9019	**484.3242**	242.6657
P	1757.8493	879.4283	**385.2558**	193.1315
L	1870.9334	935.9703	288.2030	144.6051
R	2027.0345	1014.0209	**175.1190**	88.0631

Peptide sequence 12: VPSSVTHFFANTN[Dea]GTVPLR



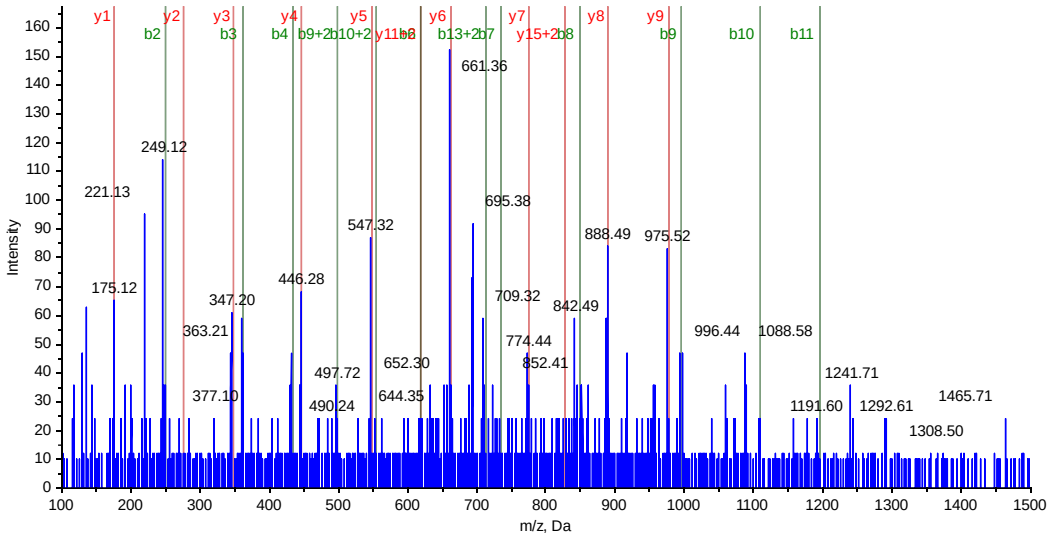
Residue	b	b+2	y	y+2
V	100.0757	50.5415	2045.0451	1023.0262
P	**197.1285**	99.0679	1945.9767	**973.4920**
S	**284.1605**	142.5839	1848.9239	**924.9656**
S	371.1925	186.0999	1761.8919	**881.4496**
V	470.2609	235.6341	1674.8598	837.9336
T	571.3086	286.1579	1575.7914	788.3993
H	**708.3675**	354.6874	1474.7437	737.8755
F	855.4359	**428.2216**	1337.6848	669.3461
F	1002.5043	**501.7558**	**1190.6164**	**595.8118**
A	**1073.5415**	**537.2744**	1043.5480	522.2776
N	**1187.5844**	**594.2958**	**972.5109**	486.7591
T	**1288.6321**	**644.8197**	**858.4680**	429.7376
N[Dea]	1403.6590	702.3331	**757.4203**	379.2138
G	1460.6805	730.8439	**642.3933**	321.7003
T	1561.7281	**781.3677**	**585.3719**	293.1896
V	1660.7966	830.9019	**484.3242**	242.6657
P	1757.8493	879.4283	**385.2558**	193.1315
L	1870.9334	935.9703	288.2030	144.6051
R	2027.0345	1014.0209	**175.1190**	88.0631

Peptide sequence 13: IAVPANVPGHFQVFFPAHSGFHQSYFN[Dea]GFSK

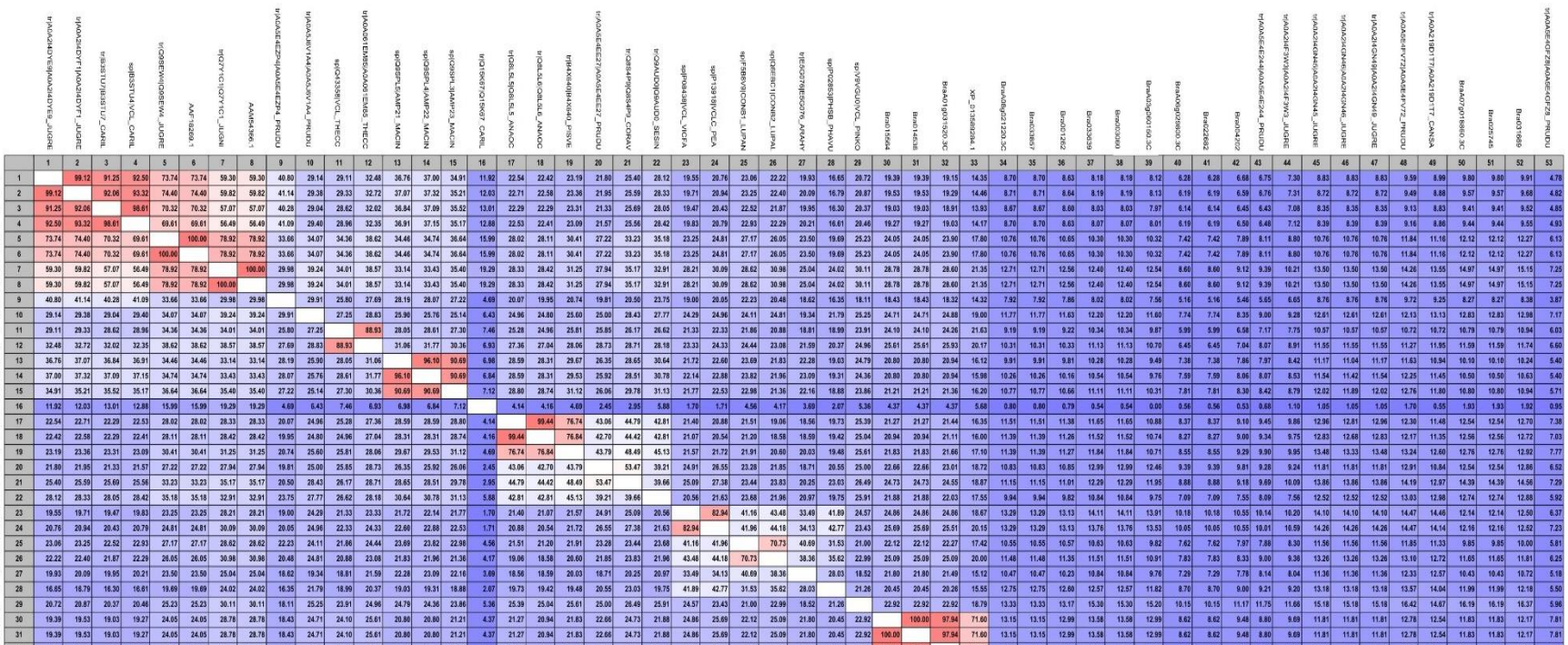


Residue	b	b+2	y	y+2
I	114.0913	57.5493	3435.6698	1718.3385
A	**185.1285**	93.0679	3322.5857	1661.7965
V	**284.1969**	142.6021	3251.5486	1626.2779
P	381.2496	191.1285	3152.4802	1576.7437
A	452.2867	226.6470	3055.4274	1528.2174
N	566.3297	283.6685	2984.3903	1492.6988
V	665.3981	333.2027	2870.3474	1435.6773
P	762.4509	381.7291	2771.2790	**1386.1431**
G	819.4723	410.2398	2674.2262	1337.6167
H	956.5312	478.7693	2617.2048	1309.1060
F	1103.5996	552.3035	2480.1458	**1240.5766**
Q	1231.6582	616.3327	2333.0774	**1167.0424**
V	1330.7266	665.8670	2205.0189	**1103.0131**
F	1477.7950	**739.4012**	2105.9504	**1053.4789**
F	1624.8635	812.9354	1958.8820	**979.9446**
P	1721.9162	861.4618	1811.8136	**906.4104**
A	1792.9533	896.9803	1714.7608	**857.8841**
H	1930.0122	965.5098	1643.7237	**822.3655**
S	2017.0443	1009.0258	1506.6648	**753.8360**
G	2074.0657	1037.5365	**1419.6328**	**710.3200**
F	2221.1342	1111.0707	**1362.6113**	681.8093
H	2358.1931	1179.6002	**1215.5429**	**608.2751**
Q	2486.2516	1243.6295	**1078.4840**	539.7456
S	2573.2837	1287.1455	**950.4254**	475.7164
Y	2736.3470	1368.6771	**863.3934**	**432.2003**
F	2883.4154	1442.2113	**700.3301**	350.6687
N[Dea]	2998.4424	1499.7248	**553.2617**	**277.1345**
G	3055.4638	1528.2355	**438.2347**	219.6210
F	3202.5322	1601.7698	**381.2132**	191.1103
S	3289.5643	1645.2858	**234.1448**	117.5761
K	3417.6592	1709.3333	**147.1128**	74.0600

Peptide sequence 14: TFLAGQDNM[Oxi]LSNINTVATR



Residue	b	b+2	y	y+2
T	102.0550	51.5311	2082.0284	1041.5179
F	**249.1234**	125.0653	1980.9808	990.9940
L	**362.2074**	181.6074	1833.9123	917.4598
A	**433.2445**	217.1259	1720.8283	860.9178
G	490.2660	245.6366	1649.7912	**825.3992**
Q	**618.3246**	309.6659	1592.7697	796.8885
D	**733.3515**	367.1794	1464.7111	732.8592
N	**847.3945**	424.2009	1349.6842	675.3457
M[Oxi]	**994.4299**	**497.7186**	1235.6412	**618.3243**
L	**1107.5139**	**554.2606**	1088.6058	544.8066
S	**1194.5459**	597.7766	**975.5218**	488.2645
N	1308.5889	654.7981	**888.4898**	444.7485
I	1421.6729	**711.3401**	**774.4468**	387.7271
N	1535.7159	768.3616	**661.3628**	331.1850
T	1636.7635	818.8854	**547.3198**	274.1636
V	1735.8320	868.4196	**446.2722**	223.6397
A	1806.8691	903.9382	**347.2037**	174.1055
T	1907.9168	954.4620	**276.1666**	138.5870
R	2064.0179	1032.5126	**175.1190**	88.0631



Employing the 48 full length 7S globulin-like vicilin sequences aligned in Supplementary Table S1, and S5 identified vicilin protein sequences in Supplementary Table S5, a pairwise analysis was undertaken using the CLC Main Workbench software (CLCbio, Katrinebjerg, AarhusN, Denmark) to obtain the number of conserved residues, *upper half* and percent identity, *bottom half*, between the proteins. Upper comparison gradient in the pairwise comparison among the sequences referred the distance

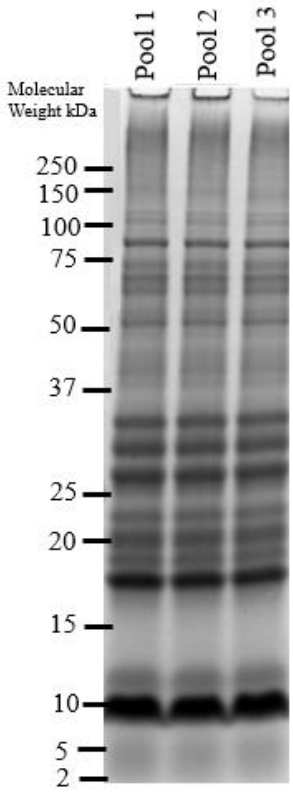
between two sequences, and lower comparison gradient indicated percentage identity between two sequences. The software guided colour gradient will be applied here. The shades of red and blue colour represent, respectively, the maximal and minimal number of identical residues, or percent of identity, between the sequences.

Distance Matrix

Uncorrected for Multiple Substitutions
Gap weighting is 0.000000

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	
0.00	91.98	92.80	91.98	92.88	94.32	94.32	94.12	93.74	92.56	93.74	92.66	95.63	91.98	91.98	91.98	91.68	95.63	92.80	89.01	93.54	91.63	93.74	VCL22_ARATH 1
	0.00	92.59	90.23	93.42	94.83	95.21	97.06	93.68	92.72	93.39	91.79	96.05	92.72	92.72	92.72	93.91	96.05	94.03	92.46	92.15	83.47	90.42	VCL43_ARATH 2
		0.00	93.83	92.60	93.42	93.42	91.18	93.42	92.59	93.00	91.58	94.80	94.03	94.03	94.03	93.21	94.80	90.12	93.53	91.98	94.44	94.24	PAP85_ARATH 3
			0.00	95.34	93.29	93.14	93.14	92.50	93.82	92.80	93.30	92.52	94.07	94.07	94.07	93.91	92.52	93.62	93.75	93.40	90.24	82.04	VCL21_ARATH 4
				0.00	94.79	94.79	98.04	94.79	92.05	94.25	93.15	87.67	90.96	90.96	90.96	92.88	87.67	32.05	91.23	94.79	94.52	93.97	XP_013589284.1 5
					0.00	4.19	95.10	94.15	94.19	93.39	94.38	93.76	93.88	93.88	93.88	94.52	93.76	93.21	93.53	95.05	94.02	93.46	A0A061EM85_THECC 6
						0.00	95.10	93.90	95.05	93.39	94.38	93.76	94.07	94.07	94.07	94.52	93.76	93.21	93.53	95.24	94.02	93.71	VCL_THECC 7
							0.00	93.14	97.06	90.20	93.14	48.04	95.10	95.10	95.10	91.18	48.04	98.04	95.10	97.06	93.14	96.08	Q15K67_CARIL 8
								0.00	96.63	94.55	93.52	94.18	94.65	94.65	94.65	94.73	94.18	93.62	94.18	93.78	94.82	93.97	A0A5J6V1A4_PRUDU 9
									0.00	88.52	94.60	93.97	93.31	93.31	93.31	67.34	93.97	93.42	91.81	94.01	93.63	93.63	A0A5E4FV72_PRUDU 10
										0.00	91.58	93.97	93.58	93.58	93.58	89.45	93.97	95.27	96.34	95.14	93.03	93.00	A0A5E4EE27_PRUDU 11
											0.00	92.66	94.60	94.60	94.60	94.60	92.66	93.95	91.58	93.52	88.98	92.87	VCL_PINKO 12
												0.00	95.01	95.01	95.01	95.84	0.00	95.01	95.69	94.80	93.76	94.39	Q7Y1C1_JUGNI 13
													0.00	0.38	0.19	89.86	95.01	92.39	93.32	93.88	93.43	92.35	A0A2I4GN46_JUGRE 14
														0.00	0.19	89.86	95.01	92.18	93.32	93.88	93.43	92.35	A0A2I4GN49_JUGRE 15
															0.00	89.86	95.01	92.18	93.32	93.88	93.43	92.35	A0A2I4GN45_JUGRE 16
																0.00	95.84	92.18	92.46	92.70	95.13	92.29	A0A219D1T7_CANSA 17
																	0.00	95.01	95.69	94.80	93.76	94.39	AAM54366.1 18
																		0.00	90.95	94.24	95.06	94.44	Bra014536 19
																			0.00	93.75	92.67	92.67	Bra025745 20
																				0.00	89.64	90.97	Bra033857 21
																					0.00	93.23	Bra003060 22
																						0.00	Bra022682 23

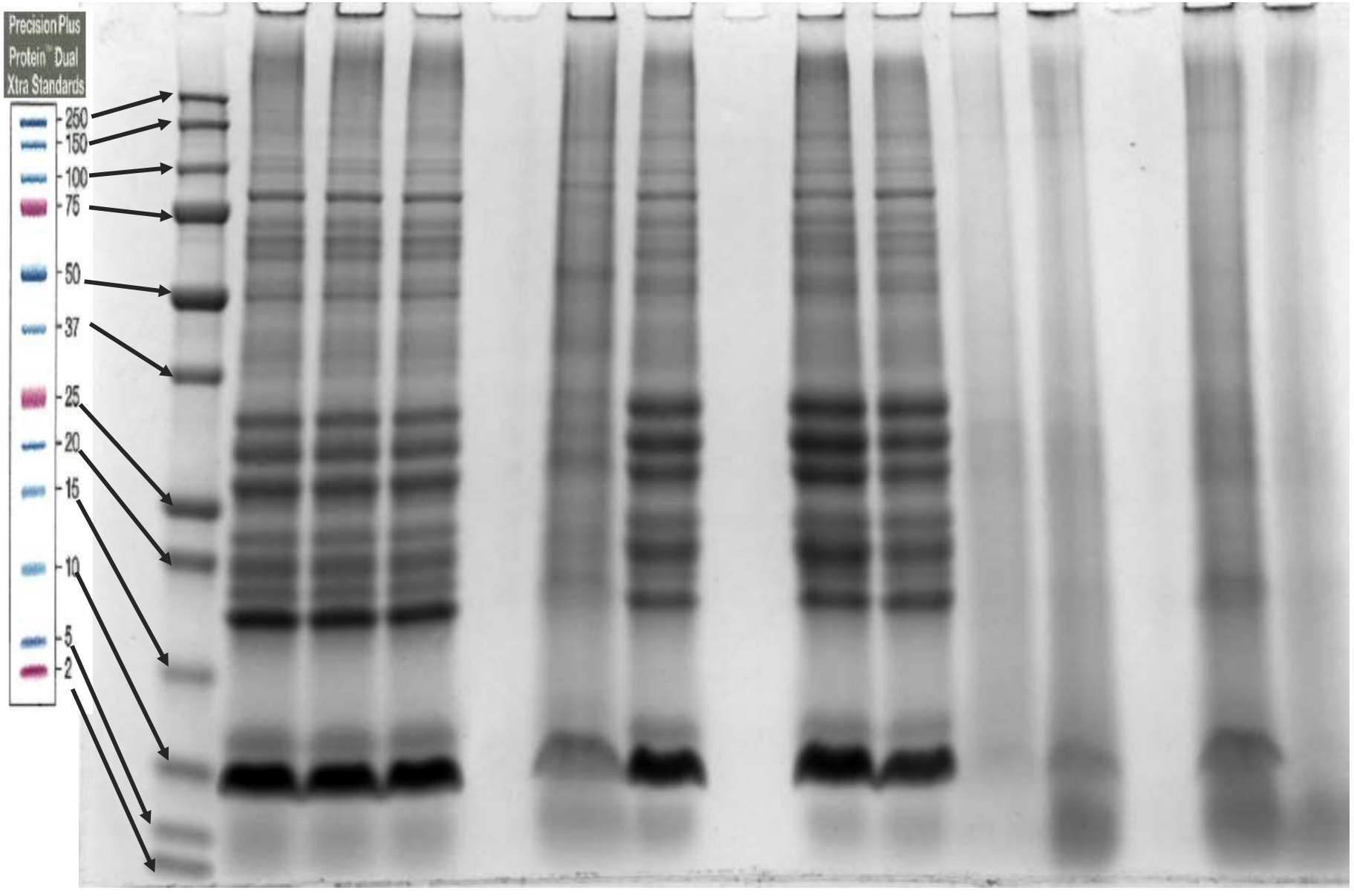
Employing the 18 full length 7S globulin-like vicilin sequences aligned in Supplementary Table S1, and S5 identified vicilin protein sequences in Supplementary Table S5, a Distance matrix was created using the distmat server (https://www.bioinformatics.nl/cgi-bin/emboss/distmat, 3, 08, 2020).


Pool 1
Pool 2
Pool 3
Molecular Weight kDa
250
150
100
75
50
37
25
20
15
10
5
2

Gel 274

Date: 19 January 2020

Lane	L-1	L-2	L- 3	L- 4	L- 5	L- 6	L- 7	L-8	L-9	L-10	L- 11	L-12	L-13	L-14	L-15
Samp	MWM	Pool -1	Pool -1	Pool -1	Blank	10 M	10 N	Blank	24 M	24 N	24 O	24 P	Blank	40 M	40 N
InsVol	Gel-274	6.5	6.5	6.5	-	15.0	6.0	-	7.5	7.0	15.0	7.0	-	13.0	15.0



S1 Table. List of 7S globulin like vicilin sequences.

Sl	Protein name	Gene name	Length	Sequences (5'-3') in FASTA format. OS= Organism species
	Brassica rapa Chiifu-401			
1	*B. rapa* Chiifu-401 Candidate-1			>BraA07g018860.3C B.rapa.Chiifu.Candidate-1 MEKNKRIFTFLLVIMFFHGVMMMRSIGYEGEEEQGGGGRERGGFMMKESRQVIKSEGGEMRVVISPRGRIIEKPMHI GFLTMEPKTLFVPQYLDSNLLIF IREATLGVICKDEFGEKRLKGGDIYWIPAGSAFYLLNTGRGQRLHVICSIDPSQSLGFETFQPFYIGGGPSSVLAGF DPDTITSALNVSRPEVQQLMTSQ VRGPIVHITEHAPTMWTDFLGLRGEEKHKHLKKLLEMKQGTSQEQEFNPWWSWKNIVSSILDVTGEKNRGSGSSKCE DSYNIYDLKNDFENDYGWSKALD YDDYEPLRYSGVGVYLVNLTAGSMMAPHMNPTATEYGIVLSGSGEIQVVLPNGTSAMNMRVSPGDVFWIPRYFAFCQ IASRIAPFEFVGFTTSAYKNRPQ FLVGSNSLLRSLNLTSLAMAFGVDEGTMKRFVEAQREAVILPTASAAPPHEGEPERFGSDHIFT
2	*B. rapa* Chiifu-401 Candidate-2			>BraA08g021220.3C B.rapa.Chiifu.Candidate-2 MIRFTVLSFFVVFVLLFACNESSAKTAKYDKSDESVENDDLAAVPSCCGFSSPLLIKKDQWKPIFANKFGQISTVQI GDGCGGMGPYKIHSITLEPNALM LPLLLHSDMVFFVDSGSGILNWVEAQATSTEIRLGDVYRLRPGTVFYLQSKPVDIFLGTKLKIYAIFSNSQECLHDP CFGAYSSVTDLLFGFDETILKSA FGVPEEIIGLMRNRTQPPLIVHDMLTTPSEANTDTDTNTWPLQTRLLKLFSGDASADSVENKKVKKKKEKKEKKKKP KKATTFNVFESEPDFQSPNGQTI TINRKDLKVLQGSMVGVSMVNLTQGSMMGPHWNPWACEISVVVRGSGMVRVLRNSISRSSSECKNMRFKVEKGDIFA VPRLHPMAQMSFLNDSLVFVGFT TSAKNNEPQFLAGKNSALWSLDREVLAASFNVSSFMIAGLLEAQKEAAVLGCPACAEGELEKLKEDEEKKESPPQQP PQPFQPQPPEEKPQQPPQPFQPQ PPQGEPQKPPQGEPQGPEKPFQPQPGQGEPQEPQASMETKMRDEERKREEEEAKKEEEERWKQEEKLWPTQPQWED
3	*B. rapa* Chiifu-401 Candidate-3			>BraA03g060150.3C B.rapa.Chiifu.Candidate-3 MGPYKIHSITLEPNALLLPLLLHSDMVFFVESGSGILNWVEAEATSSEIRRGDVYRLRPGTVFYLQSKPIDIFLGTK LRVYAIFSNTEECLHDPCFGAYS SITDLLFGFDEAILQSAFGVPEEIIGLMTNRTQPPLIVHDMLSTPGEANTYTWQLQPRLLKLFAGYVSAAEKKKKEK KTKKAKTFNVFESEPDFQSPNGR TITINRKDLEVLSGSMVGVSMVNLTQASMMGPHWNPWACEISIVLKGSGMVRVLRSSISSTSSSSECKNMRFKVEEG DIFAVPRLHPMAQMSFINESLVF IGFTTSARNNEPQFLAGQRSALRLLDQEVLAASLNVSSVMIEGLLGAQKDAVVLGCPYCAEGELEKLKVETEMKKRD DERKREEEEAKKEEEERRKREEE

		EEEEKQWPPLPQQPPE
4	*B. rapa* Chiifu -401 Candidate-4	>BraA06g029800.3C B.rapa.Chiifu.Candidate-4 MSKFTIIPLCLLTLFLCTNSFSDQNDGVPSSQSPLLVKRHQRTQLVATEFGEISAVHIGEEYTIQFITLEPNALLLP LLLHSDMVFFVHTGSGVLNWVDE EKERTLELKRGDVFRLRYGTVFYLHCNLERDEVPEKLRVYAIFDVGKCLSDQCLGAYSSIRDLLWGFDEKTLRSAFA VPKDVFGRLRDAVKPPLITHAMP KNRTQGSEEETWGSRLAKLFVRVEDSIVVDEKDMDALKGSSFGVYMVNLTKGSMMGPHWNPNACEISIVLQGEGMIR VVNHPSYQSKNESERFMVEDGDV FVVPQFYPMAQLSFVNSSFMFMGFSTSAKTNHPQFLVGQNSVLKIFNRDVLATSFNMRYATVERLLGAQKDGLLLEC VSCAEVELSRLMREIEERRRREE EEIERRKREEEEAKRQEEERRRREEEEAERKKKAEEEARKREKERERREEEAAKRREEERRRREEEEAERKRKEEEEA RKREEERKREEEAAKKREEERRK REKEEEEARKREEARERREEEEAKKREEERRKREEEEAERKRRAEEEARERREEEEAKKREEEKEAARRREEEREKEEE MAKRREEERQRKEREDVERKKRE EEEERKRREEEAMRREEERKREEEAAKRAEEERRKREEEAEHKKRPPPQGPQPPIHH
5	*B. rapa* Chiifu Candidate-5	>BraA01g031520.3C B.rapa.Chiifu.Candidate-5 MAINKLTITLFLLISFAVFHCLAFRVEVQEFEPPRQEGQEGPGGGSGEGWDEEATKNPYHFGQWSFKNFFQSKDGFV KMLPKFTKRSSTLFRGIENYRFL FQEMEPNTFLVPHHLDADYVFLVVQGKGVIGFVTDTANESFQITKGDVVRVPSSVTHFFANTNGTVPLRLAKIAVPA NVPGHFQVFFPAHSGFHQSYFTG FSKDVLTASFNIPEELLGRLIRGPQQQVGQGIIRRVSPEQIKELTEHEHATSPSNKHKDKKDKHKDKDRSTFGSPFN LLAQDAIYSNKFGRYHEAHPKRF SQLQDLDIAVGWVNMTQGSLFLPQYNSETTFVTFVENGCARYEMASPYTFQAEQQQPWFGPGQEEEVEEEMSGQVHK IVSRVCKGEVFILPAGHPFAILS QDENFVAVGFGIHASNSTRTFLAGQDNMLSNINTVATRLSFGLGSKLAEKLFTSQNYSHFAPTTPSHQFPEKPKPSF QSIFNLAGF
	Brassica rapa R-o-18	
6	*B. rapa* R-o-18 Candidate-1	>Bra031669 B.rapa.Ro18.Candidate-1 MEKNKRIFTFLLVIVFFHGVMMMRSIGYEGEEEQGGGGRERGGFMMKESRQVIKSEGGEMRVVISPRGRIIEKPMHI GFLTMEPKTLFVPQYLDSNLLIFIRQGEATLGVICKDEFGEKRLKGGDIYWIPAGSAFYLLNTGRGQRLHVICSIDP SQSLGFETFQPFYIGGGPSSVLAGFDPDTITSALNVSRPEVQQLMTSQVRGPIVHITEHAPTMWTDFLGLRGEEKHK HLKKLLELKQGTSQEQEDNPWWSWKNIVSSILDVTGEKNRGSGSSKCEDSYNIYDRKNDFENDYGWSKALDYDDYEP LRYSGVGVYLVNLTAGSMMAPHMNPTATEYGIVLSGSGEIQVVLPNGTSAMNMRVSPGDVFWIPRYFAFCQIASRIA PFEFVGFTTSAYKNRPQFLVGSNSLLRSLNLTSLAMAFGVDEGTMKRFVEAQREAVILPTASAAPPHEGEPERFGSD HIFT
7	*B. rapa* R-o-18 Candidate-2	>Bra001262 B.rapa.Ro18.Candidate-2 MIRFTVLSFFVVFVLLFACNESSAKTAKYDKSDESVENDDLAAVPSCCGFSSPLLIKKDQWKPIFANKFGQISTVQI GDGCGGMGPYKIHSITLEPNALMLPLLLHSDMVFFVDSGSGILNWVEAQATSTEIRLGDVYRLRPGTVFYLQSKPVD

			IFLGTKLKIYAIFSNSQECLHDPCFGAYSSVTDLLFGFDETILKSAFGVPEEIIGLMRNRTQPPLIVHDMLTTPGEA NTDTDTNTWPLQTRLLKLFSGDASADSVENKKVKKEKKEKKEKKKKPKKATTFNVFESEPDFQSPNGQTITINRKDL KVLQGSMVGVSMVNLTQGSMMGPHWNPWACEISVVVRGSGMVRVLRNSISRSSSECKNMRFKVEKGDIFAVPRLHPM AQMSFLNDSLVFVGFTTSAKNNEPQFLAGKNSALWSLDREVLAASFNVSSFMIAGLLEAQKEAAVLGCPACAEGELE KLKEDEEKKESPPQQPPQPFQPQPPGEKPQQPPQPFQPQPPQGEPQKPPQGEPQKPPQGEPEGPQKPFQPQPGQGEP QEPQASMETKMRDEERKREEEEAKKEEEERWKQEEKLWPTQPQWED
8	*B. rapa* R-o-18 Candidate-3		>Bra033639 B.rapa.Ro18.Candidate-3 MTKFTVLPLFVLLFLVLLCTKSWAKSEEFDESSDEENDVAAVPSCCGFSSPLLIKKDQWKPIFGTQFGQISTVQIGE GCGGMGPYKIHSITLEPNALLLPLLLHSDMVFFVESGSGILNWVEAEPTSSEIRRGDVYRLRPGTVFYLQSKPIDIF LGTKLRVYAIFSNTEECLHDPCFGAYSSITDLLFGFDEAILQSAFGVPEEIIGLMTNRTQPPLIVHDMLSTPGEANT YTWQLQVQPRLLKLFAGYVSAAEKKKKEKKTKKAKTFNVFESEPDFQSPSGRTITINRKDLEVLSGSMVGVSMVNLT QASMMGPHWNPWACEISIVLKGSGMVRVLRSSISSTSSSSSSSECKNMRFKVEEGDIFAVPRLHPMAQMSFINESLV FIGFTTSARNNEPQFLAGQRSALRLLDQEVLAASLNVSSVMIEGLLGAQKDAVVLGCPYCAEGELEKLKVETEMKKR DDERKREEEEAKKEEEERRKREEEEEEEKQWPPLPQQPPE
9	*B. rapa* R-o-18 Candidate-4		>Bra004202 B.rapa.Ro18.Candidate-4 MSKFTIIPLCLLTLFLCTNSFSDQNDGVPSSQSPLLVKRHQRTQLVATEFGEISAVHIGEEYTIQFITLEPNALLLP LLLHSDMVFFVHTGSGVLNWVDEEKERTLELKRGDVFRLRYGTVFYLHCNLERDEVPEKLRVYAIFDVGKCLSDQCL GAYSSIRDLLWGFDEKTLRSAFAVPKDVFGRLRDAVKPPLITHAMPKNRTQGSEEETWGSRLAKLFVRVEDVTDHLE MKPVVNKKKKKKKKSSAYNVFESDPDFENDNGQSIVVDEKDMDALKGSSFGVYMVNLTKGSMMGPHWNPNACEISI VLQGEGMIRVVNHPSYQSKNESERFMVEDGDVFVVPQFYPMAQLSFVNSSFMFMGFSTSAKTNHPQFLVGQNSVLKI FNRDVLATSFNMRYATVERLLGAQKDGLLLECVSCAEVELSRLMREIEERRRREEEEIERRKREEEEAKRQEEERRR REEEEAERKKKAEEEARKREKERE REEEAAKRREEERRREEEEAERKRKEEEEARKREEERKREEEAAKKREEERR KREKEEEEARKREEARE REEEEAKKREEERRKREEEEAERKRRAEEEARE REEEEAKKREEEKEAARRREEEREKEE EMAKRREEERQRKERE DVERKKREEEEERKRREEEAMRREEERKREEEAAKRAEEERRKREEEAEHKKRPPPQGPQP PIHH
10	*B. rapa* R-o-18 Candidate-5		>Bra015564 B.rapa.Ro18.Candidate-5 MAINKLTITLFLLISLAVFHCLAFRVEVQEFEPPRQEGQEGPGGGSGEGWDEEATKNPYHFGQWSFKNFFQSKDGFV KMLPKFTKRSSTLFRGIENYRFLFQEMQPNTFLVPHHLDADYVFLVVQGKGVIGFVTDTANESFQITKGDVVRVPSS VTHFFANTNGTVPLRLAKIAVPANVPGHFQVFFPAHSGFHQSYFNGFSKDVLTASFNIPEELLGRLIRGPQQEVGQG IIRRVSPEQIKELTEHEHATSPSNKHKDKKDKHKDKDRSTFGSPFNLLTQDAIYSNNFGRYHEAHPKRFSQLQDLDI AVGWVNMTQGSLFLPQYNSETTFVTFVENGCARYEMASPYTFQGEQQQPWFGPGQEEEVEEEMSGQVHKIVSRVCKG EVFILPAGHPFAILSQDENFVAVGFGIHASNSTRTFLAGQDNMLSNINTVATRLSFGLGSKMAEKLFTSQNYSHFAP TTPSHQFPEKPKPSFQSVFNLVGF
	Brassica oleracea		
11	PREDICTED: vicilin [*Brassica oleracea* var. oleracea]	N/A	>XP_013589284.1 PREDICTED: vicilin [Brassica oleracea var. oleracea] MAINKLTITLFLLISLAVFHCLAFRVEVQEFEPPQQEGQEGHGGGSGEGWDEEATKNPYHFGRWSFKNFF QSQEGFVKMLPKFTKRSSTLFRGIENYRFLFQEMQPNTFLVPHHLDADYVFLVVQGKGVIGFVTDTENES FQITKGDVVRVPSSVTHFFANTNGTVPLRLAKIAVPANVPGHFQVFFPSHSGFHQSYFTGFSKDVLTASF

				NVPEELLGRLIRRPQQQVGQGIIRRVSPDQIKELTEHAISPSNKHKNKKDKHKDKDRSTFGSPFNLLTQD AIYSNDFGRYHEAHPKKFSQLQDLDIAVGWVNMTQGSLFLPQYNSETTFVTFVENGCARYEMASPCTFQG EQQQPWFGPGQEEEV
	Pinus koraiensis (Korean pine)			
12	Vicilin Pin k 2.0101	N/A	463	>sp|V9VGU0|VCL_PINKO Vicilin Pin k 2.0101 OS=Pinus koraiensis OX=88728 PE=1 SV=1 MAFVSLLTILLAISSSSVALTEPVASMADQGVFPEQHGRGHHGVFPEEHGRGHHRGGREE EREENPYVFHSDRFRIRASSEAGEIRALPNFGEVSELLEGISRYRVTCIEMKPNTVMLPH YIDAKWILYVTGGRGYIAYVQQNELVKRKLEEGDVFGVPSGHTFYLVNNDDHNSLRIASL LRTESTMRGEYEPFYVAGGRNPETVYSAFSDDVLEAAFNTDVQKLEHIFGAHRRGVIFYA NEEQIREMMRRGGFSAESTSASEQPKPFNLRNQKPDFENDNGRFTRAGPKDNPFLDSVDV TVGFGVLNPGTMTAPSHNTKATSIAIVMEGEGRIEMACPHLGQEHGWSSPRERGHQDINY ERVRARLRTGTVYVVPAGHPITEIASTNGRLEILWFDINTSGNEREFLAGKNNVLQTLEK EVRHLSFNIPRGEEIEEVLQAQKDQVILRGPQRQRRDEPRSSS
	Prunus dulcis (Almond) (*Amygdalus dulcis*)			
13	Vicilin	N/A	547	>tr|A0A5J6V1A4|A0A5J6V1A4_PRUDU Vicilin OS=Prunus dulcis OX=3755 PE=4 SV=1 MAIKITIKASYKLPFFFFFLSTLFLASSSVTPLINALSDYHNQKCQQSICRGVGGRHSLL RSKDHPQDAREEYFYCSQSCGTSEDPEQCETECRERFDEQLKKEAEEQQKGQEEEEEEGP TFNPNPYYFPKFGLRPRFLAEEGAYFVLGSFARLSHLLRGRIQNYRAALLQTTPGTFVLP YHLDAESIFVVWNGRGTLTLVMKDTKQSFKIENGDVIRVPAGATTYLINNHTTENLSLVQ LFQPVNTPDLFEEFFPAGYKDPEPGSDYSFLHGTESYYSVFSNDLLEAAFDVPREQLEKA FGQQKREGMIIRASKEQLDALSKQAYPWWRKLVPWSMGSDLNFNLLSQRPLHSNNYGKFY EASPQEFKQLQDMNVSVAMLDINPEAMMVPHYNSKATYLMMVVDGMGYFEMACPKFTIPA SEEEMEYQEEQADQQSGVFSKVSGKLSLGDVFVIPAGHPVSIVAQNNNNNNNNNGNQNQK LRIVGFGINAGNNIRNFLAGQEGNIMKQMEREATQLTFGQEMEQVLTSQKQSYFVPASRR GSSTEKA
14	PREDICTED: vicilin	ALMOND_2B017533	534	>tr|A0A5E4FV72|A0A5E4FV72_PRUDU PREDICTED: vicilin OS=Prunus dulcis OX=3755 GN=ALMOND_2B017533 PE=4 SV=1 MGNRVLGFGVLLLVMWYGVSVAVGYTGDPDEDWGRKKEEREGRPGSGDMRRPEYEKPESE KEDWYLLPHSRQVVKTEAGEMSVVMRVGGRVVDKPMHIGFITMEPKSLFIPQYLDSNLVL FVRRGEAKVGLIYRDELGERRLKSGDVYRIPAGSPFYLVNTGEGQRLHIICSLDTSESLG LGSMQSFFIGGGSNPQSVLAGFDHDILTNAFNVSSSELMEVLTSQQKGPIVYLSDSHSPN LWAKFLQLKEQDRLQEMKKMVDFQQEPDHHQDQTQTWSWRKLLNSVFGAGSDDNKKRAED YDKGKGKAPHSYNLYDRKPDFRNNYGWSMELDESDYAPLKDSGVGVYLVNLTAGAMMAPH VNPTATEYGIVLRGSGTIQIVFPNGTSAMNTNVQDGDVFWVPRYFPFCQIASRSGALEFF GFTTSARKNRPQFLAGASSVLQTIRGPELAAAFGVSEDRLRKFIDAQREAVILPSAQAAP PYKEDRQQPREEDEKKQPREGDERKQPKGDDRGTFERVPEVIKSFGTDMFMGFD

15	PREDICTED: vicilin	ALMOND_2B023004	514	>tr|A0A5E4EE27|A0A5E4EE27_PRUDU PREDICTED: vicilin OS=Prunus dulcis OX=3755 GN=ALMOND_2B023004 PE=4 SV=1 MALKSKLLLVALLLSVLFLSVYVASATQDPELKQCRHQCEHQQGFDSKQREQCEQGCDKY IKQKREEEKHRRKSEGGGSFYPISETGRAQEEEEEFQGRQQQDQNPYFFEDEHFETRVQT EEGRFQLLQKFTERSDLLRAIENYRIGFLVTKPHAFVAPSHFDADTVLFVFQGRPAVTIV RGEKRETHNLEHGDLFRIPAGTPVYMVNRDENEKLFIVNFMKPVSVPGEYEAFYAAGGEN PESFFKAFSPQVLQAALKTEINKLERLFGQQRQGSITRASKEPIKKLSQQHGQGGSEGFL PFHGGQSSSDAFNLFSKHPSQANKFGRLFEADFNDFKQLQDLDLLVSFANITQGAMVGPY FNSRATKISFVLDGEGYFEMACPHVSSTGRQEPQPQPEQQPQPQQRRKSSPRYQKISGNL RRGAVFVAPAGHPMTAIASRNSNLQIICFEVNAHDNIRVPLVGKKNVVSQFDREAKELAF NVPAREVDRIFNNQDDEFFFEGPNEQPEHGRAYA
16	PREDICTED: vicilin	ALMOND_2B021144	811	>tr|A0A5E4EZP4|A0A5E4EZP4_PRUDU PREDICTED: vicilin OS=Prunus dulcis OX=3755 GN=ALMOND_2B021144 PE=4 SV=1 MVIHIKPRLPLFLFLSLLFLAFSVSFTLGQDREQHCQKRCQDFKRPIIHSECIYQCRMWG PWSLPPAESSNHHKQQQQHEQEQQCKQRCQPQHGHRQQQQCQQECYEQIRQQREREEMQQ MCQQSCEMQGSGGQQQQRQQCQRQCEQQVEQLKQCQLRCQMQGQGQQQEQCQRTCRQELE DQQRRQQQEQGPGGGDNKLEDETLNGEPRRRFEQCMQGCERQQQGQGEQEQCPRQCREQF DKEKRQYQQCKQSCEKSSQHDDEKRQCKQQCKQQISLQQGGGNQEEDDDALNGSGYGGAK ERFEQCKLSCQSQQGQGQQEQCPKQCKQQFEHEKHQYKQCKRGCENQARDDVQKEQCKQQ CTQQMSQQYGQQQEGSTGGGGLNQQQEEEGQMGSQGQSQSQSQSNNPFYFPSHRFQPRFQ SNEGGLYVLERFTQRQSEVLRGIKNYRLAIFEARPNTFVLPHHCDAEAIYVVLSGQCTCT LLMQDRKESFNMEHGDVIRVPAGATTYLVNNNSDKTLRIAKLLQPVNNPGRFEEFFPAGS RNSESYFSVFSNDILESAFNTPREQLEHGFKQGQQQQGQGIVMRAPREQLQALSQAASSR RRGDRQSQGPFNLRQQRPVHSNNYGQFFEARPEEFNQLQDMDASVSCIEINQQAMMVPHF NSKATHLIMVVEGKGLVEMACPYLANQSQEIMGQQEQQGEQSGRYMKVTAQLSPGDVFVI PAGHPVALVAQNQNLRILGFGLYAQNNKRNFLAGQEDNIIMHMDREARQLAFGPEMEQIF SKQQQSYFVPTQQGRSRNQHLSSILEFAGVI
17	PREDICTED: vicilin seed	ALMOND_2B032650	689	>tr|A0A5E4E244|A0A5E4E244_PRUDU PREDICTED: vicilin OS=Prunus dulcis OX=3755 GN=ALMOND_2B032650 PE=4 SV=1 MLNNKSSNQQPFPFTFFILLFIGLSLPAAKAILRNEEQYGSGASAAAAGSLVKRDQRRAL VVTEYGEISSIDISDGHRGPYHIQFITLEPNSLFLPVLLHADMVFYVHTGSGRLSWGDED DIKRVAIKRGDLFRLRPGSIFFVQSDLQAERQKLRIYAIFATNTDDDLYDPAIGAYSSVR DLVRAFDPKVLRSAFKVSDEVIESIINGTDQSGIVHAVPTKKETFWDLEARFLKTFLTGK DGSAFNKNKKKTKTYNIFDEGPDFKNCNGWSLTVNKKNSQLLKGSNIGLFMVNLTKGSMM GPHWNPRATEIAIVLHGQGMVRVVCSSTAAKKSECKSMRLRVHEGDVFAVPRFHPMAQMS FNNDSLVFMGFSTTTRRNYPQFLAGKYSVLQSLDKQVLAASFNVSNTTVDQLLAAQADSV IIDCTSCAEEEERRMMEEIEKEREEEEAKKWEEEEARKRAEEKEQRKREEEEAARKREEE EAAARKREEEAAAARQREEEAAAARQREEEEAAARQREKEQEAERQREEEQAAKQREEEE

				AKKREGEGRQREEERRQEEETERERQQQKEWERRGQEAQTEQEEARRQQEEREGKERPEE SAREEEGRQREEERRQEEETERERQQQKEWERREQEAQTEQEEARRQQEEREGKERPEES AGRQPEEREGGGRGIDVEEGRRYLRVLKV
18	PREDICTED: vicilin seed	ALMOND_2B028594	332	>tr|A0A5E4GFZ8|A0A5E4GFZ8_PRUDU PREDICTED: vicilin seed OS=Prunus dulcis OX=3755 GN=ALMOND_2B028594 PE=4 SV=1 MGKDRNGSVQERRSKSSEKEDENERKSEKAIEHSDSQSEEDRKRRKSRRKARESSQSSDE KRVRSDRRKRGSRRRYSSESDSDSDSKSESEESGSDSASESESESESDSDRRRKRKRRKE KDDDRERKRRRREKEKKRRREEERKKKKEKRKKKRKEKKEKGNKGAVTNSWGKYGIIRET DMWNKRPEFTAWLAEVKQVNLEHLPNWEEKQMFKQFMEDHNTATFPSKKYYSLDAYYRHK LEKEIKKGYKKVGQTERTVFNDEEQRRQEMMRVREKQKEEEVEALKRSMQSGLAQAMKEQ AQLREEMAYQYKIGNFEAAAAIQRRLDPDAAV
	Juglans regia (English walnut)			
19	Vicilin-like protein	N/A	593	>tr|Q9SEW4|Q9SEW4_JUGRE Vicilin-like protein (Fragment) OS=Juglans regia OX=51240 PE=2 SV=1 RGRDDDDEENPRDPREQYRQCQEYCRRQGQGQRQQQQCQIRCEERLEEDQRSQEERERRR GRDVDDQNPRDPEQRYEQCQQQCERQRRGQEQTLCRRRCEQRRQQEERERQRGRDRQDPQ QQYHRCQRRCQIQEQSPERQRQCQQRCERQYKEQQGRERGPEASPRRESRGREEEQQRHN PYYFHSQSIRSRHESEEGEVKYLERFTERTELLRGIENYRVVILDANPNTSMLPHHKDAE SVAVVTRGRATLTLVSQETRESFNLECGDVIRVPAGATVYVINQDSNERLEMVKLLQPVN NPGQFREYYAAGAKSPDQSYLRVFSNDILVAALNTPRDRLERFFDQQEQREGVIIRASQE KLRALSQHAMSAGQRPWGRRSSGGPISLKSESPSYSNQFGQFFEACPEEHRQLQEMDVLV NYAEIKRGAMMVPHYNSKATVVVYVVEGTGRYEMACPHVSSQSYEGQGRREQEEEESTGR FQKVTARLARGDIFVIPAGHPIAITASQNENLRLLGFDINGENNQRDFLAGQNNIINQLE REAKELSFNMPREEIEEIFESQMESYFVPTERQSRRGQGRDHPLASILDFAFF
20	vicilin-like seed storage protein At2g18540	LOC108995264	681	>tr|A0A2I4F3W3|A0A2I4F3W3_JUGRE vicilin-like seed storage protein At2g18540 OS=Juglans regia OX=51240 GN=LOC108995264 PE=4 SV=1 MIISSQQLSSLDHLQEKTMRNIALISPFSFLFLLLILCQYSFFNLHAAEAFNVSDVGPLV KKDERRSLVATEYGEVTATDISDGIRGLYHLQFITLEPNSLFLPVLLHADMVFYVHTGSG RLRWAEDDDNQMKRVNLRRGDIYMLQAGSIFYVKSSLEPERKKLRIHAMFSNTPDDSYDP LIGAYSSIRNLVRGFDKRVLRAAFKVPEDVIDDITQGTPAPAIVHAVQTKEENFWELEAR FLKVFLGGKGGMTFNKKKKIRAYNILDADPDFENCNGWSLTVTRRNANLLKGSNIGLFMV NLTKGSMMGPHWNPMATEIAIVLQGQGMVRVICSSSAKKPECKNMRLMVKEGDVFAVPRF HPMAQMSFNNDSFVFMGFSTTRRRNHPQFLAGKSSVLQTLDKQALAVSFNVTNSTIDQLL SGQADSFILECTSCAEEEKIILEEEIERERREEEKARKRERREERERREERERREEEARKREE EARKREEREEKEREEREEKEARKREEEARKRQEEEEARKREEEEERREKKEAESKQEEER RRREEEKEQRQEEEGRRERREERESERRERERREEQEQEERQKEEEKRRQEEAEWEEEEARR EEERRRRRQEEEEEARRERERERERKERRRWEEARRERREIQEPAGRQPEEREEQRRQNEKATS EEQEEEDSREGGRRAPRMRWI

21	vicilin-like antimicrobial peptides 2-2 isoform X1	LOC108984611	796	>tr|A0A2I4DYE9|A0A2I4DYE9_JUGRE vicilin-like antimicrobial peptides 2-2 isoform X1 OS=Juglans regia OX=51240 GN=LOC108984611 PE=4 SV=1 MVIKAKIPLFLFLSALFLALVCSSLALETEDLSNELNPHHDPESHRREFQQCQERCQREE RGQRQAQQCQRRCEEQLRERERERERERREEVVNPRDPRQQYEQCRETCEKQDPRQQPQCERR CERQFQEQEERERRERGRGKGDDDQENPRDPREQYRQCQEHCRRQGKGQRQQQQCQSRCE ERFEEEQRRQEERERRRGRDDDDEENPRDPREQYRQCQEYCRRQGQGQRQQQQCQSRCEE RLEEEQRSQEERERRRGRDVDDQNPRDPEQRYEQCQQQCERQRRGQEQTLCRRRCEQRRQ QEERERQRGRDRQDPQQQYHRCQRRCQIQEQSPERQRQCQQRCERQYKEQQGRERGPEAS PRRESRGREEEQQRHNPYYFHSQSIRSRHESEEGEVKYLERFTERTELLRGIENYRVVIL DANPNTFMLPHHKDAESVAVVTRGRATLTLVSQETRESFNLECGDVIRVPAGATVYVINQ DSNERLEMVKLLQPVNNPGQFRFEFVVLQEYYAAGAKSPDQSYLRVFSNDILVAALNTPR DRLERFFDQQEQREGVIIRASQEKLRALSQHAMSAGQRPWGRRSSGGPISLKSERPSYSN QFGQFFEACPEEHRQLQEMDVLVNYAEIKRGAMMVPHYNSKATVVVYVVEGTGRYEMACP HVSSQSYEGQGRREQEEEESTGRFQKVTARLARGDIFVIPAGHPIAITASQNENLRLLGF GINGENNQRNFLAGQNNIINQLEREAKELSFNMPREEIEEIFESQMESYFVPTERQSRRG QGRDHPLASILDFAFF
22	vicilin-like seed storage protein At2g28490 isoform X1	LOC109009328	523	>tr|A0A2I4GN49|A0A2I4GN49_JUGRE vicilin-like seed storage protein At2g28490 isoform X1 OS=Juglans regia OX=51240 GN=LOC109009328 PE=4 SV=1 MKAKMGNRATLLMLVLVLCYGMAKAMAVSFAEEEDFGREKEERKEREQRRSEREEGEEET DDRFLLQDSKSVMRTEAGEMRVIKSLGGKIWDRPLHIGFITMEPQTLFIPQYLDSSLMIF IRRGEAKIGLIYKDELGERRLKTGDLYRIPAGSAFYLVNTAEGQRLHIICSIDPSESLGI GTFQSFFIGGGKYPTSVLAGFERETLSNAFNVSFSEVQDILSRQREGPIVYVPESHSPSV WTKFLQMKERDRLQHLKKLVDFHEPRDDXEEEEEEQQQQITWSWRKLLNSVLGKEPSKRG DKRTRRTPDSYNLYKRRPDFRNNYGWSVALDESDYTPLKHSGISVFLVNLTAGSMMAPHV NPTATEYGIVLSGSGTIQIVYPNGTSAMNAKISEGDVFWVPKYFPFCQIASRTGPLEFFG FTTSARTNRPQFLVGASSILRTMLGPELAAAFGVSEDKLQRFVYAQEEAVILPSPKAAPP NEKMKSKKTGEKEKEKEKEKERMFEEVPKVIKSFGTEMIMGFD
23	vicilin-like antimicrobial peptides 2-3 isoform X2	LOC108984611	789	*Juglans regia (English walnut)* >tr|A0A2I4DYF1|A0A2I4DYF1_JUGRE vicilin-like antimicrobial peptides 2-3 isoform X2 OS=Juglans regia OX=51240 GN=LOC108984611 PE=4 SV=1 MVIKAKIPLFLFLSALFLALVCSSLALETEDLSNELNPHHDPESHRREFQQCQERCQREE RGQRQAQQCQRRCEEQLRERERERERERREEVVNPRDPRQQYEQCRETCEKQDPRQQPQCERR CERQFQEQEERERRERGRGKGDDDQENPRDPREQYRQCQEHCRRQGKGQRQQQQCQSRCE ERFEEEQRRQEERERRRGRDDDDEENPRDPREQYRQCQEYCRRQGQGQRQQQQCQSRCEE RLEEEQRSQEERERRRGRDVDDQNPRDPEQRYEQCQQQCERQRRGQEQTLCRRRCEQRRQ QEERERQRGRDRQDPQQQYHRCQRRCQIQEQSPERQRQCQQRCERQYKEQQGRERGPEAS PRRESRGREEEQQRHNPYYFHSQSIRSRHESEEGEVKYLERFTERTELLRGIENYRVVIL DANPNTFMLPHHKDAESVAVVTRGRATLTLVSQETRESFNLECGDVIRVPAGATVYVINQ

				DSNERLEMVKLLQPVNNPGQFREYYAAGAKSPDQSYLRVFSNDILVAALNTPRDRLERFF DQQEQREGVIIRASQEKLRALSQHAMSAGQRPWGRRSSGGPISLKSERPSYSNQFGQFFE ACPEEHRQLQEMDVLVNYAEIKRGAMMVPHYNSKATVVVYVVEGTGRYEMACPHVSSQSY EGQGRREQEEEESTGRFQKVTARLARGDIFVIPAGHPIAITASQNENLRLLGFGINGENN QRNFLAGQNNIINQLEREAKELSFNMPREEIEEIFESQMESYFVPTERQSRRGQGRDHPL ASILDFAFF
24	vicilin-like seed storage protein At2g28490 isoform X2	LOC109009328	523	>tr|A0A2I4GN45|A0A2I4GN45_JUGRE vicilin-like seed storage protein At2g28490 isoform X2 OS=Juglans regia OX=51240 GN=LOC109009328 PE=4 SV=1 MKAKMGNRATLLMLVLVLCYGMAKAMAVSFAEEEDFGREKEERKEREQRRSEREEGEEET DDRFLLQDSKSVMRTEAGEMRVIKSLGGKIWDRPLHIGFITMEPQTLFIPQYLDSSLMIF IRRGEAKIGLIYKDELGERRLKTGDLYRIPAGSAFYLVNTAEGQRLHIICSIDPSESLGI GTFQSFFIGGGKYPTSVLAGFERETLSNAFNVSFSEVQDILSRQREGPIVYVPESHSPSV WTKFLQMKERDRLQHLKKLVDFHEPRDDDEEEEEEQQQQITWSWRKLLNSVLGKEPSKRG DKRTRRTPDSYNLYKRRPDFRNNYGWSVALDESDYTPLKHSGISVFLVNLTAGSMMAPHV NPTATEYGIVLSGSGTIQIVYPNGTSAMNAKISEGDVFWVPKYFPFCQIASRTGPLEFFG FTTSARTNRPQFLVGASSILRTMLGPELAAAFGVSEDKLQRFVYAQEEAVILPSPKAAPP NEKMKSKKTGEKEKEKEKEKERMFEEVPKVIKSFGTEMIMGFD
25	vicilin-like seed storage protein At2g28490 isoform X3	LOC109009328	523	>tr|A0A2I4GN46|A0A2I4GN46_JUGRE vicilin-like seed storage protein At2g28490 isoform X3 OS=Juglans regia OX=51240 GN=LOC109009328 PE=4 SV=1 MKAKMGNRATLLMLVLVLCYGMAKAMAVSFAEEEDFGREKEERKEREQRRSEREEGEEET DDRFLLQDSKSVMRTEAGEMRVIKSLGGKIWDRPLHIGFITMEPQTLFIPQYLDSSLMIF IRRGEAKIGLIYKDELGERRLKTGDLYRIPAGSAFYLVNTAEGQRLHIICSIDPSESLGI GTFQSFFIGGGKYPTSVLAGFERETLSNAFNVSFSEVQDILSRQREGPIVYVPESHSPSV WTKFLQMKERDRLQHLKKLVDFHEPRDDDEEEEEEQQQQITWSWRKLLNSVLGKEPSKRG DKRTRRTPDSYNLYKRRPDFRNNYGWSVALDESDYTPLKHSGISVFLVNLTAGSMMAPHV NPTATEYGIVLRGSGTIQIVYPNGTSAMNAKISEGDVFWVPKYFPFCQIASRTGPLEFFG FTTSARTNRPQFLVGASSILRTMLGPELAAAFGVSEDKLQRFVYAQEEAVILPSPKAAPP NEKMKSKKTGEKEKEKEKEKERMFEEVPKVIKSFGTEMIMGFD
26	vicilin-like protein precursor, partial [Juglans regia]		593	>AAF18269.1 vicilin-like protein precursor, partial [Juglans regia] RGRDDDDEENPRDPREQYRQCQEYCRRQGQGQRQQQQCQIRCEERLEEDQRSQEERERRRGRDVDDQNPR DPEQRYEQCQQQCERQRRGQEQTLCRRRCEQRRQQEERERQRGRDRQDPQQQYHRCQRRCQIQEQSPERQ RQCQQRCERQYKEQQGRERGPEASPRRESRGREEEQQRHNPYYFHSQSIRSRHESEEGEVKYLERFTERT ELLRGIENYRVVILDANPNTSMLPHHKDAESVAVVTRGRATLTLVSQETRESFNLECGDVIRVPAGATVY VINQDSNERLEMVKLLQPVNNPGQFREYYAAGAKSPDQSYLRVFSNDILVAALNTPRDRLERFFDQQEQR EGVIIRASQEKLRALSQHAMSAGQRPWGRRSSGGPISLKSESPSYSNQFGQFFEACPEEHRQLQEMDVLV NYAEIKRGAMMVPHYNSKATVVVYVVEGTGRYEMACPHVSSQSYEGQGRREQEEEESTGRFQKVTARLAR GDIFVIPAGHPIAITASQNENLRLLGFDINGENNQRDFLAGQNNIINQLEREAKELSFNMPREEIEEIFE SQMESYFVPTERQSRRGQGRDHPLASILDFAFF

	Juglans nigra (Black walnut) (*Wallia nigra*)			
27	Vicilin seed storage protein	N/A	481	>tr|Q7Y1C1|Q7Y1C1_JUGNI Vicilin seed storage protein (Fragment) OS=Juglans nigra OX=16719 PE=2 SV=1 GRDRQDPQQQYHRCQRRCQIQEQSPERQRQCQQRCERQYKEQQGRERGPEASPRRESKGR EEEQQRHNPYYFHSQSIRSRHESEEGEVKYLERFAERTELLRGIENYRVVILDANPNTFM LPHHKDAESVIVVTRGRATLTLVSQETRESFNLECGDVIRVPAGATEYVINQDSNERLEM VKLLQPVNNPGQVREYYAAGAKSPDQSYLRVFSNDILVAALNTPRDRLERFFDQQEQREG VIIRASQEKLRALSQHAMSAGQRPWGRRSSGGPISLKSERPSYSNQFGQFFEACPEEHRQ LQEMDVLVNYAEIKRGAMMVPHYNSKATVVVYVVEGTGRYEMACPHVSSQSFEDQGRREQ EEEESTGRFQKVTARLARGDIFVIPAGHPIAITASQNENLRLLGFGINGENNQRNFLAGQ NSIINQLEREAKELSFNMPREEIEEIFESQMESYFVPTERQSRRGQGRDHPLASILGFAF F
28	Vicilin seed storage protein, partial [Juglans nigra]			>AAM54366.1 vicilin seed storage protein, partial [Juglans nigra] GRDRQDPQQQYHRCQRRCQIQEQSPERQRQCQQRCERQYKEQQGRERGPEASPRRESKGREEEQQRHNPY YFHSQSIRSRHESEEGEVKYLERFAERTELLRGIENYRVVILDANPNTFMLPHHKDAESVIVVTRGRATL TLVSQETRESFNLECGDVIRVPAGATEYVINQDSNERLEMVKLLQPVNNPGQVREYYAAGAKSPDQSYLR VFSNDILVAALNTPRDRLERFFDQQEQREGVIIRASQEKLRALSQHAMSAGQRPWGRRSSGGPISLKSER PSYSNQFGQFFEACPEEHRQLQEMDVLVNYAEIKRGAMMVPHYNSKATVVVYVVEGTGRYEMACPHVSSQ SFEDQGRREQEEEESTGRFQKVTARLARGDIFVIPAGHPIAITASQNENLRLLGFGINGENNQRNFLAGQ NSIINQLEREAKELSFNMPREEIEEIFESQMESYFVPTERQSRRGQGRDHPLASILGFAFF
	Carya illinoinensis (Pecan)			
29	7S vicilin	pec1a1a1	784	>tr|B3STU7|B3STU7_CARIL 7S vicilin (Fragment) OS=Carya illinoinensis OX=32201 GN=pec1a1a1 PE=2 SV=1 ARGFLSALFLALVCSSLALETEDLSNELNPHHDPESHRWEFQQCQERCQHEERGQRQAQQ CQRRCEEQLRERERERREREEIVDPREPRKQYEQCRETCEKQDPRQQPQCERRCERQFQEQ QERERRERRRGRDDDDKENPRDPREQYRQCEEHCRRQGQGQRQQQQCQSRCEERFEEEQR RQEERERRRGRDNDDEENPRDPREQYRQCQEHCRRQGQGQRQQQQCQSRCEERLEEEQRK QEERERRRGRDEDDQNPRDPEQRYEQCQQQCERQRRGQEQQLCRRRCEQQRQQEERERQR GRDRQDPQQQYHRCQRRCQTQEQSPERQRQCQQRCERQYKEQQGREWGPDQASPRRESRG REEEQQRHNPYYFHSQGLRSRHESGEGEVKYLERFTERTELLRGIENYRVVILEANPNTF VLPYHKDAESVIVVTRGRATLTFVSQERRESFNLEYGDVIRVPAGATEYVINQDSNERLE MVKLLQPVNNPGQFREYYAAGAQSTESYLRVFSNDILVAALNTPRDRLERFFDQQEQREG VIIRASQEKLRALSQHAMSAGQRPWGRRSSGGPISLKSQRSSYSNQFGQFFEACPEEHRQ LQEMDVLVNYAEIKRGAMMVPHYNSKATVVVYVVEGTGRFEMACPHDVSSQSYEYKGRRE QEEEESSTGQFQKVTARLARGDIFVIPAGHPIAITASQNENLRLVGFGINGKNNQRNFLA GQNNIINQLEREAKELSFNMPREEIEEIFERQVESYFVPMERQSRRGQGRDHPLASILDF AGFF

30	Vicilin Car i 2.0101	pec2a1a	792	>sp|B3STU4|VCL_CARIL Vicilin Car i 2.0101 OS=Carya illinoinensis OX=32201 GN=pec2a1a PE=1 SV=1 MVTKAKIPLFLFLSALFLALVCSSLALETEDLSNELNPHHDPESHRWEFQQCQERCQHEE RGQRQAQQCQRRCEEQLRERERERERREEIVDPREPRKQYEQCRETCEKQDPRQQPQCERR CERQFQEQQERERRERRRGRDDDDKENPRDPREQYRQCEEHCRRQGQGQRQQQQCQSRCE ERFEEEQRRQEERERRRGRDNDDEENPRDPREQYRQCQEHCRRQGQGQRQQQQCQSRCEE RLEEEQRKQEERERRRGRDEDDQNPRDPEQRYEQCQQQCERQRRGQEQQLCRRRCEQQRQ QEERERQRGRDRQDPQQQYHRCQRRCQTQEQSPERQRQCQQRCERQYKEQQGREWGPDQA SPRRESRGREEEQQRHNPYYFHSQGLRSRHESGEGEVKYLERFTERTELLRGIENYRVVI LEANPNTFVLPYHKDAESVIVVTRGRATLTFVSQERRESFNLEYGDVIRVPAGATEYVIN QDSNERLEMVKLLQPVNNPGQFREYYAAGAQSTESYLRVFSNDILVAALNTPRDRLERFF DQQEQREGVIIRASQEKLRALSQHAMSAGQRPWGRRSSGGPISLKSQRSSYSNQFGQFFE ACPEEHRQLQEMDVLVNYAEIKRGAMMVPHYNSKATVVVYVVEGTGRFEMACPHDVSSQS YEYKGRREQEEEESSTGQFQKVTARLARGDIFVIPAGHPIAITASQNENLRLVGFGINGK NNQRNFLAGQNNIINQLEREAKELSFNMPREEIEEIFERQVESYFVPMERQSRRGQGRDH PLASILDFAGFF
31	Putative vicilin-like seed storage protein	N/A	102	>tr|Q15K67|Q15K67_CARIL Putative vicilin-like seed storage protein (Fragment) OS=Carya illinoinensis OX=32201 PE=4 SV=1 GRDRQDPQQQYHRCQRRCQTQEQSPERQRQCQQRCERQYKEQQGREWGPDQASPRRESRG REEEQQRHNPYYFHSQGLRSRHESGEGEVKYLERFTERTELL
	Phaseolus vulgaris (Kidney bean) (French bean)			
32	Phaseolin, beta-type	N/A	421	>sp|P02853|PHSB_PHAVU Phaseolin, beta-type OS=Phaseolus vulgaris OX=3885 PE=1 SV=2 MMRARVPLLLLGILFLASLSASFATSLREEEESQDNPFYFNSDNSWNTLFKNQYGHIRVL QRFDQQSKRLQNLEDYRLVEFRSKPETLLLPQQADAELLLVVRSGSAILVLVKPDDRREY FFLTSDNPIFSDHQKIPAGTIFYLVNPDPKEDLRIIQLAMPVNNPQIHEFFLSSTEAQQS YLQEFSKHILEASFNSKFEEINRVLFEEEGQQEGVIVNIDSEQIKELSKHAKSSSRKSLS KQDNTIGNEFGNLTERTDNSLNVLISSIEMEEGALFVPHYYSKAIVILVVNEGEAHVELV GPKGNKETLEYESYRAELSKDDVFVIPAAYPVAIKATSNVNFTGFGINANNNNRNLLAGK TDNVISSIGRALDGKDVLGLTFSGSGDEVMKLINKQSGSYFVDAHHHQQEQQKGRKGAFV Y
	Theobroma cacao (Cacao)			
33	Vicilin	CSV	525	>sp|Q43358|VCL_THECC Vicilin OS=Theobroma cacao OX=3641 GN=CSV PE=2 SV=1 MVISKSPFIVLIFSLLLSFALLCSGVSAYGRKQYERDPRQQYEQCQRRCESEATEEREQE QCEQRCEREYKEQQRQQEEELQRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGE HENYHNHKKNRSEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGIN

				DYRLAMFEANPNTFILPHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVSVPAGS TVYVVSQDNQEKLTIAVLALPVNSPGKYELFFPAGNNKPESYYGAFSYEVLETVFNTQRE KLEEILEEQRGQKRQQGQQGMFRKAKPEQIRAISQQATSPRHRGGERLAINLLSQSPVYS NQNGRFFEACPEDFSQFQNMDVAVSAFKLNQGAIFVPHYNSKATFVVFVTDGYGYAQMAC PHLSRQSQGSQSGRQDRREQEEESEEETFGEFQQVKAPLSPGDVFVAPAGHAVTFFASKD QPLNAVAFGLNAQNNQRIFLAGRPFFLNHKQNTNVIKFTVKASAY
34	Vicilin-A, putative	TCM_020665	566	>tr|A0A061EM85|A0A061EM85_THECC Vicilin-A, putative OS=Theobroma cacao OX=3641 GN=TCM_020665 PE=4 SV=1 MVISKSPFIVLIFSLLLSFALLCSGVSAYGRKQYERDPRQQYEQCQRRCESEATEEREQE QCEQRCEREYKEQQRQQEEELQRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGE HENYHNHKKNRSEEEEGQQRNNPYYFPKRRSFQTRFRDEEGNFKILQRFAENSPPLKGIN DYRLAMFEANPNTFILPHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVSVPAGS TVYVVSQDNQEKLTIAVLALPVNSPGKYELFFPAGNNKPESYYGAFSYEVLETVFNTQRE KLEEILEEQRGQKRQQGQQGMFRKAKPEQIRAISQQATSPRHRGGERLAINLLSQSPVYS NQNGRFFEACPEDFSQFQNMDVAVSAFKLNQGAIFVPHYNSKATFVVFVTDGYGYAQMAC PHLSRQSQGSQSGRQDRREQEEESEEETFGEFQQVKAPLSPGDVFVAPAGHAVTFFASKD QPLNAVAFGLNAQNNQRIFLAGKKNLVRQMDSEAKELSFGVPSKLVDNIFNNPDESYFMS FSQQRQRGDERRGNPLASILDFARLF
	Vicia faba (Broad bean) (*Faba vulgaris*)			
35	Vicilin	N/A	463	>sp|P08438|VCL_VICFA Vicilin OS=Vicia faba OX=3906 PE=2 SV=1 MAATTLKDSFPLLTLLGIAFLASVCLSSRSDQDNPFVFESNRFQTLFENENGHIRLLQKF DQHSKLLENLQNYRLLEYKSKPHTIFLPQQTDADFILVVLSGKAILTVLLPNDRNSFSLE RGDTIKLPAGTIGYLVNRDDEEDLRVLDLVIPVNRPGEPQSFLLSGNQNQPSILSGFSKN ILEASFNTDYKEIEKVLLEEHGKEKYHRRGLKDRRQRGQEENVIVKISRKQIEELNKNAK SSSKKSTSSESEPFNLRSREPIYSNKFGKFFEITPKRNPQLQDLNIFVNYVEINEGSLLL PHYNSRAIVIVTVNEGKGDFELVGQRNENQQGLREEYDEEKEQGEEEIRKQVQNYKAKLS PGDVLVIPAGYPVAIKASSNLNLVGFGINAENNQRYFLAGEEDNVISQIHKPVKELAFPG SAQEVDTLLENQKQSHFANAQPRERERGSQEIKDHLYSILGSF
	Pisum sativum (Garden pea)			
36	Vicilin	N/A	459	>sp|P13918|VCLC_PEA Vicilin OS=Pisum sativum OX=3888 PE=2 SV=2 MAATTMKASFPLLMLMGISFLASVCVSSRSDPQNPFIFKSNKFQTLFENENGHIRLLQKF DQRSKIFENLQNYRLLEYKSKPHTIFLPQHTDADYILVVLSGKAILTVLKPDDRNSFNLE RGDTIKLPAGTIAYLVNRDDNEELRVLDLAIPVNRPGQLQSFLLSGNQNQQNYLSGFSKN ILEASFNTDYEEIEKVLLEEHEKETQHRRSLKDKRQQSQEENVIVKLSRGQIEELSKNAK STSKKSVSSESEPFNLRSRGPIYSNEFGKFFEITPEKNPQLQDLDIFVNSVEIKEGSLLL PHYNSRAIVIVTVNEGKGDFELVGQRNENQQEQRKEDDEEEEQGEEEINKQVQNYKAKLS

				SGDVFVIPAGHPVAVKASSNLDLLGFGINAENNQRNFLAGDEDNVISQIQRPVKELAFPG SAQEVDRILENQKQSHFADAQPQQRERGSRETRDRLSSV
37	7S vicilin-like protein	Cs7S	493	>tr|A0A219D1T7|A0A219D1T7_CANSA 7S vicilin-like protein OS=Cannabis sativa OX=3483 GN=Cs7S PE=4 SV=2 MGRIKLTLLVLMLVLSYGVLGIMGFDEDEDWTREKERKKEEEREKERERERDERGELPFIL RDSKHVMKTDAGEMRVMRSSDSKFAQGPLRIGFITMEPKTLFLPQYLDSELTIFIRRGEV KLGFIYKDQLAERKLKTGDVYRISAGSAFYLVNTGEGQRLHIICSFDTSESLRIGTFQSF FLGGGTNPASILSGFDSEILENAFNVTHAELKEILSSQQEGPIVYIPDSRSPKTWAKFLQ LKQEDKLQHLKKIVGFHQGEEEEDEEELEEDINQEQNQKTTWSWRKLLDSLFANRDKKTK DYKGKGKSPDSYNLYDGKKGFKNNYGWSIALDEFSYSPLRKSGCGVYLVNLTAGSMMAPH LNPKATEYGIILKGTGMIQVVYPNGTSAMNTEVKEGDVFWVPRYFPFCQIASRAGPMEFF GFTTSARKNRPQFLVGASSILRSMRGPELAAAFGLSLERLGNLTSYQRESVILPTSAASP PVKLAKPIRSLKE
	Arachis hypogaea (Peanut)			
38	Ara h 1 allergen	ara h 1	619	>tr|E5G076|E5G076_ARAHY Ara h 1 allergen OS=Arachis hypogaea OX=3818 GN=ara h 1 PE=4 SV=1 MRGRVSPLMLLLGILVLASVSATHAKSSPYQKKTENPCAQRCLQSCQQEPDDLKQKACES RCTKLEYDPRCVYDPRGHTGTTNQRSPPGERTRGRQPGDYDDDRRQPRREEGGRWGPAGP RERERREEDWRQPREDWRRPSHQQPRKIRPEGREGEQEWGTPGSHVREETSRNNPFYFPSR RFSTRYGNQNGRIRVLQRFDQRSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQQ GQATVTVANGNNRRALILTRAMHSESHPFHFLHLDDMTPELRVAKSHAVNTPGQFEDFFP ASSRDQSSYLQGFSRNTLEAAFNAEFNEIRRVLLEENAGGEQEERGQRRWSTRSSENNEG VIVEVSKEHVEELTKHAKSVSKKGSEEEGDITNPINLREGEPDLSDNFGRLFEVKPDKKN PQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVINKGTGNLELVAVRKEQQQRGRREQE WEEEEEDEEEEGSNREVRRYTARLKEGDVFIMPAAHPVAINASSELHLLGFGINAENNHR IFLAGDKDNVVDQIEKQAKDLAFPGSGEQVEKLIKNQRESHFVSARPQSQSPSSPEKEDQ EEENQGGKGPLLSILKAFN
	Macadamia integrifolia (Macadamia nut)			
39	Vicilin-like antimicrobial peptides 2-1	AMP2-1	666	>sp|Q9SPL5|AMP21_MACIN Vicilin-like antimicrobial peptides 2-1 OS=Macadamia integrifolia OX=60698 GN=AMP2-1 PE=2 SV=1 MAINTSNLCSLLFLLSLFLLSTTVSLAESEFDRQEYEECKRQCMQLETSGQMRRCVSQCD KRFEEDIDWSKYDNQEDPQTECQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR DPQQQYEQCQKHCQRRETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERM KEEDNKRDPQQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRY EEGEEEQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNA FVLPTHLDADAILLVIGGRGALKMIHHDNRESYNLECGDVIRIPAGTTFYLINRDNNERL

				HIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQTEKLRGVFGQQREGV IIRASQEQIRELTRDDSESRHWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYR QLQDMDLSVFIANVTQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHGGRGGGKR HEEEEDVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLLLFAFGINAQNNHENFLAGR ERNVLQQIEPQAMELAFAAPRKEVEESFNSQDQSIFFPGPRQHQQQSPRSTKQQQPLVSI LDFVGF
40	Vicilin-like antimicrobial peptides 2-2	AMP2-2	666	>sp|Q9SPL4|AMP22_MACIN Vicilin-like antimicrobial peptides 2-2 OS=Macadamia integrifolia OX=60698 GN=AMP2-2 PE=2 SV=1 MAINTSNLCSLLFLLSLFLLSTTVSLAESEFDRQEYEECKRQCMQLETSGQMRRCVSQCD KRFEEDIDWSKYDNQDDPQTDCQQCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR DPQQQYEQCQERCQRHETEPRHMQTCQQRCERRYEKEKRKQQKRYEEQQREDEEKYEERM KEEDNKRDPQQREYEDCRRRCEQQEPRQQYQCQRRCREQQRQHGRGGDLINPQRGGSGRY EEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNA FVLPTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTTFYLINRDNNERL HIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAALNTQAERLRGVLGQQREGV IISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPEDYR QLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEMACPHLSGRHGGRRGGKR HEEEEDVHYEQVKARLSKREAIVVPVGHPVVFVSSGNENLLLFAFGINAQNNHENFLAGR ERNVLQQIEPQAMELAFAAPRKEVEELFNSQDESIFFPGPRQHQQQSSRSTKQQQPLVSI LDFVGF
41	Vicilin-like antimicrobial peptides 2-3	AMP2-3	625	>sp|Q9SPL3|AMP23_MACIN Vicilin-like antimicrobial peptides 2-3 (Fragment) OS=Macadamia integrifolia OX=60698 GN=AMP2-3 PE=1 SV=1 QCMQLETSGQMRRCVSQCDKRFEEDIDWSKYDNQEDPQTECQQCQRRCRQQESDPRQQQY CQRRCKEICEEEEEYNRQRDPQQQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQ QKRYEEQQREDEEKYEERMKEGDNKRDPQQREYEDCRRHCEQQEPRLQYQCQRRCQEQQR QHGRGGDLMNPQRGGSGRYEEGEEKQSDNPYYFDERSLSTRFRTEEGHISVLENFYGRSK LLRALKNYRLVLLEANPNAFVLPTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVI RIPAGTTFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAA LNTQTERLRGVLGQQREGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKR PLYSNKYGQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADV EMACPHLSGRHGGRGGGKRHEEEEEVHYEQVRARLSKREAIVVLAGHPVVFVSSGNENLL LFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAASRKEVEELFNSQDESIFFPGPR QHQQQSPRSTKQQQPLVSILDFVGF
	Anacardium occidentale (Cashew)			
42	Vicilin-like protein	Ana o 1.0101	538	>tr|Q8L5L5|Q8L5L5_ANAOC Vicilin-like protein OS=Anacardium occidentale OX=171929 GN=Ana o 1.0101 PE=2 SV=1 MGPPTKFSFSLFLVSVLVLCLGFALAKIDPELKQCKHQCKVQRQYDEQQKEQCVKECEKY YKEKKGREREHEEEEEEWGTGGVDEPSTHEPAEKHLSQCMRQCERQEGGQQKQLCRFRCQ

				ERYKKERGQHNYKREDDEDEDEDEAEEEDENPYVFEDEDFTTKVKTEQGKVVLLPKFTQK SKLLHALEKYRLAVLVANPQAFVVPSHMDADSIFFVSWGRGTITKILENKRESINVRQGD IVSISSGTPFYIANNDENEKLYLVQFLRPVNLPGHFEVFHGPGGENPESFYRAFSWEILE AALKTSKDTLEKLFEKQDQGTIMKASKEQIRAMSRRGEGPKIWPFTEESTGSFKLFKKDP SQSNKYGQLFEAERIDYPPLEKLDMVVSYANITKGGMSVPFYNSRATKIAIVVSGEGCVE IACPHLSSSKSSHPSYKKLRARIRKDTVFIVPAGHPFATVASGNENLEIVCFEVNAEGNI RYTLAGKKNIIKVMEKEAKELAFKMEGEEVDKVFGKQDEEFFFQGPEWRKEKEGRADE
43	Vicilin-like protein	Ana o 1.0102	536	>tr|Q8L5L6|Q8L5L6_ANAOC Vicilin-like protein (Fragment) OS=Anacardium occidentale OX=171929 GN=Ana o 1.0102 PE=2 SV=1 PPTKFSFSLFLVSVLVLCLGFALAKIDPELKQCKHQCKVQRQYDEQQKEQCVKECEKYYK EKKGREREHEEEEEEWGTGGVDEPSTHEPAEKHLSQCMRQCERQEGGQQKQLCRFRCQER YKKERGQHNYKREDDEDEDEDEAEEEDENPYVFEDEDFTTKVKTEQGKVVLLPKFTQKSK LLHALEKYRLAVLVANPQAFVVPSHMDADSIFFVSWGRGTITKILENKRESINVRQGDIV SISSGTPFYIANNDENEKLYLVQFLRPVNLPGHFEVFHGPGGENPESFYRAFSWEILEAA LKTSKDTLEKLFEKQDQGTIMKASKEQVRAMSRRGEGPKIWPFTEESTGSFKLFKKDPSQ SNKYGQLFEAERIDYPPLEKLDMVVSYANITKGGMSVPFYNSRATKIAIVVSGEGCVEIA CPHLSSSKSSHPSYKKLRARIRKDTVFIVPAGHPFATVASGNENLEIVCFEVNAEGNIRY TLAGKKNIIKVMEKEAKELAFKMEGEEVDKVFGKQDEEFFFQGPEWRKEKEGRADE
	Corylus avellana (European hazel)			
44	48-kDa glycoprotein	N/A	448	>tr|Q8S4P9|Q8S4P9_CORAV 48-kDa glycoprotein OS=Corylus avellana OX=13451 PE=1 SV=1 MLPKEDPELKKCKHKCRDERQFDEQQRRDGKQICEEKARERQQEEGNSSEESYGKEQEEN PYVFQDEHFESRVKTEEGRVQVLENFTKRSRLLSGIENFRLAILEANPHTFISPAHFDAE LVLFVAKGRATITMVREEKRESFNVEHGDIIRIPAGTPVYMINRDENEKLFIVKILQPVS APGHFEAFYGAGGEDPESFYRAFSWEVLEAALKVRREQLEKVFGEQSKGSIVKASREKIR ALSQHEEGPPRIWPFGGESSGPINLLHKHPSQSNQFGRLYEAHPDDHKQLQDLDLMVSFA NITKGSMAGPYYNSRATKISVVVEGEGFFEMACPHLSSSSGSYQKISARLRRGVVFVAPA GHPVAVIASQNNNLQVLCFEVNAHGNSRFPLAGKGNIVNEFERDAKELAFNLPSREVERI FKNQDQAFFFPGPNKQQEEGGRGGRAFE
	Pistacia vera (Pistachio)			
45	Vicilin	N/A	519	>tr|B4X640|B4X640_PISVE Vicilin (Fragment) OS=Pistacia vera OX=55513 PE=2 SV=1 KTDPELKQCKHQCKVQRQYDEEQKEQCAKGCEKYYKEKKGREQEEEEEEEWGSGRGRGDE FSTHEPGEKRLSQCMKQCERQDGGQQKQLCRFRCQEKYKKERREHSYSRDEEEEEEGDEE QEEEDENPYVFEDEHFTTRVKTEQGKVVVLPKFTKRSKLLRGLEKYRLAFLVANPQAFVV PNHMDADSIFFVSWGRGTITKIRENKRESMNVKQGDIIRIRAGTPFYIVNTDENEKLYIV KLLQPVNLPGHYEVFHGPGGENPESFYRAFSREVLEAALKTPRDKLEKLFEKQDEGAIVK ASKEQIRAMSRRGEGPSIWPFTGKSTGTFNLFKKDPSQSNNYGQLFESEFKDYPPLQELD

				IMVSYVNITKGGMSGPFYNSRATKIAIVVSGEGRLEIACPHLSSSKNSGQEKSGPSYKKL SSSIRTDSVFVVPAGHPFVTVASGNQNLEILCFEVNAEGNIRYTLAGKKNIIEVMEKEAK ELAFKTKGEEVDKVFGKQDEEFFFQGPKWRQHQQGRADE
	Sesamum indicum (Oriental sesame)			
46	7S globulin	N/A	585	>tr|Q9AUD0|Q9AUD0_SESIN 7S globulin OS=Sesamum indicum OX=4182 PE=2 SV=1 MSCGGRLCLVLFALLLASAVVASESKDPELKQCKHQCKAQQQISKEQKEACIQACKEYIR QKHQGEHGRGGGDILEEEVWNRKSPIERLRECSRGCEQQHGEQREECLRRCQEEYQREKG RQDDDNPTDPEKQYQQCRLQCRRQGEGGGFSREHCERRREEKYREQQGREGGRGEMYEGR EREEEQEEQGRGRIPYVFEDQHFITGFRTQHGRMRVLQKFTDRSELLRGIENYRVAILEA EPQTFIVPNHWDAESVVFVAKGRGTISLVRQDRRESLNIKQGDILKINAGTTAYLINRDN NERLVLAKLLQPVSTPGEFELFFGAGGENPESFFKSFSDEILEAAFNTRRDRLQRIFGQQ RQGVIVKASEEQVRAMSRHEEGGIWPFGGESKGTINIYQQRPTHSNQYGQLHEVDASQYR QLRDLDLTVSLANITQGAMTAPHYNSKATKIALVVDGEGYFEMACPHMSRSRGSYQGETR GRPSYQRVASRLTRGTVVIIPAGHPFVAVASSNQNLQVLCFEVNANNNEKFPLAGRRNVM NQLEREAKELAFGMPAREVEEVSRSQQEEFFFKGPRQQQQGRADA
	Lupinus angustifolius (Narrow-leaved blue lupine)			
47	Conglutin beta 1	BETA1	611	>sp|F5B8V9|CONB1_LUPAN Conglutin beta 1 OS=Lupinus angustifolius OX=3871 GN=BETA1 PE=1 SV=1 MAKMRVRLPMLILLLGVVFLLAASIGIAYGEKDFTKNPPKEREEEEHEPRQQPRPRQQEE QEREHRREEKHDGEPSRGRSQSEESQEEEHERRREHHRREREQEQQPRPQRRQEEEEEEEE WQPRRQRPQSRREEREEREQEQGSSSGSQRGSGDERRQHRERRVHREEREQEQDSRSDSR RQRNPYHFSSNRFQTYYRNRNGQIRVLERFNQRTNRLENLQNYRIIEFQSKPNTLILPKH SDADFILVVLNGRATITIVNPDKRQVYNLEQGDALRLPAGTTSYILNPDDNQNLRVAKLA IPINNPGKLYDFYPSTTKDQQSYFSGFSKNTLEATFNTRYEEIERVLLGDDELQENEKQR RGQEQSHQDEGVIVRVSKKQIQELRKHAQSSSGEGKPSESGPFNLRSNKPIYSNKFGNFY EITPDINPQFQDLNISLTFTEINEGALLLPHYNSKAIFIVVVDEGEGNYELVGIRDQQRQ QDEQEEEYEQGEEEVRRYSDKLSKGDVFIIPAGHPLSINASSNLRLLGFGINANENQRNF LAGSEDNVIKQLDREVKELTFPGSIEDVERLIKNQQQSYFANAQPQQQQQREKEGRRGRR GPISSILNALY
	Lupinus albus (White lupine)			
48	Conglutin beta 2	N/A	533	>sp|Q6EBC1|CONB2_LUPAL Conglutin beta 2 OS=Lupinus albus OX=3870 PE=1 SV=1 MGKMRVRFPTLVLVLGIVFLMAVSIGIAYGEKDVLKSHERPEEREQEEWQPRRQRPQSRR EEREQEQEQGSPSYPRRQSGYERRQYHERSEQREEREQEQQQGSPSYSRRQRNPYHFSSQ RFQTLYKNRNGKIRVLERFDQRTNRLENLQNYRIVEFQSKPNTLILPKHSDADYVLVVLN GRATITIVNPDRRQAYNLEYGDALRIPAGSTSYILNPDDNQKLRVVKLAIPINNPGYFYD FYPSSTKDQQSYFSGFSRNTLEATFNTRYEEIQRIILGNEDEQEYEEQRRGQEQSDQDEG

	VIVIVSKKQIQKLTKHAQSSSGKDKPSDSGPFNLRSNEPIYSNKYGNFYEITPDRNPQVQ DLNISLTYIKINEGALLLPHYNSKAIYVVVVDEGEGNYELVGIRDQQRQQDEQEEKEEEV IRYSARLSEGDIFVIPAGYPISINASSNLRLLGFGINADENQRNFLAGSKDNVIRQLDRA VNELTFPGSAEDIERLIKNQQQSYFANGQPQQQQQQQSEKEGRRGRRGSSLPF

Brassica rapa candidate 7S globulins/vicilin sequences identified and characterised according to the same method described in (Rahman et al., 2020a) and sequences of 7S globulins/vicilin protein genes reported in *A. thaliana* and some other species available in the public domain databases.* Entries are included from Uniprot and NCBI protein database search with the key word “vicilin” and “7S globulin”. The entries other than these two key words were included based on the published literature (Jimenez-Lopez et al., 2016).

S2 Table. Sequences of oleosin protein genes reported in *A. thaliana* and some other species available in the public domain databases.

Sl.	Oleosins Sequence (5'-3') in FASTA format. OS= Organism species.
1	>sp|Q9LY09|GRP17_ARATH Oleosin GRP-17 OS=Arabidopsis thaliana OX=3702 GN=GRP17 PE=1 SV=1 MSEELSQKPSSAQSLSLREGRNRFPFLSLSQREGRFFPSLSLSERDGRKFSFLSMFSFLM PLLEVIKIIIASVASVIFVGFACVTLAGSAAALVVSTPVFIIFSPVLVPATIATVVLATG FTAGGSFGATALGLIMWLVKRRMGVKPKDNPPPAGLPPNSGAGAGGAQSLIKKSKAKSKG GLKAWCKKMLKSKFGGKKGKSGGGKSKFGGKGGKSEGEEGMSSGDEGMSGSEGGMSGGEG GKSKSGKGKLKAKLEKKKGMSGGSESEEGMSGSEGGMSGGGGSKSKSKKSKLKAKLGKKK GMSGGMSGSEEGMSGSEGGMSSGGGSKSKSKKSKLKAKLGKKKSMSGGMSGSEEGMSGSE GGMSGGGGGKSKSRKSKLKANLGKKKCMSGGMSGSEGGMSRSEGGISGGGMSGGSGSKHK IGGGKHGGLGGKFGKKRGMSGSGGGMSGSEGGVSGSEGSMSGGGMSGGSGSKHKIGGGKH GGLRGKFGKKRGMSGSEGGMSGSEGGMSESGMSGSGGGKHKIGGGKHKFGGGKHGGGGGH MAE
2	>sp|Q9SQ57|PXG_SESIN Peroxygenase OS=Sesamum indicum OX=4182 GN=SOP1 PE=1 SV=1 MATHVLAAAAERNAALAPDAPLAPVTMERPVRTDLETSIPKPYMARGLVAPDMDHPNGTP GHVHDNLSVLQQHCAFFDQDDNGIIYPWETYSGLRQIGFNVIASLIMAIVINVALSYPTL PGWIPSPFFPIYLYNIHKAKHGSDSGTYDTEGRYLPMNFENLFSKHARTMPDRLTLGELW SMTEANREAFDIFGWIASKMEWTLLYILARDQDGFLSKEAIRRCYDGSLFEYCAKMQRGA EDKMK
3	>sp|Q00650|OLNB1_BRANA Oleosin-B1 OS=Brassica napus OX=3708 GN=OlnB1 PE=1 SV=2 MGILRKKKHERNASFKSVLTSILATQAATFLLLISGVSLAGTAAAFIATMPLFVVFSPIL VPAGITTGLLTTGLAAAGGAGATAVTIILWLYKRATGKEPPAVLSKVLKKIIPGAAAAPR AAPAAAPAAAPAAAPAAAPAPKPAAAPAPKPAAPPAL
4	>sp|Q39165|OLEO2_ARATH Oleosin 21.2 kDa OS=Arabidopsis thaliana OX=3702 GN=At5g40420 PE=2 SV=1 MADTHRVDRTDRHFQFQSPYEGGRGQGQYEGDRGYGGGGYKSMMPESGPSSTQVLSLLIG VPVVGSLLALAGLLLAGSVIGLMVALPLFLLFSPVIVPAALTIGLAMTGFLASGMFGLTG LSSISWVMNYLRGTRRTVPEQLEYAKRRMADAVGYAGQKGKEMGQHVQNKAQDVKQYDIS KPHDTTTKGHETQGRTTAA
5	>sp|Q43402|OLNB6_BRANA Oleosin-B6 OS=Brassica napus OX=3708 GN=OlnB6 PE=1 SV=3 MKEEIQNETAQTQLQREGRMFSFLFPVIEVIKVVMASVASVVFLGFGGVTLACSAVALAV

STPLFIIFSPILVPATIATTLLATGLGAGTTLGVTGMGLLMRLIKHPGKEGAASAPAAQP
SFLSLLEMPNFIKSKMLERLIHIPGVGKKSEGRGESKGKKGKKGKSEHGRGKHEGEGKSK
GRKGHRMGVNPENNPPPAGAPPTGSPPAAPAAPEAPAAPAAPAAPAAPAAPAAPAAPEDP
AAPAAPEAPATPAAPPAPAAAPAPAAPAAPPAPAAPPRPPSFLSLLEMPSFIKSKLIEAL
INIPGFGKKSNDRGKSKGGKKSKGKGKSNGRGKHEGEGKSKSRKSKSRGKDKEKSKGKGI
FGRSSRKGSSDDESS

6 >sp|P29525|OLEO1_ARATH Oleosin 18.5 kDa OS=Arabidopsis thaliana OX=3702 GN=At4g25140 PE=2 SV=1
MADTARGTHHDIIGRDQYPMMGRDRDQYQMSGRGSDYSKSRQIAKAATAVTAGGSLLVLS
SLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWIYKYA
TGEHPQGSDKLDSARMKLGSKAQDLKDRAQYYGQQHTGGEHDRDRTRGGQHTT

7 >sp|Q42431|OLEO4_ARATH Oleosin 20.3 kDa OS=Arabidopsis thaliana OX=3702 GN=OL2 PE=2 SV=1
MANVDRDRRVHVDRTDKRVHQPNYEDDVGFGGYGGYGAGSDYKSRGPSTNQILALIAGVP
IGGTLLTLAGLTLAGSVIGLLVSIPLFLLFSPVIVPAALTIGLAVTGILASGLFGLTGLS
SVSWVLNYLRGTSDTVPEQLDYAKRRMADAVGYAGMKGKEMGQYVQDKAHEARETEFMTE
THEPGKARRGS

8 >sp|Q42626|OLNB3_BRANA Oleosin-B3 OS=Brassica napus OX=3708 GN=OlnB3 PE=1 SV=1
MRNEIQNETAQTDQTQGSMFSFFNLFPFLLPMFEVIKMVVASVASVVYLGFAGVTLSGSA
VALAVSTPLFIIFSPILLPAIAATTVLAAGLGSKKVAAAPAASPSLSLLGIPESIKPSNV
IPESIKPSNIIPESIKPSNIIPVSIKPSNIKDKIKDTIGKVKNKIKAKQEEKSKGKSEDS
SKGKGKSKGEDTTTDEDKHGKGESKHGKGESKHGKGESTHGKGGKHGSEGSSMDEGKHGG
KHGSGGSPMGGGKHGSGGKHESGGSPMGGGKHGSGGKHESGGASMGGGKHESVGKHGSGG
KHESGGSPMGGGKHGSGGKHESGGASMGGGKHGSGGRHEGGGSAMGGGKHGSGGKHGSEG
KHGGEGSSMGKNSLSKNKKEFHYRGQAMDASSTSESSDGSSSDGSSSDGSSSDGSSHGSG
GKHI

9 >sp|Q42627|OLNB4_BRANA Oleosin-B4 OS=Brassica napus OX=3708 GN=OlnB4 PE=1 SV=1
MRNEIQNETAQTDQTQGSMFSFFNLFPFLLPMFEVIKMVVASVASVVYLGFAGVTLSGSA
VALAVSTPLFIIFSPILLPAIAATTVLAAGLGGKKVAAAPEASPAASPSLSLLGIPESIK
PSNIIPESIKPSNIIPEGIKPSNIKDKIKDTIGKVKNKIKAKKEEKSKGKSEDSSKGKGK
SKGEDTTTDDDTTTDEDKHGSGAKHGKGESKHGKGESTHGKGGKHGSEGKHGSGGSSMGG
GKHGSGGKHETGGKHGSGGKHESGGSPMGGGKHGSEGKHGSGGASMGGGKHGSGGKHESG
GSAMGGGKHGSGGKHGSEGKHGGEGSSMGKNSLSKKKKEFHYRGQAMDASSTSESSDGSS

DGSSSDGSSHGSGGKHI

10 >sp|P29526|OLNB2_BRANA Oleosin-B2 (Fragment) OS=Brassica napus OX=3708 GN=OlnB2 PE=1 SV=1
QASIFSRFFRMFSFIFPFVNVIKLIIASVTSLVCLAFSCVALGGSAVALIVSTPLFIMFS
PILVPATIATTLLASGLMAGTTLGLTGIGLIMGLVRTAGGVSLLQSPLRKIIVNRIKARL
GGGGGGSRLARLKKILGLLNKLRGMGAGGAAAPAAEPAPAAEAAPAAEAAPAAAPAAAPA
AAP

11 >sp|P29531|OLEO2_SOYBN P24 oleosin isoform B OS=Glycine max OX=3847 PE=2 SV=1
MTTVPPHSVQVHTTTHRYEAGVVPPARFEAPRYEAGIKAPSSIYHSERGPTTSQVLAVVA
GLPVGGILLLLAGLTLAGTLTGLVVATPLFIIFSPVLIPATVAIGLAVAGFLTSGVFGLT
ALSSFSWILNYIRETQPASENLAAAAKHHLAEAAEYVGQKTKEVGQKTKEVGQDIQSKAQ
DTREAAARDARDAREAAARDARDAKVEARDVKRTTVTATTATA

12 >sp|P29530|OLEO1_SOYBN P24 oleosin isoform A OS=Glycine max OX=3847 PE=2 SV=2
MTTQVPPHSVQVHTTTTHRYEAGVVPPGARFETSYEAGVKAASIYHSERGPTTSQVLAVL
AGLPVGGILLLLAGLTLAGTLTGLAVATPLFVLFSPVLVPATVAIGLAVAGFLTSGAFGL
TALSSFSWILNYIRETQPASENLAAAAKHHLAEAAEYVGQKTKEVGQKTKEVGQDIQSKA
QDTREAAARDAREAAARDAREAAARDAKVEARDVKRTTVTATTATA

13 >sp|C3S7F1|OLES2_BRANA Oleosin S2-2 OS=Brassica napus OX=3708 GN=S2 PE=1 SV=1
MATVERRVQVDPTDKRIHLQPQYEGDVGYGYGYGGRADYKSSGPSSNQIVALIVGVPVGG
SLLALAGLTLAGSVIGLMLSVPLFLLFSPVIVPAAITIGLAVTAILASGLFGLTGLSSVS
WVLNYLRGTSDTVPEQLDYAKRRMADAVGYAGQKGKEMGQYVQDKAHEAHDTSLTTETTE
PGKTRRHT

14 >sp|C3S7F0|OLES1_BRANA Oleosin S1-2 OS=Brassica napus OX=3708 GN=S1 PE=1 SV=1
MADVRTHAHQVQVHPLRQHEGGIKVVYPQSGPSSTQVLAVVAGVPVGGTLLTLAGLTLAV
SVIGLILAFPLFLIFSPVIVPAAFVIGLAMTGFMASGAIGLTGLSSMSWVLNHIRRVRER
IPDELDEAKQRLADMAEYAGQRTKDAGQTIEDKAHDVRESKTYDVRDRDTKGHTASGGDR
DTKTTREVRVATT

15 >sp|P29110|OLEO3_BRANA Oleosin Bn-III OS=Brassica napus OX=3708 PE=2 SV=1
MTDTARTHHDITSRDQYPRDRDQYSMIGRDRDQYSMMGRDRDQYNMYGRDYSKSRQIAKA
VTAVTAGGSLLVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVAMLITGFLSSGGFG
IAAITVFSWIYKYATGEHPQGSDKLDSARMKLGSKAQDLKDRAQYYGQQHTGGYGQQHTG
GEHDRDRTRGTQHTT

16 >sp|P29109|OLEO5_BRANA Oleosin Bn-V (Fragment) OS=Brassica napus OX=3708 PE=2 SV=1

PARTHHDITTRDQYPLISRDRDQYGMIGRDQYNMSGQNYSKSRQIAKATTAVTAGDSLLV
LSSLTLVGTVIALIVATPLLVIFSPILVPALITVALLITGFLSSGAFGIAAITVFSWIYK
YATGEHPQGSDKLDSARMKLGSKAQDMKDRAYYYGQQHTGEEHDRDRDHRTDRDRTRGTQ
HTT

17 >sp|P29111|OLEO2_BRANA Major oleosin NAP-II (Fragment) OS=Brassica napus OX=3708 PE=1 SV=1
RRDQYPRDRDQYSMIGRDRDKYSMIGRDRDQYNMYGRDYSKSRQIAKAVTAVTAGGSLLV
LSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWIYK
YATGEHPQGSDKLDSARMKLGGKVQDMKDRAQYYGQQQTGGEDDRDRTRGTQHTT

18 >tr|Q9XI93|Q9XI93_ARATH At1g13930/F16A14.27 OS=Arabidopsis thaliana OX=3702 GN=F7A19.2 PE=1 SV=1
MNFISDQVKKLSSSTPEEPDHNKPVEGTETATRPATNAELMASAKVVAEAAQAAARNESD
KLDKGKVAGASADILDAAEKYGKFDEKSSTGQYLDKAEKYLNDYESSHSTGAGGPPPPTS
QAEPASQPEPAAKKDDEESGGGLGGYAKMAQGFLK

19 >sp|Q43284|OLEO3_ARATH Oleosin 14.9 kDa OS=Arabidopsis thaliana OX=3702 GN=OL3 PE=2 SV=2
MADQTRTHHEMISRDSTQEAHPKARQMVKAATAVTAGGSLLVLSGLTLAGTVIALTVATP
LLVIFSPVLVPAVVTVALIITGFLASGGFGIAAITAFSWLYRHMTGSGSDKIENARMKVG
SRVQDTKYGQHNIGVQHQQVS

20 >sp|Q43804|OLEO1_PRUDU Oleosin 1 OS=Prunus dulcis OX=3755 GN=OLE1 PE=2 SV=1
MADQHFQQPLHFQGSYGQQQPRSYQVAKAATAVTAGGSLLVLSGLVLAGTVIALTIATPL
LVIFSPVLVPALITVALITMGFLTSGGFGVAAVTVLSWIYKYVTGKQPPGADQLDQARHK
LAGKARDIKDRAEQFGQQHVPSGQQQSS

21 >sp|P29529|OLEO_HELAN Oleosin (Fragment) OS=Helianthus annuus OX=4232 PE=2 SV=1
TTTTYDRHFTTTQPHYRQDDRSRYDQQTHSQSTSRTLAIIALLPVGGILLGLAALTFIGT
LIGLALATPLFVIFSPIIVPAVLTIGLAVTGFLASGTFGLTGLSSLSYLFNMVRQTAGSV
PESLDYVKGTLQDAGEYAGQKTKDFGQKIQSTAHEMGDQGQVGVHAQVGGGKEGRKSGDR
T

22 >sp|Q9SS98|OLEO5_ARATH Oleosin 5 OS=Arabidopsis thaliana OX=3702 GN=At3g01570 PE=2 SV=1
MADVRTHSHQLQVHPQRQHEGGIKVLYPQSGPSSTQVLAVFVGVPIGGTLLTIAGLTLAG
SVIGLMLAFPLFLIFSPVIVPAAFVIGLAMTGFLASGAIGLTGLSSMSWVLNYIRRAGQH
IPEELEEAKHRLADMAEYVGQRTKDAGQTIEDKAHDVREAKTFDVRDRDTTKGTHNVRDT
KTT

23 >tr|Q9LY08|Q9LY08_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=ATGRP-6 PE=2 SV=1
MLSFLIPVVQFFQVVIAAVASVVFLVFAGITFGASIVGLTIATPLFVIFSPILVPATIAT
TFLVGGATAAVALGVTAFALILWLFKHRIGVKPKNNPAPKGAPTKADQPGASGGASGDKP
GEMSGAGGPSGDKPGGASGGGDKPGGASGGGPGGASGGASGGASGGASGGASGGASGGGP
GGASGGGPGGASGGGPGGASGGASGDKPEGAPGDKPGGAWGGKPGKKPGHKPEGARGGKR
LAWW
24 >tr|Q42574|Q42574_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=ATGRP19 PE=2 SV=1
MFEIIQAVFSAGVALALLTFAGITLGGSVVACIISTPLFVIFSPVLVPATIATTLLASGF
TASGSFGATAFTILSWLYKKRTGRDLPKIPGLTPPAPASNPAGSGV
25 >tr|G7I2Z9|G7I2Z9_MEDTR Oleosin OS=Medicago truncatula OX=3880 GN=11420287 PE=3 SV=1
MADTGGHYQPLRGYNQQHSTTTQQQPSSKLTQLLKSSTAVTAGGSLLILSGLVLAGTVIA
LTIATPLFLLFSPVLVPAVITVALLTLGFFVSGGFGVAAITVLAWIYRYVTGKHPPGADQ
LDTARHKLMNKAREIKDYGQQQISGTQNS
26 >tr|D7MGJ2|D7MGJ2_ARALL Oleosin OS=Arabidopsis lyrata subsp. lyrata OX=81972
GN=ARALYDRAFT_492319 PE=3 SV=1
MADTGRTTHHDIIGRDQYPMIGRDRDQYQMSGRGSDYSKSRQIAKAATAVTAGGSLLVLS
SLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWIYKYA
TGEHPQGSDRLDSARMKLGSKAQDLKDRAQYYGQQHTGGEHDRDRTRVGQHTT
27 >tr|A0A1P8BDM8|A0A1P8BDM8_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=GRP17 PE=3
SV=1
MSEELSQKPSSAQSLSLREGRNRFPFLSLSQREGRFFPSLSLSERDGRKFSFLSMFSFLM
PLLEVIKIIIASVASVIFVGFACVTLAGSAAALVVSTPVFIIFSPVLVPATIATVVLATG
FTAGGSFGATALGLIMWLVKRRMGVKPKDNPPPAGLPPNSGAGAGGAQSLIKKSKAKSKG
GLKAWCKKMLKSKFGGKKGKSGGGKSKFGGKGGKSEGEEGMSSGDEGMSGSEGGMSGGEG
GKSKSGKGKLKAKLEKKKGMSGGSESEEGMSGSEGGMSGGGGSKSKSKKSKLKAKLGKKK
GMSGGMSGSEEGMSGSEGGMSSGGGSKSKSKKSKLKAKLGKKKSMSGGMSGSEEGMSGSE
GGMSGGGGGMSGSEGGMSRSEGGISGGGMSGGSGSKHKIGGGKHGGLGGKFGKKRGMSGS
GGGMSGSEGGVSGSEGSMSGGGMSGGSGSKHKIGGGKHGGLRGKFGKKRGMSGSEGGMSG
SEGGMSESGMSGSGGGKHKIGGGKHKFGGGKHGGGGGHMAE
28 >tr|I1N747|I1N747_SOYBN Oleosin OS=Glycine max OX=3847 GN=GLYMA_19G063400 PE=3 SV=1
MTTQVPPHSVQVHTTTHRYEAGVVPPGARFEPPRYEAGVKAPSIYHSERGPTTSQVLAVL
AGLPVGGILLLLAGLTLAGTLTGLAVATPLFVLFSPVLVPATVAIGLAVAGFLTSGAFGL

TALSSFSWILNYIRETQPASENLAAAAKHHLAEAAEYVGQKTKEVGQKTKEVGQDIQSKA
QDTREAAARDAREAAARDAREAAARDAKVEARDVKRTTVTATTATA

29 >tr|M4E9X1|M4E9X1_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
MADTHRVDRTDRHLQFQSPYEGGRVNIQFEGAGGGYGQSGYGGGGGYGQSGYGGGGYKSM
MPESGPSSTQVISFLVGVPLVGSLLAIAGLLLAGSVIGLMISIPLFLLFSPVIVPAAITI
GLATTGFLTSGMFGLTGLSSISWVMNYLRRTRGSVPDQLEYAKRRMADAVGYAGQKGKEV
GQFVQDKAHDAKQYDISKPHDTTTTTTTTKGLETRTAAA

30 >tr|M4DRP3|M4DRP3_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
MTDTARTHHDITTRDPYPMMGRDRDQYAIIGRDQYQGYGQDYSKSRQIAKAATAVTAGGS
LLVLSSLTLVGTVIALIVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSW
IYKYATGEHPKGSDKLDSARMKLGSKAQDMKDRAHYYGQQHTGGEHVNTDYRNTDRDRTR
GNTT

31 >tr|M4EI43|M4EI43_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
MADTHRVDRTDRHLQFQSPYEGGRVNIQYEGGGGAGGYGGGRGGGYGAGGYKSMMPERGP
SSTQVLSFLVGVPIVGSLLAIAGLLLAGSVIGLLISIPLFLLFSPVIVPAALTIGLAATG
FLASGMFGLTGLSSVSWVMNYLRGTRKSSVPEQLEYAKKRMADAVGYAGQKGKEMGQHVQ
NKAQEAKQYDISKTHDTTTKGHETTQRTAAA

32 >tr|M4CYF6|M4CYF6_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
MLSSLIQIFQVFQVTSAVVVTAVLFALAGITLAGSVVGLIVATPLFVIFSPVLVPATIAS
TLLATNLSAGALFGVTAAALIVWLFKHRMGVHPKNNPPPAGAPPTEADKPAEGTTEKPKD
NSTGGAADKPEDKPVGGAADKPEGKPDGGATNKPESKPAGGPSNKPKDKPAGGPTDKPES
KPADKPAGGPTDKPGSKPVDKPAGGPTDKTESKLVGEASNKPKDKPAGGSTDMPEAGETS
NKPKDKSVGGPTNKPESKPAGETSHKPKDKPAGGPTDKPESKPAGETSHKPKDKLAGGPT
DKPESKPAGEASNKPKDKPAGGPTDKLAGGSVDKPKDKPAGGPTDKPTNKLTGGAANKPA
GEAANKPTGKPKNKPAGENKPPGWYR

33 >tr|M4C9X3|M4C9X3_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
MADVRTHAHQVQVHPLRQQEGGIKVVYPQSGPSSTQVLAVIAGVPVGGTLLTLAGLTLAG
SVIGLMLAFPLFLIFSPVIVPAAFVIGLAMTGFMASGAIGLTGLSSMSWVLNHIRRVRER
MPDELEEAKQRLADMAEYVGQRTKDAGQTIEEKAHDVRESKTYDVRDRDTKGHTATGGDR
DTKTTREVRVATT

34 >tr|M4DBK6|M4DBK6_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
MTDTARTHHDITSRDQYPRDRDQYSMIGRDRDKYSMIGRDRDQYNMYGRDYSKSRQIAKA

VTAVTAGGSLLVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFG
IAAITVFSWIYKYATGEHPQGSDKLDSARMKLGGKVQDMKDRAQYYGQQHTGGYGQQQTG
GEHDRDRTRGTQHTT

>tr|A0A251RPT8|A0A251RPT8_HELAN Oleosin OS=Helianthus annuus OX=4232 GN=HannXRQ_Chr17g0548541 PE=3 SV=1
MATTTYDRHHVTTTQPQYRHDQHTGDRLTHPQHQQQGPSTGKIMVIMALLPITGILFGLA
GITLVGTVIGLALATPLFVIFSPVIVPAMIAIGLAVTGFLTSGTFGLTGLSSLSYLFNMV
RRSTMSVPDQMDYVKGKLQDVGEYTGQKTKDLGQKIQHTAHEMGDQGQGQGGGKEGRKEG
GK

>tr|M4F3T3|M4F3T3_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
MANQTRTHQDIIVRDSRSTLDRDHPKTGAQMVKVATGVAAGGSLLVLSGLTLAGTVIALA
VATPLLIIFSPVLVPAVITVVLIITGFLASGGFGIAAITAFSWLYRHMTGSGSDQKIESA
RMKVGSRGYDTKSGQHNIGVHQQHQQAAS

>tr|F4K823|F4K823_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=GRP16 PE=3 SV=1
MLSFLIPVVQFFQVVIAAVASVVFLVFAGITFGASIVGLTIATPLFVIFSPILVPATIAT
TFLVGGATAAVALGVTAFALILWLFKHRIGVKPKNNPAPKGAPTKADQPGASGGASGDKP
GEMSGAGGPSGDKPGGASGGGDKPGGASGGGPGGASGGASGGATWRSVGRRTWRSVGRRT
WRSVGRSFGR

>tr|Q6WEQ9|Q6WEQ9_ARALL Oleosin OS=Arabidopsis lyrata subsp. lyrata OX=81972 GN=GRP17 PE=3 SV=1
MSEELSQNPSSAQSLSLREDKNRFPFLSLSQREGRFFPSLSLSEREGRKFSFLSMFSFLM
PLLEVIKIIIASVASVVFLGFACVTLAGSAVALAVSTPVFIIFSPVLVPATIATVVLTTG
FTAGGSFGATALGLILWLIKRRMGVKAKDNPPPAGLPPNSGAEAGGAQSLIKKSKSKGGL
KLPAWCKKMLGGKFGGKKGKSGGGKGKFGGKGGMSEGEEGMSSGDDGMSGGEGGKSKRGG
HKSGSRGGKSKSKKGMSGGSESEEGMSGSEGGMSGGGGGKSKRGGGKRGGLRDKFGKKGG
MSGGGGGMSGSEGAMSGSEGGMSGGKSKSRGGKLGGLRGKYGKKGGKSGGGGGMSGSEGG
MSESEGGMSEGGMSGGGMSGGGMSGGGMSGGGGGKHNGKGKHGGLGGKFGKKGGMSERGG
GMSGSEGGMSGSEGGMSGGGISGGGGSKHKIGGGKHGGLGSKFGKKGGMSGGGGGMSGSE
GGMSGSEGGMSEGGMSGGGGGKHKIGGGKHKLGGGKLGSGGSHMAE

>tr|A0A251SJI7|A0A251SJI7_HELAN Oleosin OS=Helianthus annuus OX=4232 GN=OLEO6 PE=3 SV=1
MATYDRDRHPQQVQVHTVHDQRIDRFGDRSHYQNQQGPSKSKVLAVMALLPVGGALLGLA
GITLVGTMIGLAVATPLFVIFSPILVPAVLMIGLAVAGFLTSGTFGLTGLSSLSYLVNSL

RQITGTVPEQVDSAKRRLQDLVEYTGQKTKDVGQTIQDKAHDIGPEGAVHAGSAVGGAKE
GRGTKA

>tr|A0A251UPB8|A0A251UPB8_HELAN Oleosin OS=Helianthus annuus OX=4232 GN=OLEO1 PE=3 SV=1
MTDIHQTYNPQHHSLGGATHQQHVSPRVHQAVKAATAATAGGSLLVLSGLILAGTVIALT
IATPLLVIFSPVLVPAVITVFLIVTGFLTSGGFGVAAVTVLSWIYRYATGGHPPGADSLD
QARDKLGYKAREMKGRAEHATGMGQHHITGGGLRADM

>tr|A0A251S7K5|A0A251S7K5_HELAN Oleosin OS=Helianthus annuus OX=4232 GN=OLEO PE=3 SV=1
MATTTTYDRHFTTTQPHYRQDDRSRYDQQTHSQSTSRTLAIIALLPVGGILLGLAGLTFI
GTLIGLALATPLFVIFSPIIVPAVLTIGLAVTGFLASGTFGLTGLSSLSYLFNMVRQTAG
SVPESLDYVKGTLQDAGEYAGQKTKDFGQKIQNTAHEMGDQGQGGQVGVHAQVGGGKEGR
KSGDRT

>tr|C3S7G3|C3S7G3_BRANA Oleosin OS=Brassica napus OX=3708 GN=S3 PE=2 SV=1
MTDTARTHHDITTRDQYPMMGRDRDQYAIIGRDQYQGYGQDYSKSRQIAKAATAVTAGGS
LLVLSSLTLVGTVIALIVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSW
IYKYATGEHPKGSDKLDSARMKLGSKAQDMKDRAHYYGQQHTGGEHVNTDYRNTDRDRTR
GTT

>tr|I1N5I8|I1N5I8_SOYBN Oleosin OS=Glycine max OX=3847 GN=100794783 PE=3 SV=1
MAEVRSQQPQHVQVHASTTHTPQQYRYYQGGAKTQHHGGEGGGVMSLFPEISLTGSQLLA
LLAGVPLGGMLLLLSGVSLIASLVGLAVATPLFIFFSPVLVPAAFVIGMAVTAVLAAGAC
GLVGLVSFSWLVNCLRQMPRGTTTKTTMMRPEQAKRHVADMEEYVGKKTKDVGQDIQTRA
HAQGTTGMV

>tr|D7LPJ0|D7LPJ0_ARALL Oleosin OS=Arabidopsis lyrata subsp. lyrata OX=81972
GN=ARALYDRAFT_484554 PE=3 SV=1
MANVDRDRRVHVDRTDKRVHLQPSYEDDVGFGGYGAGSDFKSRGPSTNQILALIAGVPIG
GTLLTLAGLTLAGSVIGLLVSIPLFLLFSPVIVPAALTIGLAVTGILASGLFGLTGLSSV
SWVLNYLRGTSDTVPEQLDYAKRRMADAVGYAGMKGKEMGQYVQDKAHEARETEFTTETH
EPGKARRLIS

>tr|Q5VKJ8|Q5VKJ8_RICCO Oleosin OS=Ricinus communis OX=3988 GN=OLE2 PE=2 SV=1
MAEHQQSPVVSHRPRVNQLVKAGTAATAGSSLLFLSGLTLTGTVIALALATPLMVLFSPV
LLPAVIIISLIGAGFLTSGGFGFGAILVLSWIYRYVTGKQPPGAESLDQARLKLAGKARE
MKDRAEQFGQHVTGQQTS

>tr|M4D1X4|M4D1X4_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1

MADTARTHHDITSRDQYPILGRDRDQYPYGRSDYQTSGQDYSKTRQIAKAATAVTAGGSL
LVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWI
YKYATGEHPQGSDKLDSARMKLGTKAQDIKDRAQYYGQQHTGGEHDRDRTRGTHHTTTTT

47 >tr|M4EW38|M4EW38_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
MANVDRRVNVDRTDKGLQLQPQYEDRVGYGYGYGGNTDYKSRGPSTNQIVALIAGVPIGG
SLLALAGLTLAGSVIGFMLSIPLFLLFSPVIVPAALTIGLAVTGILASGLFGLTGLSSVS
WVLNYIRGRSDTVPEQLDYAKRRMADAVGYAGQKGKEMGQYVQDKAHEAHDTSLTTETNG
KTRRAHIA

48 >tr|M4CYF9|M4CYF9_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
MLSFFSRLLDVIKVVVASVTSVVLFLFAGLTLSGSAVALVVSTPLFLIFSPILVPATIAT
TLLASGLTAGATLGITAISLIMGLIKTAEGSSLARLAQTPLKLFKFSGGFGGSWGGKSFS
GTFGNKGSQSSGNIPGWLKNLLNGIPAGGAVPAAGEAAPAPAAGGAAPAPAAPPG

49 >tr|A0A251UGX9|A0A251UGX9_HELAN Oleosin OS=Helianthus annuus OX=4232
GN=HannXRQ_Chr07g0205601 PE=3 SV=1
MTDIHTKEQGQQQSRWHVEPQHQSQHWTTQSQRQWNEPRAHQVVKAATAAAVGGSLLVLA
GLVLAGTVIALTLATPVLVIFSPVLVPALIAVFLLVSGFLTSGGFGVAAATVLAWMYRYV
TGEQPSGADTSDEVSHRLGAKARDIKDRGEHAGRGGHYGTAGVHTGGPGGGVGTYV

50 >tr|M4CYF7|M4CYF7_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
MVVASVASVVYLGFAGVTLSGSAVALAVSTPLFIIFSPILLPAIAATTVLAAGLGGKKVA
AAPEASPAASPSLSLLGIPESIKPSNIIPESIKPSNIIPEGIKPSNIKDKIKDTIGKVKN
KIKAKKEEKSKGKSEDSSKGKGKSKGEDTTTDDDTTTDEDKHGSGAKHGKGESKHGKGES
THGKGGKHGSEGKHGSGGSSMGGGKHGSGGKHETGGKHGSGGKHESGGSAMGGGKHGSGG
KHGSEGKHGGEGSSMGKNSLSKKKKEFHYRGQAMDASSTSESSDGSSDGSSSDGSSHGSG
GKHI

51 >tr|A0A087H670|A0A087H670_ARAAL Oleosin OS=Arabis alpina OX=50452 GN=AALP_AA3G007200 PE=3
SV=1
MADVRTHSHQVQVHPLRQHEGGIKVVYPQSGTGTGTGTGPSSTQVLTVVAGVPVGGTLLL
LAGLTLAGSVIGTILAFPLFLIFSPVIVPAAFLIGLAMAGFFTSGAIGLTGLSSMSWVLN
FFRRARENLPEELEEAKQRLADMAEYVGQRTKDAGQTIEDRAQDVRETKTDVRGDVHTKG
HARGDRDTKTTHEVRVASS

52 >tr|A0A251U5P5|A0A251U5P5_HELAN Oleosin OS=Helianthus annuus OX=4232
GN=HannXRQ_Chr08g0223251 PE=3 SV=1

MTEIHQTYNPQHQPYGGGVSHYQQQQHVSPRVHQAVKAATAITAGGSLLILSGLTLAGTV
IALTIATPLLVIFSPVLVPAAITLFLLATGFLMSGGFGVAAATVLSWIYRYATGGHPLGS
DSLDQARDKLGYKARDMKGRAEHATGGMGLHARADM

53 >tr|A0A3P5ZTB8|A0A3P5ZTB8_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA03T12417Z PE=3 SV=1
MTKRSLYQWNTLLKSLSRDKQWQQVLSQFIQMFRCEEKPDNFTIPVALKACVELRQIKCG
EIIHAFINKDASLASDLYVGSALIDMYAKCGRMTQALRVFDELEEKPDIVTWSSMVSGFE
RNGFPFEAVEFFRRMATSYHVSPDRVTLITLVSACTKLSDSKLGRCVHGFVMRRGFEKDL
SLVNSLLNCYAKSGAFKEAVHLFKVMAEKDVISWSTVIACYVQNGAAAEALPYAVFSRIP
KKDVVSWVALISGFTLNGMAHRSVEEFSKMLLENNTRPDSILMVKVLKSCSDLGFLEQAE
CFHSYLIKFGFDSNPFIGASLVELYSRCGSLGSACKVFDEITLKDTVVWTSLITGYGIHG
KGTKALETFNQMVESSEVEPNDVTFLSVLSACSHSGLIGEGLRIFELMVSQYGLVPNLEH
YAVLVDLLGRVGELDTAIEITKRMPFSPTPQVLGTLLGACRIHQNDEMAETVAKKLFELE
PNHAGYYMLMSNMYGVKGEWENVEKLRNAVRNRGIKNGLAESLIKIKRKVHRFVADDNMH
PENEPVYGLLKELDLLMKQGLEDSAYFQTEGGSLCHVSPLRLGGLMADVRTHAHQVQVHP
LRQQEGGIKVVYPQSGPSSTQVLAVIAGVPVGGTLLTLAGLTLAGSVIGLMLAFPLFLIF
SPVIVPAAFVIGLAMTGFMASGAIGLTGLSSMSWVLNHIRRVRERMPDELEEAKQRLADM
AEYVGQRTKDAGQTIEEKAHDVRESKTYDVRDRDTKGHTATGGDRDTKTTREVRVATT

54 >tr|A0A178VDK3|A0A178VDK3_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=AXX17_At3g00700 PE=3 SV=1
MADVRTHSHQLQVHPQRQHEGGIKVLYPQSGPSSTQVLAVFVGVPIGGTLLTIAGLTLAG
SVIGLMLAFPLFLIFSPVIVPAAFVIGLAMTGFLASGAIGLTGLSSMSWVLNYIRRAGQH
IPEELEEAKHRLADMAEYVGQRTKDAGQTIEDKAHDVREAKTFDVRDRDTTKGTHNVRDT
KTT

55 >tr|A0A0D3C252|A0A0D3C252_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376 GN=106340888 PE=3 SV=1
MADLHQHQQPMTRNLHESSSSPSTRQTVRFLTAATIGMSLLVLSGLTLTGTVIGLVVATP
LMVLFSPVLVPAVITMCLLTAGFLFSGGCGVAAATALSWIYRYITGKHPMGADKVDYARM
MISDNAKELGHYAQPQTDQTTTAPY

56 >tr|A0A0D3EH64|A0A0D3EH64_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376 GN=106316754 PE=3 SV=1
MLSSLIQIFQVFQVTSAVVVTAVLFALAGITLAGSVVGLIVATPLFVIFSPVLVPATIAS

TLLATNLSAGALFGVTAAALIVWLLKHRMGVHPKNNPPPAGAPPTEAAKPTDKPAEGATD
KPKDNPTGGAADNPGGKSDGGETDKPESKPAGGPVNKPKDKPAGGPTDKPGSKPADKPAG
GPTDKPENKPAEEASNKPKDKPAGEPTDKPESKPSREASNKRKDKPAGGPTDKRESKPAG
EASNKPKDKPAGGPTTKPESKPAGEVSNKPKDKPVGGPTDKPGNKPAGGPADKPKDNPAG
GPTDKPADKPTGGTENKPAEEAANKPIGKPKNKPAGENKPPAWYS

57 >tr|A0A0D3EH63|A0A0D3EH63_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376
GN=106317860 PE=3 SV=1
MRNEIQNETAQTDQTQGSMFSFFNLFPFLLPMFEVIKMVVASVASVVYLGFAGVTLSGSA
VALAVSTPLFIIFSPILLPAIAATTVLAAGLGSKKVAAAPAASPSLSLLGIPESIKPSNV
IPESIKPSNIIPESIKPSNIIPVSIKPSNIKDKIKDTIGKVKNKIKAKQEEKSKGKSEDS
SKGKGKSKGEDTTTDEDKHGKGESKHGKGESKHGKGESTHGKGGKHGSEGSSMDEGKHGG
KHGSGGSPMGGGKHGSGGKHESGGSPMGGGKHGSGGKHESGGSPMGGGKHGSGGKHESGG
SPESVGKHGSGGKHESGGSPMGGGKHGSGGKHESGGASMGGGKHGSGGRHEGGGSAMGGG
KHGSGGKHGSEGKHGGEGSSMGKNSLSKNKKEFHYRGQAMDASSTSESSDGSSSDGSSSD
GSSSDGSSHGSGGKHI

58 >tr|A0A0D3C071|A0A0D3C071_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376
GN=106337122 PE=3 SV=1
MADTHRVDRTDRHLQFQSPYEGGRVNIQFEGAGEGYGQSGYGGGGGYGQSGYGGGGYKSM
MPESGPSSTQVISFLVGVPIVGSLLAIAGLLLAGSVIGLMISIPLFLLFSPVIVPAAITI
GLATTGFLASGMFGLTGLSSISWVMNYLRRTRGGVPDQLEYAKRRMADAVGYAGQKGKEM
GQFVQDKAHDAKQYDISKPQDTTTTTTTTTKGHETRTAAA

59 >tr|A0A0D3A665|A0A0D3A665_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376
GN=106298955 PE=3 SV=1
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VTAVTAGGSLLVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVAMLITGFLSSGGFG
IAAITVFSWIYKYATGEHPQGSDKLDSARMKLGSKAQDLKDRAQYYGQQHTGGYGQQHTG
GEHDRDRTRGTQHTT

60 >tr|A0A0D3DG02|A0A0D3DG02_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376
GN=106304893 PE=3 SV=1
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LLVLSSLTLVGTVIALIVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSW
IYKYATGEHPQGSDKLDSARMKLGSKAQDMKDRAYYYGQQHTGEEHDRDRDHRTDRDRTR

GTQHTT

61 >tr|A0A078H704|A0A078H704_BRANA Oleosin OS=Brassica napus OX=3708 GN=BnaA01g14480D PE=3 SV=1
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LVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWIYKYATGE
HPQGSDKLDSARMKLGGKVQDMKDRAQYYGQQQTGGEHDRDRTRGTQHTT

62 >tr|A0A078FBB9|A0A078FBB9_BRANA Oleosin OS=Brassica napus OX=3708 GN=BnaC06g12930D PE=3 SV=1
MADTHRVDRTDRHLQFQSPYEGGRVSIQYEGGGGYGAEGYKSMMPERGPSSTQVLSFLVG
VPIVGSLLAIAGLLLAGSVIGLLISIPLFLLFSPVIVPAALTIGLAATGFLASGMFGLTG
LSSVSWVLNYLRGTRKSSVPEQLEYAKKRMADAVGYAGQKGKEMGQHVQNKAQEAKQYDI
SKTHDTTTKGHETTQRTAAA

63 >tr|C3S7F4|C3S7F4_BRANA Oleosin OS=Brassica napus OX=3708 GN=S4 PE=2 SV=1
MADTHRVDRTDRHLQFQPPYEGGRVNIQFEGAGEGYGQSGYGGGGGYGQSGYGGGGYKSM
MPESGPSSTQVISFLVGVPIVGSLLAIAGLLLAGSVIGLMISIPLFLLFSPVIVPAAITI
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GQFVQDKAHDAKQYDISKPQDTTTTTTTTKGHETRTAAA

64 >tr|C3S7F2|C3S7F2_BRANA Oleosin OS=Brassica napus OX=3708 GN=S4 PE=2 SV=1
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STQVLSFLVGVPIVGSLLAIAGLLLAGSVIGLLISIPLFLLFSPVIVPAALTIGLAATGF
LASGMFGLTGLSSVSWVLNYLRGTRKSSVPEQLEYAKKRMADAVGYAGQKGKGMGQHVQN
KAQEAKQYDISKTHDTTTKGHETTQRTAAA

65 >tr|C3S7G1|C3S7G1_BRANA Oleosin OS=Brassica napus OX=3708 GN=S3 PE=2 SV=1
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VTAVTAGGSLLVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFG
IAAITVFSWIYKYATGEHPQGSDKLDSARMKLGGKVQDMKDRAQYYGQQQTGGEHDRDRT
RGTQHTT

66 >tr|A0A078IM60|A0A078IM60_BRANA Oleosin OS=Brassica napus OX=3708 GN=BnaC04g32530D PE=3 SV=1
MADTHRVDRTDRHLQFQSPYEGGRVNIQFEGAGEGYGQSGYGGGGGYGQSGYGGGGYKSM
MPEIYIYSLTFMHTKLMRFFLGPNKTFPIVGSLLAIAGLLLAGSVIGLMISIPLFLLFSP
VIVPAAITIGLATTGFLASGMFGLTGLSSISWVMNYLRRTRGGVPDQLEYAKRRMADAVG

YAGQKGKEMGQFVQDKAHDAKQYDISKPQDTTTTTTTTTKGHETRTAAA

67 >tr|A0A078J3L4|A0A078J3L4_BRANA Oleosin (Fragment) OS=Brassica napus OX=3708 GN=BnaCnng36370D PE=3 SV=1
MLSSLIQIFQVFQVTSAVVVTAVLFALAGITLAGSVVGLIVATPLFVIFSPVLVPATIAS
TLLATNLSAGALFGVTAAALIVWLLKHRMGVHPKNNPPPAGAPPTEAAKPTDKPAEGATD
KPKDNPTGGAADNPGGKSDGGETDKPESKPAGGPVNKPKDKPAGGPTDKPGSKPADKPAG
GPTDKPENKPAEEASNKPKDKPAGEPTDKPESKPSREASNKRKDKPAGGP

68 >tr|Q9LY07|Q9LY07_ARATH Glycine-rich protein 20 OS=Arabidopsis thaliana OX=3702 GN=ATGRP20 PE=2 SV=1
MAPFPLSLIFGKKKRRRDDEIRRQKPTLKGVMTAFFATEAAICLLLLAGISLTGTAVALF
ASMPLFLVFSPVLVPAGIATTILASGLMAGGTSGVSGLTILMWLYKKYTGRDFPIKIPGA
AAAGGAAPAAPAAPAPAAPAAKPAAKPAAKPGA

69 >tr|A0A078JR26|A0A078JR26_BRANA Oleosin (Fragment) OS=Brassica napus OX=3708 GN=BnaCnng60890D PE=3 SV=1
MRNEIQNETAQTDQTQGSMFSFFNLFPFLLPMFEVIKMVVASVASVVYLGFAGVTLSGSA
VALAVSTPLFIIFSPILLPAIAATTVLAAGLGSKKVAAAPAASPSLSLLGIPESIKPSNV
IPESIKPSNIIPESIKPSNIIPVSIKPSNIKDKIKDTIGKVKNKIKAKQEEKSKGKSEDS
SKGKGKSKGEDTTTDEDKHGKGESKHGKGESKHGKGESTHGKGGKHGSEGKHGSGGSPMG
GGKHGSGGKHESGGSPM

70 >tr|C3S7F3|C3S7F3_BRANA Oleosin OS=Brassica napus OX=3708 GN=S4 PE=2 SV=1
MADTHRVDRTDRHLQFQSPYEGGRVNIQYEGGGGAGGYGGGRGGGYGAGGYKSMMPERGP
SNTQVLSFLVGVPIVGSLLAIAGLLLAGSVIGLLISIPLFLLFSPVIVPAALTIGLAATG
FLASGMFGLTGLSSVSWVMNYLRGTRKSSVPEQLEYAKKRMADAVGYAGQKGKEMGQHVQ
NKAHEAKQYDISKTHDTTTTKGHETTQRTAAA

71 >tr|C3S7E9|C3S7E9_BRANA Oleosin OS=Brassica napus OX=3708 GN=S1 PE=2 SV=1
MADVRTHAHQVQVHPLRQQEGGIKVVYPQSGPSSTQVLAVIAGVPVGGTLLTLAGLTLAG
SVIGLMLAFPLFLIFSPVIVPAAFVIGLAMTGFMASGAIGLTGLSSMSWVLNHIRRVRER
MPDELEEAKQRLADMAEYVGQRTKDAGQTIEEKAHDVRESKTYDVRDRDTKGHTATGGDR
DTKTTREVRVATT

72 >tr|Q42640|Q42640_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=GRP3 PE=2 SV=1
MRNEIQNETAQTDQTQGSMFSFFDLFPFLLPMFEVIKMVVASVASVVYLGFAGVTLSGSA
VALAVSTPLFIIFSPILLPAIAATTVLAAGLGSKKVAAAPAASPSLSLLGIPESIKPSNV

IPESIKPSNIIPESIKPSNIIPESVKPSNIKDKIKDTIGKVKNKINAKKEEKSKGKSEDS
SKGKGKSKGEDTTTDEDKPGSGGKHGKGESKHGKGESTHGKGGKHGSEGSSMDEGKHGGK
HGSGGSPMGGGKHGSGGKHESGGSPMGGGKHGSGGKHESGGASMGGGKHGSGGKHGSEGK
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I

73 >tr|C3S7G2|C3S7G2_BRANA Oleosin OS=Brassica napus OX=3708 GN=S3 PE=2 SV=1
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LLVLSSLTLVGTVIALIVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSW
IYKYATGEHPKGSDKLDSARMKPGSKAQDMKDRAHYYGQQHTGGEHVNTDYRNTDRDRTR
GTT

74 >tr|C3S7G0|C3S7G0_BRANA Oleosin OS=Brassica napus OX=3708 GN=S3 PE=2 SV=1
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VTAVTAGGSLLVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFG
IAAITVFSWIYKYATGEHPQGSDKLDSARMKLGGKVQDMKDRAQYYGQQQTGGEHDRDRT
RGTQHTT

75 >tr|Q65ZR4|Q65ZR4_BRANA Oleosin (Fragment) OS=Brassica napus OX=3708 GN=oleosin napII
PE=2 SV=1
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LSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWIYK
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76 >tr|C3S7G6|C3S7G6_BRANA Oleosin OS=Brassica napus OX=3708 GN=S3 PE=2 SV=1
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LLVLSSLTLVGTVIASIVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSW
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GTQHTT

77 >tr|A8MSB7|A8MSB7_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=GRP19 PE=3 SV=1
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78 >tr|C3S7G4|C3S7G4_BRANA Oleosin OS=Brassica napus OX=3708 GN=S3 PE=2 SV=1
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VTAVTAGGSLLVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVAMLITGFLSSGGFG
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GEHDRDRTRGTQHTT

79 >tr|Q94CI2|Q94CI2_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=GRP2 PE=3 SV=1
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80 >tr|A0A251RWY6|A0A251RWY6_HELAN Oleosin OS=Helianthus annuus OX=4232
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81 >tr|A0A0R0JP17|A0A0R0JP17_SOYBN Oleosin OS=Glycine max OX=3847 GN=GLYMA_05G004300 PE=3
SV=1
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AVLAAGACGLAGLVLFSWVVNYLRQMPRGTTMMTVLPEQAKRHVADMAEYVGQKTKEVGQ
DIQTRAHHAQGTTRMTVH

82 >tr|M4EIT0|M4EIT0_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
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83 >tr|M4CYF8|M4CYF8_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
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LIVSTPLFIMFSPILVPATIATTLLASGLMAGTTLGLTGIGLIMGLVR

84 >tr|M4CYF4|M4CYF4_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
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85 >tr|A0A178V1V3|A0A178V1V3_ARATH Oleosin OS=Arabidopsis thaliana OX=3702
GN=AXX17_At4g29040 PE=3 SV=1
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86 >tr|Q5HZ52|Q5HZ52_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=C24_LOCUS25198 PE=2 SV=1
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87 >tr|A0A384LN43|A0A384LN43_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=AXX17_At5g50000 PE=3 SV=1
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88 >tr|D7L9N5|D7L9N5_ARALL Oleosin OS=Arabidopsis lyrata subsp. lyrata OX=81972 GN=ARALYDRAFT_477358 PE=3 SV=1
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KTT

89 >tr|A0A0D3B993|A0A0D3B993_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376 PE=3 SV=1
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FPLFLIFSPVIVPAAFVIGLAMTGFMASGAIGLTGLSSMSWVLNHIRRVRERIPDELDEA

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RVATT

90 >tr|Q94FQ4|Q94FQ4_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 PE=3 SV=1
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GLKAWCKKMLKSKFGGKKGKSGGGKSKFGGKGGKSEGEEGMSSGDERMSGSEGGMSGGEG
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GGMSGGGGGKSKSRKSKLKAKLGKKKSMSGGMSGSEGGMSGSEGGMSGGGMSGGSGSKHK
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MAE

91 >tr|Q94FQ0|Q94FQ0_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 PE=3 SV=1
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92 >tr|Q9FUJ9|Q9FUJ9_SESIN Oleosin OS=Sesamum indicum OX=4182 PE=2 SV=1
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93 >tr|Q94FP9|Q94FP9_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 PE=3 SV=1
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GLKAWCKKMLKSKFGGKKGKSGGGKSKFGGKGGKSEGEEGMSSGDEGMSGSEGGMSGGEG
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MAE

94 >tr|A0A0D3CT24|A0A0D3CT24_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376 PE=3 SV=1
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95 >tr|A0A0D3DMT4|A0A0D3DMT4_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376 PE=3 SV=1
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>tr|A0A397ZZI8|A0A397ZZI8_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRARA_C02941 PE=3 SV=1
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96 >tr|A0A397YL15|A0A397YL15_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRARA_G01479 PE=3 SV=1
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97 >tr|A0A087GGK1|A0A087GGK1_ARAAL Oleosin OS=Arabis alpina OX=50452 GN=AALP_AA7G076700 PE=3 SV=1

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98 >tr|A0A087GA32|A0A087GA32_ARAAL Oleosin OS=Arabis alpina OX=50452 GN=AALP_AA8G285900 PE=3 SV=1
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99 >tr|A0A0R0FZF4|A0A0R0FZF4_SOYBN Oleosin OS=Glycine max OX=3847 GN=GLYMA_16G071800 PE=3 SV=1
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100 >tr|A0A3P6D7W5|A0A3P6D7W5_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRASC35T46007Z PE=3 SV=1
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101 >tr|A0A087G5I9|A0A087G5I9_ARAAL Oleosin OS=Arabis alpina OX=50452 GN=AALP_AA8G071100 PE=3 SV=1
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102 >tr|A0A087G5I8|A0A087G5I8_ARAAL Oleosin OS=Arabis alpina OX=50452 GN=AALP_AA8G071000 PE=3 SV=1
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103 >tr|A0A3P6DBL6|A0A3P6DBL6_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA10T44973Z PE=3 SV=1
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104 >tr|Q84WT0|Q84WT0_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=At5g51210 PE=2 SV=1
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105 >tr|Q42638|Q42638_BRAOL Oleosin (Fragment) OS=Brassica oleracea OX=3712 PE=2 SV=1
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106 >tr|Q42639|Q42639_BRAOL Oleosin (Fragment) OS=Brassica oleracea OX=3712 PE=2 SV=1
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107 >tr|Q42637|Q42637_BRAOL Oleosin OS=Brassica oleracea OX=3712 PE=2 SV=1
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108 >tr|A0A087G5I7|A0A087G5I7_ARAAL Oleosin OS=Arabis alpina OX=50452 GN=AALP_AA8G070900 PE=3
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109 >tr|Q94FR0|Q94FR0_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 PE=3 SV=1
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110 >tr|A0A178UIH4|A0A178UIH4_ARATH Oleosin OS=Arabidopsis thaliana OX=3702
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KAKSKGGLKAWCKKMLKSKFGGKKGKSGGGKSKFGGKGGKSEGEEGMSSGDEGMSGSEGG
MSGGEGGKSKSGKGKLKAKLEKKKGMSGGSESEEGMSGSEGGMSGGGGSKSKSKKSKLKA
KLGKKKGMSGGMSGSEEGMSGSEGGMSGGGGGKSKSRKSKLKAKLGKKKCMSGGMSGSEG
GMSGSEGGISGGGMSGGSGSKHKIGGGKHGGLGGKFGKKRGMSGSGGGMSGSEGGVSGSE
GSMSGGGMSGGSGSKHKIGGGKHGGLRGKFGKKRGMSGSEGGMSGSEGGMSESGMSGSGG
GKHKIGGGKHKFGGGKHGGGGGHMAE

111 >tr|Q6J1J8|Q6J1J8_ARAHY Oleosin OS=Arachis hypogaea OX=3818 GN=Ahy_A05g023475 PE=2 SV=1
MATATDRAPHQVQVHTPTTQRVDVPRRGYDVSGGGIKTLLPERGPSTSQIIAVLVGVPTG
GTLLLLSGLSLLGTIIGLAIATPVFIFFSPVIVPAVVTIGLAVTGILTAGACGLTGLMSL
SWMINFIRQVHGTTVPDQLDSVKRRMADMADYVGQKTKDAGQEIQTKAQDVKRSSS

112 >tr|A0A398AP76|A0A398AP76_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRARA_A01514
PE=3 SV=1
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VTAVTAGGSLLVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFG
IAAITVFSWIYKYATGEHPQGSDKLDSARMKLGGKVQDMKDRAQYYGQQQTGGEHDRDRT
RGTQHTT

113 >tr|A0A397ZJS4|A0A397ZJS4_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRARA_D01064
PE=3 SV=1
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ESGPSSTQVISFLVGVPLVGSLLAIAGLLLAGSVIGLMISIPLFLLFSPVIVPAAITIGL
ATTGFLTSGMFGLTGLSSISWVMNYLRRTRGSVPDQLEYAKRRMADAVGYAGQKGKEVGQ
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114 >tr|Q49L62|Q49L62_BRACM Oleosin (Fragment) OS=Brassica campestris OX=3711 PE=2 SV=1
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LVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWIYKYATGE
HPQGSDKLDSARMKLGGKVQDMKDRAQYYGQQHTGGYGQQQTGGEHDRDRTRGTQHTT

115 >tr|A0A445EPH4|A0A445EPH4_ARAHY Oleosin OS=Arachis hypogaea OX=3818 GN=Ahy_A01g001806
PE=3 SV=1
MADIQQYYQQDHQDVSATKERSSSHILALATLLPFGASLLFLAGVTLLATLIGVALATPL
FIIFSPILIPAALVIAFSVSGFLTSGAFGVTSVSSFAWMASYLRRSRLQESLLHAKDRAQ
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116 >tr|A0A445AU69|A0A445AU69_ARAHY Oleosin OS=Arachis hypogaea OX=3818 GN=Ahy_B01g054716 PE=3 SV=1
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FIIFSPILIPAALVIAFSVSGFLTSGAFGVTSVSSFAWMASYFRRSRLQESLLHAKDRAQ
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TQTRDTASTTETKDEGGGGGKSKDRKKTSS
117 >tr|A0A397KW15|A0A397KW15_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA03T14647Z PE=3 SV=1
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LLVLSSLTLVGTVIALIVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSW
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GTT
118 >tr|O82308|O82308_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=At2g25890 PE=3 SV=1
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TIGLSLLVLSGLTLTGTVIGLIVATPLMVLFSPVLVPAVITIGLLTMGFLFSGGCGVAAA
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119 >tr|Q2F3K0|Q2F3K0_BRANA Oleosin OS=Brassica napus OX=3708 PE=3 SV=1
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120 >tr|A0A445KI27|A0A445KI27_GLYSO Oleosin OS=Glycine soja OX=3848 GN=D0Y65_010876 PE=3 SV=1
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H
121 >tr|Q6V5K1|Q6V5K1_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=Bo_7530 PE=3 SV=1
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122 >tr|A0A3N6Q709|A0A3N6Q709_BRACR Oleosin OS=Brassica cretica OX=69181 GN=DY000_00001052
PE=3 SV=1
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123 >tr|A0A3N6PVU1|A0A3N6PVU1_BRACR Oleosin OS=Brassica cretica OX=69181 GN=DY000_00003179
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124 >tr|A0A3N6R1B3|A0A3N6R1B3_BRACR Oleosin OS=Brassica cretica OX=69181 GN=DY000_00015073
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125 >tr|A0A3N6S1Y1|A0A3N6S1Y1_BRACR Oleosin OS=Brassica cretica OX=69181 GN=DY000_00029368
PE=3 SV=1
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126 >tr|A0A5E4GEY2|A0A5E4GEY2_PRUDU Oleosin OS=Prunus dulcis OX=3755 GN=ALMOND_2B024808 PE=3
SV=1
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127 >tr|A0A445FCW9|A0A445FCW9_GLYSO Oleosin OS=Glycine soja OX=3848 GN=D0Y65_050659 PE=3 SV=1

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128 >tr|A0A445GFF8|A0A445GFF8_GLYSO Oleosin OS=Glycine soja OX=3848 GN=D0Y65_042947 PE=3 SV=1
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129 >tr|A0A3P6CEU7|A0A3P6CEU7_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA04T17003Z
PE=3 SV=1
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130 >tr|A0A3P6CQ91|A0A3P6CQ91_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA10T44974Z
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131 >tr|A0A3P6BRG2|A0A3P6BRG2_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA07T29727Z
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132 >tr|A0A3P6FKT4|A0A3P6FKT4_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=BOLC1T01985H PE=3
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133 >tr|A0A3P6E7Z2|A0A3P6E7Z2_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=BOLC7T45893H PE=3 SV=1
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GTQHTT

134 >tr|A0A3P6CHK0|A0A3P6CHK0_BRAOL Oleosin (Fragment) OS=Brassica oleracea OX=3712 GN=BOLC4T27103H PE=3 SV=1
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135 >tr|A0A3P6DS72|A0A3P6DS72_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=BOLC9T59710H PE=3 SV=1
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GPTDKPENKPAEEASNKPKDKPAGEPTDKPESKPSREASNKRKDKPAGGPTDKRESKPAG
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136 >tr|A0A3P6E9Q1|A0A3P6E9Q1_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=BOLC9T59709H PE=3 SV=1
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IPESIKPSNIIPESIKPSNIIPVSIKPSNIKDKIKDTIGKVKNKIKAKQEEKSKGKSEDS
SKGKGKSKGEDTTTDEDKHGKGESKHGKGESKHGKGESTHGKGGKHGSEGSSMDEGKHGG
KHGSGGSPMGGGKHGSGGKHESGGSPMGGGKHGSGGKHESGGASMGGGKHESVGKHGSGG
KHESGGSPMGGGKHGSGGKHESGGASMGGGKHGSGGRHEGGGSAMGGGKHGSGGKHGSEG
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137 >tr|A0A3P6C0K5|A0A3P6C0K5_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=BOLC4T26321H PE=3 SV=1
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GLATTGFLASGMFGLTGLSSISWVMNYLRRTRGGVPDQLEYAKRRMADAVGYAGQKGKEM
GQFVQDKAHDAKQYDISKPQDTTTTTTTTKGHETRTAAA
138 >tr|A0A3P6H0L1|A0A3P6H0L1_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=BOLC6T37105H PE=3 SV=1
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STQVTFFFTFSMLIHFLNFMHSILNLLDSIFRYGSVILFGGGPYPGLLLAGSVIGLLISI
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139 >tr|A0A3T0QHI0|A0A3T0QHI0_COCNU Oleosin OS=Cocos nucifera OX=13894 PE=2 SV=1
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140 >tr|A0A3P5Z5E2|A0A3P5Z5E2_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA01T01594Z PE=3 SV=1
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141 >tr|Q6WEQ8|Q6WEQ8_ARALL Oleosin OS=Arabidopsis lyrata subsp. lyrata OX=81972 GN=GRP16 PE=3 SV=1
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142 >tr|A0A0D3AW96|A0A0D3AW96_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376 GN=106325704 PE=3 SV=1
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143 >tr|A0A078GHK4|A0A078GHK4_BRANA Oleosin OS=Brassica napus OX=3708 GN=BnaA08g14540D PE=3 SV=1
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144 >tr|A0A078HC36|A0A078HC36_BRANA Oleosin OS=Brassica napus OX=3708 GN=BnaA04g15210D PE=3 SV=1
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145 >tr|I1JUP4|I1JUP4_SOYBN Oleosin OS=Glycine max OX=3847 GN=100301903 PE=3 SV=1
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LTGTVIGLIIATPLLVIFSPILVPAAFVLFLVASGFLFSGGCGVAAIAALSWIYNYVSGN
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146 >tr|A0A0D3EH65|A0A0D3EH65_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376 GN=106317110 PE=3 SV=1
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147 >tr|A0A0D3EH61|A0A0D3EH61_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376 GN=106316427 PE=3 SV=1
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148 >tr|C3S7G5|C3S7G5_BRANA Oleosin OS=Brassica napus OX=3708 GN=S3 PE=2 SV=1
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149 >tr|A0A078JFK5|A0A078JFK5_BRANA Oleosin OS=Brassica napus OX=3708 GN=BnaC09g47930D PE=3 SV=1

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150 >tr|M4EZN7|M4EZN7_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1
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151 >tr|A0A078JDY8|A0A078JDY8_BRANA Oleosin OS=Brassica napus OX=3708 GN=BnaA10g30190D PE=3
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152 >tr|A0A078IIH2|A0A078IIH2_BRANA Oleosin OS=Brassica napus OX=3708 GN=BnaA02g29000D PE=3
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SLLALAGLTLAGSVIGFMLSIPLFLLFSPVIVPAALTIGLAVTGILASGLFGLTGLSSVS
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153 >tr|C3S7F7|C3S7F7_BRANA Oleosin OS=Brassica napus OX=3708 GN=S5 PE=2 SV=1
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154 >tr|A0A078J6X3|A0A078J6X3_BRANA Oleosin OS=Brassica napus OX=3708 GN=BnaCnng36380D PE=3
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155 >tr|C3S7E8|C3S7E8_BRANA Oleosin OS=Brassica napus OX=3708 GN=S2 PE=2 SV=1
MANVDRRVNVDRTDKGLQLQPQYEDRVGYGYGYGGNTDYKSCGPSTNQIVALIAGVPIGG
SLLALAGLTLAGSVIGFMLSIPLFLLFSPVIVPAALTIGLAVTGILASGLFGLTGLSSVS
WVLNYIRGRSDTVPEQLDYAKRRMADAVGYAGQKGKEMGQYVQDKAHEAHDTSLTTETNG
KTRRAHIA

156 >tr|C3S7F9|C3S7F9_BRANA Oleosin OS=Brassica napus OX=3708 GN=S3 PE=2 SV=1
MADTARTHHDITSRDQYPILGRDRDQYPYGRSDYQTSGQDYSKTRQIAKAATAVTAGGSL

LVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGSLSSGGFGIAAITVFSWI
YKYATGEHPQGSDKLDSARMKLGTKAQDIKDRAQYYGQQHTGGEHDRDRTRGTHHTTTTT
157 >tr|Q94CI3|Q94CI3_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=GRP1 PE=3 SV=1
MFFQIIQGVFTGVEALALLAFAGITLGGSAVGLALSTPLFILFSPILVPATIATTLLTTG
FTTSGGLGMVALRIFWKLFKRLRKKGKGTPKIPGLAPGAPDSDPVSGG
158 >tr|Q94CI0|Q94CI0_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=GRP5 PE=3 SV=1
MFSFLSPLLDVIKVVVASVTSVVLFVFAGLTLSGSAVALVVSTPLFLIFSPILVPATIAT
TLLASGVTAGATLGITAISLIMGLIKTAEGSSLARLAQTPLKLFKFSGGFGGSWGGKPFS
GTFGNKGSQSSGNIPGWLKNLLNGIPGGGAAPAAGGAAPAPAAPAPAAPPG
159 >tr|B3H6L6|B3H6L6_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=GRP19 PE=3 SV=1
MFEIIQAVFSAGVALALLTFAGITLGGSVVACIISTPLFVIFSPVLVPATIATTLLASGN
VQGGTYQKFQD
160 >tr|Q9FLS1|Q9FLS1_ARATH Oleosin family protein OS=Arabidopsis thaliana OX=3702 GN=MBK20.3
PE=4 SV=1
MFSFLIFLLEVYKVVIAVVASIVFFVFSGLTLAGTAVGLTVTTPLFIIFSPILVPATIAI
TLLTTGFTTGGALGATAIALIRRGMGVKSKNNIPAIGAPPTMFAQFSLTPKINYEGTFKG
SWGGKSSPQATPNFSYGGTWTANWGGRSFTGKFGDQSGGGSTAGGSTPEAAGAGAGAAAA
GAGAAAAAGAAAAAVPGLGAASAGAGPGAGAGTPAPAPTGKAGKAGSKKK
161 >tr|Q494N8|Q494N8_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=At2g25890 PE=2 SV=1
MADHQQHQQQQQPIMRSLHESSPSTRQIVRFVTAATIGLSLLVLSGLTLTGTVIGLIVAT
PLMVLFSPVLVPAVITIGLLTMGFLFSGGCGVAAATALTWIYKYVTGKHPMGADKVDYAR
MRIAEKAKELGHYTHSQPQQTHQTTTTTH
162 >tr|D7MQY4|D7MQY4_ARALL Oleosin OS=Arabidopsis lyrata subsp. lyrata OX=81972
GN=ARALYDRAFT_495191 PE=3 SV=1
MADQTRTHLEMISRDSTQESHPKERQMVKAATAVTAGGSLLVLSGLTLAGTVIALTVATP
LLVIFSPVLVPAVITVALIITGFLASGGFGIAAITAFSWVYRHLTGSGSEKIENARMKVG
SRVQDTKYGQHNIGVQHQQAS
163 >tr|C3VHQ8|C3VHQ8_SOYBN Oleosin OS=Glycine max OX=3847 GN=100301903 PE=2 SV=1
MATISDQPRGSYSYGTSYGAPYGTTYETNTSINNPPSRQTVKFITAATIGITLLLLSGLT
LTGTVIGLIIATPLLVIFSPILVPAAFVLFLVASGFLFSGGCGVAAIAALSWIYNYVSGN
QPAGYDTLDYAKGYLADKARDVKERAKDYGSYAQGRINEATQGAY
164 >tr|K7KTR9|K7KTR9_SOYBN Oleosin OS=Glycine max OX=3847 GN=GLYMA_06G078700 PE=3 SV=1

MQSRHDMQSTLTSCRVTSHTSSYTTIYLSHSILSSTLGLAREKIPTMATISTDQPRGSYS
YGTSYGAPYGTTYETNSSINNPPSRQTVKFITAATIGITLLLLSGLTLTGTVIGLIIATP
LLVIFSPILVPAAFVLFLVASGFLFSGGCGVAAIAALSWIYNYVSGNQPAGSDTLDYAKG
YLTDKARDVKERAKDYGSYAQGRINEATQGTY

165 >tr|Q6WEQ7|Q6WEQ7_ARALL Oleosin OS=Arabidopsis lyrata subsp. lyrata OX=81972 GN=GRP19 PE=3 SV=1
MFEIIQAVFAAGAALALLTFSAITLGGSVVAFAISTPLFVVFSPVLVPATIATTLLASGF
TASGSFGATAFSILAWIYKRRTGRDLPKIPGLTPPAAPASNPAGSGV

166 >tr|A0A0D3EA08|A0A0D3EA08_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376 GN=106317459 PE=3 SV=1
MANQTRTHQDIIVRDSRITLDRDHPKTGAQMVKVATGVAAGGSLLVLSGLTLAGTVIAFA
VATPLLIIFSPVLVPAVITVVLIITGFLASGGFGIAAITAFSWLYRHMTGSGSDQKIESA
RMKVGSRGYDTKYGQHNIGVHQQHQQAAS

167 >tr|A0A0D3EH62|A0A0D3EH62_BRAOL Oleosin OS=Brassica oleracea var. oleracea OX=109376 GN=106316426 PE=3 SV=1
MSEELVQHESHSQASIFSRFFRMFSFIFPLLNVIKLIIASVTSLVCLAFSCVTLGGSAVA
LIVSTPLFIIFSPILVPATIATTLLASGLMAGTTLGLTGIGLITGLVRTAGGVTLAESPI
RRIIINRIKARLGGGGGSRLAMLKKILGLIKKLRGMSSGGAAPAAEAAPAAAPADGAAPA
AAPAPT

168 >tr|A0A178VRV6|A0A178VRV6_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=AXX17_At2g21730 PE=3 SV=1
MADHQQHQQQQQPIMRSLHESSPSTRQIVRFVTAATIGLSLLVLSGLTLTGTVIGLIVAT
PLMVLFSPVLVPAVITIGLLTMGFLFSGGCGVAAATALTWIYKYVTGKHPMGADKVDYAR
MRIAEKAKELGHYTHSQPQQTHQTTTTTH

169 >tr|F4K3K4|F4K3K4_ARATH Oleosin family protein OS=Arabidopsis thaliana OX=3702 GN=At5g61610 PE=4 SV=1
MHFFGTKDKAPIYAGIAVVSFMILTGLTFAGTAVALTVMIPVLVVLSPILVPAVITSSFL
ATGFLASGSLGALGIALLIWLYKKEEYSRATLHARGGRPDGPNKLAESGKQSGGDNPLKE
DKPPERDKLPRKDKPSKEDNLLKGDKPVEEDKLPAEEEKPPQKDKPAEGHKPPQKDKPAE
GDKPVEEDKPPQKDKPAEGDKHVEEDMPLGGVEHLSIPEIPKVMVVEQNPIVPKCCGPST
CTKRCHPFRFAMDANATKARSIFMKEYQKVPRVGAFAYKYFTSRDKKYVNHFHI

170 >tr|Q84WN2|Q84WN2_ARATH Oleosin (Fragment) OS=Arabidopsis thaliana OX=3702 GN=At2g25890 PE=2 SV=1
QKQHRTLNPYSLRKRKKEMADHQQHQQQQQPIMRSLHESSPSTRQIVRFVTAATIGLSLL
VLSGLTLTGTVIGLIVATPLMVLFSPVLVPAVITIGLLTMGFLFSGGCGVAAATALTWIY
KYVTGKHPMGADKVDYARMRIAEKAKELGHYTHSQPQQTHQTTTTTH
171 >tr|Q94FP8|Q94FP8_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=C24_LOCUS21470 PE=3 SV=1
MLSFLIPVVQFFQVVIAAVASVVFLVFAGITFGASIVGLTIATPLFVIFSPILVPATIAT
TFLVGGATAAVALGVTAFALILWLFKHRIGVKPKNNPAPKGAPTKADQPGASGGASGDKP
GEMSGAGGPSGDKPGGASGGGDKPGGASGGGPGGASGGASGGASGGGPGGASGGGPGGAS
GGASGDKPEGAPGDKPGGASGGKPGKKPGHKPAGARGGKRLAWW
172 >tr|A0A251RQ07|A0A251RQ07_HELAN Oleosin OS=Helianthus annuus OX=4232 GN=HannXRQ_Chr17g0549281 PE=3 SV=1
MAHNQQYYQQHQHRQPHLSHQVVKTATAATLCGSLMVLSGLTLAATVIGLVVATPLLVIF
SPVLVPALITLSLIFGGFLASGGLGATASFVCYWMYRYVTGKHPVGSRQLDMARDKIAGA
AMEARHKAEQLGHQTGRTAAAGGGVGQGHQIRVEHQAA
173 >tr|A0A2I4GNJ1|A0A2I4GNJ1_JUGRE Oleosin OS=Juglans regia OX=51240 GN=LOC109009462 PE=3 SV=1
MSDHSRPVSQALYDPSSTSSRQAVKFLTAVTIGATLLILSGLTLTGTVIALILATPVLVL
FSPILVPAGIVLFLVAAGLVVSGGCGVVAMTALSWIYNYVTGKHPMGADRLDYARMRIAD
KARDMKEKAKEYGQFVQHKAREATQGA
174 >tr|A0A397YDD7|A0A397YDD7_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA08T34077Z PE=3 SV=1
MADTARTHHDITSRDQYPILGRDRDQYPYGRSDYQTSGQDYSKTRQIAKAATAVTAGGSL
LVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWI
YKYATGEHPQGSDKLDSARMKLGTKAQDIKDRAQYYGQQHTGGEHDRDRTRGTHHTTTTT
175 >tr|A0A397XNR6|A0A397XNR6_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA10T44975Z PE=3 SV=1
MFFQIIQGVFTGVEALALLAFAGITLGGSAVGLALSTPLFILFSPILVPATIATTLLTTG
FTTSGGLGIVALRIFWKLFKRLRKKGKGTPKIPGLAPGAPDSNSVSGG
176 >tr|A0A397ZLA6|A0A397ZLA6_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA04T17591Z PE=3 SV=1

MADLHQQHQQPMTRNLHESSSSPSTRQTVRFLTAATIGMSLLVLSGLTLTGTVIGLVVAT
PLMVLFSPVLVPAVITMCLLTAGFLFSGGCGVAAATALSWIYRYVTGKHPMGADKVDYAR
MMISEKAKELGHYAQPQTDQTTTAPY

177 >tr|A0A3P6B1V9|A0A3P6B1V9_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA02T08560Z
PE=3 SV=1
MANVDRRVNVDRTDKGLQLQPQYEDRVGYGYGYGGNTDYKSRGPSTNQIVALIAGVPIGG
SLLALAGLTLAGSVIGFMLSIPLFLLFSPVIVPAALTIGLAVTGILASGLFGLTGLSSVS
WVLNYIRGRSDTVPEQLDYAKRRMADAVGYAGQKGKEMGQYVQDKAHEAHDTSLTTETNG
KTRRAHIA

178 >tr|Q94FQ5|Q94FQ5_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 PE=3 SV=1
MLSFLIPVVQFFQVVIAAVASVVFLVFAGITFGASIVGLTIATPLFVIFSPILVPATIAT
TFLVGGATAAVALGVTAFALILWLFKHRIGVKPKNNPAPKGAPTKADQPGASGGASGDKP
GEMSGAGGPSGDKPGGASGGGDKPGGASGGASGGGPGGASGGASGGGPGGASGGASGGGP
GGASGGGPGGASGGASGDKPEGAPGDKPGGASGGKPGKKPGHKPAGARGGKRLAWW

179 >tr|Q94FP7|Q94FP7_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 PE=3 SV=1
MLSFLIPVVQFFQVVIAAVASVVFFVFAGITFGASIVGLTIATPLFVIFSPILVPATIAT
TFLVGGATAAVALGVTAFALILWLFKHRIGVKPKNNPAPKGAPTKADQPGASGGASGDKP
GEMSGAGGPSGDKPGGASGGGDKPGGASGGASGGGPGGASGGASGGGPGGASGGGPGGAS
GGASGDKPEGAPGDKPGGASGGKPGKKPGHKPAGARGGKRLAWW

180 >tr|Q94FQ6|Q94FQ6_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 PE=3 SV=1
MFEIIQAVFSAGVALALLTFAGITLGGSVVACIISTPLLVIFSPVLVPATIATTLLASGF
TASGSFGATAFTILSWLYKKRTGRDLPKIPGLTPPAPASNPAGSGV

181 >tr|A0A178UC12|A0A178UC12_ARATH Oleosin OS=Arabidopsis thaliana OX=3702
GN=AXX17_At5g07240 PE=3 SV=1
MLSFLIPVVQFFQVVIAAVASVVFLVFAGITFGASIVGLTIATPLFVIFSPILVPATIAT
TFLVGGATAAVALGVTAFALILWLFKHRIGVKPKNNPAPKGAPTKADQPGASGDKPGEMS
GAGGPSGDKPGGASGGGDKPGGASGGASGGGPGGASGGASGGGPGGASGGASGGGPGGAS
GGGPGGASGGASGDKPEGAPGDKPGGASGGKPGKKPGHKPAGARGGKRLAWW

182 >tr|Q94FR1|Q94FR1_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 PE=3 SV=1
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TFLVGGATAAVALGVTAFALILWLFKHRIGVKPKNNPAPKGAPTKADQPGASGDKPGEMS
GAGGPSGDKPGGASGGGDKPGGASGGASGGGPGGASGGASGGGPGGASGGASGGGPGGAS

GGGPGGASGGASGDKPEGAPGDKPGGASGGKPGKKPGHKPAGARGGKRLAWW

183 >tr|O04925|O04925_SESIN Oleosin OS=Sesamum indicum OX=4182 PE=2 SV=1
MADEPHDQRPTDVIKSYLPEKGPSTSQVLAVVTLFPLGAVLLCLAGLILTGTIIGLAVAT
PLFVIFSPILVPAALTIALAVTGFLTSGAFGITALSSISWLLNYVRRMRGSLPEQLDHAR
RRVQETVGQKTREAGQRSQDVIRP

184 >tr|A0A398AHE7|A0A398AHE7_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRARA_B03306
PE=3 SV=1
MANVDRRVNVDRTDKGLQLQPQYEDRVGYGYGYGGNTDYKSRGPSTNQIVALIAGVPIGG
SLLALAGLTLAGSVIGFMLSIPLFLLFSPVIVPAALTIGLAVTGILASGLFGLTGLSSVS
WVLNYIRGRSDTVPEQLDYAKRRMADAVGYAGQKGKEMGQYVQDKAHEAHDTSLTTETNG
KARRAHIA

185 >tr|A0A444YZD4|A0A444YZD4_ARAHY Oleosin OS=Arachis hypogaea OX=3818 GN=Ahy_B05g074500
PE=3 SV=1
MATATDRAPHQVQVHTPTTQRVDVQRRGYDVSGGGVKTLFPDRGPSTSQIIAVLVGVPTG
GTLLLLSGLSLLGTIIGLAIATPVFIFFSPVIVPAVVTIGLAVIGILTAGACGLTGLMSL
SWMINFIRQVHGTTVPDQLDSAKRRMADMADYVGQKTKDAGQEIQTKAQDVKRSS

186 >tr|A0A397XNC0|A0A397XNC0_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA10T44971Z
PE=3 SV=1
MLSFFSPLLDVIKVVVASVTSVVLFLFAGLTLSGSAVALVVSTPLFLIFSPILVPATIAT
TLLASGLTAGATLGITAISLIMGLIKTAEGSSLARLAQTPLKLFKFSGGFGGSWGGKSFS
GTFGNKGSQSSGNIPGWLKNLLNGIPAGGAVPAAGEAAPAPAAGGAAPAPAAPPG

187 >tr|B5TMA5|B5TMA5_SESIN Oleosin OS=Sesamum indicum OX=4182 PE=2 SV=1
MAEHYGQQQQTRAPHPQLQPRAQRVVKAATAVTAGGSLLVLSGLTLAGTVIALTIATPLL
VIFSPVLVPAVITIFLLGAGFLASGGFGVAALSVLSWIYRYLTGKHPPGADQLESAKTKL
ASKAREMKDRAEQFSQQPVAGSQTS

188 >tr|A0A3N6QIR7|A0A3N6QIR7_BRACR Oleosin OS=Brassica cretica OX=69181 GN=DY000_00012937
PE=3 SV=1
MADTARTHHDITSRDQYPMLGRDRDQYPYGRSDYQTSGQDYSKTRQIAKAATAVTAGGSL
LVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWI
YKYATGEHPQGSDKLDSARMKLGSKAQDIKDRAQYYGQQHTGGEHDRDRTRGTHHTTTTT

189 >tr|A0A3N6S1W5|A0A3N6S1W5_BRACR Oleosin OS=Brassica cretica OX=69181 GN=DY000_00000294
PE=3 SV=1

MTTVDRRVNVDRTDKGLQLKPQYEDRVGYGAGYDYGYGADYKSRGPSTNQVVALIAGVPI
GGSLLALAGLTLAGSVIGLMLSIPLFLLFSPVIVPAALTIGLAVTGILASGLFGLTGLSS
VSWVLNYIRGTSDTVPEQLDYAKRRMADAVGYAGQKGKEVGQYVQDKAHEAHDTSLTTET
REPVQAKRTLA

190 >tr|Q94CI1|Q94CI1_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=GRP4 PE=3 SV=1
MSEELVRHESHSQASIFSRFFRMFSFIFPLLNVIKLIIASVTSLVCLAFSCVTLGGSAVA
LIVSTPLFIIFSPILVPATIATTLLASGLMAGTTLGLTGIGLITGLVRTAGGVTLAESPI
RRIIINRIKARLGGGGGSRLAMLKKILGLIKKLRGMSSGGAAPAAEAAPAAAPADGAAPA
AAPAPT

191 >tr|A0A3P6DW75|A0A3P6DW75_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=BOLC2T11502H PE=3
SV=1
MTTVDRRVNVDRTDKGLQLKPQYEDRVGYGAGYDYGYGADYKSRGPSTNQVVALIAGVPI
GGSLLALAGLTLAGSVIGLMLSIPLFLLFSPVIVPAALTIGLAATGILASGLFGLTGLSS
VSWVLNYIRGTSDTVPEQLDYAKRRMADAVGYAGQKGKEMGQYVQDKAHEAHDTSLTTET
REPVQAKRTLA

192 >tr|A0A3P6GN93|A0A3P6GN93_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=BOLC8T48598H PE=3
SV=1
MADTARTHHDITSRDQYPMLGRDRDQYPYGRSDYQTSGQDYSKTRQIAKAATAVTAGGSL
LVLSSLTLVGTVIALTVATPLLVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWI
YKYATGEHPQGSDKLDSARMKLGSKAQDIKDRAQYYGQQHTGGEHDRDRTRGTHHTTTTT

193 >tr|B9RAW7|B9RAW7_RICCO Oleosin 18.2 kDa, putative OS=Ricinus communis OX=3988
GN=RCOM_1509400 PE=4 SV=1
MAERLQQQQQQGHDKKGPSTSQILAVVTLLPLSGTLLFLAGATLVGALTGLGVTTPLFVI
FSPVLVPAAFVIGLAVLGFSVSGAFGITALSSLSWMLNNFRRMIGLLPQQMEHAKRRVQE
TTGQLGQKARDVGQTVQSKAQ

194 >tr|A0A251SMH6|A0A251SMH6_HELAN Putative oleosin OS=Helianthus annuus OX=4232
GN=HannXRQ_Chr14g0460941 PE=4 SV=1
MTDFYHHRGQAMHHRQYNESRAHQVVKAATAATAGGSLLVLSGLTLVGTVITLTVATPLL
VIFSPVLVPAVMTVFLLATGFLTSGGFGLAAATVFSWMYRYVTGERRTGVESYDQMRRKV
GSKGRARDDHASGKGHHATGGVQLTTGARTGLFES

195 >tr|Q9FKT7|Q9FKT7_ARATH Glycine-rich protein / oleosin OS=Arabidopsis thaliana OX=3702
GN=MDA7.16 PE=2 SV=1

MENPGGRRRRDIAITDGERTTGSSVVAATVAAVAVVGPLFGLMSFSFVATVTLFLIASPL
LLIFAPAFMVTVAVLVSAMVGVGVAAAMWMMGIAALVCCGREIGIETGLAGRMVESVVRE
LGYGRSRYLRDKSEDSYSTSSPSSRDYSSS

196 >tr|A0A397XXY0|A0A397XXY0_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRARA_J02523 PE=3 SV=1
MSEELVQHESHSQASIFSRFFRMFSFIFPLLNVIKLIIASVTSLVCLAFSCVALGGSAVA
LIVSTPLFIMFSPILVPATIATTLLASGLMAGTTLGLTGIGLIMGLVRTAGGVSLLQSPL
RKIIVNRIKARLGGGGGGSRLARLKKILGLLNKLRGMGAGGAAAPAAEPAPAAEAAPAAE
AAPAAAHAAAPAAAP

197 >tr|A0A397XIT4|A0A397XIT4_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRARA_J00613 PE=3 SV=1
MANQTRTHQDIIVRDSRSTLDRDHPKTGAQMVKVATGVAAGGSLLVLSGLTLAGTVIALA
VATPLLIIFSPVLVPAVITVVLIITGFLASGGFGIAAITAFSWLYRHMTGSGSDQKIESA
RMKVGSRGYDTKYGQHNIGVHQQHQQAAS

198 >tr|A0A398A5G3|A0A398A5G3_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRARA_B00248 PE=3 SV=1
MLSFLISLLDIIKLVIASATFLFFLAFSGLTFAGSAVALVVSTPLFIIFSPILVPATIST
TLLASGLAAGTSLGLTAIGLIMRLIKPAGGTSLLFSSPTPLNLVTYSGQFEGSVLGKTYT
GTFDNKSGGGIKWTVTWGSRTFSGTIPLPAAAAPAAAPAAPAAAPAAPAAEAAPAAPAAA
PAAPAAPAAAPAAPAAGAAPPAW

199 >tr|A0A445C916|A0A445C916_ARAHY Oleosin OS=Arachis hypogaea OX=3818 GN=Ahy_A07g033289 PE=3 SV=1
MSDQTRTGYGGGGSYGSSYGGGGTYGSSYGTSYDPSTNQPIRQAIKFMTASAIGVSFLIL
SGLILTGTVIGLIIATPLLVIFSPILVPAAITLALAAGGFLFSGGCGVAAIAALSWLYSY
VTGKHPAGSDRLDYAKGVIADKARDVKDRAKDYAGAGRAQEGTQGY

200 >tr|A0A445BU36|A0A445BU36_ARAHY Oleosin OS=Arachis hypogaea OX=3818 GN=Ahy_A08g038688 PE=3 SV=1
MSDQTRTGYGGGGSYGSSYGGGGTYGSSYGTSYDPSTNQPIRQAIKFMTASTIGVSFLIL
SGLILTGTVIGLIIATPLLVIFSPILVPAAITLALAAGGFLFSGGCGVAAIAALSWLYSY
VTGKHPAGSDRLDYAKGVIADKARDVKDRAKDYAGAGRAQEGTQGY

201 >tr|Q647G3|Q647G3_ARAHY Oleosin OS=Arachis hypogaea OX=3818 PE=2 SV=1
MSDQTRTGYGGGGSYGSSYGGGGTYGSSYGTSYDPSTNQPIRQAIKFMTASTIGVSFLIL

SGLILTGTVIGLIIATPLLVIFSPILVPAAITLALAAGGFLFSGGCGVAAIAALSWLYSY
VTGKHPAGSDRLDYAKGVIADKARDVKDRAKDYAGAGRAQEGTPGY

202 >tr|A0A5E4EAT1|A0A5E4EAT1_PRUDU Oleosin OS=Prunus dulcis OX=3755 GN=ALMOND_2B006731 PE=3 SV=1
MADQHFQQPLHFQGSYGQQQPRSYQVAKAATAVTAGGSLLVLSGLVLAGTVIALTIATPL
LVIFSPVLVPALITVALITMGFLTSGGFGVAAVTVLSWIYKYVTGKQPPGADQLDQARHK
LAGKARDIKDRAEQFGQQHVPSGQQQSS

203 >tr|A0A445FAH8|A0A445FAH8_GLYSO Oleosin OS=Glycine soja OX=3848 GN=D0Y65_050056 PE=3 SV=1
MAEVRSQQPQHVQVHASTTHTPQQYRYYQGGAKTQHHGGEGGGVMSLFPEISLTGSQLLA
LLAGVPLGGMLLLLSGVSLIASLVGLAVATPLFIFFSPVLVPAAFVIGMAVTAVLAAGAC
GLVGLVSFSWLVNCLRQMPRGTTTKTTMMRPEQAKRHVADMEEYVGKKTKDVGQDIQTRA
HAQGTTGMLGLWVWVFDAVLVVVWVWVFDAVLVVVWVFGVGLAASGDLVEQDWTGKIGSD
PTSHHKHSAIFNGDDATRVYQNSDGVKSAATDGE

204 >tr|A0A3P6EKY2|A0A3P6EKY2_BRAOL Oleosin OS=Brassica oleracea OX=3712 GN=BOLC9T59708H PE=3 SV=1
MSEELVQHESHSQASIFSRFFRMFSFIFPLLNVIKLIIASVTSLVCLAFSCVTLGGSAVA
LIVSTPLFIIFSPILVPATIATTLLASGLMAGTTLGLTGIGLITGLVRTAGGVTLAESPI
RRIIINRIKARLGGGGGSRLAMLKKILGLIKKLRGMSSGGAAPAAEAAPAAAPADGAAPA
AAPAPT

205 >tr|C3S7F6|C3S7F6_BRANA Oleosin OS=Brassica napus OX=3708 GN=S5 PE=2 SV=1
MANQTRTHQDIIVRDSRITLDRDHPKTGAQMVKVATGVAAGGSLLVLSGLTLAGTVIAFA
VATPLLIIFSPVLVPAVITVVLIITGFLASGGFGIAAITAFSWLYRHMTGSGSDQKIESA
RMKVGSRGYDTKYGQHNIGVHQQHQQAAS

206 >tr|A0A5E4FAC4|A0A5E4FAC4_PRUDU Oleosin OS=Prunus dulcis OX=3755 GN=ALMOND_2B028251 PE=3 SV=1
MADQSRHVTLKLQDHDHSAAPPSSLRLTGKFLTAGAAGTTLLVLSGLTLTGTVMALIMAT
PVLVVFSPILVPAGIVVFLTAAGLVFSGGCGVAAVTTLTLMYKYISSYVATKKRAYLYGQ
YFCPF

207 >tr|B9RE45|B9RE45_RICCO Oleosin, putative OS=Ricinus communis OX=3988 GN=RCOM_1618240 PE=4 SV=1
MADRDRASNPAQRPTRTATSNATPNNHVSTFLRKLQSHAPNSTQFMGILTLLISGSILLL
LIGITVTALVMGLVFFTPLIIVSSPIWFPIGVLLFFAAAGFFSVCGFLVATIGGLSWMYR

YYRGMHPPGSDRFDYARSRIYDTASHVKDYAREYGGYLQSKVKDAAPGA

S3 Table. Identification yield at false discovery rate (FDR) threshold for *B. rapa* R-o-18 database used to analyses mass spectroscopic data.

Data level	FDR	Brassica rapa R-o-18 database			
Sample number		10	16	19	49
Number of spectra in search		20712	18200	16257	15282
FDR type: Local					
FDR of protein	1%	449	418	315	332
	5%	449	436	315	332
	10%	449	449	315	332
FDR of distinct peptide	1%	1677	1751	1246	1236
	5%	1784	1891	1330	1333
	10%	1833	1952	1367	1377
False discovery rate of spectra	1%	7871	8324	5679	6316
	5%	8587	9017	6036	6694
	10%	8916	9666	6197	6869
Number of identified proteins			323		
Number of non-redundant proteins identified in at least 3 out of 4 biological replicates with at least 2 unique peptides and a p value of < 0.05			233		

FDR=False discovery rate.

S4 Table. List of proteins identified from liquid chromatography–mass spectrometry (LC/MS) analysis using *Brassica rapa* R-o-18 database.

#	Identified Proteins	Accession Number	Molecular Weight	Total Spectrum Count Uncategorized Sample Pool 1	Total Spectrum Count Uncategorized Sample Pool 2	Total Spectrum Count Uncategorized Sample Pool 3	Total Spectrum Count Uncategorized Sample Pool 4
1	Brassica rapa ro18 1.5 Candidate 4 cruciferin	Bra022801 (+5)		656	452	367	343
2	PREDICTED: Brassica napus embryonic protein DC-8-like (LOC106447584), transcript variant X1, mRNA ; PREDICTED: Brassica napus embryonic protein DC-8-like (LOC106447584), transcript variant X2, mRNA ; Similar to SBP65 Seed biotin-containing protein SBP65 (Glycine max)::Bra040977:0-729	Bra040977	78 kDa	347	428	450	213
3	Brassica rapa ro18 1.5 Candidate 3 cruciferin	Bra035434 (+5)		429	306	209	236
4	Brassica rapa ro18 1.5 Candidate 1 cruciferin	Bra002906 (+2)		364	278	293	225
5	PREDICTED: Brassica napus jacalin-related lectin 36-like (LOC106376924), mRNA ; PREDICTED: Brassica napus jacalin-related lectin 36-like	Bra014461	49 kDa	250	290	271	268

	(LOC106454993), mRNA ; PREDICTED: Brassica oleracea var. oleracea jacalin-related lectin 36 (LOC106324420), mRNA ; PREDICTED: Brassica rapa jacalin-related lectin 36 (LOC103835222), mRNA ; Similar to JAL36 Jacalin-related lectin 36 (Arabidopsis thaliana)::Bra014461:0-460 PREDICTED: Brassica rapa oleosin S2-2 (LOC103854221), mRNA ; Similar to S2 Oleosin S2-2 (Brassica napus)::Bra019493:0-188						
6	Similar to JAL5 Jacalin-related lectin 5 (Arabidopsis thaliana)::Bra029497:0-970 PREDICTED: Brassica oleracea var. oleracea oleosin S2-2 (LOC106316842), mRNA ; PREDICTED: Brassica rapa oleosin S2-2 (LOC103837001), mRNA ; Similar to S2 Oleosin S2-2 (Brassica napus)::Bra000167:0-188	Bra019493 (+1)	20 kDa	220	300	250	174
7	Oleosin OS=Brassica napus OX=3708 GN=BnaA08g14540D PE=3 SV=1	Bra029497		286	294	95	205
8	PREDICTED: Brassica napus jacalin-related lectin 36-like	Bra000167 (+1)	20 kDa	337	391	375	338
9		A0A078GHK4_BRANA (+3)	20 kDa	150	202	136	233
10		Bra021102	34 kDa	237	294	304	300

	(LOC106397692), mRNA ; PREDICTED: Brassica napus jacalin-related lectin 36 (LOC106346621), mRNA ; PREDICTED: Brassica napus jacalin-related lectin 36 (LOC106397691), mRNA ; PREDICTED: Brassica rapa jacalin-related lectin 36-like (LOC103872285), mRNA ; Similar to JAL36 Jacalin-related lectin 36 (Arabidopsis thaliana)::Bra021102:0-312						
11	Similar to At5g40420 Oleosin 21.2 kDa (Arabidopsis thaliana)::Bra039545:0-220	Bra039545 (+1)	23 kDa	245	335	312	225
12	Brassica napus beta-glucosidase 19 (LOC106376923), mRNA ; PREDICTED: Brassica napus beta-glucosidase 19 (LOC106376923), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea beta-glucosidase 19 (LOC106295008), mRNA ; PREDICTED: Brassica rapa beta-glucosidase 19 (LOC103835230), mRNA ; Similar to BGLU19 Beta-glucosidase 19 (Arabidopsis thaliana)::Bra014460:0-528	Bra014460	60 kDa	239	185	57	150

13	Brassica napus oleosin S3-5 (S3) mRNA, complete cds ; Brassica napus oleosin S3-6 (S3) mRNA, complete cds ; PREDICTED: Brassica napus oleosin 18.5 kDa (LOC106361728), mRNA ; PREDICTED: Brassica rapa oleosin 18.5 kDa-like (LOC103861532), mRNA ; Similar to Oleosin Bn-V (Fragment) (Brassica napus)::Bra011140:0-183 PREDICTED: Brassica napus late embryogenesis abundant protein At3g53040-like (LOC106399842), mRNA ; PREDICTED: Brassica napus late embryogenesis abundant protein At3g53040-like (LOC106409388), mRNA ; PREDICTED: Brassica oleracea var. oleracea embryonic protein DC-8 (LOC106340390), mRNA ; PREDICTED: Brassica rapa embryonic protein DC-8 (LOC103872167), mRNA ; Similar to Embryonic protein DC-8 (Daucus carota)::Bra039225:0-451	Bra011140 (+3)	20 kDa	141	190	88	227
14	Brassica rapa chiifu v2 candidate 8 cruciferin	Bra039225	49 kDa	102	120	133	94
15		BraA09006896	49 kDa	157	143	72	96

16	Oleosin OS=Brassica campestris OX=3711 GN=BRARA_C02941 PE=3 SV=1	A0A397ZZI8_BRACM (+3)	21 kDa	94	135	110	114
17	Similar to PER1 1-Cys peroxiredoxin PER1 (Arabidopsis thaliana)::Bra029708:0-231	Bra029708	26 kDa	92	126	125	105
18	Brassica napus oleosin S3-3 (S3) mRNA, complete cds ; Brassica napus oleosin S3-4 (S3) mRNA, complete cds ; Brassica napus oleosin S3-7 (S3) mRNA, complete cds ; Brassica rapa oleosin-like protein mRNA, partial cds ; PREDICTED: Brassica napus major oleosin NAP-II-like (LOC106442597), mRNA ; PREDICTED: Brassica napus oleosin Bn-III-like (LOC106346567), mRNA ; PREDICTED: Brassica napus oleosin Bn-III (LOC111202192), mRNA ; PREDICTED: Brassica oleracea var. oleracea oleosin Bn-III (LOC106298955), transcript variant X1, misc_RNA ; PREDICTED: Brassica oleracea var. oleracea oleosin Bn-III (LOC106298955), transcript variant X2, mRNA ; PREDICTED: Brassica rapa oleosin Bn-III (LOC103862927),	Bra012836 (+1)	22 kDa	91	122	46	113

	mRNA ; Similar to Oleosin Bn-III (Brassica napus)::Bra012836:0-195						
19	Similar to HSD1 11-beta-hydroxysteroid dehydrogenase 1A (Arabidopsis thaliana)::Bra017248:0-349	Bra017248	39 kDa	100	101	49	62
20	PREDICTED: Brassica napus late embryogenesis abundant protein (LOC106365978), mRNA ; PREDICTED: Brassica rapa late embryogenesis abundant protein (LOC103842523), mRNA ; Similar to Late embryogenesis abundant protein (Raphanus sativus)::Bra005778:0-183	Bra005778	19 kDa	87	96	76	96
21	PREDICTED: Brassica napus vicilin-like seed storage protein At3g22640 (LOC106454009), mRNA ; PREDICTED: Brassica oleracea var. oleracea vicilin (LOC106297624), mRNA ; PREDICTED: Brassica rapa vicilin-like seed storage protein At3g22640 (LOC103834417), mRNA ; Similar to PAP85 Vicilin-like seed storage protein At3g22640 (Arabidopsis thaliana)::Bra014536:0-486	Bra014536 (+1)	55 kDa	124	90	68	53
22	PREDICTED: Brassica napus dehydrin Rab18-like	Bra000838	18 kDa	66	87	113	62

	(LOC106366343), mRNA ; PREDICTED: Brassica oleracea var. oleracea dehydrin Rab18-like (LOC106315749), mRNA ; PREDICTED: Brassica rapa dehydrin Rab18-like (LOC103837679), mRNA ; Similar to RAB18 Dehydrin Rab18 (Arabidopsis thaliana)::Bra000838:0-179						
23	Brassica rapa R-o-18 V1.5 candidate 1 napin PREDICTED: Brassica napus vicilin-like seed storage protein At2g28490 (LOC106352587), mRNA ; PREDICTED: Brassica napus vicilin-like seed storage protein At2g28490 (LOC111204718), mRNA ; PREDICTED: Brassica oleracea var. oleracea vicilin-like antimicrobial peptides 2-2 (LOC106333272), mRNA ; PREDICTED: Brassica rapa vicilin-like seed storage protein At2g28490 (LOC103829747), mRNA ; Similar to At2g28490 Vicilin-like seed storage protein At2g28490 (Arabidopsis	Bra041165 (+1)		84	93	101	66
24	thaliana)::Bra025745:0-466	Bra025745 (+2)	52 kDa	95	81	94	73

25	Brassica napus peroxygenase 1 (LOC106429504), mRNA ; Similar to PXG1 Peroxygenase 1 (Arabidopsis thaliana)::Bra033733:0-245	Bra033733	28 kDa	74	106	67	83
26	Brassica oleracea HDEM genome, scaffold: C1 ; Brassica rapa genome, scaffold: A01 ; Brassica rapa ME-leaC4 mRNA for late embryogenesis-abundant protein, complete cds ; PREDICTED: Brassica napus late embryogenesis abundant protein 76-like (LOC106349612), mRNA ; PREDICTED: Brassica rapa late embryogenesis abundant protein 76 (LOC103840578), mRNA ; Similar to Late embryogenesis abundant protein 76 (Brassica napus)::Bra014978:0-226	Bra014978	25 kDa	65	73	99	57
27	Similar to Late embryogenesis abundant protein D-34 (Gossypium hirsutum)::Bra030208:0-262	Bra030208	27 kDa	108	139	52	75
28	PREDICTED: Brassica napus NADPH-dependent aldehyde reductase 1, chloroplastic (LOC106392387), mRNA ; PREDICTED: Brassica napus NADPH-dependent aldehyde reductase 1, chloroplastic	Bra013750	31 kDa	138	105	20	47

	(LOC111212037), mRNA ; PREDICTED: Brassica oleracea var. oleracea glucose and ribitol dehydrogenase homolog 1 (LOC106297131), mRNA ; PREDICTED: Brassica rapa glucose and ribitol dehydrogenase homolog 1 (LOC103844522), mRNA ; Similar to At1g54870 Glucose and ribitol dehydrogenase homolog 1 (Arabidopsis thaliana)::Bra013750:0-289 PREDICTED: Brassica napus oil body-associated protein 1A (BNAA10G03690D), mRNA ; PREDICTED: Brassica napus oil body-associated protein 1A (BNAC05G03600D), mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterized LOC106294119 (LOC106294119), mRNA ; PREDICTED: Brassica rapa oil body-associated protein 1A (LOC103844119), mRNA ;						
29	Protein of unknown function::Bra036039:0-264	Bra036039	30 kDa	83	83	69	46
30	PREDICTED: Brassica napus late embryogenesis abundant protein 31-like (LOC106366934), mRNA ; PREDICTED: Brassica napus	Bra010153	27 kDa	66	91	59	38

31	late embryogenesis abundant protein 31-like (LOC106439628), mRNA ; PREDICTED: Brassica oleracea var. oleracea late embryogenesis abundant protein D-34-like (LOC106335925), mRNA ; PREDICTED: Brassica rapa late embryogenesis abundant protein 31-like (LOC103859958), mRNA ; Similar to Late embryogenesis abundant protein D-34 (Gossypium hirsutum)::Bra010153:0-256 Brassica oleracea HDEM genome, scaffold: C5 ; Brassica rapa genome, scaffold: A06 ; PREDICTED: Brassica napus heat shock 70 kDa protein 5-like (LOC106346793), mRNA ; PREDICTED: Brassica napus heat shock 70 kDa protein 5-like (LOC106396610), mRNA ; PREDICTED: Brassica oleracea var. oleracea heat shock 70 kDa protein 5 (LOC106295243), mRNA ; PREDICTED: Brassica rapa heat shock 70 kDa protein 5 (LOC103872405), mRNA ; Similar to HSP70-5 Heat shock 70 kDa protein 5 (Arabidopsis thaliana)::Bra021189:0-647	Bra021189	71 kDa	80	72	39	54

32	Similar to GAPC Glyceraldehyde-3-phosphate dehydrogenase, cytosolic (Sinapis alba)::Bra034599:0-290	Bra034599	32 kDa	80	76	14	48
33	PREDICTED: Brassica napus vicilin-like seed storage protein At4g36700 (LOC106359072), partial mRNA ; PREDICTED: Brassica napus vicilin-like seed storage protein At4g36700 (LOC106361437), transcript variant X1, mRNA ; PREDICTED: Brassica napus vicilin-like seed storage protein At4g36700 (LOC106361437), transcript variant X2, mRNA ; PREDICTED: Brassica rapa vicilin-like seed storage protein At4g36700 (LOC103834998), mRNA ; Similar to At4g36700 Vicilin-like seed storage protein At4g36700 (Arabidopsis thaliana)::Bra033857:0-585	Bra033857 (+2)	65 kDa	73	77	21	31
34	PREDICTED: Brassica napus protein disulfide isomerase-like 1-1 (LOC106425960), mRNA ; PREDICTED: Brassica napus protein disulfide isomerase-like 1-1 (LOC106425964), mRNA ; PREDICTED: Brassica napus protein disulfide isomerase-like 1-	Bra034333	56 kDa	66	79	13	50

	1 (LOC106431998), mRNA ; PREDICTED: Brassica napus protein disulfide isomerase-like 1-1 (LOC106432001), mRNA ; PREDICTED: Brassica oleracea var. oleracea protein disulfide isomerase-like 1-1 (LOC106312445), mRNA ; PREDICTED: Brassica rapa protein disulfide isomerase-like 1-1 (LOC103835729), mRNA ; Similar to PDIL1-1 Protein disulfide isomerase-like 1-1 (Arabidopsis thaliana)::Bra034333:0-501 PREDICTED: Brassica napus late seed maturation protein P8B6 (LOC106438038), transcript variant X1, mRNA ; PREDICTED: Brassica napus late seed maturation protein P8B6 (LOC106438038), transcript variant X2, mRNA ; PREDICTED: Brassica rapa late seed maturation protein P8B6-like (LOC103857913), mRNA ; Similar to Late seed maturation protein P8B6 (Raphanus						
35	sativus)::Bra008633:0-88	Bra008633	10 kDa	41	41	49	16
36	Brassica oleracea HDEM genome, scaffold: C4 ; Brassica rapa	Bra029133	18 kDa	31	46	46	36

	genome, scaffold: A05 ; PREDICTED: Brassica napus 17.6 kDa class I heat shock protein 2-like (LOC106451531), mRNA ; PREDICTED: Brassica napus 17.6 kDa class I heat shock protein 2 (LOC106451510), mRNA ; PREDICTED: Brassica oleracea var. oleracea 17.6 kDa class I heat shock protein 2 (LOC106342847), mRNA ; PREDICTED: Brassica rapa 17.6 kDa class I heat shock protein 2 (LOC103868031), mRNA ; Similar to HSP17.8 17.8 kDa class I heat shock protein (Arabidopsis thaliana) ; Zea mays clone 10568 mRNA sequence::Bra029133:0-156						
37	Similar to A1 Elongation factor 1-alpha 1 (Arabidopsis thaliana)::Bra020415:0-1456	Bra020415	162 kDa	45	67	31	28
38	Similar to Putative invertase inhibitor (Platanus acerifolia)::Bra018664:0-761	Bra018664	82 kDa	65	62	26	33
39	PREDICTED: Brassica napus chaperone protein ClpB1-like (LOC106354381), mRNA ; PREDICTED: Brassica napus chaperone protein ClpB1 (LOC106354344), mRNA ; PREDICTED: Brassica rapa	Bra027348	101 kDa	50	66	22	34

	chaperone protein ClpB1 (LOC103831900), mRNA ; Similar to CLPB1 Chaperone protein ClpB1 (Arabidopsis thaliana)::Bra027348:0-911 PREDICTED: Brassica napus oil body-associated protein 2A (BNACNNG34690D), mRNA ; PREDICTED: Brassica napus oil body-associated protein 2A (LOC106386443), mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterized LOC106305268 (LOC106305268), mRNA ; PREDICTED: Brassica rapa oil body-associated protein 2A (LOC103827782), mRNA ;						
40	Protein of unknown function::Bra023699:0-246	Bra023699	28 kDa	57	60	20	29
41	PREDICTED: Brassica napus GDSL esterase/lipase At1g54020-like (LOC106345820), transcript variant X1, mRNA ; PREDICTED: Brassica napus GDSL esterase/lipase At1g54020 (LOC106348443), transcript variant X1, mRNA ; PREDICTED: Brassica rapa GDSL esterase/lipase At1g54020-like (LOC103871087), transcript	Bra020125	43 kDa	49	45	29	28

42	variant X1, mRNA ; Similar to At1g54020 GDSL esterase/lipase At1g54020 (Arabidopsis thaliana)::Bra020125:0-383 PREDICTED: Brassica rapa low-temperature-induced 65 kDa protein-like (LOC103857129), mRNA ; Similar to LTI65 Low-temperature-induced 65 kDa protein (Arabidopsis thaliana)::Bra007884:0-674	Bra007884	73 kDa	30	52	39	40
43	Brassica napus late embryogenesis abundant protein 76-like (LOC106403035), mRNA ; Brassica napus lea3-1 gene for group 3 late embryogenesis abundant protein, exons 1-2 ; Brassica oleracea HDEM genome, scaffold: C5 ; Brassica oleracea HDEM genome, scaffold: C5 ; Brassica rapa genome, scaffold: A05 ; Brassica rapa subsp. pekinensis clone KBrB021B05, complete sequence ; PREDICTED: Brassica napus late embryogenesis abundant protein 76-like (LOC106397930), mRNA ; PREDICTED: Brassica napus late embryogenesis abundant protein 76-like (LOC106403035), transcript variant X1, mRNA ;	Bra030867	29 kDa	43	59	63	39

44	PREDICTED: Brassica oleracea var. oleracea late embryogenesis abundant protein 76 (LOC106294785), mRNA ; PREDICTED: Brassica rapa late embryogenesis abundant protein 76-like (LOC103869890), mRNA ; Similar to Late embryogenesis abundant protein 76 (Brassica napus)::Bra030867:0-265 Similar to Aldose reductase (Hordeum vulgare)::Bra006614:0-322	Bra006614	37 kDa	50	53	31	26
45	Brassica oleracea HDEM genome, scaffold: C7 ; Brassica rapa cultivar Tsuda peptidylprolyl isomerase (ROC1) mRNA, complete cds ; Brassica rapa genome, scaffold: A06 ; PREDICTED: Brassica napus peptidyl-prolyl cis-trans isomerase CYP18-3-like (LOC106349476), mRNA ; PREDICTED: Brassica napus peptidyl-prolyl cis-trans isomerase CYP18-3-like (LOC106349478), mRNA ; PREDICTED: Brassica napus peptidyl-prolyl cis-trans isomerase CYP18-3-like (LOC106410133), mRNA ; PREDICTED: Brassica oleracea var. oleracea peptidyl-	Bra023885	18 kDa	38	51	27	26

	prolyl cis-trans isomerase CYP18-3-like (LOC106305761), mRNA ; PREDICTED: Brassica rapa peptidyl-prolyl cis-trans isomerase CYP18-3-like (LOC103828088), mRNA ; Similar to CYP18-3 Peptidyl-prolyl cis-trans isomerase CYP18-3 (Arabidopsis thaliana) ; Zea mays clone 9139 mRNA sequence::Bra023885:0-172 PREDICTED: Brassica napus alcohol dehydrogenase class-P-like (LOC106356941), mRNA ; PREDICTED: Brassica napus alcohol dehydrogenase class-P (LOC106386015), transcript variant X2, misc_RNA ; PREDICTED: Brassica rapa alcohol dehydrogenase class-P-like (LOC103830574), transcript variant X1, mRNA ; PREDICTED: Brassica rapa alcohol dehydrogenase class-P-like (LOC103830574), transcript variant X2, mRNA ; Similar to ADH1 Alcohol dehydrogenase class-P (Arabidopsis						
46	thaliana)::Bra026424:0-413	Bra026424	45 kDa	65	46	4	29
47	Brassica rapa 17.6 kDa class II heat shock protein (LOC103249161), mRNA ;	Bra007053	18 kDa	36	29	9	19

48	Brassica rapa genome, scaffold: A03 ; PREDICTED: Brassica napus 17.6 kDa class II heat shock protein (LOC106419901), mRNA ; Similar to HSP17.6 17.6 kDa class II heat shock protein (Arabidopsis thaliana)::Bra007053:0-154 PREDICTED: Brassica napus nitrilase 2 (LOC106387438), transcript variant X1, mRNA ; PREDICTED: Brassica napus nitrilase 2 (LOC106387438), transcript variant X2, mRNA ; PREDICTED: Brassica napus nitrilase 2 (LOC106403172), mRNA ; PREDICTED: Brassica oleracea var. oleracea nitrilase 2-like (LOC106333257), mRNA ; PREDICTED: Brassica rapa nitrilase 2 (LOC103856931), mRNA ; Similar to NIT2 Nitrilase 2 (Arabidopsis thaliana)::Bra007719:0-343	Bra007719	38 kDa	45	39	37	13
49	PREDICTED: Brassica napus em-like protein GEA1 (LOC106437913), mRNA ; PREDICTED: Brassica rapa em-like protein GEA1 (LOC103848642), mRNA ; Similar to EM1 Em-like protein	Bra014069	19 kDa	38	37	32	11

50	GEA1 (Arabidopsis thaliana)::Bra014069:0-172 PREDICTED: Brassica napus poly [ADP-ribose] polymerase 3 (LOC106371650), mRNA ; PREDICTED: Brassica oleracea var. oleracea poly [ADP-ribose] polymerase 3 (LOC106316987), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea poly [ADP-ribose] polymerase 3 (LOC106316987), transcript variant X2, mRNA ; PREDICTED: Brassica rapa poly [ADP-ribose] polymerase 3 (LOC103845539), mRNA ; Similar to PARP3 Poly [ADP-ribose] polymerase 3 (Arabidopsis thaliana)::Bra036910:0-809	Bra036910	91 kDa	27	42	19	38
51	PREDICTED: Brassica napus glutathione S-transferase F9 (LOC106387849), transcript variant X2, mRNA ; PREDICTED: Brassica napus glutathione S-transferase F9 (LOC106437571), mRNA ; PREDICTED: Brassica napus glutathione S-transferase F9 (LOC106437572), mRNA ; PREDICTED: Brassica rapa glutathione S-transferase F9	Bra008026	24 kDa	42	53	9	18

	(LOC103857341), mRNA ; Similar to GSTF9 Glutathione S-transferase F9 (Arabidopsis thaliana)::Bra008026:0-215 Brassica oleracea var. viridis disulfide isomerase-like protein 1-2 mRNA, complete cds ; PREDICTED: Brassica napus protein disulfide isomerase-like 1-2 (LOC106354602), mRNA ; PREDICTED: Brassica napus protein disulfide isomerase-like 1-2 (LOC106389517), mRNA ; PREDICTED: Brassica napus protein disulfide isomerase-like 1-2 (LOC106400427), mRNA ; PREDICTED: Brassica oleracea var. oleracea protein disulfide isomerase-like 1-2 (LOC106300838), mRNA ; PREDICTED: Brassica rapa protein disulfide isomerase-like 1-2 (LOC103832197), mRNA ; Similar to PDIL1-2 Protein disulfide isomerase-like 1-2 (Arabidopsis						
52	thaliana)::Bra027552:0-509	Bra027552	56 kDa	31	51	15	37
53	PREDICTED: Brassica napus aspartyl protease AED3-like (LOC106419485), mRNA ; PREDICTED: Brassica napus	Bra037658	47 kDa	34	35	20	26

54	aspartyl protease AED3-like (LOC106446100), mRNA ; PREDICTED: Brassica oleracea var. oleracea protein ASPARTIC PROTEASE IN GUARD CELL 2 (LOC106319255), mRNA ; PREDICTED: Brassica rapa aspartyl protease AED3 (LOC103847097), mRNA ; Protein of unknown function::Bra037658:0-439 PREDICTED: Brassica napus UPF0098 protein CT_736-like (LOC106435166), mRNA ; PREDICTED: Brassica napus UPF0098 protein CT_736-like (LOC106435872), mRNA ; PREDICTED: Brassica oleracea var. oleracea UPF0098 protein CT_736 (LOC106317405), mRNA ; Protein of unknown function::Bra038002:0-162	Bra038002	18 kDa	30	42	24	23
55	Brassica oleracea HDEM genome, scaffold: C4 ; Brassica rapa genome, scaffold: A05 ; PREDICTED: Brassica napus late embryogenesis abundant protein 18 (BNAC04G09820D), mRNA ; PREDICTED: Brassica napus late embryogenesis abundant protein 18-like (LOC106414888), mRNA	Bra028656	11 kDa	36	39	35	6

56	; PREDICTED: Brassica napus late embryogenesis abundant protein 18-like (LOC111211095), mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterized LOC106341460 (LOC106341460), mRNA ; PREDICTED: Brassica rapa uncharacterized LOC103867375 (LOC103867375), mRNA ; Protein of unknown function::Bra028656:0-98 Brassica napus oleosin 21.2 kDa-like (LOC106352688), mRNA ; Brassica napus oleosin 21.2 kDa-like (LOC106402820), mRNA ; PREDICTED: Brassica rapa oleosin 21.2 kDa-like (LOC103850173), mRNA ; Similar to At5g40420 Oleosin 21.2 kDa (Arabidopsis thaliana)::Bra025845:0-211	Bra025845 (+2)	22 kDa	183	234	260	139
57	Similar to GSTF3 Glutathione S-transferase F3 (Arabidopsis thaliana)::Bra000078:0-216	Bra000078	25 kDa	43	38	16	16
58	PREDICTED: Brassica napus GDSL esterase/lipase At5g14450-like (LOC106418385), mRNA ; PREDICTED: Brassica napus GDSL esterase/lipase At5g14450 (LOC106372098), mRNA ;	Bra037317	43 kDa	31	35	21	26

59	PREDICTED: Brassica oleracea var. oleracea GDSL esterase/lipase At5g14450 (LOC106318861), mRNA ; PREDICTED: Brassica rapa GDSL esterase/lipase At5g14450 (LOC103846482), mRNA ; Similar to At5g14450 GDSL esterase/lipase At5g14450 (Arabidopsis thaliana)::Bra037317:0-389 PREDICTED: Brassica napus mediator of RNA polymerase II transcription subunit 37a-like (LOC106387846), misc_RNA ; PREDICTED: Brassica napus mediator of RNA polymerase II transcription subunit 37f-like (LOC106437759), mRNA ; PREDICTED: Brassica oleracea var. oleracea mediator of RNA polymerase II transcription subunit 37f-like (LOC106335110), mRNA ; PREDICTED: Brassica rapa mediator of RNA polymerase II transcription subunit 37f (LOC103857349), mRNA ; PREDICTED: Raphanus sativus mediator of RNA polymerase II transcription subunit 37f-like (LOC108847038), mRNA ;	Bra008034 (+1)	74 kDa	49	54	32	32

60	Similar to MED37A Mediator of RNA polymerase II transcription subunit 37a (Arabidopsis thaliana)::Bra008034:0-669 Brassica oleracea HDEM genome, scaffold: C4 ; Brassica rapa genome, scaffold: A05 ; PREDICTED: Brassica napus heme-binding protein 2-like (LOC106362450), mRNA ; PREDICTED: Brassica napus heme-binding protein 2-like (LOC106372750), mRNA ; PREDICTED: Brassica rapa uncharacterized LOC103867148 (LOC103867148), mRNA ; Protein of unknown function::Bra028439:0-199	Bra028439	22 kDa	27	36	22	19
61	Similar to ADH1 Alcohol dehydrogenase class-P (Arabidopsis thaliana)::Bra027518:0-415	Bra027518 (+1)	45 kDa	65	47	4	20
62	PREDICTED: Brassica napus phosphoglycerate kinase 3, cytosolic-like (LOC106381505), transcript variant X1, mRNA ; PREDICTED: Brassica napus phosphoglycerate kinase 3, cytosolic-like (LOC106430726), mRNA ; PREDICTED: Brassica napus phosphoglycerate kinase 3,	Bra027664	42 kDa	42	31	11	21

63	cytosolic (LOC106354791), mRNA ; PREDICTED: Brassica oleracea var. oleracea phosphoglycerate kinase, cytosolic-like (LOC106300883), mRNA ; PREDICTED: Brassica rapa phosphoglycerate kinase, cytosolic (LOC103832426), transcript variant X1, mRNA ; PREDICTED: Brassica rapa phosphoglycerate kinase, cytosolic (LOC103832426), transcript variant X2, mRNA ; Similar to Phosphoglycerate kinase, cytosolic (Nicotiana tabacum)::Bra027664:0-401 Brassica oleracea HDEM genome, scaffold: C2 ; Brassica rapa genome, scaffold: A02 ; Brassica rapa subsp. pekinensis clone KBrH010D15, complete sequence ; PREDICTED: Brassica napus histone H2B.7-like (LOC106357790), mRNA ; PREDICTED: Brassica napus histone H2B.7-like (LOC106385623), mRNA ; PREDICTED: Brassica oleracea var. oleracea histone H2B.7-like (LOC106322833), mRNA ; PREDICTED: Brassica rapa	Bra016706	15 kDa	31	35	9	13

64	histone H2B.7-like (LOC103851535), mRNA ; Similar to H2B-3 Histone H2B.3 (Fragment) (Solanum lycopersicum) ; Zea mays clone 10590 mRNA sequence::Bra016706:0-142 Brassica rapa Chiifu-401 V2 candidate 4 napin	BraA01001883 (+1)	20 kDa	89	92	82	91
65	Similar to TIL Temperature-induced lipocalin-1 (Arabidopsis thaliana)::Bra016829:0-333	Bra016829	39 kDa	21	25	35	18
66	PREDICTED: Brassica napus glutathione S-transferase DHAR1, mitochondrial (LOC106346950), mRNA ; PREDICTED: Brassica napus glutathione S-transferase DHAR1, mitochondrial (LOC106401061), mRNA ; PREDICTED: Brassica oleracea var. oleracea glutathione S-transferase DHAR1, mitochondrial (LOC106295217), mRNA ; PREDICTED: Brassica rapa glutathione S-transferase DHAR1, mitochondrial (LOC103872760), mRNA ; Similar to DHAR1 Glutathione S-transferase DHAR1, mitochondrial (Arabidopsis thaliana)::Bra021474:0-213	Bra021474	24 kDa	21	42	16	20

67	PREDICTED: Brassica napus myrosinase-binding protein 2-like (LOC111201427), mRNA ; PREDICTED: Brassica oleracea var. oleracea myrosinase-binding protein 2-like (LOC106316347), mRNA ; PREDICTED: Brassica rapa myrosinase-binding protein 2-like (LOC103845081), transcript variant X1, mRNA ; PREDICTED: Brassica rapa myrosinase-binding protein 2-like (LOC103845081), transcript variant X2, mRNA ; PREDICTED: Brassica rapa myrosinase-binding protein 2-like (LOC103845081), transcript variant X3, mRNA ; Similar to MBP2 Myrosinase-binding protein 2 (Arabidopsis thaliana)::Bra036569:0-550	Bra036569	58 kDa	23	23	17	20
68	PREDICTED: Brassica napus probable inactive serine/threonine-protein kinase fnkC (LOC106365884), mRNA ; PREDICTED: Brassica napus probable inactive serine/threonine-protein kinase fnkC (LOC106440360), mRNA ; PREDICTED: Brassica rapa probable inactive serine/threonine-	Bra000418	42 kDa	48	23	2	21

69	protein kinase fnkC (LOC103837118), mRNA ; Protein of unknown function::Bra000418:0-367 Similar to MSD2 Superoxide dismutase [Mn] 2, mitochondrial (Arabidopsis thaliana)::Bra005106:0-430	Bra005106	49 kDa	40	22	17	13
70	PREDICTED: Brassica napus actin-7 (LOC106384924), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea actin-7-like (LOC106335398), mRNA ; PREDICTED: Brassica rapa actin-7-like (LOC103855835), mRNA ; Similar to ACT7 Actin-7 (Arabidopsis thaliana)::Bra006948:0-377	Bra006948 (+2)	42 kDa	35	26	13	13
71	PREDICTED: Brassica napus 11-beta-hydroxysteroid dehydrogenase-like 5 (LOC106436433), mRNA ; PREDICTED: Brassica oleracea var. oleracea 11-beta-hydroxysteroid dehydrogenase-like 5 (LOC106328447), mRNA ; Similar to HSD5 11-beta-hydroxysteroid dehydrogenase-like 5 (Arabidopsis thaliana)::Bra009101:0-461	Bra009101	52 kDa	17	24	17	13

72	Similar to SSL9 Protein STRICTOSIDINE SYNTHASE-LIKE 9 (Arabidopsis thaliana)::Bra040149:0-853 PREDICTED: Brassica napus oleosin 14.9 kDa (LOC106375666), mRNA ; PREDICTED: Brassica napus oleosin 14.9 kDa (LOC106402530), mRNA ; PREDICTED: Brassica rapa oleosin 14.9 kDa (LOC103864856), mRNA ;	Bra040149	96 kDa	30	27	10	25
73	Similar to OL3 Oleosin 14.9 kDa (Arabidopsis thaliana)::Bra035756:0-205 PREDICTED: Brassica napus late seed maturation protein P8B6-like (LOC106450837), mRNA ; PREDICTED: Brassica napus late seed maturation protein P8B6 (LOC106397804), mRNA ; PREDICTED: Brassica oleracea var. oleracea late seed maturation protein P8B6 (LOC106342772), mRNA ; PREDICTED: Brassica rapa late seed maturation protein P8B6 (LOC103866975), mRNA ;	Bra035756	22 kDa	25	19	20	12
74	Similar to EM6 Em-like protein GEA6 (Arabidopsis thaliana)::Bra028273:0-84	Bra028273	9 kDa	46	35	49	17

	PREDICTED: Brassica napus non-specific lipid-transfer protein-like 1 (LOC106402434), mRNA ; PREDICTED: Brassica napus non-specific lipid-transfer protein-like 1 (LOC106447070), transcript variant X1, mRNA ; PREDICTED: Brassica napus non-specific lipid-transfer protein-like 1 (LOC106447070), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea non-specific lipid-transfer protein-like 1 (LOC106315711), mRNA ; PREDICTED: Brassica rapa non-specific lipid-transfer protein-like 1 (LOC103839274), mRNA ;						
75	Protein of unknown function::Bra001600:0-123	Bra001600	14 kDa	17	20	20	21
76	PREDICTED: Brassica napus late embryogenesis abundant protein 46 (LOC106419166), mRNA ; PREDICTED: Brassica rapa 18 kDa seed maturation protein (LOC103847016), mRNA ; Similar to GMPM1 18 kDa seed maturation protein (Glycine max)::Bra037704:0-159	Bra037704	16 kDa	26	28	18	8
77	Brassica oleracea var. botrytis peroxidase 7 mRNA, complete cds	Bra027198	40 kDa	18	26	4	22

78	; Brassica rapa peroxidase 12 mRNA, partial cds ; PREDICTED: Brassica napus peroxidase 12 (LOC106354161), mRNA ; PREDICTED: Brassica napus peroxidase 12 (LOC106381085), mRNA ; PREDICTED: Brassica oleracea var. oleracea peroxidase 12 (LOC106300904), mRNA ; PREDICTED: Brassica rapa peroxidase 12 (LOC103249149), mRNA ; PREDICTED: Raphanus sativus peroxidase 12 (LOC108828655), mRNA ; Similar to PER12 Peroxidase 12 (Arabidopsis thaliana)::Bra027198:0-362 Brassica oleracea HDEM genome, scaffold: C2 ; Brassica oleracea HDEM genome, scaffold: C3 ; Brassica oleracea HDEM genome, scaffold: C3 ; Brassica rapa genome, scaffold: A02 ; Brassica rapa genome, scaffold: A08 ; Brassica rapa genome, scaffold: A08 ; Brassica rapa subsp. pekinensis clone KBrB027K16, complete sequence ; Brassica rapa subsp. pekinensis clone KBrB027K16, complete sequence	Bra034035 (+1)	94 kDa	21	30	4	16

	; PREDICTED: Brassica napus elongation factor 2-like (LOC106361586), mRNA ; PREDICTED: Brassica napus elongation factor 2-like (LOC106382668), mRNA ; PREDICTED: Brassica napus elongation factor 2-like (LOC106418012), mRNA ; PREDICTED: Brassica napus elongation factor 2-like (LOC111213817), mRNA ; PREDICTED: Brassica napus elongation factor 2 (LOC106361587), mRNA ; PREDICTED: Brassica rapa elongation factor 2 (LOC103835224), mRNA ; Similar to LOS1 Elongation factor 2 (Arabidopsis thaliana)::Bra034035:0-843						
79	Protein of unknown function::Bra016576:0-634	Bra016576	69 kDa	13	33	8	16
80	PREDICTED: Brassica napus cell division control protein 48 homolog D-like (LOC106352759), mRNA ; PREDICTED: Brassica napus cell division control protein 48 homolog D (LOC106452445), mRNA ; PREDICTED: Brassica	Bra025942	90 kDa	26	26	11	6

81	oleracea var. oleracea cell division control protein 48 homolog D (LOC106296744), mRNA ; PREDICTED: Brassica rapa cell division control protein 48 homolog D (LOC103829916), mRNA ; Similar to CDC48D Cell division control protein 48 homolog D (Arabidopsis thaliana)::Bra025942:0-810 PREDICTED: Brassica napus adenylate kinase 3 (LOC106388427), mRNA ; PREDICTED: Brassica napus adenylate kinase 3 (LOC106388472), mRNA ; PREDICTED: Brassica oleracea var. oleracea adenylate kinase 3 (LOC106334666), mRNA ; PREDICTED: Brassica rapa adenylate kinase 3 (LOC103858450), mRNA ; Similar to ADK2 Adenylate kinase 3 (Arabidopsis thaliana)::Bra009032:0-245	Bra009032	27 kDa	10	23	16	22
82	Brassica rapa genome, scaffold: A01 ; Brassica rapa subsp. pekinensis clone KBrB061L05, complete sequence ; PREDICTED: Brassica napus 23.6 kDa heat shock protein,	Bra012843	17 kDa	21	25	12	11

83	mitochondrial (LOC106443195), mRNA ; PREDICTED: Brassica rapa 23.6 kDa heat shock protein, mitochondrial (LOC103862989), mRNA ; Similar to HSP23.6 23.6 kDa heat shock protein, mitochondrial (Arabidopsis thaliana)::Bra012843:0-149 PREDICTED: Brassica napus fructose-bisphosphate aldolase 8, cytosolic (LOC106367801), mRNA ; PREDICTED: Brassica napus fructose-bisphosphate aldolase 8, cytosolic (LOC106367922), transcript variant X1, mRNA ; PREDICTED: Brassica napus fructose-bisphosphate aldolase 8, cytosolic (LOC106367922), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea fructose-bisphosphate aldolase, cytoplasmic isozyme-like (LOC106312678), mRNA ; PREDICTED: Brassica rapa fructose-bisphosphate aldolase, cytoplasmic isozyme-like (LOC103841225), mRNA ; Similar to Fructose-bisphosphate aldolase, cytoplasmic isozyme	Bra004845	38 kDa	26	20	9	12

	(Spinacia oleracea)::Bra004845:0-358 Brassica juncea basic glucanase mRNA, complete cds ; Brassica rapa genome, scaffold: A07 ; Brassica rapa subsp. pekinensis glucanase 1 (Glu1) mRNA, complete cds ; PREDICTED: Brassica napus probable glucan endo-1,3-beta-glucosidase BG3 (LOC106353239), mRNA ; PREDICTED: Brassica napus probable glucan endo-1,3-beta-glucosidase BG3 (LOC106410962), mRNA ; PREDICTED: Brassica napus probable glucan endo-1,3-beta-glucosidase BG3 (LOC106445917), mRNA ; PREDICTED: Brassica napus probable glucan endo-1,3-beta-glucosidase BG3 (LOC106445918), mRNA ; PREDICTED: Brassica oleracea var. oleracea glucan endo-1,3-beta-glucosidase, acidic isoform-like (LOC106296725), mRNA ; PREDICTED: Brassica rapa probable glucan endo-1,3-beta-glucosidase BG3						
84	(LOC103830091), mRNA ;	Bra026071	38 kDa	10	27	11	18

85	PREDICTED: Raphanus sativus probable glucan endo-1,3-beta-glucosidase BG3 (LOC108815042), mRNA ; Similar to BG3 Probable glucan endo-1,3-beta-glucosidase BG3 (Arabidopsis thaliana)::Bra026071:0-341 PREDICTED: Brassica napus nitrogen regulatory protein P-II homolog (LOC106438650), mRNA ; PREDICTED: Brassica rapa nitrogen regulatory protein P-II homolog (LOC103858794), mRNA ; Similar to GLB1 Nitrogen regulatory protein P-II homolog (Arabidopsis thaliana)::Bra009285:0-196	Bra009285	21 kDa	15	21	19	11
86	B.napus mRNA for myrosinase MC ; PREDICTED: Brassica napus myrosinase-like (LOC106366548), transcript variant X1, mRNA ; PREDICTED: Brassica napus myrosinase-like (LOC106366548), transcript variant X2, mRNA ; PREDICTED: Brassica napus myrosinase-like (LOC106382308), mRNA ; PREDICTED: Brassica oleracea	Bra034560	59 kDa	30	12	5	10

87	var. oleracea myrosinase-like (LOC106310472), mRNA ; PREDICTED: Brassica rapa myrosinase-like (LOC103836047), mRNA ; Similar to TGG1 Myrosinase 1 (Arabidopsis thaliana)::Bra034560:0-510 PREDICTED: Brassica napus 60S ribosomal protein L7a-2-like (LOC106415818), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L7a-2-like (LOC106420535), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L7a-2-like (LOC106307692), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L7a-2-like (LOC103842092), mRNA ; Similar to RPL7AA 60S ribosomal protein L7a-1 (Arabidopsis thaliana) ; Zea mays clone 14482 mRNA sequence::Bra005473:0-242	Bra005473 (+3)	28 kDa	12	17	12	15
88	Similar to Embryonic protein DC-8 (Daucus carota)::Bra040652:0-387	Bra040652	42 kDa	18	36	33	19
89	PREDICTED: Brassica napus heat shock 70 kDa protein 10,	Bra006940	73 kDa	15	23	8	14

	mitochondrial-like (LOC106430600), mRNA ; PREDICTED: Brassica napus heat shock 70 kDa protein 10, mitochondrial (LOC106384930), mRNA ; PREDICTED: Brassica oleracea var. oleracea heat shock 70 kDa protein 10, mitochondrial (LOC106335389), mRNA ; PREDICTED: Brassica rapa heat shock 70 kDa protein 10, mitochondrial-like (LOC103855827), mRNA ; Similar to HSP70-10 Heat shock 70 kDa protein 10, mitochondrial (Arabidopsis thaliana)::Bra006940:0-681 PREDICTED: Brassica napus embryo-specific protein ATS3 (LOC106419203), mRNA ; PREDICTED: Brassica rapa uncharacterized LOC103847082 (LOC103847082), mRNA ;						
90	Protein of unknown function::Bra037669:0-205	Bra037669	22 kDa	1	15	26	15
91	Similar to OEP162 Outer envelope pore protein 16-2, chloroplastic (Arabidopsis thaliana)::Bra013303:0-179	Bra013303	19 kDa	26	14	0	16
92	Brassica rapa genome, scaffold: A01 ; PREDICTED: Brassica	Bra042033	10 kDa	10	13	21	8

	napus uncharacterized BNAA01G30160D (BNAA01G30160D), mRNA ; PREDICTED: Brassica rapa uncharacterized LOC103849726 (LOC103849726), mRNA ; Protein of unknown function::Bra042033:0-88 PREDICTED: Brassica napus AIG2-like protein A (LOC106351782), mRNA ; PREDICTED: Brassica napus AIG2-like protein A (LOC106356653), mRNA ; PREDICTED: Brassica oleracea var. oleracea AIG2-like protein (LOC106299568), mRNA ; PREDICTED: Brassica rapa AIG2-like protein (LOC103850151), mRNA ; Similar to At5g39720 AIG2-like protein (Arabidopsis						
93	thaliana)::Bra025831:0-169	Bra025831	20 kDa	10	17	10	9
94	Similar to At1g53240 Malate dehydrogenase 1, mitochondrial (Arabidopsis thaliana)::Bra031854:0-338	Bra031854	35 kDa	27	22	1	7
95	Brassica rapa chiifu v2 candidate 4 cruciferin	BraA08002105 (+3)	55 kDa	127	0	0	0

96	Similar to FER2 Ferritin-2, chloroplastic (Arabidopsis thaliana)::Bra031179:0-633	Bra031179	72 kDa	19	20	7	10
97	12S seed storage protein CRB OS=Arabidopsis thaliana OX=3702 GN=CRB PE=1 SV=2 cruciferin	CRU2_ARATH	51 kDa	109	82	43	42
98	PREDICTED: Brassica napus malate dehydrogenase 1, cytoplasmic-like (LOC106366626), misc_RNA ; PREDICTED: Brassica napus malate dehydrogenase 1, cytoplasmic (LOC106366627), mRNA ; PREDICTED: Brassica oleracea var. oleracea malate dehydrogenase, cytoplasmic 1 (LOC106319444), mRNA ; PREDICTED: Brassica rapa malate dehydrogenase, cytoplasmic 1 (LOC103839246), mRNA ; Similar to MDH1 Malate dehydrogenase, cytoplasmic 1 (Arabidopsis thaliana)::Bra001572:0-332	Bra001572	36 kDa	34	15	1	5
99	PREDICTED: Brassica napus late embryogenesis abundant protein 1-like (LOC106348819), mRNA ; PREDICTED: Brassica napus late embryogenesis abundant protein 1-like (LOC106373675), mRNA ;	Bra012478	29 kDa	16	14	16	3

100	Protein of unknown function::Bra012478:0-264 PREDICTED: Brassica napus late embryogenesis abundant protein 46-like (LOC106413949), mRNA ; PREDICTED: Brassica napus late embryogenesis abundant protein 46-like (LOC106426361), mRNA ; PREDICTED: Brassica oleracea var. oleracea 18 kDa seed maturation protein-like (LOC106335780), transcript variant X1, mRNA ; PREDICTED: Brassica rapa 18 kDa seed maturation protein-like (LOC103855696), mRNA ; Similar to GMPM1 18 kDa seed maturation protein (Glycine max)::Bra006839:0-159	Bra006839	16 kDa	23	30	19	10
101	PREDICTED: Brassica napus glycine-rich RNA-binding protein 2-like (LOC106433663), mRNA ; PREDICTED: Brassica rapa glycine-rich RNA-binding protein 10-like (LOC103846048), mRNA ; Similar to Glycine-rich RNA-binding protein (Daucus carota)::Bra024171:0-159	Bra024171	16 kDa	10	19	7	10
102	Similar to PEC-2 Thioredoxin H-type (Brassica campestris)::Bra001593:0-123	Bra001593	14 kDa	22	11	10	11

	PREDICTED: Brassica napus probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial (LOC106380476), mRNA ; PREDICTED: Brassica napus probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial (LOC106396928), mRNA ; PREDICTED: Brassica oleracea var. oleracea probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial (LOC106321579), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial (LOC106321579), transcript variant X2, mRNA ; Similar to GPX6 Probable phospholipid hydroperoxide glutathione peroxidase 6, mitochondrial (Arabidopsis						
103	thaliana)::Bra018546:0-229	Bra018546	25 kDa	12	19	10	12
104	Brassica rapa Chiifu-401 V2 candidate 6 napin	BraA01001887 (+1)	20 kDa	72	0	75	0
105	Brassica rapa Chiifu-401 V2 candidate 8 napin	BraA03000889 (+3)	21 kDa	0	62	57	50

106	Brassica rapa genome, scaffold: A03 ; PREDICTED: Brassica napus late embryogenesis abundant protein 29-like (LOC106439419), mRNA ; PREDICTED: Brassica rapa late embryogenesis abundant protein 76-like (LOC103859635), mRNA ; Similar to Late embryogenesis abundant protein 76 (Brassica napus)::Bra009893:0-204	Bra009893	22 kDa	47	57	66	36
107	PREDICTED: Brassica napus UTP--glucose-1-phosphate uridylyltransferase 2-like (LOC106450527), mRNA ; PREDICTED: Brassica napus UTP--glucose-1-phosphate uridylyltransferase 2 (LOC106450722), mRNA ; PREDICTED: Brassica napus UTP--glucose-1-phosphate uridylyltransferase 2 (LOC111207933), mRNA ; PREDICTED: Brassica oleracea var. oleracea probable UTP--glucose-1-phosphate uridylyltransferase 2 (LOC106343185), mRNA ; PREDICTED: Brassica rapa UTP--glucose-1-phosphate uridylyltransferase 2-like	Bra031582	52 kDa	18	22	7	3

	(LOC103855145), mRNA ; Similar to At3g03250 Probable UTP--glucose-1-phosphate uridylyltransferase 2 (Arabidopsis thaliana)::Bra031582:0-469 PREDICTED: Brassica napus aconitate hydratase 1-like (LOC106351933), mRNA ; PREDICTED: Brassica napus aconitate hydratase 1 (LOC106347211), mRNA ; PREDICTED: Brassica oleracea var. oleracea aconitate hydratase 1 (LOC106308688), mRNA ; PREDICTED: Brassica rapa aconitate hydratase 1 (LOC103873312), mRNA ; PREDICTED: Raphanus sativus aconitate hydratase 1-like (LOC108842639), misc_RNA ; Similar to ACO1 Aconitate hydratase 1 (Arabidopsis						
108	thaliana)::Bra011617:0-898	Bra011617	98 kDa	18	16	7	8
109	Similar to GSTU21 Glutathione S-transferase U21 (Arabidopsis thaliana)::Bra027601:0-450	Bra027601	52 kDa	13	13	9	9
110	Brassica rapa genome, scaffold: A03 ; Brassica rapa heat shock protein 18 (hsp18) mRNA, complete cds ; Brassica rapa subsp. pekinensis cultivar inbred	Bra007554	18 kDa	12	25	23	14

111	line Chiifu HSP18.2C (HSP18.2C) gene, partial cds ; Brassica rapa subsp. pekinensis cultivar inbred line Kenshin HSP18.2C (HSP18.2C) gene, partial cds ; PREDICTED: Brassica napus 18.1 kDa class I heat shock protein (LOC106443275), mRNA ; Similar to HSP18.1 18.1 kDa class I heat shock protein (Arabidopsis thaliana)::Bra007554:0-160 PREDICTED: Brassica napus 17.4 kDa class III heat shock protein-like (LOC106443219), mRNA ; PREDICTED: Brassica rapa 17.4 kDa class III heat shock protein-like (LOC103832638), mRNA ; Similar to HSP17.4B 17.4 kDa class III heat shock protein (Arabidopsis thaliana)::Bra031806:0-154	Bra031806	17 kDa	13	21	2	6
112	PREDICTED: Brassica napus probable histone H2AXa (LOC106346303), mRNA ; PREDICTED: Brassica rapa probable histone H2AXa (LOC103871626), mRNA ; Similar to At1g08880 Probable histone H2AXa (Arabidopsis thaliana)::Bra020481:0-142	Bra020481 (+1)	15 kDa	10	11	11	7

113	PREDICTED: Brassica napus desiccation-related protein PCC13-62-like (LOC111213365), transcript variant X2, mRNA ; PREDICTED: Brassica napus desiccation-related protein PCC13-62 (LOC106351214), mRNA ; PREDICTED: Brassica oleracea var. oleracea desiccation-related protein PCC13-62 (LOC106299167), mRNA ; PREDICTED: Brassica rapa desiccation-related protein PCC13-62 (LOC103871506), mRNA ; Similar to Desiccation-related protein PCC13-62 (Craterostigma plantagineum)::Bra020390:0-309	Bra020390	34 kDa	15	16	3	10
114	Similar to GRXC1 Glutaredoxin-C1 (Arabidopsis thaliana)::Bra022411:0-120	Bra022411	13 kDa	11	12	13	7
115	PREDICTED: Brassica napus uncharacterized protein At5g02240-like (LOC106372572), mRNA ; PREDICTED: Brassica napus uncharacterized protein At5g02240 (LOC106433551), mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterized protein At5g02240 (LOC106318266),	Bra037977	27 kDa	13	18	5	5

116	mRNA ; PREDICTED: Brassica rapa uncharacterized protein At5g02240 (LOC103847467), mRNA ; Similar to At5g02240 Uncharacterized protein At5g02240 (Arabidopsis thaliana)::Bra037977:0-253 Similar to FBA Fructose-bisphosphate aldolase cytoplasmic isozyme (Oryza sativa subsp. japonica)::Bra040649:0-1556	Bra040649	170 kDa	31	14	5	13
117	Similar to GRP10 Glycine-rich RNA-binding protein 10 (Brassica napus)::Bra011387:0-146	Bra011387	14 kDa	9	10	13	3
118	Similar to XYLA Xylose isomerase (Arabidopsis thaliana)::Bra036666:0-654	Bra036666	73 kDa	11	13	1	15
119	PREDICTED: Brassica napus 60S ribosomal protein L17-2-like (LOC106372951), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L17-2 (LOC106392065), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L17-2-like (LOC106323561), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L17-2 (LOC103852402), mRNA ; Similar to RPL17B 60S ribosomal	Bra017394 (+2)	20 kDa	10	13	6	11

120	protein L17-2 (Arabidopsis thaliana)::Bra017394:0-179 Amphidasya ambigua voucher Clark & Watt 736 (QCNE, MO, UPS) ATP synthase F1 subunit 1 (atp1) gene, complete cds; mitochondrial ; Anthospermum spathulatum voucher Bremer et al. 4405 (UPS) ATP synthase F1 subunit 1 (atp1) gene, complete cds; mitochondrial ; Arabidopsis thaliana ATPase, F1 complex, alpha subunit protein (AT2G07698), mRNA ; Arabidopsis thaliana chromosome 2 BAC T18C6 genomic sequence, complete sequence ; Arabidopsis thaliana chromosome 2 sequence ; Arabidopsis thaliana ecotype C24 mitochondrion, complete genome ; Arabidopsis thaliana ecotype Col-0 mitochondrion, complete genome ; Arabidopsis thaliana ecotype Col-0 mitochondrion, complete genome ; Arabidopsis thaliana ecotype Columbia ATPase subunit 1 mRNA, partial cds; mitochondrial ; Arabidopsis thaliana ecotype Landsberg erecta mitochondrion, complete genome ; Arabidopsis thaliana	Bra014393	55 kDa	10	12	5	11

	mitochondrial genome ; Arabidopsis thaliana other for ATSL087910 ; Arabidopsis thaliana other::Bra014393:0-507 PREDICTED: Brassica napus aldehyde dehydrogenase family 2 member B4, mitochondrial (LOC106408937), mRNA ; PREDICTED: Brassica oleracea var. oleracea aldehyde dehydrogenase family 2 member B4, mitochondrial (LOC106311632), mRNA ; PREDICTED: Brassica rapa aldehyde dehydrogenase family 2 member B4, mitochondrial (LOC103873180), mRNA ; Similar to ALDH2B4 Aldehyde dehydrogenase family 2 member B4, mitochondrial (Arabidopsis						
121	thaliana)::Bra021698:0-539	Bra021698	59 kDa	10	17	3	9
	PREDICTED: Brassica napus superoxide dismutase [Cu-Zn] (LOC106420167), mRNA ; PREDICTED: Brassica rapa superoxide dismutase [Cu-Zn] (LOC103843378), mRNA ; Similar to SODCC Superoxide dismutase [Cu-Zn] (Brassica						
122	oleracea var. capitata) ; Zea mays	Bra006323	15 kDa	8	12	13	4

	clone 20042 mRNA sequence::Bra006323:0-152						
123	Similar to ATL5 60S ribosomal protein L5-1 (Arabidopsis thaliana)::Bra024735:0-302	Bra024735	35 kDa	8	8	11	8
124	Similar to HSP90-2 Heat shock protein 90-2 (Arabidopsis thaliana)::Bra016954:0-324	Bra016954 (+1)	36 kDa	7	15	2	9
125	Similar to CSD1 Superoxide dismutase [Cu-Zn] 1 (Arabidopsis thaliana)::Bra020480:0-446	Bra020480	49 kDa	10	14	9	4
126	PREDICTED: Brassica napus myrosinase-like (LOC106397816), mRNA ; Similar to TGG2 Myrosinase 2 (Arabidopsis thaliana)::Bra026687:0-546	Bra026687	62 kDa	34	13	4	10
127	PREDICTED: Brassica napus uncharacterized BNAANNG12230D (BNAANNG12230D), mRNA ; PREDICTED: Brassica rapa uncharacterized LOC103843642 (LOC103843642), mRNA ; Protein of unknown function::Bra006472:0-183	Bra006472	20 kDa	12	9	5	7
128	Similar to LTI65 Low-temperature-induced 65 kDa protein (Arabidopsis thaliana)::Bra017183:0-1131	Bra017183	122 kDa	14	26	16	14

129	Brassica oleracea HDEM genome, scaffold: C3 ; Brassica rapa genome, scaffold: A03 ; Brassica rapa subsp. pekinensis clone KBrH007P05, complete sequence ; PREDICTED: Brassica napus 60S ribosomal protein L12-2-like (LOC106392722), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L12-2-like (LOC106441066), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L12-2 (LOC106335634), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L12-2 (LOC103857662), mRNA ; Similar to RPL12A 60S ribosomal protein L12-1 (Arabidopsis thaliana)::Bra008329:0-166	Bra008329 (+2)	18 kDa	0	17	6	11
130	PREDICTED: Brassica napus 60S ribosomal protein L4-1-like (LOC111215776), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L4-1 (LOC106452757), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L4-1-like (LOC106295520), mRNA ; PREDICTED: Brassica rapa 60S	Bra031264	45 kDa	4	14	8	6

	ribosomal protein L4-1-like (LOC103870529), mRNA ; Similar to RPL4A 60S ribosomal protein L4-1 (Arabidopsis thaliana)::Bra031264:0-406 PREDICTED: Brassica napus 40S ribosomal protein S18-like (LOC106360957), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S18-like (LOC111210018), transcript variant X1, mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S18-like (LOC111210018), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea 40S ribosomal protein S18 (LOC106313634), mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S18 (LOC103838875), mRNA ; Similar to RPS18A 40S ribosomal protein S18 (Arabidopsis						
131	thaliana)::Bra002515:0-173	Bra002515 (+3)	20 kDa	10	15	4	6
132	Similar to Endochitinase CH25 (Brassica napus)::Bra031091:0-536	Bra031091	59 kDa	10	14	1	7
133	Brassica rapa genome, scaffold: A03 ; PREDICTED: Brassica napus eukaryotic initiation factor	Bra009832 (+2)	48 kDa	10	14	1	8

134	4A-1-like (LOC106389163), transcript variant X1, mRNA ; PREDICTED: Brassica napus eukaryotic initiation factor 4A-1-like (LOC106389163), transcript variant X2, mRNA ; PREDICTED: Brassica napus eukaryotic initiation factor 4A-1-like (LOC106390450), mRNA ; PREDICTED: Brassica oleracea var. oleracea eukaryotic initiation factor 4A-1-like (LOC106335974), mRNA ; PREDICTED: Brassica rapa eukaryotic initiation factor 4A-1-like (LOC103859548), transcript variant X1, mRNA ; PREDICTED: Brassica rapa eukaryotic initiation factor 4A-1-like (LOC103859548), transcript variant X2, mRNA ; Similar to TIF4A-1 Eukaryotic initiation factor 4A-1 (Arabidopsis thaliana)::Bra009832:0-426 Similar to ENO2 Bifunctional enolase 2/transcriptional activator (Arabidopsis thaliana)::Bra028552:0-363	Bra028552	39 kDa	12	9	5	9
135	Brassica oleracea HDEM genome, scaffold: C3 ; Brassica rapa genome, scaffold: A03 ;	Bra007556 (+4)	11 kDa	14	13	1	3

136	PREDICTED: Brassica napus histone H4-like (LOC106386836), mRNA ; PREDICTED: Brassica napus histone H4 (LOC106436220), mRNA ; PREDICTED: Brassica oleracea var. oleracea histone H4 (LOC106331525), mRNA ; PREDICTED: Brassica rapa histone H4 (LOC103856615), mRNA ; Similar to Histone H4 (Glycine max)::Bra007556:0-103 PREDICTED: Brassica napus triosephosphate isomerase, cytosolic-like (LOC106445356), mRNA ; PREDICTED: Brassica rapa triosephosphate isomerase, cytosolic (LOC103863163), mRNA ; Similar to CTIMC Triosephosphate isomerase, cytosolic (Arabidopsis thaliana)::Bra038454:0-254	Bra038454	27 kDa	14	12	3	5
137	PREDICTED: Brassica napus uncharacterized BNAA10G02700D (BNAA10G02700D), mRNA ; PREDICTED: Brassica napus uncharacterized BNAC05G02680D (BNAC05G02680D), transcript variant X1, mRNA ;	Bra035274	20 kDa	8	14	6	5

138	PREDICTED: Brassica rapa uncharacterized LOC103844243 (LOC103844243), mRNA ; Protein of unknown function::Bra035274:0-185 PREDICTED: Brassica napus glutathione S-transferase U19 (LOC106418428), mRNA ; PREDICTED: Brassica oleracea var. oleracea glutathione S-transferase U19-like (LOC106324691), mRNA ; Similar to GSTU19 Glutathione S-transferase U19 (Arabidopsis thaliana)::Bra017892:0-219	Bra017892	26 kDa	15	2	3	9
139	PREDICTED: Brassica napus vicilin-like seed storage protein At4g36700 (LOC106407622), mRNA ; PREDICTED: Brassica napus vicilin-like seed storage protein At4g36700 (LOC106451973), mRNA ; PREDICTED: Brassica oleracea var. oleracea provicilin-like (LOC106305419), mRNA ; PREDICTED: Brassica rapa vicilin-like seed storage protein At4g36700 (LOC103862486), mRNA ; Similar to At4g36700 Vicilin-like seed storage protein	Bra003060 (+1)	56 kDa	17	19	3	15

140	At4g36700 (Arabidopsis thaliana)::Bra003060:0-502 Brassica oleracea HDEM genome, scaffold: C3 ; Brassica rapa genome, scaffold: A03 ; PREDICTED: Brassica napus 40S ribosomal protein S2-2-like (LOC106437974), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S2-2 (LOC106388267), mRNA ; PREDICTED: Brassica oleracea var. oleracea 40S ribosomal protein S2-2-like (LOC106335906), mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S2-2-like (LOC103857998), mRNA ; Similar to RPS2A 40S ribosomal protein S2-1 (Arabidopsis thaliana)::Bra008698:0-282	Bra008698 (+1)	31 kDa	9	8	6	9
141	PREDICTED: Brassica napus 60S acidic ribosomal protein P2-2-like (LOC106352563), mRNA ; PREDICTED: Brassica napus 60S acidic ribosomal protein P2-2-like (LOC106352564), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S acidic ribosomal protein P2-2-like (LOC106339404), mRNA ;	Bra025686	11 kDa	7	10	11	4

142	PREDICTED: Brassica rapa 60S acidic ribosomal protein P2-2-like (LOC103829681), mRNA ; Similar to RPP2A 60S acidic ribosomal protein P2A (Zea mays)::Bra025686:0-113 Brassica oleracea HDEM genome, scaffold: C5 ; PREDICTED: Brassica napus stress-response A/B barrel domain-containing protein DABB1 (BNAA05G15190D), mRNA ; PREDICTED: Brassica napus stress-response A/B barrel domain-containing protein DABB1-like (LOC106356988), mRNA ; PREDICTED: Brassica napus stress-response A/B barrel domain-containing protein DABB1-like (LOC106397779), mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterized LOC106344145 (LOC106344145), mRNA ; PREDICTED: Brassica rapa stress-response A/B barrel domain-containing protein UP3 (LOC103868574), mRNA ; Protein of unknown function::Bra042262:0-121	Bra042262	13 kDa	9	7	8	7

143	Similar to PRXIIF Peroxiredoxin-2F, mitochondrial (Arabidopsis thaliana)::Bra042236:0-433	Bra042236	48 kDa	3	11	8	9
144	PREDICTED: Brassica napus 60S ribosomal protein L24-2 (LOC106367917), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L24-2 (LOC106382591), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L24-2-like (LOC103841233), mRNA ; Similar to RPL24B 60S ribosomal protein L24-2 (Arabidopsis thaliana)::Bra004854:0-180	Bra004854 (+3)	21 kDa	7	7	9	8
145	Brassica napus 11-beta-hydroxysteroid dehydrogenase 1B-like (LOC106388429), mRNA ; PREDICTED: Brassica napus 11-beta-hydroxysteroid dehydrogenase 1B (LOC106388464), mRNA ; PREDICTED: Brassica oleracea var. oleracea 11-beta-hydroxysteroid dehydrogenase 1B-like (LOC106333477), mRNA ; PREDICTED: Brassica rapa 11-beta-hydroxysteroid dehydrogenase 1B-like (LOC103858452), mRNA ; PREDICTED: Raphanus sativus	Bra009034	38 kDa	46	44	8	37

	11-beta-hydroxysteroid dehydrogenase 1B-like (LOC108846709), mRNA ; Similar to HSD1 11-beta-hydroxysteroid dehydrogenase 1A (Arabidopsis thaliana)::Bra009034:0-341 PREDICTED: Brassica napus plastid-lipid-associated protein 6, chloroplastic (LOC106357886), transcript variant X1, mRNA ; PREDICTED: Brassica napus plastid-lipid-associated protein 6, chloroplastic (LOC106357886), transcript variant X2, mRNA ; PREDICTED: Brassica rapa probable plastid-lipid-associated protein 6, chloroplastic (LOC103828744), mRNA ; Similar to PAP6 Probable plastid-lipid-associated protein 6, chloroplastic (Arabidopsis						
146	thaliana)::Bra024890:0-277	Bra024890	30 kDa	11	8	2	8
147	PREDICTED: Brassica napus protein disulfide-isomerase like 2-1 (LOC106438331), transcript variant X1, mRNA ; PREDICTED: Brassica napus protein disulfide-isomerase like 2-1 (LOC106438331), transcript variant X2, mRNA ;	Bra008871	44 kDa	6	13	2	9

148	PREDICTED: Brassica napus protein disulfide-isomerase like 2-1 (LOC106438331), transcript variant X3, mRNA ; PREDICTED: Brassica oleracea var. oleracea protein disulfide-isomerase like 2-1-like (LOC106328378), mRNA ; PREDICTED: Brassica rapa protein disulfide-isomerase like 2-1 (LOC103858248), mRNA ; Similar to PDIL2-1 Protein disulfide-isomerase like 2-1 (Arabidopsis thaliana)::Bra008871:0-397 PREDICTED: Brassica napus nascent polypeptide-associated complex subunit alpha-like protein 1 (LOC106351941), mRNA ; PREDICTED: Brassica napus nascent polypeptide-associated complex subunit alpha-like protein 1 (LOC106436932), mRNA ; PREDICTED: Brassica oleracea var. oleracea nascent polypeptide-associated complex subunit alpha-like protein 1 (LOC106341702), mRNA ; PREDICTED: Brassica rapa nascent polypeptide-associated complex subunit alpha-like protein 1 (LOC103845577),	Bra015175	19 kDa	7	8	7	6

149	mRNA ; Similar to At3g12390 Nascent polypeptide-associated complex subunit alpha-like protein 1 (Arabidopsis thaliana)::Bra015175:0-172 PREDICTED: Brassica napus late embryogenesis abundant protein 76 (LOC111200976), transcript variant X1, mRNA ; Similar to ECU03_1610 Uncharacterized protein ECU03_1610 (Encephalitozoon cuniculi (strain GB-M1))::Bra001919:0-351	Bra001919	40 kDa	8	5	13	3
150	Brassica rapa peroxiredoxin-2B (LOC103852305), mRNA ; Brassica rapa subsp. pekinensis type 2 peroxiredoxin (PrxII) mRNA, complete cds ; PREDICTED: Brassica napus peroxiredoxin-2B-like (LOC106441213), mRNA ; PREDICTED: Brassica napus peroxiredoxin-2B (LOC106381333), mRNA ; PREDICTED: Brassica oleracea var. oleracea peroxiredoxin-2B (LOC106322672), mRNA ; Similar to PRXIIB Peroxiredoxin-2B (Arabidopsis thaliana)::Bra017320:0-162	Bra017320	17 kDa	7	8	4	9

151	PREDICTED: Brassica rapa 40S ribosomal protein S24-1 (LOC103837315), mRNA ; Similar to RPS24A 40S ribosomal protein S24-1 (Arabidopsis thaliana)::Bra000338:0-133	Bra000338 (+2)	15 kDa	7	10	12	4
152	Brassica napus epithiospecifier protein-like (LOC111207173), mRNA ; PREDICTED: Brassica rapa epithiospecifier protein-like (LOC103827899), mRNA ; Similar to ESP Epithiospecifier protein (Arabidopsis thaliana)::Bra023756:0-357	Bra023756	39 kDa	20	6	2	1
153	Brassica napus probable mediator of RNA polymerase II transcription subunit 37e (LOC106361615), mRNA ; Brassica oleracea HDEM genome, scaffold: C4 ; Brassica oleracea HDEM genome, scaffold: C9 ; Brassica rapa genome, scaffold: A10 ; Brassica rapa genome, scaffold: A10 ; PREDICTED: Brassica napus probable mediator of RNA polymerase II	Bra037958 (+1)	70 kDa	41	26	20	22

154	transcription subunit 37e (LOC106361614), mRNA ; PREDICTED: Brassica napus probable mediator of RNA polymerase II transcription subunit 37e (LOC106372589), misc_RNA ; PREDICTED: Brassica oleracea var. oleracea probable mediator of RNA polymerase II transcription subunit 37e (LOC106317538), mRNA ; PREDICTED: Brassica oleracea var. oleracea probable mediator of RNA polymerase II transcription subunit 37e (LOC106341975), mRNA ; PREDICTED: Brassica rapa probable mediator of RNA polymerase II transcription subunit 37e (LOC103847444), mRNA ; Similar to MED37E Probable mediator of RNA polymerase II transcription sub::Bra037958:0-634 PREDICTED: Brassica napus SNF1-related protein kinase regulatory subunit gamma-like PV42a (LOC106346666), transcript variant X1, mRNA ; PREDICTED: Brassica napus SNF1-related protein kinase	Bra021133	39 kDa	17	5	1	5

	regulatory subunit gamma-like PV42a (LOC106346666), transcript variant X2, mRNA ; PREDICTED: Brassica napus SNF1-related protein kinase regulatory subunit gamma-like PV42a (LOC106452179), mRNA ; PREDICTED: Brassica oleracea var. oleracea SNF1-related protein kinase regulatory subunit gamma-like PV42a (LOC106292693), mRNA ; PREDICTED: Brassica rapa SNF1-related protein kinase regulatory subunit gamma-like PV42a (LOC103872324), mRNA ; Similar to PV42A SNF1-related protein kinase regulatory subunit gamma-like PV42a (Arabidopsis thaliana)::Bra021133:0-355 PREDICTED: Brassica napus S-formylglutathione hydrolase-like (LOC106396216), mRNA ; PREDICTED: Brassica napus S-formylglutathione hydrolase-like (LOC106450663), mRNA ; PREDICTED: Brassica rapa S-formylglutathione hydrolase-like (LOC103866563), mRNA ; Similar to SFGH S-						
155	formylglutathione hydrolase	Bra027961	31 kDa	7	14	0	7

156	(Arabidopsis thaliana)::Bra027961:0-281 Similar to Acyl-CoA-binding protein (Brassica napus)::Bra030139:0-92 PREDICTED: Brassica napus reticulon-like protein B1 (LOC106438459), transcript variant X1, mRNA ; PREDICTED: Brassica napus reticulon-like protein B1 (LOC106438459), transcript variant X2, misc_RNA ; PREDICTED: Brassica rapa reticulon-like protein B1 (LOC103861418), mRNA ;	Bra030139	10 kDa	12	8	4	4
157	Similar to RTNLB1 Reticulon-like protein B1 (Arabidopsis thaliana)::Bra011059:0-268 Brassica napus seed specific protein Bn15D33A mRNA, complete cds ; PREDICTED: Brassica napus uncharacterized BNAA02G24090D (BNAA02G24090D), mRNA ; PREDICTED: Brassica napus uncharacterized LOC106379664 (LOC106379664), mRNA ;	Bra011059 (+2)	30 kDa	8	7	1	8
158	PREDICTED: Brassica rapa uncharacterized LOC103853665 (LOC103853665), mRNA ;	Bra018166 (+1)	13 kDa	17	8	0	3

159	Protein of unknown function::Bra018166:0-116 PREDICTED: Brassica napus 40S ribosomal protein S4-1-like (LOC106411885), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S4-1-like (LOC106426312), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S4-1-like (LOC106429399), mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S4-1-like (LOC103855714), mRNA ; Similar to RPS4A 40S ribosomal protein S4-1 (Arabidopsis thaliana)::Bra006848:0-279	Bra006848 (+4)	32 kDa	8	10	4	5
160	Similar to pyrH Uridylate kinase (Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131))::Bra031240:0-703	Bra031240	77 kDa	2	10	7	4
161	Brassica oleracea HDEM genome, scaffold: C1 ; Brassica rapa genome, scaffold: A01 ; PREDICTED: Brassica napus uncharacterized BNAA01G05030D (BNAA01G05030D), mRNA ; PREDICTED: Brassica napus uncharacterized LOC106371401	Bra011941	11 kDa	10	12	5	0

	(LOC106371401), mRNA ; PREDICTED: Brassica napus uncharacterized LOC106375395 (LOC106375395), mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterized LOC106303707 (LOC106303707), mRNA ; PREDICTED: Brassica rapa uncharacterized LOC103851502 (LOC103851502), mRNA ; Protein of unknown function::Bra011941:0-100 PREDICTED: Brassica napus uncharacterized LOC106365887 (LOC106365887), transcript variant X1, mRNA ; PREDICTED: Brassica napus uncharacterized LOC106365887 (LOC106365887), transcript variant X2, mRNA ; PREDICTED: Brassica napus uncharacterized LOC106440359 (LOC106440359), transcript variant X1, mRNA ; PREDICTED: Brassica napus uncharacterized LOC106440359 (LOC106440359), transcript variant X3, misc_RNA ; PREDICTED: Brassica oleracea						
162	var. oleracea uncharacterized	Bra000417	40 kDa	24	2	0	1

163	LOC106316619 (LOC106316619), mRNA ; PREDICTED: Brassica rapa uncharacterized LOC103837119 (LOC103837119), mRNA ; Protein of unknown function::Bra000417:0-346 PREDICTED: Brassica napus 60S ribosomal protein L7-2 (LOC106381922), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L7-2 (LOC106388681), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L7-2 (LOC106322552), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L7-2 (LOC103832784), mRNA ; Similar to RPL7B 60S ribosomal protein L7-2 (Arabidopsis thaliana)::Bra019175:0-242	Bra019175 (+1)	28 kDa	9	11	4	1
164	PREDICTED: Brassica napus ATP synthase subunit beta-1, mitochondrial-like (LOC106380543), transcript variant X1, mRNA ; PREDICTED: Brassica napus ATP synthase subunit beta-1, mitochondrial-like (LOC106380543), transcript	Bra000218 (+6)	57 kDa	12	5	3	5

variant X2, mRNA ;
PREDICTED: Brassica napus
ATP synthase subunit beta-1,
mitochondrial-like
(LOC106396303), mRNA ;
PREDICTED: Brassica napus
ATP synthase subunit beta-1,
mitochondrial-like
(LOC106396307), mRNA ;
PREDICTED: Brassica napus
ATP synthase subunit beta-2,
mitochondrial-like
(LOC106380544), mRNA ;
PREDICTED: Brassica napus
ATP synthase subunit beta-2,
mitochondrial (LOC106377686),
mRNA ; PREDICTED: Brassica
oleracea var. oleracea ATP
synthase subunit beta-1,
mitochondrial-like
(LOC106327128), mRNA ;
PREDICTED: Brassica oleracea
var. oleracea ATP synthase
subunit beta-1, mitochondrial
(LOC106327662), mRNA ;
PREDICTED: Brassica rapa ATP
synthase subunit beta-1,
mitochondrial-like
(LOC103850708), misc_RNA ;
PREDIC::Bra000218:0-533

165	Brassica juncea mRNA for O-acetylserine(thiol) lyase, clone OAS-TL4 ; Brassica rapa subsp. chinensis O-acetylserine(thiol)lyase isoform A4 (OASA4) mRNA, complete cds ; PREDICTED: Brassica napus cysteine synthase-like (LOC106435443), transcript variant X1, mRNA ; PREDICTED: Brassica napus cysteine synthase-like (LOC106435443), transcript variant X2, mRNA ; PREDICTED: Brassica napus cysteine synthase (LOC106360617), transcript variant X1, mRNA ; PREDICTED: Brassica napus cysteine synthase (LOC106360617), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea cysteine synthase (LOC106307369), mRNA ; PREDICTED: Brassica rapa cysteine synthase (OASA4), transcript variant X1, mRNA ; PREDICTED: Brassica rapa cysteine synthase (OASA4), transcript variant X2, mRNA ;	Bra041810	34 kDa	9	13	1	3

	Similar to Cysteine synthase (Brassica juncea)::Bra041810:0-322 PREDICTED: Brassica napus 60S ribosomal protein L10-3-like (LOC106406321), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L10-3-like (LOC106432562), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L10-3-like (LOC106300530), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L10-3-like (LOC103831514), mRNA ; Similar to RPL10C 60S ribosomal protein L10-3 (Arabidopsis						
166	thaliana)::Bra027071:0-220	Bra027071	25 kDa	10	9	4	2
167	Similar to At1g47710 Serpin-ZX (Arabidopsis thaliana)::Bra036377:0-550	Bra036377	61 kDa	12	7	0	5
168	Similar to SUS3 Sucrose synthase 3 (Arabidopsis thaliana)::Bra000059:0-822	Bra000059	94 kDa	19	5	0	1
169	PREDICTED: Brassica napus 40S ribosomal protein S13-2 (LOC106411904), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S13-2 (LOC106412000), mRNA ;	Bra005344 (+4)	17 kDa	7	7	4	6

170	PREDICTED: Brassica oleracea var. oleracea 40S ribosomal protein S13-2 (LOC106309894), mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S13-2 (LOC103841918), mRNA ; Similar to RPS13B 40S ribosomal protein S13-2 (Arabidopsis thaliana) ; Zea mays clone 11839 mRNA sequence::Bra005344:0-151 Similar to PIN5 Putative auxin efflux carrier component 5 (Arabidopsis thaliana)::Bra037288:0-653	Bra037288	71 kDa	8	8	4	4
171	Protein of unknown function::Bra017629:0-127	Bra017629	14 kDa	4	5	12	3
172	Similar to ANN1 Annexin D1 (Arabidopsis thaliana)::Bra029908:0-370	Bra029908	42 kDa	12	5	6	1
173	Similar to UREG Urease accessory protein G (Arabidopsis thaliana)::Bra040534:0-435	Bra040534	49 kDa	4	10	4	1
174	PREDICTED: Brassica napus germin-like protein subfamily 2 member 1 (LOC106419894), mRNA ; PREDICTED: Brassica rapa germin-like protein subfamily 2 member 1 (LOC103843347), mRNA ; Similar to GLP4 Germin-like protein subfamily 2 member 1	Bra006300	23 kDa	8	9	4	2

175	(Arabidopsis thaliana)::Bra006300:0-216 Similar to RPL18B 60S ribosomal protein L18-2 (Arabidopsis thaliana)::Bra019708:0-397 Brassica juncea clone 575 60S ribosomal protein L13-2 mRNA, partial sequence ; Brassica napus 60S ribosomal protein L13-1 (LOC106447867), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L13-1 (LOC106447867), transcript variant X1, mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L13-2-like (LOC111197723), transcript variant X1, mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L13-2-like (LOC111197723), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L13-2-like (LOC106311292), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L13-1 (LOC103874976), mRNA ;	Bra019708 (+1)	44 kDa	5	4	5	7
176	Similar to 60S ribosomal protein L13-1 (Brassica napus) ; Zea mays	Bra013909 (+1)	24 kDa	7	8	3	1

177	clone 14550 mRNA sequence::Bra013909:0-206 PREDICTED: Brassica napus 40S ribosomal protein S6-2 (LOC106384903), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S6-2 (LOC106430360), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S6-2 (LOC106430367), mRNA ; PREDICTED: Brassica oleracea var. oleracea 40S ribosomal protein S6-2 (LOC106328438), mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S6-2 (LOC103855860), mRNA ; Similar to RPS6B 40S ribosomal protein S6-2 (Arabidopsis thaliana) ; Zea mays clone 13559 mRNA sequence::Bra006969:0-249	Bra006969	28 kDa	4	2	1	9
178	PREDICTED: Brassica napus aspartyl protease AED3 (LOC106431380), mRNA ; PREDICTED: Brassica napus aspartyl protease AED3 (LOC106445461), mRNA ; PREDICTED: Brassica oleracea var. oleracea protein ASPARTIC PROTEASE IN GUARD CELL 2-	Bra038558	50 kDa	4	8	3	4

	like (LOC106342769), mRNA ; PREDICTED: Brassica rapa aspartyl protease AED3-like (LOC103863237), mRNA ; Protein of unknown function::Bra038558:0-466						
179	Similar to DJ1A Protein DJ-1 homolog A (Arabidopsis thaliana)::Bra030915:0-407	Bra030915	43 kDa	9	8	1	4
180	PREDICTED: Brassica napus ADP,ATP carrier protein 3, mitochondrial-like (LOC106361198), transcript variant X1, mRNA ; PREDICTED: Brassica napus ADP,ATP carrier protein 3, mitochondrial-like (LOC106361198), transcript variant X2, mRNA ; PREDICTED: Brassica napus ADP,ATP carrier protein 3, mitochondrial-like (LOC106361198), transcript variant X3, mRNA ; PREDICTED: Brassica rapa ADP,ATP carrier protein 3, mitochondrial (LOC103834762), transcript variant X1, mRNA ; PREDICTED: Brassica rapa ADP,ATP carrier protein 3, mitochondrial (LOC103834762),	Bra033682	44 kDa	13	5	0	4

181	transcript variant X2, mRNA ; Similar to AAC3 ADP,ATP carrier protein 3, mitochondrial (Arabidopsis thaliana)::Bra033682:0-402 Similar to RPS25E 40S ribosomal protein S25-4 (Arabidopsis thaliana)::Bra011385:0-108	Bra011385 (+2)	12 kDa	0	10	5	7
182	Brassica oleracea HDEM genome, scaffold: C4 ; Brassica rapa genome, scaffold: A05 ; PREDICTED: Brassica napus heat shock 70 kDa protein 8-like (LOC106451327), mRNA ; PREDICTED: Brassica napus heat shock 70 kDa protein 8 (LOC106396657), transcript variant X1, mRNA ; PREDICTED: Brassica napus heat shock 70 kDa protein 8 (LOC106396657), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea heat shock 70 kDa protein 8 (LOC106342916), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea heat shock 70 kDa protein 8 (LOC106342916), transcript variant X2, mRNA ; PREDICTED: Brassica rapa heat	Bra028928	61 kDa	11	8	0	3

183	shock 70 kDa protein 8 (LOC103867668), mRNA ; Similar to HSP70-8 Heat shock 70 kDa protein 8 (Arabidopsis thaliana)::Bra028928:0-564 PREDICTED: Brassica napus universal stress protein PHOS34 (LOC106410769), mRNA ; PREDICTED: Brassica oleracea var. oleracea universal stress protein YxiE-like (LOC106296807), mRNA ; Protein of unknown function ; Zea mays clone 13463 mRNA sequence ; Zea mays clone 14034 mRNA sequence::Bra025973:0-159	Bra025973	18 kDa	8	11	0	3
184	PREDICTED: Brassica napus early nodulin-like protein 2 (LOC106376112), mRNA ; PREDICTED: Brassica oleracea var. oleracea early nodulin-like protein 2 (LOC106327489), mRNA ; PREDICTED: Brassica rapa early nodulin-like protein 2 (LOC103867244), mRNA ; Similar to At4g27520 Early nodulin-like protein 2 (Arabidopsis thaliana)::Bra013070:0-328	Bra013070	33 kDa	3	8	6	2

185	PREDICTED: Brassica napus GDSL esterase/lipase At3g09930 (LOC111213910), mRNA ; PREDICTED: Brassica oleracea var. oleracea GDSL esterase/lipase At3g09930 (LOC106292495), mRNA ; PREDICTED: Brassica rapa GDSL esterase/lipase At3g09930 (LOC103870502), mRNA ; Similar to At3g09930 GDSL esterase/lipase At3g09930 (Arabidopsis thaliana)::Bra031244:0-354	Bra031244	40 kDa	1	8	6	4
186	PREDICTED: Brassica napus low-temperature-induced 65 kDa protein-like (LOC106440851), transcript variant X1, mRNA ; PREDICTED: Brassica rapa low-temperature-induced 65 kDa protein (LOC103861574), mRNA ; Similar to LTI65 Low-temperature-induced 65 kDa protein (Arabidopsis thaliana)::Bra011172:0-559	Bra011172	60 kDa	7	7	6	1
187	Similar to LRP 40S ribosomal protein SA (Brassica napus)::Bra017597:0-296	Bra017597 (+4)	32 kDa	7	7	2	3
188	PREDICTED: Brassica napus uncharacterized LOC106346992 (LOC106346992), transcript variant X3, mRNA ;	Bra017274	25 kDa	1	5	10	4

	PREDICTED: Brassica napus uncharacterized LOC106402967 (LOC106402967), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterized LOC106324852 (LOC106324852), transcript variant X3, mRNA ; Protein of unknown function::Bra017274:0-233 PREDICTED: Brassica napus dehydrin Xero 1-like (LOC106454853), mRNA ; PREDICTED: Brassica napus dehydrin Xero 1 (LOC106399795), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea dehydrin Xero 1-like (LOC106311856), mRNA ; PREDICTED: Brassica rapa dehydrin Xero 1-like (LOC103841019), mRNA ; Similar to XERO1 Dehydrin Xero 1 (Arabidopsis						
189	thaliana)::Bra004681:0-134	Bra004681	14 kDa	6	6	7	0
190	Similar to MBP2 Myrosinase-binding protein 2 (Arabidopsis thaliana)::Bra031923:0-334	Bra031923	37 kDa	16	2	0	3

191	PREDICTED: Brassica napus protein disulfide-isomerase like 2-1-like (LOC106450433), mRNA ; PREDICTED: Brassica rapa protein disulfide-isomerase like 2-1 (LOC103866377), transcript variant X1, mRNA ; Similar to PDIL2-1 Protein disulfide-isomerase like 2-1 (Arabidopsis thaliana)::Bra027783:0-361	Bra027783	39 kDa	9	10	4	10
192	PREDICTED: Brassica napus probable pectinesterase/pectinesterase inhibitor 36 (LOC106414961), mRNA ; PREDICTED: Brassica oleracea var. oleracea probable pectinesterase/pectinesterase inhibitor 36 (LOC106311324), mRNA ; PREDICTED: Brassica rapa probable pectinesterase/pectinesterase inhibitor 36 (LOC103841916), transcript variant X1, misc_RNA ; PREDICTED: Brassica rapa probable pectinesterase/pectinesterase inhibitor 36 (LOC103841916), transcript variant X2, mRNA ; Similar to PME36 Probable pectinesterase/pectinesterase	Bra005342	58 kDa	1	8	3	6

193	inhibitor 36 (Arabidopsis thaliana)::Bra005342:0-521 PREDICTED: Brassica napus dnaJ homolog subfamily B member 13 (LOC106368780), mRNA ; PREDICTED: Brassica napus dnaJ homolog subfamily B member 13 (LOC106436699), mRNA ; PREDICTED: Brassica oleracea var. oleracea dnaJ homolog subfamily B member 13 (LOC106312462), mRNA ; PREDICTED: Brassica rapa dnaJ homolog subfamily B member 13 (LOC103842598), mRNA ; Similar to DNAJB6 DnaJ homolog subfamily B member 6 (Homo sapiens)::Bra005828:0-338	Bra005828	37 kDa	7	8	4	1
194	PREDICTED: Brassica napus uncharacterized LOC106395796 (LOC106395796), mRNA ; PREDICTED: Brassica napus uncharacterized LOC106433462 (LOC106433462), mRNA ; PREDICTED: Brassica napus uncharacterized LOC106433482 (LOC106433482), mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterized LOC106325614 (LOC106325614), mRNA ;	Bra017618	51 kDa	2	9	6	2

195	PREDICTED: Brassica rapa uncharacterized LOC103852751 (LOC103852751), mRNA ; Protein of unknown function::Bra017618:0-459 PREDICTED: Brassica napus 60S ribosomal protein L6-1-like (LOC106369059), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L6-1 (LOC106436769), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L6-1 (LOC106309544), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L6-1 (LOC103842696), mRNA ; Similar to RPL6A 60S ribosomal protein L6-1 (Arabidopsis thaliana)::Bra005912:0-234	Bra005912	26 kDa	1	9	7	1
196	PREDICTED: Brassica napus desiccation-related protein PCC13-62-like (LOC106412444), misc_RNA ; PREDICTED: Brassica napus desiccation-related protein PCC13-62-like (LOC106429407), misc_RNA ; PREDICTED: Brassica napus desiccation-related protein PCC13-62 (LOC106420540), mRNA ; PREDICTED: Brassica	Bra005466	34 kDa	7	4	5	4

197	oleracea var. oleracea desiccation-related protein PCC13-62 (LOC106310506), mRNA ; PREDICTED: Brassica rapa desiccation-related protein PCC13-62 (LOC103842077), mRNA ; Similar to Desiccation-related protein PCC13-62 (Craterostigma plantagineum)::Bra005466:0-311 PREDICTED: Brassica napus probable elongation factor 1-gamma 1 (LOC106420176), mRNA ; PREDICTED: Brassica rapa probable elongation factor 1-gamma 1 (LOC103843341), mRNA ; Similar to At1g09640 Probable elongation factor 1-gamma 1 (Arabidopsis thaliana)::Bra006296:0-413	Bra006296	46 kDa	6	8	3	2
198	Similar to At3g53970 Probable proteasome inhibitor (Arabidopsis thaliana)::Bra025972:0-325	Bra025972	35 kDa	6	5	3	4
199	PREDICTED: Brassica napus transketolase-1, chloroplastic-like (LOC106414826), mRNA ; PREDICTED: Brassica napus transketolase-1, chloroplastic-like (LOC106414846), mRNA ; PREDICTED: Brassica oleracea var. oleracea transketolase-1,	Bra005343 (+1)	79 kDa	7	8	0	3

200	chloroplastic (LOC106311760), mRNA ; PREDICTED: Brassica rapa transketolase-1, chloroplastic (LOC103841917), mRNA ; Similar to TKL-1 Transketolase-1, chloroplastic (Arabidopsis thaliana)::Bra005343:0-736 Similar to APA1 Aspartic proteinase A1 (Arabidopsis thaliana)::Bra006206:0-588	Bra006206	64 kDa	6	6	0	5
201	PREDICTED: Brassica napus probable inactive serine/threonine-protein kinase fnkC (LOC106389282), transcript variant X1, mRNA ; PREDICTED: Brassica napus probable inactive serine/threonine-protein kinase fnkC (LOC106389282), transcript variant X2, mRNA ; PREDICTED: Brassica napus probable inactive serine/threonine-protein kinase fnkC (LOC106424470), transcript variant X1, mRNA ; PREDICTED: Brassica napus probable inactive serine/threonine-protein kinase fnkC (LOC106424470), transcript variant X2, mRNA ; PREDICTED: Brassica rapa	Bra010074	44 kDa	11	0	0	0

	probable inactive serine/threonine-protein kinase fnkC (LOC103859852), transcript variant X1, mRNA ; PREDICTED: Brassica rapa probable inactive serine/threonine-protein kinase fnkC (LOC103859852), transcript variant X2, mRNA ; Protein of unknown function::Bra010074:0-382						
202	Similar to At5g07830 Heparanase-like protein 1 (Arabidopsis thaliana)::Bra037650:0-525	Bra037650	58 kDa	2	6	5	3
203	Similar to At1g23190 Probable phosphoglucomutase, cytoplasmic 1 (Arabidopsis thaliana)::Bra034284:0-583	Bra034284	63 kDa	6	9	1	1
204	PREDICTED: Brassica napus vicilin-like seed storage protein At2g18540 (LOC106348195), mRNA ; PREDICTED: Brassica napus vicilin-like seed storage protein At2g18540 (LOC106385437), mRNA ; PREDICTED: Brassica oleracea var. oleracea nuclear speckle splicing regulatory protein 1 (LOC106333178), mRNA ; PREDICTED: Brassica rapa vicilin-like seed storage protein	Bra022682 (+2)	83 kDa	9	3	2	1

	At2g18540 (LOC103874069), mRNA ; Similar to At2g18540 Vicilin-like seed storage protein At2g18540 (Arabidopsis thaliana)::Bra022682:0-697 PREDICTED: Brassica napus uncharacterized BNACNNG75970D (BNACNNG75970D), mRNA ; PREDICTED: Brassica napus uncharacterized LOC106356495 (LOC106356495), mRNA ; PREDICTED: Brassica napus uncharacterized LOC106358345 (LOC106358345), mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterized LOC106306577 (LOC106306577), mRNA ; PREDICTED: Brassica rapa uncharacterized LOC103829566 (LOC103829566), mRNA ; Protein of unknown						
205	function::Bra025598:0-117 Similar to ADH2 Alcohol dehydrogenase class-3 (Arabidopsis	Bra025598	13 kDa	8	6	2	0
206	thaliana)::Bra001897:0-399 Similar to EMB2247 Valine--tRNA ligase,	Bra001897 (+1)	43 kDa	5	6	0	5
207	chloroplastic/mitochondrial 2	Bra037183	134 kDa	0	8	8	0

208	(Arabidopsis thaliana)::Bra037183:0-1183 Similar to RRP5 rRNA biogenesis protein RRP5 (Arabidopsis thaliana)::Bra015151:0-2134 PREDICTED: Brassica napus 60S ribosomal protein L8-3-like (LOC106451593), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L8-3-like (LOC111215659), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L8-3-like (LOC106307103), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L8-3-like (LOC103862457), mRNA ;	Bra015151	237 kDa	4	9	1	1
209	Similar to RPL8C 60S ribosomal protein L8-3 (Arabidopsis thaliana)::Bra003034:0-258 PREDICTED: Brassica napus heat shock 70 kDa protein 14-like (LOC106345936), transcript variant X1, mRNA ; PREDICTED: Brassica napus heat shock 70 kDa protein 14-like (LOC106345936), transcript variant X2, mRNA ;	Bra003034 (+2)	28 kDa	2	3	2	0
210	PREDICTED: Brassica rapa heat shock 70 kDa protein 14	Bra020199	90 kDa	6	5	0	4

211	(LOC103871120), transcript variant X1, mRNA ; PREDICTED: Brassica rapa heat shock 70 kDa protein 14 (LOC103871120), transcript variant X2, mRNA ; Similar to HSP70-14 Heat shock 70 kDa protein 14 (Arabidopsis thaliana)::Bra020199:0-818 PREDICTED: Brassica napus 3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic-like (LOC106381762), transcript variant X1, mRNA ; PREDICTED: Brassica napus 3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic-like (LOC106381763), transcript variant X1, mRNA ; PREDICTED: Brassica napus 3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic (LOC106411349), mRNA ; PREDICTED: Brassica rapa 3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic-like (LOC103853696), mRNA ; Similar to KAS1 3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic (Arabidopsis thaliana)::Bra018214:0-521	Bra018214	56 kDa	10	4	0	1

212	Brassica napus enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic-like (LOC106439777), mRNA ; PREDICTED: Brassica napus enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic-like (LOC106439776), mRNA ; PREDICTED: Brassica napus enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic-like (LOC106439777), transcript variant X1, mRNA ; PREDICTED: Brassica napus enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic-like (LOC106439777), transcript variant X2, mRNA ; Similar to Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic (Brassica napus)::Bra010588:0-394	Bra010588	42 kDa	5	6	0	4
213	Brassica oleracea var. alboglabra S-adenosyl-L-homocystein hydrolase mRNA, complete cds ; PREDICTED: Brassica napus adenosylhomocysteinase 1-like (LOC106399668), transcript variant X1, mRNA ; PREDICTED: Brassica napus adenosylhomocysteinase 1-like	Bra032371 (+1)	53 kDa	6	6	0	3

	(LOC106437676), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea adenosylhomocysteinase 1-like (LOC106311804), transcript variant X1, mRNA ; Similar to SAHH1 Adenosylhomocysteinase 1 (Arabidopsis thaliana)::Bra032371:0-485 Similar to PIMT2 Protein-L-isoaspartate O-methyltransferase 2 (Arabidopsis						
214	thaliana)::Bra009023:0-301 PREDICTED: Brassica napus probable protein phosphatase 2C 39 (LOC106397444), mRNA ; PREDICTED: Brassica napus probable protein phosphatase 2C 39 (LOC106403039), mRNA ; PREDICTED: Brassica oleracea var. oleracea probable protein phosphatase 2C 39 (LOC106344001), mRNA ; PREDICTED: Brassica rapa probable protein phosphatase 2C 39 (LOC103869944), mRNA ; Similar to At3g15260 Probable protein phosphatase 2C 39 (Arabidopsis	Bra009023	32 kDa	6	6	0	3
215	thaliana)::Bra030903:0-288	Bra030903	31 kDa	5	9	0	1

216	PREDICTED: Brassica napus 60S ribosomal protein L23a-1 (LOC106438085), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L23a-1-like (LOC103857868), mRNA ; Similar to RPL23AA 60S ribosomal protein L23a-1 (Arabidopsis thaliana)::Bra008599:0-233	Bra008599 (+3)	26 kDa	0	2	9	4
217	PREDICTED: Brassica napus probable voltage-gated potassium channel subunit beta (LOC111200420), transcript variant X1, mRNA ; PREDICTED: Brassica napus probable voltage-gated potassium channel subunit beta (LOC111200420), transcript variant X2, mRNA ; PREDICTED: Brassica rapa probable voltage-gated potassium channel subunit beta (LOC103836560), mRNA ; Similar to KAB1 Probable voltage-gated potassium channel subunit beta (Arabidopsis thaliana)::Bra034911:0-328	Bra034911 (+1)	37 kDa	9	6	0	0
218	Similar to At4g30910 Leucine aminopeptidase 2, chloroplastic	Bra039978	55 kDa	15	0	0	0

219	(Arabidopsis thaliana)::Bra039978:0-523 PREDICTED: Brassica napus 60S ribosomal protein L11-1 (LOC106406958), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L11-1 (LOC106315662), mRNA ; Similar to RPL11A 60S ribosomal protein L11-1 (Arabidopsis thaliana) ; Zea mays clone 19991 mRNA sequence::Bra003588:0-182	Bra003588 (+6)	21 kDa	3	2	4	5
220	PREDICTED: Brassica napus 40S ribosomal protein S14-2 (LOC106388134), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S14-2 (LOC106391301), transcript variant X1, mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S14-2 (LOC106391301), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea 40S ribosomal protein S14-2 (LOC106331850), mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S14-2 (LOC103857606), mRNA ; Similar to RPS14B 40S ribosomal	Bra008277 (+4)	16 kDa	3	4	5	2

	protein S14-2 (Arabidopsis thaliana)::Bra008277:0-150 PREDICTED: Brassica napus non-classical arabinogalactan protein 31-like (LOC106358056), mRNA ; PREDICTED: Brassica rapa non-classical arabinogalactan protein 31-like (LOC103829021), mRNA ; Similar to AGP31 Non-classical arabinogalactan protein 31 (Arabidopsis						
221	thaliana)::Bra025193:0-328 PREDICTED: Brassica napus 40S ribosomal protein S20-1-like (LOC106345888), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S20-1 (LOC106387934), mRNA ; PREDICTED: Brassica oleracea var. oleracea 40S ribosomal protein S20-1-like (LOC106335881), mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S20-1-like (LOC103857176), mRNA ; Similar to RPS20A 40S ribosomal protein S20-1 (Arabidopsis	Bra025193	35 kDa	2	3	7	2
222	thaliana)::Bra007923:0-123 PREDICTED: Brassica napus cinnamoyl-CoA reductase 1-like	Bra007923 (+1)	14 kDa	4	4	2	4
223	(LOC106367237), mRNA ;	Bra040499	36 kDa	6	7	1	0

224	PREDICTED: Brassica oleracea var. oleracea cinnamoyl-CoA reductase 1 (LOC106342015), mRNA ; PREDICTED: Brassica rapa cinnamoyl-CoA reductase 1 (LOC103865283), mRNA ; Similar to CCR1 Cinnamoyl-CoA reductase 1 (Arabidopsis thaliana)::Bra040499:0-321 Similar to MFT Protein MOTHER of FT and TF 1 (Arabidopsis thaliana)::Bra005928:0-173 PREDICTED: Brassica napus 40S ribosomal protein S19-1-like (LOC106388645), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S19-1-like (LOC106438916), mRNA ; PREDICTED: Brassica oleracea var. oleracea 40S ribosomal protein S19-1-like (LOC106328670), mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S19-1-like (LOC103858939), mRNA ; PREDICTED: Raphanus sativus 40S ribosomal protein S19-1-like (LOC108856952), mRNA ;	Bra005928	19 kDa	5	2	7	0
225	Similar to RPS19A 40S ribosomal protein S19-1 (Arabidopsis thaliana) ; Zea mays clone 9201	Bra009396	16 kDa	5	8	1	0

	mRNA sequence::Bra009396:0-143 PREDICTED: Brassica oleracea var. oleracea HVA22-like protein b (LOC106326526), mRNA ; Similar to HVA22B HVA22-like protein b (Arabidopsis						
226	thaliana)::Bra019937:0-165 Similar to HSP70-10 Heat shock 70 kDa protein 10, mitochondrial (Arabidopsis	Bra019937	19 kDa	4	3	1	5
227	thaliana)::Bra015956:0-1090 Similar to AAC2 ADP,ATP carrier protein 2, mitochondrial (Arabidopsis	Bra015956	119 kDa	12	20	3	13
228	thaliana)::Bra007113:0-395 PREDICTED: Brassica napus peroxiredoxin Q, chloroplastic (LOC106436659), transcript variant X1, mRNA ; PREDICTED: Brassica napus peroxiredoxin Q, chloroplastic (LOC106436659), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea peroxiredoxin Q, chloroplastic (LOC106320257), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea peroxiredoxin Q,	Bra007113 (+2)	43 kDa	6	5	0	3
229	chloroplastic (LOC106320257),	Bra022015	24 kDa	1	6	6	0

	transcript variant X2, mRNA ; PREDICTED: Brassica rapa peroxiredoxin Q, chloroplastic (LOC103854405), transcript variant X1, mRNA ; PREDICTED: Brassica rapa peroxiredoxin Q, chloroplastic (LOC103854405), transcript variant X2, mRNA ; Similar to PRXQ Peroxiredoxin Q, chloroplastic (Arabidopsis thaliana)::Bra022015:0-216 Similar to SSL9 Protein STRICTOSIDINE SYNTHASE-LIKE 9 (Arabidopsis						
230	thaliana)::Bra026064:0-1565	Bra026064	175 kDa	11	10	0	4
231	PREDICTED: Brassica napus aspartic proteinase A3 (LOC106366922), mRNA ; PREDICTED: Brassica napus aspartic proteinase A3 (LOC106376996), transcript variant X1, mRNA ; PREDICTED: Brassica napus aspartic proteinase A3 (LOC106376996), transcript variant X2, mRNA ; PREDICTED: Brassica napus aspartic proteinase A3 (LOC106376996), transcript variant X3, mRNA ;	Bra002262	58 kDa	9	4	0	0

232	PREDICTED: Brassica oleracea var. oleracea aspartic proteinase A3 (LOC106312989), mRNA ; PREDICTED: Brassica rapa aspartic proteinase A3 (LOC103839838), transcript variant X1, mRNA ; PREDICTED: Brassica rapa aspartic proteinase A3 (LOC103839838), transcript variant X2, mRNA ; Similar to APA3 Aspartic proteinase A3 (Arabidopsis thaliana)::Bra002262:0-532 PREDICTED: Brassica napus protein usf (LOC106447086), mRNA ; Protein of unknown function::Bra040434:0-239	Bra040434	26 kDa	0	8	0	3
233	Similar to NUCL1 Nucleolin 1 (Arabidopsis thaliana)::Bra020321:0-419	Bra020321 (+1)	45 kDa	1	7	3	1
234	Similar to RPS15A 40S ribosomal protein S15a (Brassica napus)::Bra007545:0-292	Bra007545 (+3)	33 kDa	0	8	0	3
235	PREDICTED: Brassica napus probable desiccation-related protein LEA14 (LOC106407032), mRNA ; PREDICTED: Brassica oleracea var. oleracea probable desiccation-related protein LEA14 (LOC106329308), mRNA ;	Bra034987	16 kDa	10	0	0	2

236	PREDICTED: Brassica rapa probable desiccation-related protein LEA14 (LOC103836663), mRNA ; Similar to LEA14 Probable desiccation-related protein LEA14 (Arabidopsis thaliana)::Bra034987:0-151 PREDICTED: Brassica napus 40S ribosomal protein S8-1-like (LOC106371762), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S8-1-like (LOC106439493), mRNA ; PREDICTED: Brassica oleracea var. oleracea 40S ribosomal protein S8-1 (LOC106313191), mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S8-1 (LOC103845690), mRNA ; Similar to RPS8A 40S ribosomal protein S8-1 (Arabidopsis thaliana)::Bra036995:0-228	Bra036995	26 kDa	2	4	1	4
237	PREDICTED: Brassica napus uncharacterized protein At2g27730, mitochondrial-like (LOC106352562), transcript variant X1, mRNA ; PREDICTED: Brassica rapa uncharacterized protein At2g27730, mitochondrial-like (LOC103829682), transcript	Bra025687	12 kDa	2	2	5	1

238	variant X1, mRNA ; Similar to At2g27730 Uncharacterized protein At2g27730, mitochondrial (Arabidopsis thaliana)::Bra025687:0-114 Similar to CFIS2 Pre-mRNA cleavage factor Im 25 kDa subunit 2 (Arabidopsis thaliana)::Bra033759:0-453	Bra033759	51 kDa	3	2	6	0
239	Brassica oleracea HDEM genome, scaffold: C1 ; Brassica rapa genome, scaffold: A01 ; PREDICTED: Brassica napus peptidyl-prolyl cis-trans isomerase (LOC106375290), mRNA ; PREDICTED: Brassica napus peptidyl-prolyl cis-trans isomerase (LOC106434732), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea peptidyl-prolyl cis-trans isomerase CYP18-4 (LOC106341430), mRNA ; PREDICTED: Brassica rapa peptidyl-prolyl cis-trans isomerase (LOC103833770), mRNA ; Similar to PCKR1 Peptidyl-prolyl cis-trans isomerase (Catharanthus roseus) ; Zea mays clone 13538 mRNA sequence ; Zea mays clone	Bra011689	18 kDa	0	6	2	3

	93630 mRNA sequence::Bra011689:0-171 PREDICTED: Brassica napus 60S ribosomal protein L13a-2-like (LOC106434833), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L13a-2-like (LOC106435375), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L13a-2-like (LOC106301537), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L13a-2-like (LOC103828595), mRNA ; PREDICTED: Raphanus sativus 60S ribosomal protein L13a-2-like (LOC108856366), mRNA ; Similar to RPL13AB 60S ribosomal protein L13a-2 (Arabidopsis thaliana) ; Zea mays clone 12538 mRNA						
240	sequence::Bra024793:0-206 PREDICTED: Brassica napus glutaredoxin-C2 (LOC106446144), mRNA ; PREDICTED: Brassica rapa glutaredoxin-C2 (LOC103863982), mRNA ;	Bra024793	24 kDa	4	5	0	2
241	Similar to GRXC2 Glutaredoxin-C2 (Arabidopsis thaliana) ; Zea	Bra039532	12 kDa	0	6	2	2

242	mays clone 11723 mRNA sequence::Bra039532:0-111 PREDICTED: Brassica napus fasciclin-like arabinogalactan protein 1 (LOC106371391), mRNA ; PREDICTED: Brassica napus fasciclin-like arabinogalactan protein 1 (LOC106390893), mRNA ; PREDICTED: Brassica oleracea var. oleracea fasciclin-like arabinogalactan protein 1 (LOC106319394), mRNA ; PREDICTED: Brassica rapa fasciclin-like arabinogalactan protein 1 (LOC103845019), mRNA ; Similar to FLA1 Fasciclin-like arabinogalactan protein 1 (Arabidopsis thaliana)::Bra036516:0-426	Bra036516	45 kDa	7	0	1	3
243	PREDICTED: Brassica napus 60S ribosomal protein L34-2-like (LOC106394022), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L34-2 (LOC106372741), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L34-2 (LOC106324938), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L34-2-	Bra017546 (+3)	14 kDa	0	6	2	3

244	like (LOC103852598), mRNA ; Similar to RPL34B 60S ribosomal protein L34-2 (Arabidopsis thaliana)::Bra017546:0-120 Similar to AGAL1 Alpha-galactosidase 1 (Arabidopsis thaliana)::Bra006906:0-741	Bra006906 (+1)	82 kDa	4	4	0	3
245	Brassica oleracea HDEM genome, scaffold: C7 ; Brassica rapa genome, scaffold: A03 ; PREDICTED: Brassica napus 60S ribosomal protein L26-1-like (LOC106402150), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L26-1-like (LOC106439994), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L26-1-like (LOC106451943), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L26-1-like (LOC106301991), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L26-1-like (LOC103860635), mRNA ; PREDICTED: Raphanus sativus 60S ribosomal protein L26-1 (LOC108852068), mRNA ; PREDICTED: Raphanus sativus 60S ribosomal protein L26-1	Bra010383 (+1)	17 kDa	0	7	0	4

	(LOC108852079), mRNA ; Similar to RPL26A 60S ribosomal protein L26-1 (Arabidopsis thaliana)::Bra010383:0-146 PREDICTED: Brassica napus ATP-citrate synthase beta chain protein 2 (LOC106365855), transcript variant X1, mRNA ; PREDICTED: Brassica napus ATP-citrate synthase beta chain protein 2 (LOC106365855), transcript variant X2, mRNA ; PREDICTED: Brassica napus ATP-citrate synthase beta chain protein 2 (LOC111197906), transcript variant X1, mRNA ; PREDICTED: Brassica napus ATP-citrate synthase beta chain protein 2 (LOC111197906), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea ATP-citrate synthase beta chain protein 2 (LOC106318884), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea ATP-citrate synthase beta chain protein 2 (LOC106318884), transcript variant X2, mRNA ;						
246	PREDICTED: Brassica rapa ATP-	Bra000310 (+1)	81 kDa	11	0	0	0

	citrate synthase beta chain protein 2 (LOC103837286), transcript variant X1, mRNA ; PREDICTED: Brassica rapa ATP-citrate synthase beta chain protein 2 (LOC103837286), transcript variant X2, mRNA ; Similar::Bra000310:0-738 PREDICTED: Brassica napus hsp70 nucleotide exchange factor fes1-like (LOC111215787), mRNA ; PREDICTED: Brassica rapa uncharacterized LOC103870549 (LOC103870549), mRNA ;						
247	Protein of unknown function::Bra031278:0-372	Bra031278	41 kDa	3	3	1	2
248	PREDICTED: Brassica napus 2-hydroxyacyl-CoA lyase-like (LOC106445967), mRNA ; PREDICTED: Brassica rapa 2-hydroxyacyl-CoA lyase (LOC103833165), mRNA ; Similar to HACL 2-hydroxyacyl-CoA lyase (Arabidopsis thaliana)::Bra037154:0-574	Bra037154	61 kDa	1	5	1	3
249	Brassica oleracea HDEM genome, scaffold: C9 ; Brassica rapa genome, scaffold: A09 ; PREDICTED: Brassica napus 40S ribosomal protein S28-2	Bra000692 (+4)	7 kDa	3	3	1	3

	(LOC106357658), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S28-2 (LOC106364133), mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S28-2 (LOC106364145), transcript variant X1, mRNA ; PREDICTED: Brassica napus 40S ribosomal protein S28-2 (LOC106364145), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea 40S ribosomal protein S28-2 (LOC106317812), mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S28-2 (LOC103837515), transcript variant X1, mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S28-2 (LOC103837515), transcript variant X2, mRNA ; PREDICTED: Raphanus sativus 40S ribosomal protein S28-2 (LOC108827482), mRNA ; Similar to RPS28C 40S ribosomal protein S28-2 (Arabidopsis thaliana)::Bra000692:0-64						
250	Brassica rapa copper/zinc superoxide dismutase (CSD)	Bra040196	21 kDa	5	2	1	2

	mRNA, partial cds ; PREDICTED: Brassica napus superoxide dismutase [Cu-Zn] 2, chloroplastic (LOC106446718), mRNA ; PREDICTED: Brassica oleracea var. oleracea superoxide dismutase [Cu-Zn] 2, chloroplastic (LOC106336916), mRNA ; PREDICTED: Brassica rapa superoxide dismutase [Cu-Zn] 2, chloroplastic (LOC103864828), mRNA ; Similar to CSD2 Superoxide dismutase [Cu-Zn] 2, chloroplastic (Arabidopsis thaliana) ; Zea mays clone 13950 mRNA sequence::Bra040196:0-207 PREDICTED: Brassica napus aspartyl protease AED3-like (LOC106415755), mRNA ; PREDICTED: Brassica napus aspartyl protease AED3 (LOC106415612), mRNA ; PREDICTED: Brassica oleracea var. oleracea protein ASPARTIC PROTEASE IN GUARD CELL 2-like (LOC106312619), mRNA ; PREDICTED: Brassica rapa aspartyl protease AED3-like (LOC103841353), mRNA ;						
251	PREDICTED: Raphanus sativus	Bra004945	46 kDa	2	2	0	2

	aspartyl protease AED3-like (LOC108862032), transcript variant X1, mRNA ; PREDICTED: Raphanus sativus aspartyl protease AED3-like (LOC108862032), transcript variant X2, mRNA ; Protein of unknown function::Bra004945:0-430 Brassica oleracea HDEM genome, scaffold: C8 ; Brassica rapa genome, scaffold: A08 ; PREDICTED: Brassica napus major oleosin NAP-II-like (LOC106419670), mRNA ; PREDICTED: Brassica napus major oleosin NAP-II-like (LOC111208674), mRNA ; PREDICTED: Brassica oleracea var. oleracea major oleosin NAP-II-like (LOC106319905), mRNA ; PREDICTED: Brassica rapa oleosin 16 kDa-like (LOC103832967), mRNA ; Protein of unknown						
252	function::Bra032113:0-166 PREDICTED: Brassica napus uncharacterized protein ECU03_1610 (BNAA02G22630D), mRNA ;	Bra032113	18 kDa	4	0	3	2
253	PREDICTED: Brassica rapa	Bra018080	28 kDa	4	2	2	0

254	uncharacterized protein ECU03_1610-like (LOC103848870), mRNA ; Similar to ECU03_1610 Uncharacterized protein ECU03_1610 (Encephalitozoon cuniculi (strain GB-M1))::Bra018080:0-253 PREDICTED: Brassica napus tubulin alpha-3 chain-like (LOC106425816), transcript variant X1, mRNA ; PREDICTED: Brassica napus tubulin alpha-3 chain-like (LOC106425817), transcript variant X1, mRNA ; PREDICTED: Brassica rapa tubulin alpha-3 chain-like (LOC103851297), mRNA ; Similar to TUBA5 Tubulin alpha-5 chain (Arabidopsis thaliana)::Bra016485:0-450	Bra016485 (+5)	50 kDa	0	5	1	4
255	Similar to RPP0B 60S acidic ribosomal protein P0-2 (Arabidopsis thaliana)::Bra009661:0-690	Bra009661 (+1)	77 kDa	3	0	1	6
256	PREDICTED: Brassica napus 60S ribosomal protein L3-1-like (LOC106371594), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L3-1-like	Bra018503	32 kDa	5	5	0	0

257	(LOC106418390), transcript variant X1, mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L3-1-like (LOC106418390), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L3-1-like (LOC106327742), transcript variant X1, mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L3-1 (LOC103848547), mRNA ; Similar to ARP1 60S ribosomal protein L3-1 (Arabidopsis thaliana)::Bra018503:0-280 PREDICTED: Brassica napus basic transcription factor 3 (LOC106369038), mRNA ; PREDICTED: Brassica oleracea var. oleracea transcription factor BTF3 homolog 4-like (LOC106309603), mRNA ; PREDICTED: Brassica rapa basic transcription factor 3-like (LOC103842730), mRNA ; Similar to BTF3L4 Transcription factor BTF3 homolog 4 (Bos taurus)::Bra005936:0-169	Bra005936 (+1)	18 kDa	4	4	1	0

258	PREDICTED: Brassica napus 60S ribosomal protein L9-2-like (LOC106381958), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L9-2-like (LOC106391789), transcript variant X1, mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L9-2-like (LOC106391789), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L9-2 (LOC106313639), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L9-2-like (LOC103838914), mRNA ; Similar to RPL9D 60S ribosomal protein L9-2 (Arabidopsis thaliana)::Bra002476:0-194	Bra002476 (+1)	22 kDa	6	2	1	0
259	PREDICTED: Brassica napus glycerophosphodiester phosphodiesterase GDPDL4-like (LOC106371412), mRNA ; PREDICTED: Brassica napus glycerophosphodiester phosphodiesterase GDPDL4-like (LOC106418457), mRNA ; PREDICTED: Brassica oleracea var. oleracea glycerophosphodiester	Bra036498	84 kDa	5	3	0	1

	phosphodiesterase GDPDL4 (LOC106318551), mRNA ; PREDICTED: Brassica rapa glycerophosphodiester phosphodiesterase GDPDL4 (LOC103844984), mRNA ; Similar to GDPDL4 Glycerophosphodiester phosphodiesterase GDPDL4 (Arabidopsis thaliana)::Bra036498:0-768 PREDICTED: Brassica napus V-type proton ATPase catalytic subunit A-like (LOC106381450), mRNA ; PREDICTED: Brassica napus V-type proton ATPase catalytic subunit A-like (LOC106381541), mRNA ; PREDICTED: Brassica napus V-type proton ATPase catalytic subunit A (LOC106353430), mRNA ; PREDICTED: Brassica napus V-type proton ATPase catalytic subunit A (LOC106405672), transcript variant X1, mRNA ; PREDICTED: Brassica napus V-type proton ATPase catalytic subunit A (LOC106405672), transcript variant X2, mRNA ;						
260	PREDICTED: Brassica oleracea	Bra017919	77 kDa	4	4	0	1

	var. oleracea V-type proton ATPase catalytic subunit A-like (LOC106327423), mRNA ; PREDICTED: Brassica oleracea var. oleracea V-type proton ATPase catalytic subunit A (LOC106300466), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea V-type proton ATPase catalytic subunit A (LOC106300466), transcript variant X2, mRNA ; PREDICTED: Brassica rapa V-type proton ATPase catalytic subunit A-like (LO::Bra017919:0-697 PREDICTED: Brassica napus AIG2-like protein A (LOC106432325), mRNA ; PREDICTED: Brassica napus AIG2-like protein A (LOC106446035), mRNA ; PREDICTED: Brassica oleracea var. oleracea AIG2-like protein (LOC106342351), mRNA ; PREDICTED: Brassica rapa AIG2-like protein (LOC103863913), mRNA ;						
261	Similar to At5g39720 AIG2-like	Bra039463	19 kDa	3	3	0	3

	protein (Arabidopsis thaliana)::Bra039463:0-166 Brassica oleracea HDEM genome, scaffold: C9 ; Brassica rapa genome, scaffold: A09 ; Brassica rapa subsp. pekinensis sulfotransferase 5b (ST5b-7) gene, complete cds ; PREDICTED: Brassica napus cytosolic sulfotransferase 18-like (LOC106447906), mRNA ; PREDICTED: Brassica napus cytosolic sulfotransferase 18 (LOC106405028), mRNA ; PREDICTED: Brassica oleracea var. oleracea cytosolic sulfotransferase 18-like (LOC106314384), mRNA ; PREDICTED: Brassica rapa cytosolic sulfotransferase 18-like (LOC103838473), mRNA ; Similar to SOT18 Cytosolic sulfotransferase 18 (Arabidopsis						
262	thaliana)::Bra001541:0-368	Bra001541	42 kDa	3	4	0	2
263	PREDICTED: Brassica napus probable pectinesterase/pectinesterase inhibitor 16 (LOC106351635), mRNA ; PREDICTED: Brassica napus probable pectinesterase/pectinesterase	Bra000006	56 kDa	4	4	0	0

	inhibitor 16 (LOC106391703), mRNA ; PREDICTED: Brassica oleracea var. oleracea probable pectinesterase/pectinesterase inhibitor 16 (LOC106339744), mRNA ; PREDICTED: Brassica rapa probable pectinesterase/pectinesterase inhibitor 16 (LOC103866037), mRNA ; Similar to PME16 Probable pectinesterase/pectinesterase inhibitor 16 (Arabidopsis thaliana)::Bra000006:0-516						
264	Similar to SULTR3;1 Sulfate transporter 3.1 (Arabidopsis thaliana)::Bra004751:0-794	Bra004751	88 kDa	8	1	0	0
265	Similar to NAP1;2 Nucleosome assembly protein 1;2 (Arabidopsis thaliana)::Bra024503:0-308	Bra024503 (+1)	35 kDa	6	3	0	0
266	Similar to RAD23C Ubiquitin receptor RAD23c (Arabidopsis thaliana)::Bra009412:0-359	Bra009412	38 kDa	1	2	2	0
267	PREDICTED: Brassica napus alpha-L-fucosidase 2-like (LOC106396165), mRNA ; PREDICTED: Brassica napus alpha-L-fucosidase 2 (LOC106354862), mRNA ; PREDICTED: Brassica oleracea var. oleracea alpha-L-fucosidase 2	Bra011731	93 kDa	2	3	0	1

268	(LOC106308629), mRNA ; PREDICTED: Brassica rapa alpha-L-fucosidase 2 (LOC103839946), mRNA ; Similar to FUC95A Alpha-L-fucosidase 2 (Arabidopsis thaliana)::Bra011731:0-836 PREDICTED: Brassica napus 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 (LOC106386536), transcript variant X1, mRNA ; PREDICTED: Brassica napus 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 (LOC106386536), transcript variant X2, mRNA ; PREDICTED: Brassica napus 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 (LOC106386536), transcript variant X3, mRNA ; PREDICTED: Brassica napus 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 (LOC106433609), transcript variant X1, mRNA ;	Bra007311 (+1)	84 kDa	2	4	2	0

	PREDICTED: Brassica napus 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 (LOC106433609), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1 (LOC106332023), mRNA ; PREDICTED: Brassica rapa 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase::Bra007311:0-765 PREDICTED: Brassica napus phosphoglycerate kinase 1, chloroplastic-like (LOC106353104), mRNA ; PREDICTED: Brassica rapa phosphoglycerate kinase 1, chloroplastic (LOC103859466), mRNA ; Similar to PGK1 Phosphoglycerate kinase 1, chloroplastic (Arabidopsis						
269	thaliana)::Bra009772:0-484	Bra009772 (+2)	50 kDa	3	4	0	5
270	PREDICTED: Brassica napus 26S proteasome non-ATPase regulatory subunit 1 homolog A-	Bra040450	109 kDa	1	0	4	2

271	like (LOC106447099), mRNA ; PREDICTED: Brassica napus 26S proteasome non-ATPase regulatory subunit 1 homolog A (LOC106427681), mRNA ; PREDICTED: Brassica oleracea var. oleracea 26S proteasome non-ATPase regulatory subunit 1 homolog A-like (LOC106341990), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea 26S proteasome non-ATPase regulatory subunit 1 homolog A-like (LOC106341990), transcript variant X2, mRNA ; PREDICTED: Brassica rapa 26S proteasome non-ATPase regulatory subunit 1 homolog A-like (LOC103865226), mRNA ; Similar to RPN2A 26S proteasome non-ATPase regulatory subunit 1 homolog A (Arabidopsis thaliana)::Bra040450:0-1004 PREDICTED: Brassica napus glutathione S-transferase F8, chloroplastic-like (LOC106438339), transcript variant X1, mRNA ;	Bra008877	24 kDa	4	3	0	0

272	PREDICTED: Brassica napus glutathione S-transferase F8, chloroplastic-like (LOC106438339), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea glutathione S-transferase F8, chloroplastic-like (LOC106335128), mRNA ; PREDICTED: Brassica rapa glutathione S-transferase F8, chloroplastic-like (LOC103858256), mRNA ; Similar to GSTF8 Glutathione S-transferase F8, chloroplastic (Arabidopsis thaliana)::Bra008877:0-215 Similar to GSTL1 Glutathione S-transferase L1 (Arabidopsis thaliana)::Bra015689:0-411	Bra015689	47 kDa	4	0	0	4
273	PREDICTED: Brassica rapa beta-glucosidase 19-like (LOC103872284), mRNA ; Similar to BGLU19 Beta-glucosidase 19 (Arabidopsis thaliana)::Bra021101:0-574	Bra021101	65 kDa	0	124	0	0
274	PREDICTED: Brassica napus ATP synthase subunit d, mitochondrial (LOC106440060), mRNA ; PREDICTED: Brassica rapa ATP synthase subunit d,	Bra010299 (+1)	20 kDa	1	3	2	1

	mitochondrial (LOC103860757), mRNA ; Similar to At3g52300 ATP synthase subunit d, mitochondrial (Arabidopsis thaliana)::Bra010299:0-168 Similar to CYS4 Cysteine proteinase inhibitor 4 (Arabidopsis						
275	thaliana)::Bra041705:0-281	Bra041705	32 kDa	4	1	1	0
276	PREDICTED: Brassica napus pyruvate kinase 1, cytosolic (LOC106367797), mRNA ; PREDICTED: Brassica napus pyruvate kinase 1, cytosolic (LOC106367920), mRNA ; PREDICTED: Brassica oleracea var. oleracea pyruvate kinase, cytosolic isozyme-like (LOC106311653), mRNA ; PREDICTED: Brassica rapa pyruvate kinase 1, cytosolic-like (LOC103841229), transcript variant X1, mRNA ; PREDICTED: Brassica rapa pyruvate kinase 1, cytosolic-like (LOC103841229), transcript variant X2, mRNA ; Similar to OsI_35105 Pyruvate kinase 1, cytosolic (Oryza sativa subsp. indica)::Bra004850:0-527	Bra004850 (+2)	58 kDa	2	3	0	2
277	PREDICTED: Brassica napus 2-oxoglutarate dehydrogenase,	Bra022629	115 kDa	4	1	0	1

278	mitochondrial-like (LOC106348097), transcript variant X1, mRNA ; PREDICTED: Brassica napus 2-oxoglutarate dehydrogenase, mitochondrial-like (LOC106348097), transcript variant X2, mRNA ; PREDICTED: Brassica napus 2-oxoglutarate dehydrogenase, mitochondrial-like (LOC106348184), mRNA ; PREDICTED: Brassica oleracea var. oleracea 2-oxoglutarate dehydrogenase, mitochondrial (LOC106334854), mRNA ; PREDICTED: Brassica rapa 2-oxoglutarate dehydrogenase, mitochondrial (LOC103874014), mRNA ; Similar to sucA 2-oxoglutarate dehydrogenase E1 component (Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni (strain Fiocruz L1-130))::Bra022629:0-1014 Brassica oleracea HDEM genome, scaffold: C5 ; Brassica rapa genome, scaffold: A06 ; PREDICTED: Brassica napus germin-like protein subfamily T	Bra021427	23 kDa	0	1	3	1

	member 2 (LOC106400858), mRNA ; PREDICTED: Brassica napus germin-like protein subfamily T member 2 (LOC111199002), mRNA ; PREDICTED: Brassica oleracea var. oleracea germin-like protein subfamily T member 2 (LOC106344049), mRNA ; PREDICTED: Brassica rapa germin-like protein subfamily T member 2 (LOC103872702), mRNA ; PREDICTED: Raphanus sativus germin-like protein subfamily T member 2 (LOC108854527), mRNA ; Similar to At1g18980 Germin-like protein subfamily T member 2 (Arabidopsis thaliana)::Bra021427:0-214 Similar to INO80 Putative DNA helicase INO80 (Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056))::Bra014441:0-691						
279	PREDICTED: Brassica napus proteasome subunit alpha type-5-A-like (LOC106360399), transcript variant X5, mRNA ;	Bra014441	79 kDa	3	1	0	1
280	PREDICTED: Brassica rapa proteasome subunit alpha type-5-	Bra031823	26 kDa	4	3	0	0

	A-like (LOC103832649), transcript variant X2, mRNA ; Similar to PAE1 Proteasome subunit alpha type-5-A (Arabidopsis thaliana)::Bra031823:0-237 PREDICTED: Brassica napus kynurenine formamidase-like (LOC106393997), mRNA ; PREDICTED: Brassica napus kynurenine formamidase-like (LOC106441136), mRNA ; PREDICTED: Brassica napus kynurenine formamidase-like (LOC111207619), mRNA ; PREDICTED: Brassica oleracea var. oleracea kynurenine formamidase (LOC106306226), mRNA ; PREDICTED: Brassica rapa kynurenine formamidase (LOC103862325), mRNA ; Protein of unknown						
281	function::Bra002912:0-259	Bra002912	29 kDa	6	1	0	0
282	PREDICTED: Brassica napus 10 kDa chaperonin-like (LOC106364276), mRNA ; PREDICTED: Brassica napus 10 kDa chaperonin-like (LOC106382313), mRNA ; PREDICTED: Brassica rapa 10 kDa chaperonin	Bra034561	11 kDa	0	0	4	2

	(LOC103836048), mRNA ; Similar to 10 kDa chaperonin (Brassica napus)::Bra034561:0-98 PREDICTED: Brassica napus ras-related protein RABD2b (LOC106430002), mRNA ; PREDICTED: Brassica rapa ras-related protein RABD2b (LOC103839540), mRNA ; PREDICTED: Brassica rapa ras-related protein RABD2b (LOC103853792), mRNA ; PREDICTED: Raphanus sativus ras-related protein RABD2b-like (LOC108812580), transcript variant X2, mRNA ; PREDICTED: Raphanus sativus ras-related protein RABD2b-like (LOC108824031), mRNA ; Similar to RABD2B Ras-related protein RABD2b (Arabidopsis						
283	thaliana)::Bra003498:0-202 PREDICTED: Brassica napus 60S ribosomal protein L28-1-like (LOC106447120), mRNA ; Similar to RPL28A 60S ribosomal protein L28-1 (Arabidopsis	Bra003498 (+2)	22 kDa	7	0	0	0
284	thaliana)::Bra001082:0-203 PREDICTED: Brassica napus 40S ribosomal protein S3-2	Bra001082	23 kDa	1	3	2	0
285	(LOC106437728), mRNA ;	Bra008066 (+2)	27 kDa	1	4	0	1

286	PREDICTED: Brassica rapa 40S ribosomal protein S3-2-like (LOC103857385), transcript variant X1, mRNA ; PREDICTED: Brassica rapa 40S ribosomal protein S3-2-like (LOC103857385), transcript variant X2, mRNA ; Similar to RPS3B 40S ribosomal protein S3-2 (Arabidopsis thaliana)::Bra008066:0-249 PREDICTED: Brassica napus 40S ribosomal protein S15-1 (LOC106369246), mRNA ; Similar to RPS15A 40S ribosomal protein S15-1 (Arabidopsis thaliana)::Bra006484:0-152	Bra006484 (+2)	17 kDa	3	3	0	0
287	PREDICTED: Brassica napus protein disulfide isomerase-like 1-4 (LOC106365754), mRNA ; PREDICTED: Brassica napus protein disulfide isomerase-like 1-4 (LOC106371613), mRNA ; PREDICTED: Brassica oleracea var. oleracea protein disulfide isomerase-like 1-4 (LOC106318458), mRNA ; PREDICTED: Brassica rapa protein disulfide isomerase-like 1-4 (LOC103845478), mRNA ; Similar to PDIL1-4 Protein	Bra036870	66 kDa	0	2	3	0

	disulfide isomerase-like 1-4 (Arabidopsis thaliana)::Bra036870:0-596 PREDICTED: Brassica napus proteasome subunit alpha type-7-A-like (LOC111200303), mRNA ; PREDICTED: Brassica napus proteasome subunit alpha type-7-A (LOC106367724), mRNA ; PREDICTED: Brassica oleracea var. oleracea proteasome subunit alpha type-7-A (LOC106307482), mRNA ; PREDICTED: Brassica rapa proteasome subunit alpha type-7-A (LOC103841046), mRNA ; Similar to PAD1 Proteasome subunit alpha type-7-A (Arabidopsis						
288	thaliana)::Bra004701:0-250	Bra004701 (+1)	27 kDa	3	3	0	0
289	PREDICTED: Brassica napus 6-phosphogluconate dehydrogenase, decarboxylating 3-like (LOC106352176), transcript variant X1, mRNA ; PREDICTED: Brassica napus 6-phosphogluconate dehydrogenase, decarboxylating 3-like (LOC106352176), transcript variant X2, mRNA ; PREDICTED: Brassica napus 6-phosphogluconate dehydrogenase,	Bra015223 (+1)	54 kDa	4	2	0	0

290	decarboxylating 3-like (LOC106352176), transcript variant X3, mRNA ; PREDICTED: Brassica napus 6-phosphogluconate dehydrogenase, decarboxylating 3 (LOC106349212), transcript variant X1, mRNA ; PREDICTED: Brassica napus 6-phosphogluconate dehydrogenase, decarboxylating 3 (LOC106349212), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea 6-phosphogluconate dehydrogenase, decarboxylating 3 (LOC106340355), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea 6-phosphogluconate dehydrogenase, decarboxylating 3 (LOC106340355), transcript variant X5, mRNA ; PREDICTED: Brassica rapa 6-phosphog::Bra015223:0-486 Similar to PGIC Glucose-6-phosphate isomerase, cytosolic (Arabidopsis thaliana)::Bra001613:0-542	Bra001613	60 kDa	4	0	0	2

291	Similar to PAB8 Polyadenylate-binding protein 8 (Arabidopsis thaliana)::Bra020285:0-627 PREDICTED: Brassica napus glycine--tRNA ligase, mitochondrial 1-like (LOC111206420), misc_RNA ; PREDICTED: Brassica napus glycine--tRNA ligase, mitochondrial 1 (LOC106367376), mRNA ; PREDICTED: Brassica oleracea var. oleracea glycine--tRNA ligase 1, mitochondrial (LOC106295514), mRNA ; PREDICTED: Brassica rapa glycine--tRNA ligase, mitochondrial 1 (LOC103840454), mRNA ;	Bra020285	68 kDa	3	1	1	0
292	Similar to At1g29880 Glycine--tRNA ligase, mitochondrial 1 (Arabidopsis thaliana)::Bra003997:0-690 PREDICTED: Brassica napus alpha-xylosidase 1-like (LOC106354019), misc_RNA ; PREDICTED: Brassica napus alpha-xylosidase 1-like (LOC106405609), mRNA ;	Bra003997 (+1)	77 kDa	2	2	1	0
293	PREDICTED: Brassica oleracea var. oleracea alpha-xylosidase 1	Bra026970	103 kDa	2	3	0	0

	(LOC106300147), mRNA ; PREDICTED: Brassica rapa alpha-xylosidase 1 (LOC103831266), mRNA ; Similar to XYL1 Alpha-xylosidase 1 (Arabidopsis thaliana)::Bra026970:0-926 PREDICTED: Brassica napus dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic-like (LOC106452022), mRNA ; PREDICTED: Brassica napus dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic (LOC106427199), mRNA ; PREDICTED: Brassica rapa dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic (LOC103869649), mRNA ; Similar to PYD1 Dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic (Arabidopsis						
294	thaliana)::Bra030728:0-431	Bra030728	47 kDa	3	1	0	0
295	PREDICTED: Brassica napus FAM10 family protein At4g22670-like (LOC106376536), transcript variant X1, mRNA ; PREDICTED: Brassica napus FAM10 family protein At4g22670-like (LOC106376536),	Bra012611	45 kDa	3	2	0	0

	transcript variant X2, mRNA ; PREDICTED: Brassica rapa FAM10 family protein At4g22670 (LOC103860206), transcript variant X1, mRNA ; PREDICTED: Brassica rapa FAM10 family protein At4g22670 (LOC103860206), transcript variant X2, mRNA ; Similar to At4g22670 FAM10 family protein At4g22670 (Arabidopsis thaliana)::Bra012611:0-416 PREDICTED: Brassica napus ubiquitin carboxyl-terminal hydrolase 3-like (LOC111214250), mRNA ; PREDICTED: Brassica rapa ubiquitin carboxyl-terminal hydrolase 3-like (LOC103860918), mRNA ; Similar to UCH3 Ubiquitin carboxyl-terminal hydrolase 3 (Arabidopsis						
296	thaliana)::Bra010752:0-234	Bra010752	26 kDa	0	0	1	4
	Similar to VDAC1 Mitochondrial outer membrane protein porin 1 (Arabidopsis						
297	thaliana)::Bra031639:0-326	Bra031639	35 kDa	0	1	0	4
	Similar to LAZ1 Protein LAZ1 (Arabidopsis						
298	thaliana)::Bra011359:0-1735	Bra011359	194 kDa	3	2	0	0

299	PREDICTED: Brassica napus uncharacterized BNAC03G41230D (BNAC03G41230D), mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterized LOC106334556 (LOC106334556), mRNA ; PREDICTED: Brassica rapa uncharacterized LOC103859827 (LOC103859827), mRNA ; Protein of unknown function::Bra010054:0-416	Bra010054	45 kDa	0	3	0	2
300	PREDICTED: Brassica napus adenylate kinase 4-like (LOC106347908), mRNA ; PREDICTED: Brassica napus adenylate kinase 4-like (LOC106431226), mRNA ; PREDICTED: Brassica napus adenylate kinase 4-like (LOC106431257), mRNA ; PREDICTED: Brassica napus adenylate kinase 4-like (LOC111208808), mRNA ; PREDICTED: Brassica oleracea var. oleracea adenylate kinase 4-like (LOC106328009), mRNA ; PREDICTED: Brassica rapa adenylate kinase 4-like (LOC103873752), mRNA ;	Bra022431	26 kDa	8	0	6	0

301	Similar to ADK1 Adenylate kinase 4 (Arabidopsis thaliana)::Bra022431:0-240 Similar to MNR1 (+)-neomenthol dehydrogenase (Capsicum annuum)::Bra035009:0-295 PREDICTED: Brassica napus nucleoside diphosphate kinase 1 (LOC106366685), mRNA ;	Bra035009	32 kDa	5	0	0	0
302	Similar to NDK1 Nucleoside diphosphate kinase 1 (Arabidopsis thaliana)::Bra001958:0-148 PREDICTED: Brassica napus 60S ribosomal protein L35-1-like (LOC106388959), mRNA ; PREDICTED: Brassica napus 60S ribosomal protein L35-1 (LOC106439191), mRNA ; PREDICTED: Brassica oleracea var. oleracea 60S ribosomal protein L35-1-like (LOC106331644), mRNA ; PREDICTED: Brassica rapa 60S ribosomal protein L35-1 (LOC103859293), mRNA ;	Bra001958	16 kDa	5	0	0	0
303	Similar to RPL35A 60S ribosomal protein L35-1 (Arabidopsis thaliana) ; Zea mays clone 10876 mRNA sequence::Bra009646:0-123	Bra009646 (+3)	14 kDa	0	5	0	0

304	Brassica rapa subsp. campestris polygalacturonase inhibitory protein (MF19) mRNA, complete cds ; PREDICTED: Brassica napus leucine-rich repeat protein FLOR 1 (LOC106351771), mRNA ; PREDICTED: Brassica napus leucine-rich repeat protein FLOR 1 (LOC106416600), mRNA ; PREDICTED: Brassica oleracea var. oleracea polygalacturonase inhibitor 1-like (LOC106323568), mRNA ; PREDICTED: Brassica rapa polygalacturonase inhibitor 1-like (LOC103845755), mRNA ; Similar to PGIP Polygalacturonase inhibitor (Pyrus communis)::Bra015163:0-325	Bra015163	36 kDa	0	5	0	0
305	PREDICTED: Brassica napus heat shock 70 kDa protein 6, chloroplastic-like (LOC106348936), mRNA ; PREDICTED: Brassica napus heat shock 70 kDa protein 6, chloroplastic (LOC106440803), transcript variant X1, mRNA ; PREDICTED: Brassica napus heat shock 70 kDa protein 6, chloroplastic (LOC106440803), transcript variant X2, mRNA ;	Bra011095 (+1)	76 kDa	3	1	0	1

306	PREDICTED: Brassica oleracea var. oleracea heat shock 70 kDa protein 6, chloroplastic-like (LOC106306084), mRNA ; PREDICTED: Brassica rapa heat shock 70 kDa protein 6, chloroplastic-like (LOC103861480), mRNA ; Similar to HSP70-6 Heat shock 70 kDa protein 6, chloroplastic (Arabidopsis thaliana)::Bra011095:0-711 PREDICTED: Brassica napus 26S proteasome regulatory subunit 6A homolog (LOC106388875), mRNA ; PREDICTED: Brassica napus 26S proteasome regulatory subunit 6A homolog (LOC111214163), mRNA ; PREDICTED: Brassica oleracea var. oleracea 26S protease regulatory subunit 6A homolog (LOC106328377), mRNA ; PREDICTED: Brassica rapa 26S protease regulatory subunit 6A homolog (LOC103859097), mRNA ; PREDICTED: Raphanus sativus 26S protease regulatory subunit 6A homolog (LOC108861240), mRNA ; Similar to TBP1 26S protease	Bra009512 (+2)	47 kDa	2	0	1	1

	regulatory subunit 6A homolog (Brassica campestris)::Bra009512:0-424 PREDICTED: Brassica napus peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic-like (LOC106391832), mRNA ; PREDICTED: Brassica napus peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic-like (LOC106424086), mRNA ; PREDICTED: Brassica napus peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic (LOC106391828), mRNA ; PREDICTED: Brassica oleracea var. oleracea peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic (LOC106337573), mRNA ; PREDICTED: Brassica rapa peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic-like (LOC103866085), mRNA ; Similar to FKBP16-3 Peptidyl-prolyl cis-trans isomerase FKBP16-3, chloroplastic (Arabidopsis						
307	thaliana)::Bra041096:0-216	Bra041096	23 kDa	2	2	0	0
308	PREDICTED: Brassica napus late embryogenesis abundant protein	Bra033313	27 kDa	0	7	13	0

	1-like (LOC106359738), mRNA ; PREDICTED: Brassica rapa late embryogenesis abundant protein 1-like (LOC103848743), mRNA ; Protein of unknown function::Bra033313:0-248 PREDICTED: Brassica napus beta-D-xylosidase 4-like (LOC106371739), mRNA ; PREDICTED: Brassica napus beta-D-xylosidase 4-like (LOC106402417), mRNA ; PREDICTED: Brassica napus beta-D-xylosidase 4 (LOC106366244), mRNA ; PREDICTED: Brassica oleracea var. oleracea beta-D-xylosidase 4 (LOC106319519), mRNA ; PREDICTED: Brassica rapa beta-D-xylosidase 4-like (LOC103837535), mRNA ; Similar to BXL4 Beta-D-xylosidase 4 (Arabidopsis						
309	thaliana)::Bra000708:0-776 PREDICTED: Brassica napus V-type proton ATPase subunit B3 (LOC106347084), transcript variant X1, mRNA ; PREDICTED: Brassica napus V-type proton ATPase subunit B3	Bra000708 (+1)	84 kDa	4	0	0	0
310	(LOC106347084), transcript	Bra021536 (+4)	54 kDa	4	0	0	0

variant X2, mRNA ;
PREDICTED: Brassica napus V-type proton ATPase subunit B3 (LOC106433719), transcript variant X1, mRNA ;
PREDICTED: Brassica napus V-type proton ATPase subunit B3 (LOC106433719), transcript variant X2, mRNA ;
PREDICTED: Brassica oleracea var. oleracea V-type proton ATPase subunit B3-like (LOC106295185), transcript variant X1, mRNA ;
PREDICTED: Brassica oleracea var. oleracea V-type proton ATPase subunit B3-like (LOC106295185), transcript variant X2, mRNA ;
PREDICTED: Brassica rapa V-type proton ATPase subunit B3 (LOC103872821), transcript variant X1, mRNA ;
PREDICTED: Brassica rapa V-type proton ATPase subunit B3 (LOC103872821), transcript variant X2, mRNA ; Similar to VHA-B3 V-type proton ATPase subunit B3 (Arabidopsis thaliana)::Bra021536:0-486

311	PREDICTED: Brassica napus tripeptidyl-peptidase 2-like (LOC106421156), mRNA ; PREDICTED: Brassica napus tripeptidyl-peptidase 2-like (LOC106440420), misc_RNA ; PREDICTED: Brassica oleracea var. oleracea tripeptidyl-peptidase 2 (LOC106303335), partial mRNA ; PREDICTED: Brassica rapa tripeptidyl-peptidase 2-like (LOC103861204), mRNA ; Similar to TPP2 Tripeptidyl-peptidase 2 (Arabidopsis thaliana)::Bra010903:0-1310	Bra010903	144 kDa	2	1	0	0
312	Brassica oleracea HDEM genome, scaffold: C6 ; Brassica rapa genome, scaffold: A05 ; PREDICTED: Brassica napus phospholipase D alpha 2-like (LOC106449389), mRNA ; PREDICTED: Brassica napus phospholipase D alpha 2 (LOC106405207), mRNA ; PREDICTED: Brassica oleracea var. oleracea phospholipase D alpha 2 (LOC106299943), mRNA ; PREDICTED: Brassica rapa phospholipase D alpha 2 (LOC103868492), mRNA ; Similar to PLDALPHA1	Bra029460 (+1)	88 kDa	1	2	0	0

313	Phospholipase D alpha 1 (Arabidopsis thaliana)::Bra029460:0-779 Similar to HOP2 Hsp70-Hsp90 organizing protein 2 (Arabidopsis thaliana)::Bra001413:0-575 PREDICTED: Brassica napus benzaldehyde dehydrogenase (NAD(+))-like (LOC106371001), mRNA ; PREDICTED: Brassica napus benzaldehyde dehydrogenase (NAD(+)) (LOC106402186), transcript variant X1, mRNA ; PREDICTED: Brassica napus benzaldehyde dehydrogenase (NAD(+)) (LOC106402186), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea benzaldehyde dehydrogenase (NAD(+)) (LOC106295510), transcript variant X1, mRNA ; PREDICTED: Brassica oleracea var. oleracea benzaldehyde dehydrogenase (NAD(+)) (LOC106295510), transcript variant X2, mRNA ; PREDICTED: Brassica rapa benzaldehyde dehydrogenase	Bra001413	65 kDa	1	0	2	0
314	(NAD(+)) (LOC103844240),	Bra035276	155 kDa	3	0	0	0

	transcript variant X1, mRNA ; PREDICTED: Brassica rapa benzaldehyde dehydrogenase (NAD(+)) (LOC103844240), transcript variant X2, mRNA ; Similar to AAO4 Benzaldehyde dehydrogenase (NAD(+)) (Arabidopsis thaliana)::Bra035276:0-1411 PREDICTED: Brassica napus lysine--tRNA ligase, cytoplasmic-like (LOC106450425), mRNA ; PREDICTED: Brassica napus lysine--tRNA ligase, cytoplasmic (LOC106351199), mRNA ; PREDICTED: Brassica oleracea var. oleracea lysine--tRNA ligase (LOC106336618), mRNA ; PREDICTED: Brassica rapa lysine--tRNA ligase, cytoplasmic (LOC103846034), mRNA ; Similar to At3g11710 Lysine--tRNA ligase, cytoplasmic (Arabidopsis						
315	thaliana)::Bra015138:0-623	Bra015138	71 kDa	0	3	0	0
316	Similar to HSP90-7 Endoplasmin homolog (Arabidopsis thaliana)::Bra012756:0-719	Bra012756	82 kDa	2	0	0	0
317	PREDICTED: Brassica napus 26.5 kDa heat shock protein, mitochondrial (LOC106376590),	Bra021021	27 kDa	0	2	0	0

	mRNA ; PREDICTED: Brassica napus 26.5 kDa heat shock protein, mitochondrial (LOC106404842), transcript variant X1, mRNA ; PREDICTED: Brassica napus 26.5 kDa heat shock protein, mitochondrial (LOC106404842), transcript variant X2, mRNA ; PREDICTED: Brassica oleracea var. oleracea 26.5 kDa heat shock protein, mitochondrial (LOC106299182), mRNA ; PREDICTED: Brassica rapa 26.5 kDa heat shock protein, mitochondrial (LOC103871208), mRNA ; Similar to HSP26.5 26.5 kDa heat shock protein, mitochondrial (Arabidopsis thaliana)::Bra021021:0-232						
318	Similar to At3g01520 Universal stress protein A-like protein (Arabidopsis thaliana)::Bra026122:0-204	Bra026122	23 kDa	2	0	0	0
319	Similar to RPT2A 26S proteasome regulatory subunit 4 homolog A (Arabidopsis thaliana)::Bra033654:0-901	Bra033654	99 kDa	2	0	0	0
320	PREDICTED: Brassica napus 60S ribosomal protein L15-1 (LOC106440269), mRNA ;	Bra010723 (+3)	30 kDa	2	0	0	0

321	PREDICTED: Brassica rapa 60S ribosomal protein L15-1-like (LOC103860880), mRNA ; Similar to RPL15A 60S ribosomal protein L15-1 (Arabidopsis thaliana)::Bra010723:0-264 PREDICTED: Brassica napus hsp70-Hsp90 organizing protein 3-like (LOC106362025), mRNA ; PREDICTED: Brassica napus hsp70-Hsp90 organizing protein 3 (LOC106402021), mRNA ; PREDICTED: Brassica rapa hsp70-Hsp90 organizing protein 3 (LOC103868140), mRNA ; Similar to HOP3 Hsp70-Hsp90 organizing protein 3 (Arabidopsis thaliana)::Bra018790:0-553	Bra018790	63 kDa	2	0	0	0
322	PREDICTED: Brassica napus 14-3-3-like protein GF14 kappa (LOC106347979), transcript variant X1, mRNA ; PREDICTED: Brassica napus 14-3-3-like protein GF14 kappa (LOC106347979), transcript variant X2, mRNA ; Similar to GRF8 14-3-3-like protein GF14 kappa (Arabidopsis thaliana)::Bra022594:0-223	Bra022594	25 kDa	2	0	0	0
323	PREDICTED: Brassica napus dihydrolipoyl dehydrogenase 1,	Bra009942 (+1)	66 kDa	2	0	0	0

chloroplastic (LOC106358154), mRNA ; PREDICTED: Brassica napus dihydrolipoyl dehydrogenase 1, chloroplastic (LOC106439448), transcript variant X1, mRNA ; PREDICTED: Brassica napus dihydrolipoyl dehydrogenase 1, chloroplastic (LOC106439448), transcript variant X2, mRNA ; PREDICTED: Brassica napus dihydrolipoyl dehydrogenase 1, chloroplastic (LOC106439448), transcript variant X3, mRNA ; PREDICTED: Brassica napus dihydrolipoyl dehydrogenase 1, chloroplastic (LOC106439448), transcript variant X4, mRNA ; PREDICTED: Brassica oleracea var. oleracea dihydrolipoyl dehydrogenase 1, chloroplastic (LOC106328211), mRNA ; PREDICTED: Brassica rapa dihydrolipoyl dehydrogenase 1, chloroplastic (LOC103859689), transcript variant X1, mRNA ; PREDICTED: Brassica rapa dihydrolipoyl dehydrogenase 1, chloroplastic (LOC103859689), transcript variant X2, mRNA ; PREDICTED: Brassica rapa

dihydrolipoyl
dehydrog::Bra009942:0-618

S5 Table. List of protein sequences of identified vicilin, oleosin and oil-body proteins *Brassica rapa* R-o-18 seed samples.

Protein name (identified in *Brassica rapa* R-o-18) by LC-MS/MS	Amino acid length	Molecular weight (Da)	% identity	% coverage	Sequences (5'-3') in FASTA format
Identified vicilins					
Bra014536	486	54,657.4 Da	100% with *B. napus* vicilin-like SSP At3g22640	40%	>Bra014536 MAINKLTITLFLLISLAVFHCLAFRVEVQE FEPPRQEGQEGPGGGSGEGWDEEATKNP YHFGQWSFKNFFQSKDGFVKMLPKFTKRSS TLFRGIENYRFLFQEMQPNTFLVPHHLD ADYVFLVVQGKGVIGFVTDTANESFQITKG DVVRVPSSVTHFFANTNGTVPLRLAKIA VPANVPGHFQVFFPAHSGFHQSYFNGFSKD VLTASFNIPEELLGRLIRGPQQEVGQGI IRRVSPEQIKELTEHEHATSPSNKHKDKKD KHKDKDRSTFGSPFNLLTQDAIYSNNFG RYHEAHPKRFSQLQDLDIAVGWVNMTQGSL FLPQYNSETTFVTFVENGCARYEMASPY TFQGEQQQPWFGPGQEEEVEEEMSGQVHKI VSRVCKGEVFILPAGHPFAILSQDENFV AVGFGIHASNSTRTFLAGQDNMLSNINTVA TRLSFGLGSKMAEKLFTSQNYSHFAPTT PSHQFPEKPKPSFQSVFNLVGF
Bra025745	464	52,074.5 Da	100% with *B. napus* vicilin-like SSP At2g28490	27%	>Bra025745 MEKNKRIFTFLLVIMFFHGVMMMRSIGYEG EEEQGGGGRERGGFMMKESRQVIKSEGG EMRVVISPRGRIIEKPMHIGFLTMEPKTLF VPQYLDSNLLIFIREATLGVICKDEFGE KRLKGGDIYWIPAGSAFYLLNTGRGQRLHV ICSIDPSQSLGFETFQPFYIGGGPSSVL AGFDPDTITSALNVSRPEVQQLMTSQVRGP IVHITEHAPTMWTDFLGLRGEEKHKHLK KLLEMKQGTSQEQEFNPWWSWKNIVSSILD VTGEKNRGSGSSKCEDSYNIYDLKNDFE NDYGWSKALDYDDYEPLRYSGVGVYLVNLT AGSMMAPHMNPTATEYGIVLSGSGEIQV VLPNGTSAMNMRVSPGDVFWIPRYFAFCQI ASRIAPFEFVGFTTSAYKNRPQFLVGSN SLLRSLNLTSLAMAFGVDEGTMKRFVEAQR EAVILPTASAAPPHEGEPERFGSDHIFT

Bra033857	576	65,332.1 Da	100% with *B. napus* vicilin-like SSP At4g36700	18%	>Bra033857 MIRFTVLSFFVVFVLLFACNESSAKTAKYD KSDESVENDDLAAVPSCCGFSSPLLIKK DQWKPIFANKFGQISTVQIGDGCGGMGPYK IHSITLEPNALMLPLLLHSDMVFFVDSG SGILNWVEAQATSTEIRLGDVYRLRPGTVF YLQSKPVDIFLGTKLKIYAIFSNSQECL HDPCFGAYSSVTDLLFGFDETILKSAFGVP EEIIGLMRNRTQPPLIVHDMLTTPSEAN TDTDTNTWPLQTRLLKLFSGDASADSVENK KVKKKKEKKEKKKKPKKATTFNVFESEP DFQSPNGQTITINRKDLKVLQGSMVGVSMV NLTQGSMMGPHWNPWACEISVVVRGSGM VRVLRNSISRSSSECKNMRFKVEKGDIFAV PRLHPMAQMSFLNDSLVFVGFTTSAKNN EPQFLAGKNSALWSLDREVLAASFNVSSFM IAGLLEAQKEAAVLGCPACAEGELEKLK EDEEKKESPPQQPPQPFQPQPPEEKPQQPP QPFQPQPPQGEPQKPPQGEPQGPEKPFQ PQPGQGEPQEPQASMETKMRDEERKREEEE AKKEEEERWKQEEKLWPTQPQWED
Bra003060	502	56,142.3 Da	98% with *B. napus* vicilin-like SSP At4g36700	3%	>Bra003060 MTKFTVLPLFVLLFLVLLCTKSWAKSEEFD ESSDEENDVAAVPSCCGFSSPLLIKKDQ WKPIFGTQFGQISTVQIGEGCGGMGPYKIH SITLEPNALLLPLLLHSDMVFFVESGSG ILNWVEAEPTSSEIRRGDVYRLRPGTVFYL QSKPIDIFLGTKLRVYAIFSNTEECLHD PCFGAYSSITDLLFGFDEAILQSAFGVPEE IIGLMTNRTQPPLIVHDMLSTPGEANTY TWQLQVQPRLLKLFAGYVSAAEKKKKEKKT KKAKTFNVFESEPDFQSPSGRTITINRK DLEVLSGSMVGVSMVNLTQASMMGPHWNPW ACEISIVLKGSGMVRVLRSSISSTSSSS SSSECKNMRFKVEEGDIFAVPRLHPMAQMS FINESLVFIGFTTSARNNEPQFLAGQRS ALRLLDQEVLAASLNVSSVMIEGLLGAQKD AVVLGCPYCAEGELEKLKVETEMKKRDD ERKREEEEAKKEEEERRKREEEEEEEKQWP PLPQQPPE
Bra022682	657	83,300.9 Da	100% with *B. napus* vicilin-like SSP At2g18540	3%	>Bra022682 MSKFTIIPLCLLTLFLCTNSFSDQNDGVPS SQSPLLVKRHQRTQLVATEFGEISAVHI GEEYTIQFITLEPNALLLPLLLHSDMVFFV HTGSGVLNWVDEEKERTLELKRGDVFRL RYGTVFYLHCNLERDEVPEKLRVYAIFDVG KCLSDQCLGAYSSIRDLLWGFDEKTLRS AFAVPKDVFGRLRDAVKPPLITHAMPKNRT QGSEEETWGSRLAKLFVRVEDSIVVDEK DMDALKGSSFGVYMVNLTKGSMMGPHWNPN ACEISIVLQGEGMIRVVNHPSYQSKNES ERFMVEDGDVFVVPQFYPMAQLSFVNSSFM FMGFSTSAKTNHPQFLVGQNSVLKIFNR DVLATSFNMRYATVERLLGAQKDGLLLECV SCAEVELSRLMREIEERRRREEEEIERR KREEEEAKRQEEERRRREEEEAERKKKAEE EARKREKEREREEEAAKRREEERRRREE EEAERKRKEEEEARKREEERKREEEAAKKR EEERRKREKEEEEARKREEAREREEEEA

					KKREEERRKREEEEAERKRRAEEEARERE EEAKKREEEKEAARRREEEREKEEEMAK RREEERQRKEREDVERKKREEEEERKRREE EAMRREEERKREEEAAKRAEEERRKREE EAEHKKRPPPQGPQPPIHH
Identified oleosins					
Bra019493	188	19,972.4 Da	100% identity with Bra019493 :0-188	44%	>Bra019493 PREDICTED: Brassica rapa oleosin S2-2 (LOC103854221), mRNA ; Similar to S2 Oleosin S2-2 (Brassica napus)::Bra019493:0-188 MANVDRRVNVDRTDKGLQLQPQYEDRVGYG YGYGGNTDYKSRGPSTNQIVALIAGVPIGG SLLALAGLTLAGSVIGFMLSIPLFLLFSPV IVPAALTIGLAVTGILASGLFGLTGLSSVS WVLNYIRGRSDTVPEQLDYAKRRMADAVGY AGQKGKEMGQYVQDKAHEAHDTSLTTETNG KARRAHIA
Bra000167	188	19,879.9 Da	100% identity with Bra000167	46%	>Bra000167 PREDICTED: Brassica oleracea var. oleracea oleosin S2-2 (LOC106316842), mRNA ; PREDICTED: Brassica rapa oleosin S2-2 (LOC103837001), mRNA ; Similar to S2 Oleosin S2-2 (Brassica napus)::Bra000167:0-188 MATVERRVQVDPTDKRIHLQPQYEGDVGYG YGYGGRADYKSSGPSSNQIVALIVGVPVGG SLLALAGLTLAGSVIGLMLSVPLFLLFSPV IVPAAITIGLAVTAILASGLFGLTGLSSVS WVLNYLRGTSDTVPEQLDYAKRRMADAVGY AGQKGKEMGQYVQDKAHEAHDTSLTTETTE PGKTRRHT
A0A078GHK4	180	19,515.6 Da	100% identity with A0A078GHK4_BRANA	42%	>tr|A0A078GHK4|A0A078GHK4_BRANA Oleosin OS=Brassica napus OX=3708 GN=BnaA08g14540D PE=3 SV=1 MADTARTHHDITSRDQYPILGRDRDQYPYG RSDYQTSGQDYSKTRQIAKAATAVTAGGSL LVLSSLTLVGTVIALTVATPLLVIFSPILV PALITVALLITGFLSSGGFGIAAITVFSWI YKYATGEHPQGSDKLDSARMKLGTKAQDIK DRAQYYGQQHTGGEHDRDRTRGTHHTTTTT
M4E9X1	220	23,024.7 Da	100% identity with BRARP Oleosin	50%	>tr|M4E9X1|M4E9X1_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1 MADTHRVDRTDRHLQFQSPYEGGRVNIQFE GAGGGYGQSGYGGGGGYGQSGYGGGGYKSM MPESGPSSTQVISFLVGVPLVGSLLAIAGL LLAGSVIGLMISIPLFLLFSPVIVPAAITI GLATTGFLTSGMFGLTGLSSISWVMNYLRR TRGSVPDQLEYAKRRMADAVGYAGQKGKEV GQFVQDKAHDAKQYDISKPHDTTTTTTTTT KGLETRTAAA
A0A397KW15	183	20,0002.4 Da	100% identity with A0A397K	36%	>tr|A0A397KW15|A0A397KW15_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRAA03T14647Z PE=3 SV=1

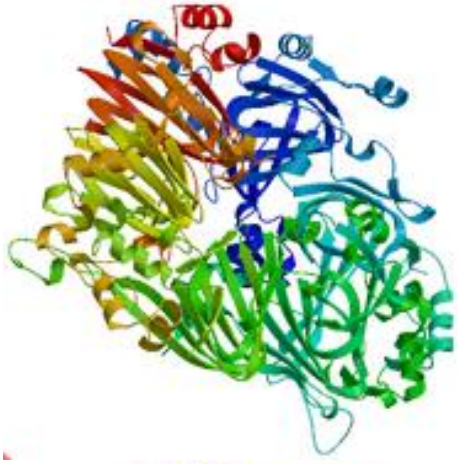
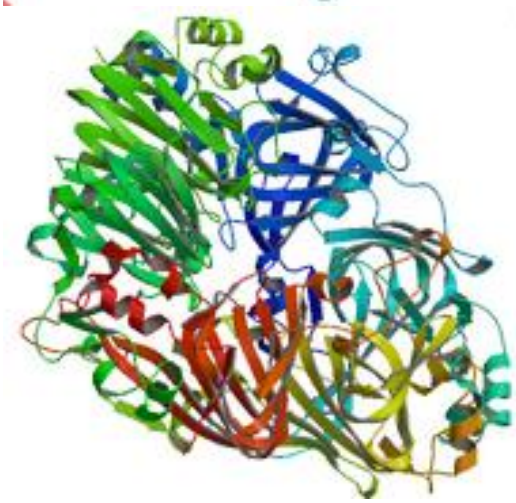
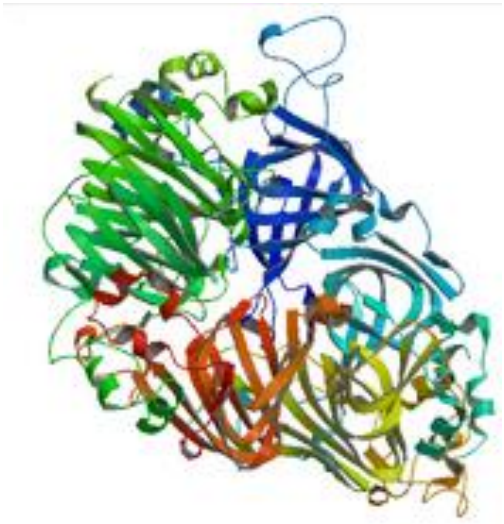
			W15_BRACM Oleosin		MTDTARTHHDITTRDQYPMMGRDRDQYAII GRDQYQGYGQDYSKSRQIAKAATAVTAGGS LLVLSSLTLVGTVIALIVATPLLVIFSPIL VPALITVALLITGFLSSGGFGIAAITVFSW IYKYATGEHPKGSDKLDSARMKLGSKAQDM KDRAHYYGQQHTGGEHVNTDYRNTDRDRTR GTT
A0A397ZZI8	193	20,790.6 Da	100% identity with A0A397ZZI8_BRACM Oleosin	24%	>tr|A0A397ZZI8|A0A397ZZI8_BRACM Oleosin OS=Brassica campestris OX=3711 GN=BRARA_C02941 PE=3 SV=1 MADVRTHAHQVQVHPLRQQEGGIKVVYPQS GPSSTQVLAVIAGVPVGGTLLTLAGLTLAG SVIGLMLAFPLFLIFSPVIVPAAFVIGLAM TGFMASGAIGLTGLSSMSWVLNHIRRVRER MPDELEEAKQRLADMAEYVGQRTKDAGQTI EEKAHDVRESKTYDVRDRDTKGHTATGGDR DTKTTREVRVATT
M4DBK6	195	21,511.9 Da	100% identity with M4DBK6_BRARP Oleosin	44%	>tr|M4DBK6|M4DBK6_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1 MTDTARTHHDITSRDQYPRDRDQYSMIGRD RDKYSMIGRDRDQYNMYGRDYSKSRQIAKA VTAVTAGGSLLVLSSLTLVGTVIALTVATP LLVIFSPILVPALITVALLITGFLSSGGFG IAAITVFSWIYKYATGEHPQGSDKLDSARM KLGGKVQDMKDRAQYYGQQHTGGYGQQQTG GEHDRDRTRGTQHTT
M4EI43	211	22,095.6 Da	100% identity with M4EI43_BRARP Oleosin	35%	>tr|M4EI43|M4EI43_BRARP Oleosin OS=Brassica rapa subsp. pekinensis OX=51351 PE=3 SV=1 MADTHRVDRTDRHLQFQSPYEGGRVNIQYE GGGGAGGYGGGRGGGYGAGGYKSMMPERGP SSTQVLSFLVGVPIVGSLLAIAGLLLAGSV IGLLISIPLFLLFSPVIVPAALTIGLAATG FLASGMFGLTGLSSVSWVMNYLRGTRKSSV PEQLEYAKKRMADAVGYAGQKGKEMGQHVQ NKAQEAKQYDISKTHDTTTKGHETTQRTAA A
Bra035756	205	21734.5 Da	100% identity with Bra035756	24%	>Bra035756 PREDICTED: Brassica napus oleosin 14.9 kDa (LOC106375666), mRNA ; PREDICTED: Brassica napus oleosin 14.9 kDa (LOC106402530), mRNA ; PREDICTED: Brassica rapa oleosin 14.9 kDa (LOC103864856), mRNA ; Similar to OL3 Oleosin 14.9 kDa (Arabidopsis thaliana)::Bra035756:0-205 MKTFSTRGTDKQRGLTSFLPISLIHISSLL TPNILLSNLPLLSSSIFVSERSQQESMANQ TRTHQDVIVRDSRSTLDRDHPKTGAQMVKV ATGVAAGGSLLVLSGLTLAGTVIALAVATP LLIIFSPVLVPAVITVVLIITGFLASGGFG IAAITAFSWLYRHMTGSGSDQKIESARMKV GSRGYDTKSGQHNIGVHQQHQQAAS

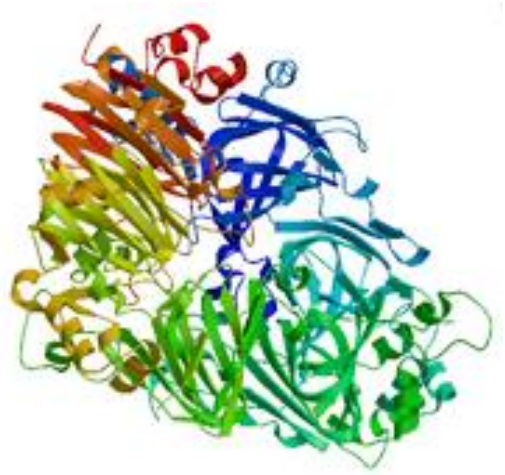
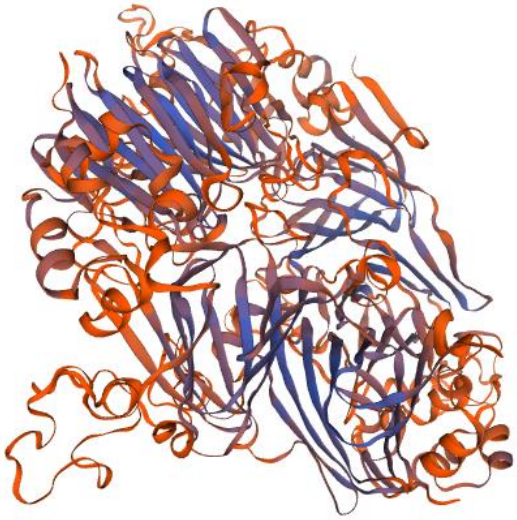
Bra032113	166	18,301.4 Da	100% identity with Bra032113	19%	>Bra032113 Brassica oleracea HDEM genome, scaffold: C8 ; Brassica rapa genome, scaffold: A08 ; PREDICTED: Brassica napus major oleosin NAP-II-like (LOC106419670), mRNA ; PREDICTED: Brassica napus major oleosin NAP-II-like (LOC111208674), mRNA ; PREDICTED: Brassica oleracea var. oleracea major oleosin NAP-II-like (LOC106319905), mRNA ; PREDICTED: Brassica rapa oleosin 16 kDa-like (LOC103832967), mRNA ; Protein of unknown function::Bra032113:0-166 MADRTSPSHIQQRPYGSPIAPPRGNNINHP IASFLRQLQSQSPEHSRQRFGLLAFFISGG ILLLLTGITVTAFVLGFIAFLPIIIISSPI WIPLFLLVTGFLSVAGFLFSTAIVMSWMYR YFKGMHPVGSEQVDYARSRIYDTAAHVKDY AGGYFHGKLKDAAPGA
Identified oil-body proteins					
Bra036039	264	30,002.6 Da	100% identity with Bra036039	35%	>Bra036039 PREDICTED: Brassica napus oil body-associated protein 1A (BNAA10G03690D), mRNA ; PREDICTED: Brassica napus oil body-associated protein 1A (BNAC05G03600D), mRNA ; PREDICTED: Brassica oleracea var. oleracea uncharacterised LOC106294119 (LOC106294119), mRNA ; PREDICTED: Brassica rapa oil body-associated protein 1A (LOC103844119), mRNA ; Protein of unknown function::Bra036039:0-264 MFFFTIRLNNSRDREGSRESICAMEKAVHL STKAGPEVPGEPTKMGTSMVDSAAAAVQSF TPINQIHQHLCAFHFYAYDMTRQVEAHHFC GHINEDMRQCLIYDGPDANARLIGLEYIVS EKLFMTLPDDEKKLWHTHEWEVKGGFLFMP GVPEPIQRQDLEIVAKTYGKVYHFWQVDLG HELPIGLPNIMMAVTRDGQLYPEMVKETEK KFGISIDKERESRAYMTGPDHGIHPLANGG GKGLKLEMREVDIKPVESVPRVFV
Bra036099	562	27,737.6 Da	100% identity with Bra036099	56%	>Bra036099 PREDICTED: Brassica napus putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1D (LOC106371146), mRNA ; Similar to FAB1D Putative 1-phosphatidylinositol-3-phosphate 5-kinase FAB1D (Arabidopsis thaliana)::Bra036099:0-562 MEEAAERLRQFLLTSANSLGIKDDWIIPCA DLLEIVAKERDGLHNYIKFKCVATSDSPSL

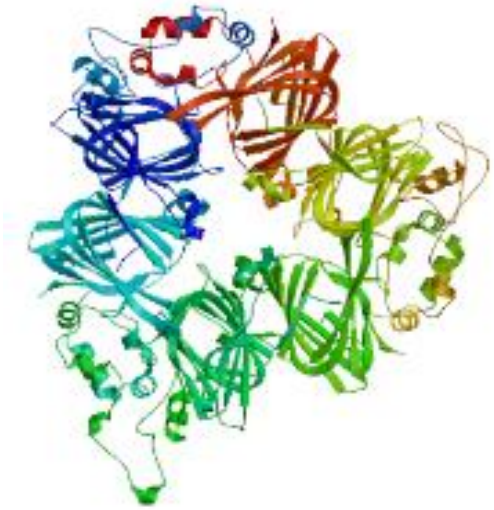
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LGYSCTALRCEKTIESLNDPINEKPLMFLD
GCGSLTILLKGSSTAELKLMKRMLKTGYNQ
FRNELLSSDYFLVALPPSKIIPWEMDGGQD
EVVTIREEEVSSYIAYSLQQVHDESSESRP
KSSVFCQHRDSFHELRSKCNMTESQYISSL
SRCDTWEAKGGKSGALFAKSRDTRLIIKEI
NQAEFESFAKFGPMYFEYMKEANKTFLTKI
YGVYKVTLGQAKFLMVMENLNFDRRIAMQY
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RLHLNPYLKQDLQTVIRNDTAFLSGINVMD
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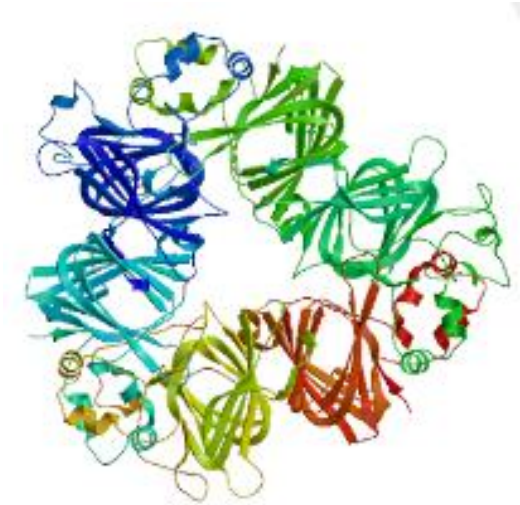
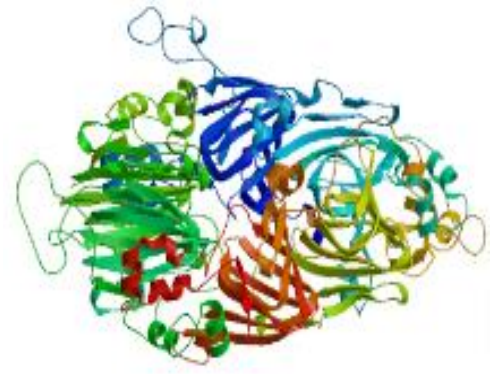
List of protein sequences of identified vicilin, oleosin and oil-body proteins in *Brassica rapa* R-o-18 seed samples using liquid chromatography–mass spectrometry (LC-MS/MS) analysis.

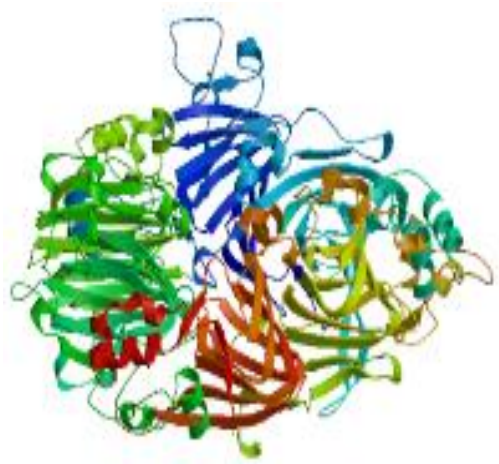
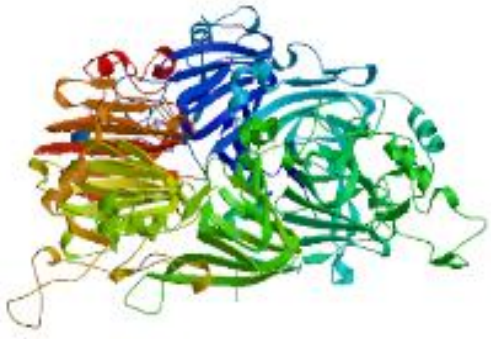
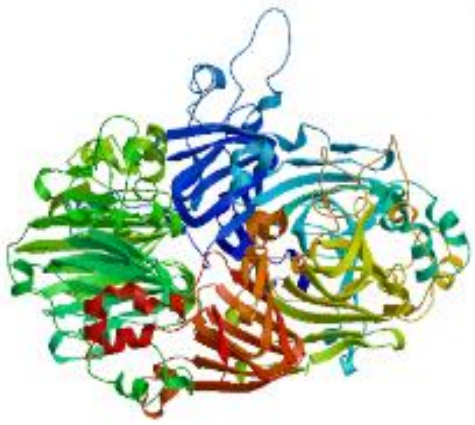
S6 Table. Three dimensional models of vicilin candidate proteins.

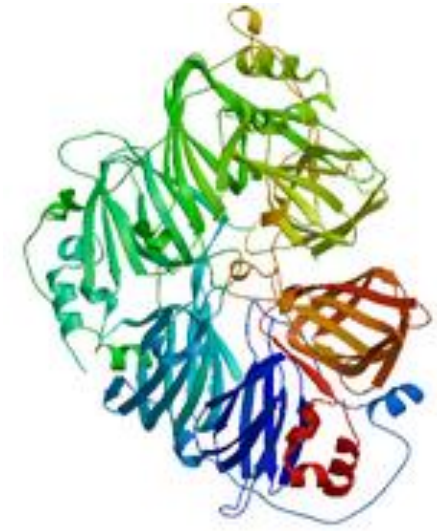
3D model for *Brassica rapa* R-o-18	Template	Seqence Identity	GMQE	QMEAN	Oligo-State
Brassica rapa R-o-18 vicilin-1					
	3smh.1.A (Allergen Ara h 1, clone P41B)	34.51%	0.57	-1.57	Homo-trimer (matching prediction)
	2ea7.1.A (Adzuki Bean 7S globulin-1)	34.55%	0.58	-2.18	Homo-trimer (matching prediction)
	4lej.1 (Korean pine vicilin)	30.38%	0.50	-2.35	Homo-trimer (matching prediction)

	5e1r.1.A (pecan 7S vicilin)	37.32%	0.56	-2.13	Homo-trimer (matching prediction)
Predicted vicilin-2, *Brassica rapa* R-o-18					
	4lej.1.A (Korean pine vicilin)	24.59%	0.51	-2.96	Homo-trimer (matching prediction)
	2ea7.1.A (Adzuki Bean 7S globulin-1)	20.22%	0.51	-3.99	Homo-trimer (matching prediction)

	3smh.1.A (Allergen Ara h 1, clone P41B)	21.22%	0.49	-4.49	Homo-trimer (matching prediction)
	5e1r.1.A (pecan 7S vicilin)	22.65%	0.49	-4.46	Homo-trimer (matching prediction)
Predicted vicilin-3, *Brassica rapa* R-o-18					
	3smh.1.A (Allergen Ara h 1, clone P41B)	21.19%	0.41	-3.52	Homo-trimer (matching prediction)

	4lej.1.A (Korean pine vicilin)	23.37%	0.40	-4.68	Homo-trimer (matching prediction)
	5e1r.1.A (pecan 7S vicilin)	21.62%	0.40	-4.97	Homo-trimer (matching prediction)
Predicted vicilin-4, *Brassica rapa* R-o-18					
	4lej.1.A (Korean pine vicilin)	22.99%	0.46	-3.88	Homo-trimer (matching prediction)

	2ea7.1.A (Adzuki Bean 7S globulin-1)	22.04%	0.48	-3.64	Homo-trimer (matching prediction)
	3smh.1.A (Allergen Ara h 1, clone P41B)	25.54%	0.42	-4.44	Homo-trimer (matching prediction)
	4lej.1 (Korean pine vicilin)	27.65%	0.41	-5.17	Homo-trimer (matching prediction)

Predicted vicilin-5, *Brassica rapa* R-o-18					
	3smh.1.A (Allergen Ara h 1, clone P41B)	29.11%	0.24	-3.78	Homo-trimer (matching prediction)
	2ea7.1.A (Adzuki Bean 7S globulin-1)	27.10%	0.26	-4.96	Homo-trimer (matching prediction)
	3s7i.1 (Major Peanut Allergen Ara h 1)	29.45%	0.23	-4.47	Homo-trimer (matching prediction)

	4lej.1 (Korean pine vicilin)	30.45%	0.26	-5.08	Homo-trimer (matching prediction)

Three dimensional models of vicilin candidate proteins identified in the seed samples using liquid chromatography–mass spectrometry (LC/MS) analysis. Analysis found in at least 3 out of 4 biological replicates with at least 2 unique peptides and a p value of < 0.05 using *Brassica rapa* R-o-18 database. The candidate proteins were identified according to the method described in (Rahman et al., 2020a). The three dimensional models are cyphered using the automated SWISS-MODEL server homology modelling pipeline. The GMQE (Global Model Quality Estimation) was based on the QSQE (Quaternary Structure Quality Estimation) while local estimates of the model quality based on the QMEAN (Qualitative Model Energy Analysis) scoring function, both were used for the model rankings. The sequence identity represents target–template sequence identity.

S7 Table. List of protein sequences *Arabidopsis thaliana* oleosins representing four different lineages.

Lineages	Representing *Arabidopsis thaliana* oleosin	Molecular weight	Sequences
U	AtOLE5	169	>tr|Q9M9A1|Q9M9A1_ARATH F27J15.22 OS=Arabidopsis thaliana OX=3702 GN=At1g48990 PE=1 SV=1 MADRTNPSSHTQQRPIYNSTTVPRSNTTTNHPLSSLLRQLLQSQSPNHSGQLFGFLAFFI SGGILLLLTGITVTAFVLGFIAFLPLIIISSPIWIPLFLIVTGFLSLAGLILATGAVVSW LYRYFKGMHPLRSDQVDYARSRIHDTAAHVKDYAGGYFHGTLKDAAPGA
SL	AtOLE4	191	>sp|Q42431|OLEO4_ARATH Oleosin 20.3 kDa OS=Arabidopsis thaliana OX=3702 GN=OL2 PE=2 SV=1 MANVDRDRRVHVDRTDKRVHQPNYEDDVGFGGYGGYGAGSDYKSRGPSTNQILALIAGVP IGGTLLTLAGLTLAGSVIGLLVSIPLFLLFSPVIVPAALTIGLAVTGILASGLFGLTGLS SVSWVLNYLRGTSDTVPEQLDYAKRRMADAVGYAGMKGKEMGQYVQDKAHEARETEFMTE THEPGKARRGS
SH	AtOLEO6	149	>tr|Q494N8|Q494N8_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=At2g25890 PE=1 SV=1 MADHQQHQQQQQPIMRSLHESSPSTRQIVRFVTAATIGLSLLVLSGLTLTGTVIGLIVAT PLMVLFSPVLVPAVITIGLLTMGFLFSGGCGVAAATALTWIYKYVTGKHPMGADKVDYAR MRIAEKAKELGHYTHSQPQQTHQTTTTTH
T	AtOLE13	106	>tr|Q42574|Q42574_ARATH Oleosin OS=Arabidopsis thaliana OX=3702 GN=ATGRP19 PE=1 SV=1 MFEIIQAVFSAGVALALLTFAGITLGGSVVACIISTPLFVIFSPVLVPATIATTLLASGF TASGSFGATAFTILSWLYKKRTGRDLPKIPGLTPPAPASNPAGSGV

Adapted from (Chen et al., 2019).

S8 Table. Status of *B. rapa* R-o-18 putative napins corresponding to the identified proteins.

Sl	*Brassica rapa*	Protein name	Length	Status of putative napins corresponding to the identified proteins using LC-MS/MS
R-o-18				
1	Candidate napin 1	Bra041165	178	Identified in LC-MS/MS data. BraA03000889: 100% cov and 87.0% pid, BraA01001883: 100% cov and 93.9% pid.
2	Candidate napin 2	Bra022319	166	Bra041165: 88.2 % cov and 51.3% pid, BraA03000889: 94.6 % cov and 47.7% pid, BraA01001883: 94.0 % cov and 94.0% pid.
3	Candidate napin 3	Bra022317	135	Bra041165: 74.2 % cov and 65.7% pid, BraA03000889: 98.5 % cov and 49.7% pid, BraA01001883: 97.0 % cov and 50.0% pid.
4	Candidate napin 4	Bra001100	121	Bra041165: 68.0 % cov and 62.3% pid, BraA03000889: 100 % cov and 41.3% pid, BraA01001883: 99.2 % cov and 42.5% pid.
5	Candidate napin 5	Bra029497	546	Bra041165: 99.4 % cov and 29.6% pid, BraA03000889: 98.4 % cov and 30.3% pid, BraA01001883: 99.4 % cov and 30.9% pid.
Chiifu				
6	Candidate napin 1	BraA03005709	173	Bra041165: 95.5 % cov and 71.3% pid, BraA03000889: 92.9 % cov and 67.7% pid, BraA01001883: 94.4 % cov and 69.4% pid.
7	Candidate napin 2	BraA01002186	179	Bra041165: 100 % cov and 99.4% pid, indicating identified in LC-MS/MS data. BraA03000889: 97.3 % cov and 89.1% pid, BraA01001883: 99.4 % cov and 94.4% pid.
8	Candidate napin 3	BraA01001885	180	Bra041165: 100 % cov and 94.4% pid, BraA03000889: 97.8 % cov and 92.9% pid, BraA01001883: 100 % cov and 96.7% pid indicating identified in LC-MS/MS data.
9	Candidate napin 4	BraA01001883	180	Identified in LC-MS/MS data, Bra041165: 100 % cov and 93.9% pid, BraA03000889: 97.8 % cov and 92.9% pid.
10	Candidate napin 5	BraA01001886	179	Bra041165: 99.4 % cov and 93.3% pid, BraA03000889: 97.3 % cov and 92.9% pid, BraA01001883: 99.4 % cov and 95.6% pid indicating identified in LC-MS/MS data.
11	Candidate napin 6	BraA01001887	182	Bra041165: 99.4 % cov and 90.7% pid, BraA03000889: 98.4 % cov and 92.4% pid, BraA01001883: 99.4% cov and 94.5% pid.
12	Candidate napin 7	BraA03005713	158	Bra041165: 88.2 % cov and 53.6% pid, BraA03000889: 85.3 % cov and 50.0% pid, BraA01001883: 87.2 % cov and 52.5% pid.
13	Candidate napin 8	BraA03000889	184	Identified in LC-MS/MS data. Bra041165: 100% cov and 87.0% pid, BraA01001883: 100 % cov and 92.4% pid.

14	Candidate napin 9	BraA08002165	171	Bra041165: 94.9 % cov and 64.4% pid, BraA03000889: 92.4 % cov and 57.8% pid, BraA01001883: 93.9 % cov and 62.1% pid.
15	Candidate napin 10	BraA03000890	76	Bra041165: 42.7 % cov and 94.7% pid, BraA03000889:41.3 % cov and 98.7% pid, BraA01001883: 42.2 % cov and 94.7% pid.
16	Candidate napin 11	BraA01001889	325	Bra041165: 99.4 % cov and 48.2% pid, BraA03000889: 98.9 % cov and 49.2% pid, BraA01001883: 99.4 % cov and 50.3% pid.

Status of *B. rapa* putative napins characterised in (Rahman, Baten, et al., 2020) corresponding to the identified proteins using LC-MS/MS analysis in *B. rapa* R-o-18 seeds. Bra041165 (length 178), BraA03000889 (length 184) and BraA01001883 (length 180) are the identified napin in *B. rapa* R-o-18 seed using LC-MS/MS analysis. Cov=coverage, pid=percent identity.The coverage and percent identity among the putative napins characterised in (Rahman, Baten, et al., 2020) and the napin sequences identified in *B. rapa* R-o-18 seeds using LC-MS/MS analysis (S4 Table) were determined using Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo/) (Madeira et al., 2019) and MView (Brown et al., 1998) tools. The proteins that had complete match in LC-MS/MS analysis are marked as “Identified in LC-MS/MS data” and those which had over 95.0%pid are referred as “indicating identified in LC-MS/MS data”.

S9 Table. Sequence analysis outcome of the identified 7S globulin-like vicilins.

Amino acid	Bra014536	Bra025745	Bra033857	Bra003060	Bra022682	Side Chain Acidity / Basicity	% count
A=Ala	26	22	32	27	43	Neutral	5.584512
C=Cys	3	4	10	10	8	Neutral	1.303053
D=Asp	16	18	26	18	21	Acidic	3.685778
E=Glu	33	35	51	52	143	Acidic	11.69025
F=Phe	47	28	32	26	25	Neutral	5.882353
G=Gly	39	47	35	32	25	Neutral	6.626955
H=His	19	10	6	6	12	Basic (weakly)	1.973194
I=Ile	19	29	22	25	17	Neutral	4.169769
K=Lys	26	21	48	33	53	Basic (weakly)	6.738645
L=Leu	33	36	46	51	45	Basic	7.855547
M=Met	8	20	17	15	16	Neutral	2.829486
N=Asn	25	17	22	15	16	Neutral	3.536858
P=Pro	29	25	50	29	22	Neutral	5.770663
Q=Gln	31	16	37	20	18	Neutral	4.54207
R=Arg	18	25	19	22	92	Basic (strong)	6.552494
S=Ser	36	37	46	48	32	Neutral	7.408786
T=Thr	29	24	27	25	19	Neutral	4.61653
V=Val	35	28	35	33	37	Neutral	6.254654
W=Trp	4	7	9	8	4	Neutral	1.191363
Y=Tyr	10	15	6	8	9	Neutral	1.787044
Residue	486	464	576	502	657	-	100
Molecular weight	54657.59	51927.33	64442.47	56141.32	78666.16	-	-
Isoelectric point	6.9	6.19	5.2668	4.8806	5.3778	-	-

Amino acid composition and isoelectric point of 7S globulin type vicilins were calculated using (https://www.ebi.ac.uk/Tools/seqstats/emboss_pepstats/, 30/08/2020). % amino acid count is calculated from total number of amino acids of five vicilins. Side chain acidity / basicity is from (http://www.thinkpeptides.com/aminoacidproperties.html, 30/08/2020).