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(54) Title: METHOD OF PROTEIN EXTRACTION FROM CANNABIS PLANT MATERIAL

(57) Abrégé/Abstract:

The present invention relates generally to a method for extracting cannabis-derived proteins from cannabis plant material, including the preparation of samples of extracted cannabis-derived proteins for proteomic analysis and methods for analysing a cannabis plant proteome.

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(54) Title: METHOD OF PROTEIN EXTRACTION FROM CANNABIS PLANT MATERIAL

(57) Abstract: The present invention relates generally to a method for extracting cannabis-derived proteins from cannabis plant material, including the preparation of samples of extracted cannabis-derived proteins for proteomic analysis and methods for analysing a cannabis plant proteome.

**WO 2020/124128 A1**

- 1 -

METHOD OF PROTEIN EXTRACTION FROM CANNABIS PLANT MATERIAL

[0001] The present application claims priority from both Australian Provisional Patent Application 2018904869 filed 20 December 2018 and Australian Provisional Patent Application 2019902643 filed 25 July 2019, the disclosure of which is hereby expressly incorporated herein by reference in its entirety.

FIELD

[0002] The present invention relates generally to a method for extracting cannabis-derived proteins from cannabis plant material, including the preparation of samples of extracted cannabis-derived proteins for proteomic analysis and methods for analysing a cannabis plant proteome.

BACKGROUND

[0003] Cannabis is an herbaceous flowering plant of the *Cannabis* genus (*Rosale*) that has been used for its fibre and medicinal properties for thousands of years. The medicinal qualities of cannabis have been recognised since at least 2800 BC, with use of cannabis featuring in ancient Chinese and Indian medical texts. Although use of cannabis for medicinal purposes has been known for centuries, research into the pharmacological properties of the plant has been limited due to its illegal status in most jurisdictions.

[0004] The chemistry of cannabis is varied. It is estimated that cannabis plants produce more than 400 different molecules, including phytocannabinoids, terpenes and phenolics. Cannabinoids, such as Δ -9-tetrahydrocannabinol (THC) and cannabidiol (CBD) are the most well-known and researched cannabinoids. CBD and THC are naturally present in their acidic forms, Δ -9-tetrahydrocannabinolic acid (THCA) and cannabidiolic acid (CBDA), *in planta* which are alternative products of a shared precursor, cannabigerolic acid (CBGA). Since different cannabinoids are likely to have different therapeutic potential, it is important to be able to identify and extract different cannabinoids that are suitable for medicinal use.

- 2 -

[0005] Quantitative proteomic techniques allow for the quantitation of abundance, form, location, or activity of proteins that are involved in developmental changes or responses to alterations in environmental conditions. Initially, proteomic techniques included traditional two-dimensional (2D) gel electrophoresis and protein staining. While these techniques have been, and continue to be, informative about biological systems, there are a number of problems with sensitivity, throughput and reproducibility which limits their application for comparative proteomic analysis. Advancements in platform technology have allowed mass spectroscopy (MS) to develop into the primary detection method used in proteomics, which has greatly expanded depth and improved reliability of proteomic analysis when compared to 2D techniques.

[0006] The ability for MS-based techniques to accurately resolve the diversity and complexity of cellular proteomes is associated with the development of different protocols to support analysis by MS. For the most part, these protocols have been developed to improve the depth of proteome coverage through the optimisation of conditions that are favourable for proteolytic digestion and sample recovery. The careful selection of solutions and enrichment methods during sample preparation is essential to ensure compatibility with downstream workflows and detection platforms. In the context of cannabis, this also includes the sampling of appropriate plant material at different stages of plant development.

[0007] Previous studies of the cannabis proteome have largely focused on the analysis of non-reproductive organs from immature cannabis plants such as roots and hypocotyls (Bona *et al.* 2007, *Proteomics* 7:1121-30; Behr *et al.* 2018, *BMC Plant Biol.* 18:1) or processed seeds from hemp (Aiello *et al.* 2016, *J. Proteomics* 147:187-96). Furthermore, these previous studies did not employ any standardised sample preparation method to maximise the recovery of cannabis-derived proteins for proteomic analysis. This is reflected in the types of analysis methods employed. For example, in the study conducted by Bona *et al.*, protein extracts were then analysed by two-dimensional electrophoresis (2-DE), while Aiello *et al.* used one-dimensional polyacrylamide gel electrophoresis (1-D PAGE).

[0008] There remains, therefore, an urgent need for improved methods for extracting cannabis-derived proteins from cannabis plant material in a manner that optimises the

- 3 -

recovery of cannabis-derived proteins for proteomic analysis.

SUMMARY

[0009] In an aspect disclosed herein, there is provided a method of extracting cannabis-derived proteins from cannabis plant material, the method comprising:

- (a) suspending cannabis plant material in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution; and
- (b) separating the solution comprising the cannabis-derived proteins from residual plant material.

[00010] In another aspect disclosed herein, there is provided a method of extracting cannabis-derived proteins from cannabis plant material, the method comprising:

- (a) pre-treating the cannabis plant material with an organic solvent to precipitate the cannabis-derived proteins;
- (b) suspending the precipitated cannabis-derived proteins of (a) in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution; and
- (c) separating the solution comprising the cannabis-derived proteins from residual plant material.

[0010] In another aspect disclosed herein, there is provided a method of preparing a sample of cannabis-derived proteins from cannabis plant material for proteomic analysis, the method comprising:

- (a) pre-treating the cannabis plant material with an organic solvent to precipitate the cannabis-derived proteins;
- (b) suspending the precipitated cannabis-derived proteins of (a) in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution;
- (c) separating the solution comprising the cannabis-derived proteins from residual plant material; and
- (d) digesting the solution of (c) with a protease.

- 4 -

[0011] In another aspect disclosed herein, there is provided a method of preparing a sample of cannabis-derived proteins from cannabis plant material for proteomic analysis, the method comprising:

- (a) pre-treating the cannabis plant material with an organic solvent to precipitate the cannabis-derived proteins;
- (b) suspending the precipitated cannabis-derived proteins of (a) in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution; and
- (c) separating the solution comprising the cannabis-derived proteins from residual plant material.

[0012] In an embodiment, the charged chaotropic acid is guanidine hydrochloride.

[0013] The present disclosure also extends to methods of analysing a cannabis plant proteome, the methods comprising preparing a sample of cannabis-derived proteins in accordance with the methods disclosed herein; and subjecting the sample to proteomic analysis.

BRIEF DESCRIPTION OF THE DRAWINGS

[0014] **Figure 1** is a graphical representation of intact proteins extracted using urea-or guanidine-HCl-based extraction methods, data was compared by Principal Component Analysis (PCA) of PC1 (60.7% variance; x-axis) against PC2 (32.9% variance; y-axis) using top-down proteomics data from 571 proteins.

[0015] **Figure 2** is a graphical representation of peptides extracted using urea-or guanidine-HCl-based extraction methods, data was compared by PCA of PC1 (65.2% variance; x-axis) against PC2 (11.6% variance; y-axis) using bottom-up proteomics data from 43,972 proteomic clusters.

[0016] **Figure 3** is a graphical representation of the comparison of the number of tryptic peptides identified from (A) trichomes and apical buds, extraction methods 1 and 2 (AB1, AB2, T1 and T2); (B), apical buds, extraction methods 1-6 (AB1-AB6); and (C) AB1-AB6 and T1-T2.

- 5 -

[0017] **Figure 4** is a graphical representation of a pathway analysis of cannabis proteins identified from (A) apical buds; and (B) trichomes.

[0018] **Figure 5** is a graphical representation of the distribution of UniprotKB entries from *C. sativa* entries (y-axis) from 1986 to 2018 (x-axis).

[0019] **Figure 6** shows the impact of extraction methods on enzymes involved in cannabinoid biosynthesis: (A) The cannabinoid biosynthesis pathway; (B) Two-dimensional hierarchical clustering of enzymes involved in cannabinoid synthesis. Columns represent extraction method per tissue types (AB, apical bud; T, trichomes), rows represent the peptides identified from enzymes of interest. Peptides from the same enzymes bear the same shade of grey.

[0020] **Figure 7** is a graphical representation of FTMS and FTMS/MS spectra from infused myoglobin. (A) Fragmentation of all ions by SID; (B) Fragmentation of ion 942.68 m/z ($z=+18$) by ETD, CID and HCD; (C) Fragmentation of ion 1211.79 m/z ($z=+14$) by ETD, CID and HCD.

[0021] **Figure 8** shows the matching ions achieved for myoglobin using Prosight Lite. (A-C) A graphical representation of the number of ions (y-axis) against myoglobin amino acid position (x-axis) for every MS/MS parameter tested (A) summed across all five charge states listed in Table 5; (B) summed by MS/MS mode along myoglobin amino acid sequence; (C) summed globally across all the data obtained for myoglobin along its amino acid sequence; (D) A schematic representation of global amino acid sequence coverage when all MS/MS data is considered; and (E) a graphical representation of sequence coverage achieved for each of the five myoglobin charge states.

[0022] **Figure 9** shows excerpts of results for β -lactoglobulin (β -LG), α -S1-casein (α -S1-CN), and bovine serum albumin (BSA). (A) Graphical representations of examples of FTMS and FTMS/MS spectra using SID, ETD, CID and HCD; and (B) global AA sequence coverage when all MS/MS data is considered.

[0023] **Figure 10** is a graphical representation of the relationship between the observed mass (kD; left y-axis) and coverage (%; right y-axis) of the protein standards (x-axis) analysed and their sequencing results by top-down proteomics.

[0024] **Figure 11** shows the Mascot search results of protein standards MS/MS peak

- 6 -

lists using (A) the homemade database and (B) Swissprot database.

[0025] **Figure 12** shows the profiles of medicinal cannabis protein samples. (A) Graphical representations of total ion chromatograms (TIC) representing elution time (min; x-axis) and signal intensity (y-axis) for each biological replicate (buds 1 to 3), $n = 2$; (B) Graphical representations of LC-MS pattern representing elution time (min; y-axis) and mass range (500-2000 m/z; x-axis) of each biological replicate (buds 1 to 3), $n = 1$; (C) Graphical representations of deconvoluted LC-MS map representing elution time (min; y-axis) and mass range (3-30 kDa; x-axis) of each biological replicate (buds 1 to 3), $n = 1$; (D) Graphical representations of zoom-in the area boxed in (C) representing elution time (15-45 min; y-axis) and mass range (9-11.5 kDa; x-axis) corresponding to abundant proteins; and (E) Graphical representations of triplicated LC-MS/MS patterns from biological replicate bud 1; dots represents MS/MS events.

[0026] **Figure 13** is a graphical representation of the distribution of cannabis proteins according to their accurate masses (Da; y-axis) and occurrence (x-axis).

[0027] **Figure 14** shows multivariate statistical analyses using LC-MS data from cannabis protein samples using (A) PCA; and (B) Hierarchical Clustering Analysis (HCA).

[0028] **Figure 15** shows the statistics on parent ions from cannabis proteins analysed by LC-MS/MS. (A) A graphical representation on the distribution of deconvoluted mass (Da; y-axis) according to their charge state (z ; x-axis); (B) A graphical representation of the distribution of deconvoluted masses (Da; y-axis) according to their base peak intensity (x-axis); and (C) A graphical representation of the distribution of deconvoluted masses (Da; y-axis) according to their elution times (min; x-axis).

[0029] **Figure 16** shows the top-down sequencing results from Mascot for *C. sativa* Cytochrome b559 subunit alpha (A0A0C5ARS8). (A) Protein view; and (B) Peptide view.

[0030] **Figure 17** shows the top-down sequencing summary for *C. sativa* Photosystem I iron-sulphur centre (PS I Fe-S centre, accession A0A0C5AS17). (A) A graphical representation of FTMS spectra showing relative abundance (y-axis) and mass (m/z; x-axis) at 30.8 min, lightning bolts depicts the two most abundant charge states chosen for MS/MS fragmentation; (B) Graphical representations of FTMS/MS spectra showing relative abundance (y-axis) and mass (m/z; x-axis) for “low”, “mid” and “high” charge

- 7 -

states using each of the three MS/MS methods; spectra in grey represent the energy level for a particular MS/MS mode that yields the best sequencing information; and (C) AA sequence coverage for each of the charge state and then combined.

[0031] **Figure 18** shows the experimental design for a multiple protease strategy to optimise shotgun proteomics.

[0032] **Figure 19** shows the LC-MS patterns of BSA. Graphical representations of elution time (min; y-axis) and mass (m/z; x-axis) for BSA digested with various proteases on their own or in combination. A graphical representation of the number of MS peaks (y-axis) observed using the various proteases on their own or in combination (x-axis; in triplicate) is provided in the bottom right-hand panel.

[0033] **Figure 20** is a graphical representation of MS peak statistics from BSA samples. Percentage of MS peaks that underwent MS/MS fragmentation (light grey bars), MS/MS spectra that were annotated in Mascot (black bars) and MS peaks that led to an identification in SEQUEST (dark grey bars) (%; left-hand y-axis) are shown relative to the protease digestion strategy (x-axis). The number of MS peaks obtained for each protease digestion strategy (right-hand y-axis) is also shown.

[0034] **Figure 21** shows the amino acid composition of BSA. (A) A graphical representation of the theoretical amino acid composition (x-axis) and abundance (%; y-axis) of BSA mature protein sequence using ExPASy ProtParam. (B) A graphical representation of predicted (black bars) and observed (grey bars) cleavage sites (%; y-axis) for amino acids targeted by proteases (x-axis).

[0035] **Figure 22** shows that each protease on their own or combined yield high sequence coverage of BSA. (A) A graphical representation of PCA of the identified peptides. (B) A graphical representation of HCA of the identified peptides. (C) A schematic representation of the sequence alignment of identified peptides to the amino acid sequence of the mature BSA protein. (D) A graphical representation of the percentage sequence coverage (%; x-axis) achieved using the various proteases on their own or in combination (y-axis). (E) A graphical representation of the average mass (peptide mass, Da; y-axis) of identified proteins using the various proteases on their own or in combination (x-axis). (F) A graphical representation of the distribution of the number of

- 8 -

identified peptides (y-axis) and the number of miscleavages that they contain (x-axis). Vertical bars denote standard deviation (SD). Downward arrowhead denotes the minimum peptide mass and upward arrowhead denotes the maximum peptide mass.

[0036] **Figure 23** is a graphical representation of the distribution of BSA peptides (y-axis) according to the number of miscleavages per digestion combination (x-axis).

[0037] **Figure 24** shows that the LC-MS patterns of cannabis are protein-rich and complex. Graphical representations of elution time (min; y-axis) and mass (m/z; x-axis) in cannabis-derived protein samples digested with various proteases on their own or in combination. A graphical representation of the number of MS peaks (y-axis) observed using the various proteases on their own or in combination (x-axis; in triplicate) is also provided in the bottom right-hand panel.

[0038] **Figure 25** shows that peptides isolated from cannabis can be grouped by digestion type. (A) A graphical representation of PCA projection of PC1 (x-axis) and PC2 (y-axis) for the 42 digest samples resulting from the action of one protease (T, G or C), or two (T->G, T->C, or G-C), or three proteases (T->G->C) applied sequentially. (B) A graphical representation of PCA loading of PC1 (x-axis) and PC2 (y-axis) for the 27,635 cannabis peptides identified and coloured according to their deconvoluted masses. (C) A graphical representation of PLS score of LV1 (x-axis) and LV2 (y-axis) featuring the 42 digest samples using the digestion type as a response. (D) A graphical representation of PLS loading of LV1 (x-axis) and LV2 (y-axis) featuring the 3,349 most significant peptides from the linear model testing the response to proteases, and coloured according to their retention time (min) and m/z values. T, trypsin; G, GluC; C, chymotrypsin; RT, retention time.

[0039] **Figure 26** is a graphical representation of MS peak statistics from medicinal cannabis samples. Percentage of MS peaks that underwent MS/MS fragmentation (light grey bars), MS/MS spectra that were annotated in Mascot (black bars) and MS peaks that led to an identification in SEQUEST (dark grey bars) (%; left-hand y-axis) are shown relative to the protease digestion strategy (x-axis). The number of MS peaks obtained for each protease digestion strategy (right-hand y-axis) is also shown.

- 9 -

[0040] **Figure 27** shows that each protease behaves differently when applied to cannabis-derived samples. (A) A graphical representation of the ion score (average score; y-axis) per amino acid residue targeted by the three proteases (x-axis). Maximum is represented by the triangles. Vertical bars denote SD. (B) A graphical representation of the distribution (occurrence; y-axis) of the number of missed cleavages (x-axis) per protease. (C) A graphical representation of the distribution of the average peptide mass (y-axis) of the cannabis peptides according to the number of missed cleavages (x-axis). Vertical bars denote SD. (D) A graphical representation of extreme peptide mass (y-axis) according to the number of missed cleavages (x-axis). Minimum peptide mass is represented as circles and maximum peptide mass is represented as triangles.

[0041] **Figure 28** shows the annotated MS/MS spectra of the illustrative example peptides from ribulose biphosphate carboxylase large chain (RBCL, UniProtID A0A0C5B2I6). (A) Features of the peptides selected to illustrate MS/MS annotation. (B) Comparison of the same sequence area (peptide alignment provided) resulting from the action of GluC, chymotrypsin, trypsin/LysC proteases. (C) Example post-translational modification (PTM) annotation such as oxidation or phosphorylation.

[0042] **Figure 29** is a graphical representation of the pathways in which identified cannabis proteins are involved.

DETAILED DESCRIPTION OF THE INVENTION

[0043] Throughout this specification, unless the context requires otherwise, the word “comprise”, or variations such as “comprises” or “comprising”, will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

[0044] The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgement or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

- 10 -

[0045] Unless specifically defined otherwise, all technical and scientific terms used herein shall be taken to have the same meaning as commonly understood by one of ordinary skill in the art.

[0046] Unless otherwise indicated the molecular biology, cell culture, laboratory, plant breeding and selection techniques utilised in the present invention are standard procedures, well known to those skilled in the art. Such techniques are described and explained throughout the literature in sources such as, J. Perbal, *A Practical Guide to Molecular Cloning*, John Wiley and Sons (1984), J. Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press (1989), T.A. Brown (editor), *Essential Molecular Biology: A Practical Approach*, Volumes 1 and 2, IRL Press (1991), D.M. Glover and B.D. Hames (editors), *DNA Cloning: A Practical Approach*, Volumes 1-4, IRL Press (1995 and 1996), and F.M. Ausubel *et al.* (editors), *Current Protocols in Molecular Biology*, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present); Janick, J. (2001) *Plant Breeding Reviews*, John Wiley & Sons, 252 p.; Jensen, N.F. ed. (1988) *Plant Breeding Methodology*, John Wiley & Sons, 676 p.; Richard, A.J. ed. (1990) *Plant Breeding Systems*, Unwin Hyman, 529 p.; Walter, F.R. ed. (1987) *Plant Breeding*, Vol. I, Theory and Techniques, MacMillan Pub. Co.; Slavko, B. ed. (1990) *Principles and Methods of Plant Breeding*, Elsevier, 386 p.; and Allard, R.W. ed. (1999) *Principles of Plant Breeding*, John-Wiley & Sons, 240 p. The ICAC Recorder, Vol. XV no. 2: 3-14; all of which are incorporated by reference. The procedures described are believed to be well known in the art and are provided for the convenience of the reader. All other publications mentioned in this specification are also incorporated by reference in their entirety.

[0047] As used in the subject specification, the singular forms “a”, “an” and “the” include plural aspects unless the context clearly dictates otherwise. Thus, for example, reference to “a protein” includes a single protein, as well as two or more proteins; reference to “an apical bud” includes a single apical bud, as well as two or more apical buds; and so forth.

[0048] The present disclosure is predicated, at least in part, on the unexpected finding that an optimised protein extraction methods for cannabis bud and trichome material improves proteomic analysis of cannabis plant by enhancing the coverage of proteins of

- 11 -

relevance to the biosynthesis of cannabinoids and terpenes that underpin the therapeutic value of medicinal cannabis.

[0049] Therefore, in an aspect disclosed herein, there is provided a method of extracting cannabis-derived proteins from cannabis plant material, the method comprising:

- (a) suspending cannabis plant material in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution; and
- (b) separating the solution comprising the cannabis-derived proteins from residual plant material.

Cannabis

[0050] As used herein, the term "cannabis plant" means a plant of the genus *Cannabis*, illustrative examples of which include *Cannabis sativa*, *Cannabis indica* and *Cannabis ruderalis*. *Cannabis* is an erect annual herb with a dioecious breeding system, although monoecious plants exist. Wild and cultivated forms of *cannabis* are morphologically variable, which has resulted in difficulty defining the taxonomic organisation of the genus. In an embodiment, the cannabis plant is *C. sativa*.

[0051] The terms "plant", "cultivar", "variety", "strain" or "race" are used interchangeably herein to refer to a plant or a group of similar plants according to their structural features and performance (*i.e.*, morphological and physiological characteristics).

[0052] The reference genome for *C. sativa* is the assembled draft genome and transcriptome of "Purple Kush" or "PK" (van Bakal *et al.* 2011, *Genome Biology*, 12:R102). *C. sativa*, has a diploid genome ($2n = 20$) with a karyotype comprising nine autosomes and a pair of sex chromosomes (X and Y). Female plants are homogametic (XX) and males heterogametic (XY) with sex determination controlled by an X-to-autosome balance system. The estimated size of the haploid genome is 818 Mb for female plants and 843 Mb for male plants.

[0053] As used herein, the terms "plant material" or "cannabis plant material" are to be understood to mean any part of the cannabis plant, including the leaves, stems, roots, and buds, or parts thereof, as described elsewhere herein, as well as extracts, illustrative examples of which include kief or hash, which includes trichomes and glands. In a

- 12 -

preferred embodiment, the plant material is an apical bud. In another preferred embodiment, the plant material comprises trichomes.

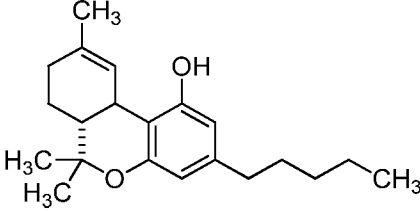
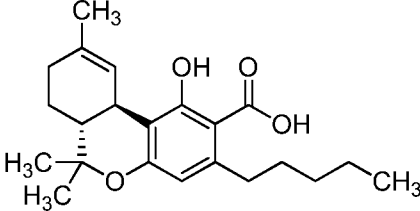
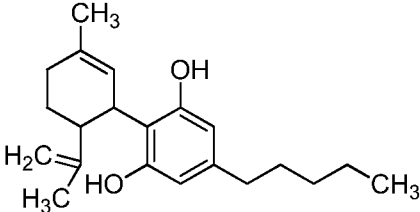
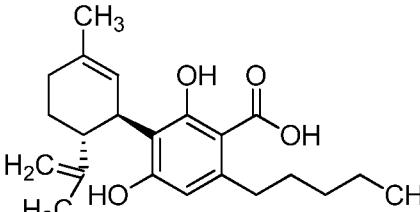
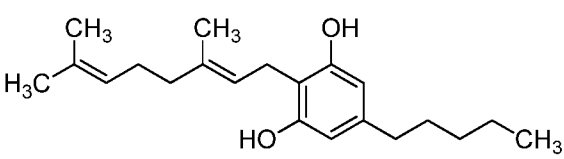
[0054] In an embodiment, the plant material is derived from a female cannabis plant. In another embodiment, the plant material is derived from a mature female cannabis plant.

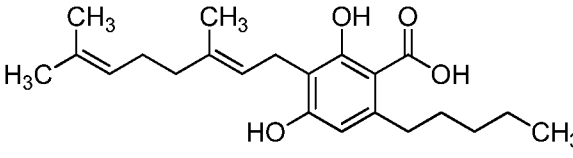
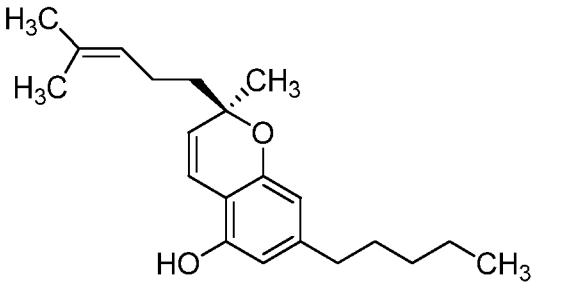
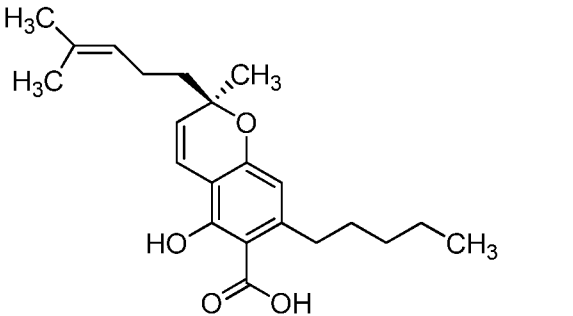
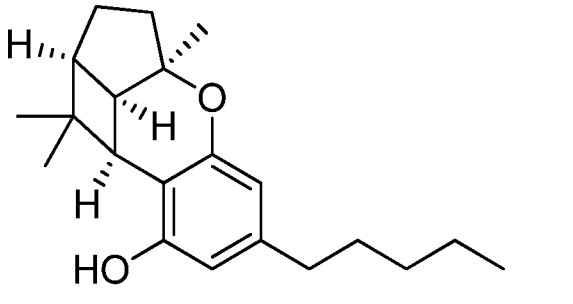
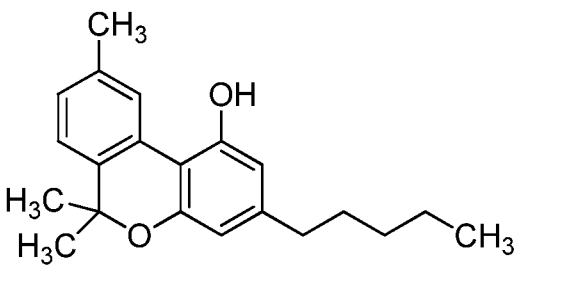
Cannabis-derived proteins

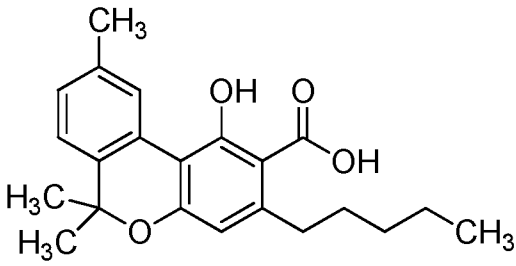
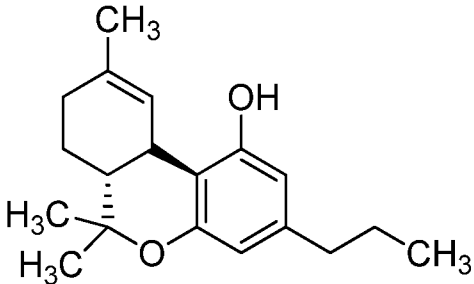
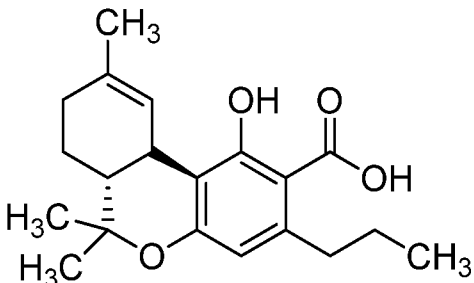
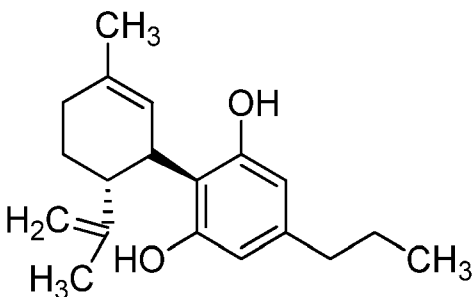
[0055] As used herein, the term "cannabis-derived protein" refers to any protein produced by a cannabis plant. Cannabis-derived proteins will be known to persons skilled in the art, illustrative examples of which include cannabinoids, terpenes, terpinoids, flavonoids, and phenolic compounds.

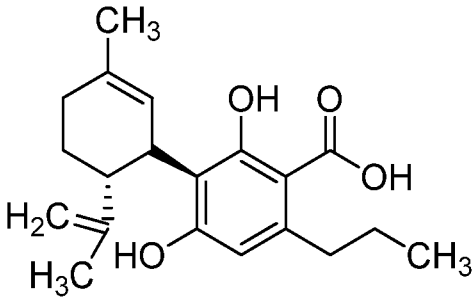
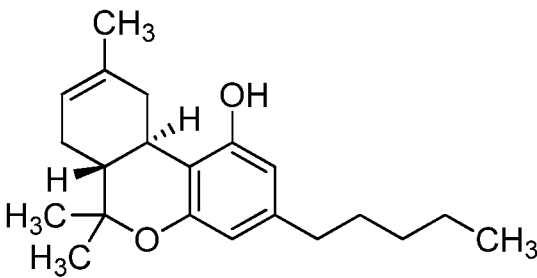
[0056] The term "cannabinoid", as used herein, refers to a family of terpeno-phenolic compounds, of which more than 100 compounds are known to exist in nature. Cannabinoids will be known to persons skilled in the art, illustrative examples of which are provided in Table 1, below, including acidic and decarboxylated forms thereof.

Table 1: Cannabinoids and their properties.

Name	Structure	Chemical properties/ [M+H] ⁺ ESI MS
Δ^9 -tetrahydrocannabinol (THC)		Psychoactive, decarboxylation product of THCA <i>m/z</i> 315.2319
Δ^9 -tetrahydrocannabinolic acid (THCA/THCA-A)		<i>m/z</i> 359.2217
cannabidiol (CBD)		decarboxylation product of CBDA <i>m/z</i> 315.2319
cannabidiolic acid (CBDA)		<i>m/z</i> 359.2217
cannabigerol (CBG)		Non- intoxicating, decarboxylation product of CBGA <i>m/z</i> 317.2475

Name	Structure	Chemical properties/ [M+H] ⁺ ESI MS
cannabigerolic acid (CBGA)		<i>m/z</i> 361.2373
cannabichromene (CBC)		Non- psychotropic, converts to cannabicyclol upon light exposure <i>m/z</i> 315.2319
cannabichromene acid (CBCA)		<i>m/z</i> 359.2217
cannabicyclol (CBL)		Non- psychoactive, 16 isomers known. Derived from non-enzymatic conversion of CBC <i>m/z</i> 315.2319
cannabinol (CBN)		Likely degradation product of THC <i>m/z</i> 311.2006

Name	Structure	Chemical properties/ [M+H] ⁺ ESI MS
cannabinolic acid (CBNA)		<i>m/z</i> 355.1904
tetrahydrocannabivarin (THCV)		decarboxylation product of THCVA <i>m/z</i> 287.2006
tetrahydrocannabivarinic acid (THCVA)		<i>m/z</i> 331.1904
cannabidivarin (CBDV)		<i>m/z</i> 287.2006

Name	Structure	Chemical properties/ [M+H] ⁺ ESI MS
cannabidivarinic acid (CBDVA)		<i>m/z</i> 331.1904
Δ8-tetrahydrocannabinol (d8-THC)		<i>m/z</i> 315.2319

[0057] Cannabinoids are synthesised in cannabis plants as carboxylic acids. Acid forms of cannabinoids will be known to persons skilled in the art, illustrative examples of which are described in Papaset *et al.* (*Int. J. Med. Sci.*, 2018; 15(12): 1286–1295) and *Cannabis and Cannabinoids (PDQ®): Health Professional Version*; PDQ Integrative, Alternative, and Complementary Therapies Editorial Board; Bethesda (MD): National Cancer Institute (US); 2002-2018).

[0058] The precursors of cannabinoids originate from two distinct biosynthetic pathways: the polyketide pathway, giving rise to olivetolic acid (OLA) and the plastidal 2-C-methyl-D-erythritol 4-phosphate (MEP) pathway, leading to the synthesis of geranyl diphosphate (GPP). OLA is formed from hexanoyl-CoA, derived from the short-chain fatty acid hexanoate, by aldol condensation with three molecules of malonyl-CoA. This reaction is catalysed by a polyketide synthase (PKS) enzyme and an olivetolic acid cyclase (OAC). The geranylpyrophosphate:olivetolate geranyltransferase catalyses the alkylation of OLA with GPP leading to the formation of CBGA, the central precursor of various

- 17 -

cannabinoids. Three oxidocyclases are responsible for the diversity of cannabinoids: THCA synthase (THCAS) converts CBGA to THCA, while CBDA synthase (CBDAS) forms CBDA, and CBCA synthase (CBCAS) produces CBCA. Propyl cannabinoids (cannabinoids with a C3 side-chain, instead of a C5 side-chain), such as tetrahydrocannabivarinic acid (THCVA), are synthesised from a divarinolic acid precursor.

[0059] "Δ-9-tetrahydrocannabinolic acid" or "THCA-A" is synthesised from the CBGA precursor by THCA synthase. The neutral form "Δ-9-tetrahydrocannabinol" or "THC" is associated with psychoactive effects of cannabis, which are primarily mediated by its activation of CB1G-protein coupled receptors, which result in a decrease in the concentration of cyclic AMP (cAMP) through the inhibition of adenylate cyclase. THC also exhibits partial agonist activity at the cannabinoid receptors CB1 and CB2. CB1 is mainly associated with the central nervous system, while CB2 is expressed predominantly in the cells of the immune system. As a result, THC is also associated with pain relief, relaxation, fatigue, appetite stimulation, and alteration of the visual, auditory and olfactory senses. Furthermore, more recent studies have indicated that THC mediates an anti-cholinesterase action, which may suggest its use for the treatment of Alzheimer's disease and myasthenia (Eubanks *et al.*, 2006, *Molecular Pharmaceuticals*, 3(6): 773-7).

[0060] "Cannabidiolic acid" or "CBDA" is also a derivative of cannabigerolic acid (CBGA), which is converted to CBDA by CBDA synthase. Its neutral form, "cannabidiol" or "CBD" has antagonist activity on agonists of the CB1 and CB2 receptors. CBD has also been shown to act as an antagonist of the putative cannabinoid receptor, GPR55. CBD is commonly associated with therapeutic or medicinal effects of cannabis and has been suggested for use as a sedative, anti-inflammatory, anti-anxiety, anti-nausea, atypical anti-psychotic, and as a cancer treatment. CBD can also increase alertness, and attenuate the memory impairing effect of THC.

[0061] The terms "terpene" and "terpenoids" as used herein, refer to a family of non-aromatic compounds that are typically found as components of essential oil present in many plants. Terpenes contain a carbon and hydrogen scaffold, while terpenoids contain a carbon, hydrogen and oxygen scaffold. Terpenes and terpenoids will be known to persons skilled in the art, illustrative examples of which include α-pinene, α-bisabolol, β-pinene, guaiene, guaiol, limonene, myrcene, ocimene, α-mumulene, terpinolene, 3-carene,

myrcene, α -terpineol and linalool.

[0062] Terpenes are classified according to the number of repeating units of 5-carbon building blocks (isoprene units), such as monoterpenes with 10 carbons, sesquiterpenes with 15 carbons, and triterpenes derived from a 30-carbon skeleton. Terpene yield and distribution in the plant vary according to numerous parameters, such as processes for obtaining essential oil, environmental conditions, or maturity of the plant. Mono- and sesqui-terpenes have been detected in flowers, roots, and leaves of cannabis, while triterpenes have been detected in hemp roots, fibers and in hempseed oil.

[0063] Two different biosynthetic pathways contribute, in their early steps, to the synthesis of plant-derived terpenes. The cytosolic mevalonic acid (MVA) pathway is involved in the biosynthesis of sesqui-, and tri-terpenes, and the plastid-localized MEP pathway contributes to the synthesis of mono-, di-, and tetraterpenes. MVA and MEP are produced through various and distinct steps, from two molecules of acetyl-coenzyme A and from pyruvate and D-glyceraldehyde-3-phosphate, respectively. They are further converted to isopentenyl diphosphate (IPP) and isomerised to dimethylallyl diphosphate (DMAPP), the end point of the MVA and MEP pathways. In the cytosol, two molecules of IPP (C5) and one molecule of DMAPP (C5) are condensed to produce farnesyl diphosphate (FPP, C15) by farnesyl diphosphate synthase (FPS). FPP serves as a precursor for sesquiterpenes (C15), which are formed by terpene synthases and can be decorated by other various enzymes. Two FPP molecules are condensed by squalene synthase (SQS) at the endoplasmic reticulum to produce squalene (C30), the precursor for triterpenes and sterols, which are generated by oxidosqualene cyclases (OSC) and are modified by various tailoring enzymes. In the plastid, one molecule of IPP and one molecule of DMAPP are condensed to form GPP (C10) by GPP synthase (GPS). GPP is the immediate precursor for monoterpenes.

[0064] The term "chemotype", as used herein, refers to a representation of the type, amount, level, ratio and/or proportion of cannabis-derived proteins that are present in the cannabis plant or part thereof, as typically measured within plant material derived from the plant or plant part, including an extract therefrom.

- 19 -

[0065] The chemotype of a cannabis plant typically predominantly comprises the acidic form of the cannabinoids, but may also comprise some decarboxylated (neutral) forms thereof, at various concentrations or levels at any given time (*e.g.*, at propagation, growth, harvest, drying, curing, *etc.*) together with other cannabis-derived proteins such as terpenes, flavonoids and phenolic compounds.

[0066] The terms "level", "content", "concentration" and the like, are used interchangeably herein to describe an amount of the cannabis-derived protein, and may be represented in absolute terms (*e.g.*, mg/g, mg/ml, *etc.*) or in relative terms, such as a ratio to any or all of the other proteins in the cannabis plant material or as a percentage of the amount (*e.g.*, by weight) of any or all of the other proteins in the cannabis plant material.

[0067] As noted elsewhere herein, cannabinoids are synthesised in cannabis plants predominantly in acid form (*i.e.*, as carboxylic acids). While some decarboxylation may occur in the plant, decarboxylation typically occurs post-harvest and is increased by exposing the plant material to heat.

Protein extraction

[0068] Protein extraction methods are typically optimised based on the intended use of the extract, such as whether the extract is to be further processed to isolate specific constituents, produce an enriched extract or for use in proteomic analysis. For example, methods for the extraction of specific constituents of plant material may include steps such as maceration, decoction, and extraction with aqueous and non-aqueous solvents, distillation and sublimation. By contrast, methods for the extraction of plant-derived proteins for proteomic analysis desirably require the preservation of proteins and peptides, including post-translational modifications, hydrophobic membrane proteins and low-abundance proteins. Such methods typically include steps such as the homogenisation, cell lysis, solubilisation, precipitation, separation, enrichment, *etc.*, depending on the starting material and downstream analysis method.

[0069] In an embodiment, the methods described herein comprise suspending cannabis plant material in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution.

- 20 -

[0070] The term "chaotropic agent" as used herein refers to a substance that disrupts the structure of proteins to enable proteins to unfold with all ionisable groups exposed to solution. Chaotropic agents are used during the sample solubilisation process to break down interactions involved in protein aggregation (*e.g.*, disulphide/hydrogen bonds, van der Waals forces, ionic and hydrophobic interactions) to enable the disruption of proteins into a solution of individual polypeptides, thereby promoting their solubilisation. Suitable chaotropic agents would be known to persons skilled in the art, illustrative examples of which include n-butanol, ethanol, guanidine hydrochloride, guanidine isothiocyanate, lithium perchlorate, lithium acetate, magnesium chloride, phenol, 2-propanol, sodium dodecyl sulphate, thiourea and urea.

[0071] In an embodiment, the chaotropic agent is a charged chaotropic agent selected from the group consisting of guanidine hydrochloride, guanidine isothiocyanate. In another embodiment, the charged chaotropic agent is guanidine hydrochloride.

[0072] In an embodiment, the solution comprises from about 5.5M to about 6.5M, preferably about 5.6 M to about 6.5 M, preferably about 5.7 M to about 6.5M, preferably about 5.8M to about 6.5M, preferably about 5.9M to about 6.5M, preferably about 6.0M to about 6.5M, preferably about 5.5M to about 6.4M, preferably about 5.5M to about 6.3M, preferably about 5.5M to about 6.2M, preferably about 5.5M to about 6.1M, preferably about 5.5M to about 6.0M, or more preferably about 6.0M guanidine hydrochloride.

[0073] In an embodiment, the solution further comprises a reducing agent.

[0074] The terms "reducing agent" and "reductant" may be used interchangeably herein to refer to substances that disrupt disulphide bonds between cysteine residues, thereby promoting unfolding of proteins to enable analysis of single subunits of proteins. Suitable reducing agents would be known to persons skilled in the art, illustrative examples of which include dithiothreitol (DTT) and dithioerythritol (DTE).

[0075] In an embodiment, the reducing agent is DTT.

[0076] In an embodiment, the solution comprises from about 5mM to about 20mM, preferably about 5 mM to about 19 mM, about 5 mM to about 18 mM, about 5 mM to about 17 mM, about 5 mM to about 16 mM, about 5 mM to about 15 mM, about 5 mM to about 14 mM, about 5 mM to about 13 mM, about 5 mM to about 12 mM, about 5 mM to

- 21 -

about 11 mM, about 5 mM to about 10 mM, about 6 mM to about 20 mM, about 7 mM to about 20 mM, about 8 mM to about 20 mM, about 9 mM to about 20 mM, about 10 mM to about 20 mM, or more preferably about 10mM DTT.

[0077] In an embodiment, the cannabis plant material is pre-treated with an organic solvent before step (a) for a period of time to precipitate the cannabis-derived proteins.

[0078] Protein precipitation followed by resuspension in sample solution is commonly used to remove contaminants such as salts, lipids, polysaccharides, detergents, nucleic acids, *etc.* thereby promoting unfolding of proteins to enable analysis of single subunits of proteins. Suitable protein precipitation agents and methods would be known to persons skilled in the art, illustrative examples of which include precipitation with organic solvents such as trichloroacetic acid, acetone, chloroform, methanol, ammonium sulphate, ethanol, isopropanol, diethylether, polyethylene glycol or combinations thereof.

[0079] In an embodiment, the organic solvent is selected from the group consisting of trichloroacetic acid (TCA)/acetone and TCA/ethanol.

[0080] In an embodiment, the organic solvent comprises from about 5% to about 20%, preferably about 5% to about 19%, about 5% to about 18%, about 5% to about 17%, about 5% to about 16%, about 5% to about 15%, about 5% to about 14%, about 5% to about 13%, about 5% to about 12%, about 5% to about 11%, about 5% to about 10%, about 6% to about 20%, about 7% to about 20%, about 8% to about 20%, about 9% to about 20%, about 10% to about 20%, or more preferably about 10% TCA/acetone or TCA/ethanol.

[0081] In an embodiment, the cannabis-derived proteins separated by step (b), as described elsewhere herein, are subsequently digested by a protease in preparation for proteomic analysis.

[0082] The process of protein digestion is an important step in the preparation of samples for bottom-up proteomic analysis (also referred to as “shotgun” proteomics), as described elsewhere herein. The process of protein digestion is also an important step in the preparation of samples for middle-down proteomic analysis, as described elsewhere herein. The digestion of proteins into peptides by a protease facilitates protein identification using proteomic techniques and allows coverage of proteins that would be problematic due to, for example, poor solubility and heterogeneity.

- 22 -

[0083] The term "protease" as used herein refers to an enzyme that catabolise protein by hydrolysis of peptide bonds. Suitable proteases would be known to persons skilled in the art, illustrative examples of which include trypsin, trypsin/LysC, chymotrypsin, GluC, pepsin, Proteinase K, enterokinase, ficin, papain and bromelain.

[0084] As described elsewhere herein, the use of multiple proteases of various specificity can result in higher coverage of amino acid sequences. In particular, the generation of peptides using multiple proteases can increase the resolution of bottom-up and middle-down proteomic analysis to enable discrimination between closely related protein isoforms and detection of various post-translational modification (PTM) sites.

[0085] Thus, in an embodiment, the cannabis-derived proteins separated by step (b) are digested by two or more proteases, preferably two or more proteases, preferably three or more proteases, preferably four or more proteases, or more preferably five or more proteases.

[0086] In an embodiment, the two or more proteases comprise orthogonal proteases.

[0087] In accordance with the methods disclosed herein, the cannabis-derived proteins separated by step (b) may be digested by the two or more proteases sequentially or simultaneously, as part of the same digestion or as separate digestions (*e.g.*, single-, double-, and triple-digests).

[0088] In an embodiment, the cannabis-derived proteins separated by step (b) are digested by the two or more proteases sequentially.

[0089] By "sequentially" it is meant that there is an interval between digestion with a first protease and digestion with a second protease. The interval between the sequential digestions may be seconds, minutes, hours, or days. In a preferred embodiment, the interval between sequential protease digestions is at least 18 hours (*i.e.*, overnight). The sequential digestions may be in any order.

[0090] In an embodiment, the cannabis-derived proteins separated by step (b) are digested by trypsin/LysC followed by GluC ("T→G").

[0091] In an embodiment, the cannabis-derived proteins separated by step (b) are digested by trypsin/LysC followed by chymotrypsin ("T→C").

- 23 -

[0092] In an embodiment, the cannabis-derived proteins separated by step (b) are digested by GluC followed by chymotrypsin (“G→C”).

[0093] In an embodiment, the cannabis-derived proteins separated by step (b) are digested by trypsin/LysC followed by GluC followed by chymotrypsin (“T→G→C”).

[0094] In an embodiment, the cannabis-derived proteins separated by step (b) are digested by the two or more proteases simultaneously (*i.e.*, multiple proteases in a single digest).

[0095] In an embodiment, the cannabis-derived proteins separated by step (b) are digested by trypsin/LysC and GluC simultaneously (“T:G”).

[0096] In an embodiment, the cannabis-derived proteins separated by step (b) are digested by trypsin/LysC and chymotrypsin simultaneously (“T:C”).

[0097] In an embodiment, the cannabis-derived proteins separated by step (b) are digested by GluC digest and chymotrypsin simultaneously (“G:C”).

[0098] In an embodiment, the cannabis-derived proteins separated by step (b) are digested by trypsin/LysC, GluC and chymotrypsin simultaneously (“T:G:C”).

[0099] The skilled person would appreciate that the amounts of each protease used simultaneously may vary according to the intended use of the digested protein sample (*i.e.*, incomplete digestion for middle-down proteomics). In a preferred embodiment, however, the same volume of each protease is applied to the the cannabis-derived proteins separated by step (c).

[0100] In an embodiment, the protease is selected from the group consisting of trypsin, trypsin/LysC, chymotrypsin, GluC and pepsin. In another embodiment, the protease is selected from the group consisting of trypsin/LysC, chymotrypsin and GluC.

[0101] In yet another embodiment, the protease is trypsin/LysC.

[0102] In an embodiment, the cannabis-derived proteins separated by step (b), as described elsewhere herein, are subsequently alkylated in preparation for proteomic analysis.

- 24 -

[0103] The process of alkylation is typically desirable in the preparation of samples for top-down proteomic analysis, as described elsewhere herein. The alkylation of protein thiols reduces disulphide bonds and generally improves the resolution of proteomic techniques by reducing, for example, the generation of artefacts from disulphide-bonded dipeptides that are not selected and fragmented.

[0104] Reagents for the alkylation of proteins would be known to persons skilled in the art, illustrative examples of which include iodoacetamide (IAA), iodoacetic acid, acrylamide monomers and 4-vinylpyridine.

[0105] In an embodiment, the cannabis-derived proteins separated by step (b) are alkylated by IAA.

[0106] In another aspect, there is provided a method of extracting cannabis-derived proteins from cannabis plant material, the method comprising:

- (a) pre-treating the cannabis plant material with an organic solvent to precipitate the cannabis-derived proteins;
- (b) suspending the precipitated cannabis-derived proteins of (a) in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution; and
- (c) separating the solution comprising the cannabis-derived proteins from residual plant material.

Proteomic analysis and sample preparation

[0107] The methods disclosed herein may also suitably be used to prepare a sample for proteomic analysis that will enhance coverage of proteins of relevance to the biosynthesis of cannabis-derived proteins of therapeutic value (*e.g.*, cannabinoids and terpenes). The advantageously allows for the improvement of genome annotation and genomic selective breeding strategies to enable the production of cannabis plants with desirable chemotype(s).

- 25 -

[0108] Thus, in an aspect disclosed herein, there is provided a method of preparing a sample of cannabis-derived proteins from cannabis plant material for proteomic analysis, the method comprising:

- (a) pre-treating the cannabis plant material with an organic solvent to precipitate the cannabis-derived proteins;
- (b) suspending the precipitated cannabis-derived proteins of (a) in a solution comprising a charged chaotropic agent from a period of time to allow for extraction of cannabis-derived proteins into the solution;
- (c) separating the solution comprising the cannabis-derived proteins from residual plant material; and
- (d) digesting the solution of (c) with a protease.

[0109] In an embodiment, step (d) comprises digesting the solution of (c) with two or more proteases.

[0110] In another aspect disclosed herein, there is provided a method of preparing a sample of cannabis-derived proteins from cannabis plant material for proteomic analysis, the method comprising:

- (a) pre-treating the cannabis plant material with an organic solvent to precipitate the cannabis-derived proteins;
- (b) suspending the precipitated cannabis-derived proteins of (a) in a solution comprising a charged chaotropic agent from a period of time to allow for extraction of cannabis-derived proteins into the solution; and
- (c) separating the solution comprising the cannabis-derived proteins from residual plant material.

[0111] In an embodiment, the charged chaotropic acid is guanidine hydrochloride.

[0112] Proteomic analysis methods would be known to persons skilled in the art, illustrative examples of which include two-dimensional gel electrophoresis (2DE), capillary electrophoresis, capillary isoelectric focusing, Fourier-transform mass spectrometry (FT-MS), liquid chromatography-mass spectrometry (LC-MS), isotope coded affinity tag (ICAT) analysis, ultra-performance LC-MS (UPLC-MS), nano liquid

- 26 -

chromatography-tandem mass spectrometry (nLC-MS/MS), MALDI-MS, SELDI, and electrospray ionisation.

[0113] In an embodiment, the proteomic analysis method is selected from the group consisting of LC-MS, UPLC-MS and nLC-MS/MS.

[0114] LC-based proteomic methods may be used for top-down, middle-down and bottom-up proteomics methods, as described elsewhere herein.

[0115] The term "top-down proteomics" as used herein refers to a proteomic method where a protein sample is separated and then individual, intact proteins are identified directly by means of tandem mass spectrometry. Using this approach, liquid chromatography may be used for separation of proteins prior to mass spectrometry analysis. Persons skilled in the art would be aware of suitable top-down proteomic approaches, illustrative embodiments of which include the methods of Wang *et al.* (2005, *Journal of Chromatography A*, 1073(1-2): 35-41) and Moritz *et al.* (2005, *Proteomics* 5, 3402: 1746-1757).

[0116] The term "bottom-up proteomics" or "shotgun proteomics" as used herein refers to a proteomic method where a protein, or protein mixture is digested. Single- or multidimensional liquid chromatography coupled to mass spectrometry is then used for separation of peptide mixtures and identification of their compounds. Persons skilled in the art would be aware of suitable bottom-up proteomic approaches, illustrative embodiments of which include the method of Rappsilber *et al.* (2003, *Analytical Chemistry*, 75(3): 663-670).

[0117] The term "middle-down proteomics", as used herein, refers to a hybrid technique that incorporates aspects of both top-down and bottom-up proteomics approaches. While top-down proteomics typically explores intact proteins of about 10-30 kDa and trypsin-based bottom-up proteomics generally yields short peptides of about 0.7-3 kDa, middle-down proteomics is used to analyse peptide fragments of about 3-10 kDa. Middle-down proteomics can be achieved by, for example, performing limited proteolysis through reduced incubation times and/or increased protease:proteins ratio to achieve partial digestion, or by using proteases with greater specificity and/or lesser efficiency, which

- 27 -

cleave less frequently. Persons skilled in the art would be aware of suitable middle-down proteomics approaches, an illustrative example of which is described by Pandeswaria and Sabareesh (2019, *RSC Advances*, 9: 313-344).

[0118] In another aspect disclosed herein, there is provided a method of analysing a cannabis plant proteome, the method comprising:

- (a) preparing a sample of cannabis-derived proteins in accordance with the methods described herein; and
- (b) subjecting the sample to proteomic analysis.

[0119] The skilled person will appreciate that when a sample of cannabis-derived proteins is digested using one, two, three or more proteases, proteolysis is often incomplete, and non-standard protease cleavages (*i.e.*, miscleavages) can occur.

[0120] Number of miscleavages is commonly used in proteomics analysis to discriminate between correct and incorrect matches based upon the protease used. For example, up to four miscleavages are recommended for chymotrypsin and GluC, and other two for trypsin (see, *e.g.*, Giansanti *et al.*, 2016, *Nature Protocols*, 11: 993-1006).

[0121] In an embodiment, the proteomic analysis comprises a parameter setting the maximum number of missed cleavages to between about 2 and about 10. In another embodiment, the proteomic analysis comprises a parameter setting the maximum number of missed cleavages to between about 6 and about 10.

[0122] In an embodiment, the method of analysing a cannabis plant proteome comprises subjecting the sample to a first proteomic analysis, followed by one or more additional proteomic analyses (*i.e.*, re-analysis of the sample). The re-analysis of the sample may deepen the proteome analysis and increase the proportion of annotated MS/MS spectra (*i.e.*, successful hits), as described elsewhere herein. Such re-analysis may be achieved using iterative exclusion lists from the precursor ions already fragmented.

[0123] Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications which fall

- 28 -

within the spirit and scope. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

[0124] Unless otherwise defined, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs.

[0125] The various embodiments enabled herein are further described by the following non-limiting examples.

EXAMPLES

Materials and methods

Plant materials

Apical bud sampling and grinding

[0126] Fresh plant material was obtained from the Victorian Government Medicinal Cannabis Cultivation Facility. The top three centimetres of the apical bud was excised using secateurs, placed into a labelled paper bag, snap frozen in liquid nitrogen and stored at -80°C until grinding. Samples were collected in triplicates. Frozen buds were ground in liquid nitrogen using a mortar and pestle. The ground frozen powder was transferred into a 15 mL tube and stored at stored at -80°C until protein extraction.

Trichome recovery

[0127] The top three centimetres of the apical bud was cut using secateurs and placed into a labelled paper bag. Samples were collected in triplicates. Trichome recovery was performed using the procedure of Yerger *et al.* (1992, *Plant Physiology*, 99: 1-7), with modifications. The bud was further trimmed with the secateurs into smaller pieces and placed into a 50 mL tube. Approximately 10 mL liquid nitrogen was added to the tube and the cap was loosely attached. The tube was then vortexed for 1 min. The cap was removed, and the content of the tube was discarded by inverting the tube and tapping it on the bench, while the trichomes stuck to the walls of the tube. The process was repeated in the same

- 29 -

tube until all the apical bud was trimmed. Tubes were stored at -80°C until protein extraction.

Protein extraction methods

[0128] For the apical bud extraction, one 50 mg scoop of ground frozen powder was transferred into a 2 mL microtube kept on ice pre-filled with 1.8 mL precipitant or 0.5 mL resuspension buffer depending on the extraction method employed, as described elsewhere herein. All six extraction methods described hereafter were applied to the apical bud samples. For the trichome extraction, all trichomes stuck to the walls of the tubes were resuspended into the solutions and volumes specified below. Due the limited amount of trichomes recovered, only extraction methods 1 and 2 were attempted.

Extraction 1: Resuspension in urea buffer

[0129] Plant material was resuspended in 0.5 mL of urea buffer (6M urea, 10mM DTT, 10mM Tris-HCl pH 8.0, 75mM NaCl, and 0.05% SDS). The tubes were vortexed for 1 min, sonicated for 5 min, vortexed again for 1 min. The tubes were centrifuged for 10 min at 13,500 rpm. The supernatant was transferred into fresh 1.5 mL tubes and stored at -80°C until protein assay.

Extraction 2: Resuspension in guanidine-hydrochloride buffer

[0130] Plant material was resuspended in 0.5 mL of guanidine-HCl buffer (6M guanidine-HCl, 10mM DTT, 5.37 mM sodium citrate tribasic dihydrate, and 0.1 M Bis-Tris). The tubes were vortexed for 1 min, sonicated for 5 min, vortexed again for 1 min. The tubes were centrifuged for 10 min at 13,500 rpm and at 4°C. The supernatant was transferred into fresh 1.5 mL tubes and stored at -80C until protein assay.

Extraction 3: TCA/acetone precipitation followed by resuspension in urea buffer

[0131] Plant material was resuspended in 1.8 mL ice-cold 10% TCA/10mM DTT/acetone (w/w/v) by vortexing for 1 min. Tubes were left at -20°C overnight. The next day, tubes were centrifuged for 10 min at 13,500 rpm and at 4°C. The supernatant was removed, and the pellet was resuspended in ice-cold 10mM DTT/acetone (w/v) by vortexing for 1 min. Tubes were left at -20°C for 2 h. The tubes were centrifuged as

- 30 -

specified before and the supernatant removed. This washing step of the pellet was repeated once more. The pellets were dried for 30 min under a fume hood. The dry pellet resuspended in 0.5 mL of urea buffer as described in Extraction 1.

Extraction 4: TCA/acetone precipitation followed by resuspension in guanidine-hydrochloride buffer

[0132] Plant material was processed as detailed in Extraction 3, except that the dry pellet was resuspended in 0.5 mL of guanidine-HCl buffer.

Extraction 5: TCA/ethanol precipitation followed by resuspension in urea buffer

[0133] Plant material was processed as detailed in Extraction 3, except that acetone was replaced with ethanol.

Extraction 6: TCA/ethanol precipitation followed by resuspension in guanidine-hydrochloride buffer

[0134] Plant material was processed as detailed in Extraction 4, except that acetone was replaced with ethanol.

Protein assay

[0135] Protein extracts from apical buds were diluted ten times into their respective resuspension buffer and protein extracts from trichomes were diluted four times. The protein concentrations were measured in triplicates using the Microplate BCA protein assay kit (Pierce) following the manufacturer's instructions. Bovine Serum Albumin (BSA) was used a standard.

Trypsin/LysC protein digestion and desalting

Protease digestion

[0136] An aliquot corresponding to 100 µg of plant proteins was used for protein digestion as follows. The DTT-reduced and IAA-alkylated proteins were diluted six times using 50 mM Tris-HCl pH 8 to drop the resuspension buffer molarity below 1 M. Trypsin/LysC protease (Mass Spectrometry Grade, 100 µg, Promega) was carefully solubilised in 1 mL of 50 mM Tris-HCl pH 8. A 40 µL aliquot of trypsin/LysC solution

- 31 -

was added and gently mixed with the plant extracts thus achieving a 1:25 ratio of protease:plant proteins. The mixture was left to incubate overnight (19 h) at 37°C in the dark. The digestion reaction was stopped by lowering the pH of the mixture using a 10% formic acid (FA) in H₂O (v/v) to a final concentration of 1% FA.

[0137] Bovine serum albumin (BSA) was also digested under the same conditions to be used as a control for digestion and nLC-MS/MS analysis.

Desalting

[0138] The 25 tryptic digests were desalted using solid phase extraction (SPE) cartridges (Sep-Pak C18 1cc Vac Cartridge, 50 mg sorbent, 55-105 µm particle size, 1 mL, Waters) by gravity as described in (Vincent *et al.* 2015, 2015, *Frontiers in Genetics*, 6: 360).

[0139] A 90 µL aliquot of peptide digest was mixed with 10 µL 1ng/µL Glu-Fibrinopeptide B (Sigma), as an internal standard. The peptide/internal standard mixture was transferred into a 100 µL glass insert placed into a glass vial. The vials were positioned into the autosampler at 4°C for immediate analyses by nLC-MS/MS.

Intact protein analysis by Ultra performance liquid chromatography mass spectrometry (UPLC-MS)

UPLC separation

[0140] The UPLC-MS analyses of the 24 plant protein extracts were performed in duplicates for a total of 48 MS files. Protein extracts were chromatographically separated using the UHPLC 1290 Infinity Binary LC system (Agilent) and a Aeris™ WIDEPORE XB-C8 column (Phenomenex) kept at 75°C as described in Vincent *et al.* (2016, *PLoS One*, 11: e0163471). Mobile phase A contained 0.1% formic acid in water and mobile phase B contained 0.1% formic acid in acetonitrile. UPLC gradient was as follows: starting conditions 3% B, held for 2.5 min, ramping to 60% B in 27.5 min, ramping to 99% B in 1 min and held at 99% B for 4 min, lowering to 3% B in 0.1 min, equilibration at 3% B for 4.9 min. A 10 µL injection volume was applied to each protein extract, irrespective of their protein concentration. Each extract was injected twice.

- 32 -

MS acquisition

[0141] During the 40 min chromatographic separation, plant intact proteins were analysed using an Orbitrap Velos hybrid ion trap-Orbitrap mass spectrometer (ThermoFisher Scientific) online with the UPLC and fitted with a heated electrospray ionisation (HESI) source. HESI parameters were: capillary heated to 300°C, source heated to 250°C, sheath gas flow 30, auxiliary gas flow 10, sweep gas flow 2, 3.6 kV, 100 µA, and S-Lens RF level 60%. SID was set at 15V.

[0142] For the first 2.5 min, nLC flow was sent to waste, then switched to source from 2.5 to 38 min, and finally switched back to waste for the last minute of the 40 min run. Spectra were acquired in positive ion mode using the full MS scan mode of the Fourier Transform (FT) Orbitrap mass analyser at a resolution of 60,000 using a 500-2000 m/z mass window and 6 microscans. FT Penning gauge difference was set at 0.05 E-10 Torr.

[0143] All LC-MS files will be available from the stable public repository MassIVE at the following URL: <http://massive.ucsd.edu/ProteoSAFe/datasets.jsp> with the accession number MSV000083191.

Peptide analysis by nano liquid chromatography-tandem mass spectrometry (nLC-MS/MS)

[0144] The nLC-ESI-MS/MS analyses were performed on 25 peptide digests in duplicates thus yielding 50 MS/MS files. Chromatographic separation of the peptides was performed by reverse phase (RP) using an Ultimate 3000 RSLCnano System (Dionex) online with an Orbitrap Velos hybrid ion trap-Orbitrap mass spectrometer (ThermoFisher Scientific). The parameters for nLC and MS/MS have been described in Vincent *et al.*, *supra*. Each digest was injected twice. Blanks (1 µL of mobile phase A) were injected in between each set of six extraction replicates and analysed over a 20 min nLC run to minimise carry-over.

Database search for protein identification

[0145] Database searching of the 50 MS .RAW files was performed in Proteome Discoverer (PD) 1.4 using MASCOT 2.6.1. All 589 *C. sativa* protein sequences publicly

- 33 -

available on 13 December 2018 from UniprotKB (www.uniprot.org; key word used “*Cannabis sativa*”) were downloaded as a FASTA file. These also included 77 sequences from the European hop, *Humulus lupulus*, the closest relative to *C. sativa*, as well as 72 sequences from the Chinese grass, *Boehmeria nivea*, which also closely related to *C. sativa*. The GOT sequence was retrieved from WO 2011/017798 A1 and included in the FASTA file (590 entries). The FASTA file was imported and indexed in PD 1.4. The SEQUEST algorithm was used to search the indexed FASTA file. The database searching parameters specified trypsin as the digestion enzyme and allowed for up to two missed cleavages. The precursor mass tolerance was set at 10 ppm, and fragment mass tolerance set at 0.5 Da. Peptide absolute Xcorr threshold was set at 0.4 and protein relevance threshold was set at 1.5. Carbamidomethylation (C) was set as a static modification. Oxidation (M), phosphorylation (STY), conversion from Gln to pyro-Glu (N-term Q) and Glu to pyro-Glu (N-term E), and deamination (NQ) were set as dynamic modifications. The target decoy peptide-spectrum match (PSM) validator was used to estimate false discovery rates (FDR). At the peptide level, peptide confidence value set at high was used to filter the peptide identification, and the corresponding FDR on peptide level was less than 1 %. At the protein level, protein grouping was enabled.

[0146] All nLC-MS/MS files will be available from the stable public repository MassIVE at the following URL: <http://massive.ucsd.edu/ProteoSAFe/datasets.jsp> with the accession number MSV000083191.

Data processing and statistical analyses

[0147] The data files obtained following UPLC-MS analysis were processed in the Refiner MS module of Genedata Expressionist® 11.0 with the following parameters: 1/ RT Structure Removal using a 5 scan minimum RT length, 2/ m/z Structure Removal using 8 points minimum m/z length, 3/ Chromatogram Chemical Noise Reduction using 7 scan smoothing, and a moving average estimator, 4/ Spectrum Smoothing using a Savitzky-Golay algorithm with 5 points m/z window and a polynomial order of 3, 5/ Chromatogram RT Alignment using a pairwise alignment-based tree and 50 RT scan search interval, 6/ Chromatogram Peak Detection using a 0.3 min minimum peak size, 0.02 Da maximum merge distance, a boundaries merge strategy, a 30% gap/peak ratio, a curvature-based

- 34 -

algorithm, using both local maximum and inflection points to determine boundaries, 7/ Chromatogram Isotope Clustering using a 4 scan RT tolerance, a 20 ppm m/z tolerance, a peptide isotope shaping method with protonation, charges from 2-25, mono-isotopic masses and variable charge dependency, 8/ Singleton Filter, 9/ Charge and Adduct Grouping (*i.e.*, deconvolution) using a 50 ppm mass tolerance, a 0.1 min RT tolerance, a dynamic adduct list containing ions (H), and neutrals (-H₂O, K-H, and Na-H), 10/ Export Analyst using group volumes.

[0148] The data files obtained following nLC-MS/MS analysis were processed in the Refiner MS module of Genedata Expressionist® 11.0 with the following parameters: 1/ RT Structure Removal applying a minimum of 4 scans, 2/ m/z Structure Removal applying a minimum of 8 points, 3/ Chromatogram Chemical Noise Reduction using 5 scan smoothing, a moving average estimator, a 25 scan RT window, a 30% quantile, and clipping an intensity of 20, 4/ Grid using an adaptive grid with 10 scans and 10% deltaRT smoothing, 5/ Chromatogram RT Alignment using a pairwise alignment-based tree and 50 RT scan search interval, 6/ Chromatogram Peak Detection using a 0.1 min minimum peak size, 0.03 Da maximum merge distance, a boundaries merge strategy, a 20% gap/peak ratio, a curvature-based algorithm, intensity-weighted and using inflection points to determine boundaries, 7/ Chromatogram Isotope Clustering using a 0.3 min RT tolerance, a 0.1 Da m/z tolerance, a peptide isotope shaping method with protonation, charges from 2-6 and mono-isotopic masses; 8/ Singleton Filter, 9/ MS/MS Consolidation, 10/ Proteome Discoverer Import using a Xcorr above 1.5, 11/ Peak Annotation, 12/ Export Analyst using cluster volumes.

[0149] Statistical analyses were performed using the Analyst module of Genedata Expressionist® 11.0 where columns denote plant samples and rows denote intact proteins or tryptic digest peptides. Principal Component Analyses (PCA) were performed on rows using a covariance matrix with 50% valid values and row mean as imputation. Two-dimension hierarchical clustering (2-D HCA) was performed on both columns and rows using positive correlation and Ward linkage method. Venn diagrams were produced by exporting quantitative data of the identified peptides to Microsoft Excel 2016 (Office 365) spreadsheet and using the Excel function COUNT to establish the frequency of the

- 35 -

peptides in the samples and across extraction methods. Venn diagrams were drawn in Microsoft Powerpoint 2016 (Office 365).

Protein standards for top-down proteomics

[0150] Protein standards were purchased from Sigma and include: α -casein (α -CN 23.6 kDa) from bovine milk (C6780-250MG, 70% pure), β -lactoglobulin (β -LG, 18.7 kDa) from bovine milk (L3908-250MG, 90% pure), albumin from bovine serum (BSA, 66.5 kDa, A7906-10G, 98% pure), and myoglobin from horse skeletal muscle (Myo, 16.9 kDa, M0630-250MG, 95-100% pure and salt-free).

[0151] Lyophilised protein standards were solubilised at a 10mg/mL concentration in 50% acetonitrile (ACN)/0.1% formic acid (FA)/10 mM dithiothreitol (DTT). Standards were dissolved by vortexing for 1 min and sonication for 10 min followed by another 1 min vortexing. An iodoacetamide (IAA) solution was added to reach a final concentration of 20 mM, vortexed for 1 min, and left to incubate for 30 min at room temperature in the dark. Apart from BSA and β -lactoglobulin, none of the standards needed reduction and alkylation steps as they bear no disulfide bridges; yet, these steps were still performed to emulate plant sample processing.

[0152] Standard solutions were then desalted using a solid phase extraction (SPE) cartridges (Sep-Pak C18 1cc Vac Cartridge, 50 mg sorbent, 55–105 μ m particle size, 1 mL, Waters) by gravity as described in Vincent *et al.*, *supra*. Bound intact proteins were desalted using 1 mL of 0.1% FA solution and eluted into a 2 mL microtube using 1 mL of 80% ACN/0.1% FA solution.

Up-scaled cannabis protein extraction for top-down proteomics

[0153] Protein extraction for Cannabis mature apical buds was performed according to the method of Extraction 4, as described at [00132] above. This method was up-scaled for top-down proteomics, as detailed below.

- 36 -

[0154] One 500 mg scoop of ground frozen powder of plant material from apical buds was transferred into a 15 mL tube kept on ice prefilled with 12 mL ice-cold 10% trichloroacetic acid (TCA)/10mM dithiothreitol (DTT)/acetone (w/w/v). The tubes were vortexed for 1 min and left at -20 °C overnight. The next day, tubes were centrifuged for 30 min at 4 °C and at maximum speed (5000 rpm) using a swing rotor centrifuge (Sigma 4-16k). The supernatant was removed, and the pellet was resuspended in 12 mL ice-cold 10mM DTT/acetone (w/v) by vortexing for 1 min. Tubes were left at -20 °C for 2 h. The tubes were centrifuged as specified before and the supernatant removed. This washing step of the pellet was repeated once more. The pellets were dried for 30 min under a fume hood. The dry pellet resuspended in 2 mL of guanidine-HCl buffer (6 M guanidine-HCl, 10 mM DTT, 5.37 mM sodium citrate tribasic dihydrate and 0.1 M Bis-Tris).

Protein assay and cannabis protein alkylation

[0155] Protein extracts from apical buds were diluted ten times in guanidine-HCl buffer. The protein concentrations were measured in triplicates using the Microplate BCA protein assay kit (Pierce) following the manufacturer's instructions. Bovine Serum Albumin (BSA) from the kit was used as a standard as per instructions. Protein extract concentrations ranked from 2.84 to 3.72 mg of proteins per mL of extract.

[0156] Following protein assay, the concentrations of the DTT-reduced protein samples were adjusted to the least concentrated one (2.84 mg/mL) by adding an appropriate volume of guanidine-HCl buffer. The protein extracts were then alkylated by adding a volume of 1M iodoacetamide (IAA)/water (w/v) solution to reach a 20 mM final IAA concentration. The tubes were vortexed for 1 min and left to incubate at room temperature in the dark for 60 min.

Cannabis protein desalting and evaporation

[0157] A volume of 0.5 mL of alkylated protein extract (1.42 mg proteins) was then desalted, as described above at [0138] above.

[0158] The 1 mL eluates were then evaporated using a SpeedVac concentrator (Savant SPD2010) for 90 min until the volume reached 0.2 mL. The evaporated samples were

- 37 -

transferred into a 100 μ L glass insert placed into a glass vial. The vials were positioned into the autosampler at 4 °C for immediate analyses by UPLC-MS.

Mass spectrometry analyses for top-down proteomics

[0159] MS analyses were performed on an Orbitrap Elite hybrid ion trap-Orbitrap mass spectrometer (Thermo Fisher Scientific) composed of a Linear Ion Trap Quadrupole (ITMS) mass spectrometer hosting the source and a Fourier-Transform mass spectrometer (FTMS) with a resolution of 240,000 at 400 m/z. Both ITMS and FTMS were calibrated in positive mode and the ETD was tuned prior to all MS and MS/MS experiments. All MS and MS/MS files (RAW, mzXML, MGF) and fasta files from known protein standards and cannabis samples are available from the stable public repository MassIVE at the following URL: <http://massive.ucsd.edu/ProteoSAFe/datasets.jsp> with the accession number MSV000083970.

[0160] Protein standard solutions were individually infused using a 0.5 mL Gastight #1750 syringe (Hamilton Co.) at a 20-30 μ L/min flow rate using the built-in syringe pump of the LTQ mass spectrometer, to achieve at least 1e6 ion signal intensity. Protein standard solutions were pushed through first a 30 cm red PEEK tube (0.005 in. ID), then through a metal union and a PEEK VIPER tube (6041-5616, 130 μ m x 150 mm, Thermo Fischer Scientific), eventually to the heated electrospray ionisation (HESI) source where proteins were electrosprayed through a HESI needle insert 0.32 gauge (Thermo Fisher Scientific 70005-60155).

[0161] The source parameters were: capillary temperature 300 °C, source heater temperature 250 °C, sheath gas flow 30, auxiliary gas flow 10, sweep gas flow 2, FTMS injection waveforms on, FTMS full AGC target 1e6, FTMS MSn AGC target 1e6, positive polarity, source voltage 4kV, source current 100 μ A, S-lens RF level 70%, reagent ion source CI pressure 10, reagent vial ion time 200 ms, reagent vial AGC target 5e5, supplemental activation energy 15V, FTMS full micro scans 16, FTMS full max ion time 100 ms, FTMS MSn micro scans 8, and FTMS MSn max ion time 1000 ms. SID was set at 15V and FT Penning gauge pressure difference was set at 0.01 E-10 Torr to improve signal intensity. Mass window was 600-2000 m/z for FTMS1 and 300-2000 m/z for FTMS2.

- 38 -

[0162] Various fragmentation parameters were tested on individual protein standards. In-source fragmentation (SID) potentials varied from 0 to 100 V (maximum potential). Collision-Induced Dissociation (CID) normalized collision energy (NCE) varied from 30 to 50 eV with constant activation Q of 0.400 and an activation time of 100 ms. High energy CID (HCD) NCE varied from 10 to 30 eV with constant activation time of 0.1 ms. Electron Transfer Dissociation (ETD) activation times varied from 5 to 25 ms with constant activation Q of 0.250. Data files were acquired on the fly using the Acquire Data function of Tune Plus software 2.7 (Thermo Fisher Scientific) for up to 3 min at a time.

Separation of cannabis intact proteins by UPLC

[0163] Intact proteins from cannabis mature buds were chromatographically separated using a UHPLC 1290 Infinity Binary LC system (Agilent) and a bioZen XB-C4 column (3.6 μ m, 200 Å, 150 $\times$ 2.1 mm, Phenomenex) kept at 90 °C. Flow rate was 0.2 mL/min and total duration was 120 min. Mobile phase A contained 0.1% FA in water and mobile phase B contained 0.1% FA in acetonitrile.

[0164] Chromatographic separation was optimised and optimum UPLC gradient for cannabis proteins was as follows: starting conditions 3% B, ramping to 15% B in 2 min, ramping to 40% B in 89 min, ramping to 50% B in 5 min, ramping to 99% B in 5 min and held at 99% B for 10 min, lowering to 3% B in 1.1 min, equilibration at 3% B for 7.9 min. A 20 μ L injection volume was applied to each protein extract. Each extract was injected five times with blank in between the extracts.

Analyses of cannabis intact protein extracts using MS online with UPLC

[0165] The UPLC outlet line was connected to the switching valve of the LTQ mass spectrometer. During the 119 min acquisition time by mass spectrometry, the first two minutes and the last minute of the run were directed to the waste whereas the rest of the run was directed to the source.

Full Scan FTMSI

[0166] Tune parameters have been described above. Data was acquired in positive polarity with profile and normal scan modes at a resolution of 240,000 at 400 m/z along a

- 39 -

mass window of 500-2000 m/z. SID was set at 15V. Full scan files were acquired in duplicate at the first and last injections of the 5 sample injections. The three intermediate injections were dedicated to tandem MS (see below).

FTMS2

[0167] Three MS/MS methods were applied in which the energy applied to each fragmentation modes varied between what we call “Low”, “High”, and intermediate “Mid”. SID was set to 15V throughout. One segment was defined with four scan events. The first scan event applied full scan FTMS in profile and normal modes at a resolution of 120,000 for 400 m/z, scanning a mass window of 500-2000 m/z. The most abundant ion whose intensity was above 500 and m/z above 700 from the first scan was selected for subsequent fragmentation in a data-dependent manner with an isolation width of 15 and a default charge state of 10. FTMS2 spectra were acquired along a mass window of 300-2000 m/z at a resolution of 60,000 at 400 m/z. Scan events 2 to 4 are described below as their energy levels varied. The parameters that changed are in bold.

[0168] In the “Low” energy FTMS2 method, the precursor underwent an ETD fragmentation during the second scan event with an activation time of 5 ms and an activation Q of 0.250; a CID fragmentation in the third scan event with a NCE of 35 eV, an activation Q of 0.400 and an activation time of 100 ms; and a HCD fragmentation with a NCE of 19 eV and an activation time of 0.1 ms.

[0169] In the “Mid” energy FTMS2 method, the precursor underwent an ETD fragmentation during the second scan event with an activation time of 10 ms and an activation Q of 0.250; a CID fragmentation in the third scan event with a NCE of 42 eV, an activation Q of 0.400 and an activation time of 100 ms; and a HCD fragmentation with a NCE of 23 eV and an activation time of 0.1 ms.

[0170] In the “High” energy FTMS2 method, the precursor underwent an ETD fragmentation during the second scan event with an activation time of 15 ms and an activation Q of 0.250; a CID fragmentation in the third scan event with a NCE of 50 eV, an activation Q of 0.400 and an activation time of 100 ms; and a HCD fragmentation with a NCE of 27 eV and an activation time of 0.1 ms.

Data processing and statistical analyses for top-down proteomics***Analysis of infusion MS/MS spectra***

[0171] Given the MW of myoglobin, β -lactoglobulin, α -S1-casein and the 240,000 resolution of the instrument, the spectra of these proteins were isotopically resolved. BSA is too large for isotopic resolution, therefore only average mass was obtained. Isotopically resolved RAW files were opened using the Qual Browser module of Xcalibur software version 3.1 (Thermo scientific) and deconvoluted using Xtract algorithm (Thermo scientific) with the following parameters: M masses mode, 60000 resolution at 400 m/z 3 S/N threshold, 44 fit factor, 25% remainder, averagine method and 40 max charges. In the deconvoluted spectra, the second scan corresponding to the monoisotopic zero-charge (deisotoped) mass spectrum was selected for export as explained in DeHart *et al. Methods Mol. Biol.* 2017, 1558: 381-394.

[0172] Deconvoluted exact masses were then exported to Excel 2016 (Microsoft) to generate pivot tables and charts. VBA macros were used to compile lists of masses corresponding to different MS/MS modes and parameters, and parent ions from the same protein. The deconvoluted deisotoped masses were copied and pasted into ProSight Lite version 1.4 (Northwestern University, USA) with the following parameters: S-carboxamidomethyl-L-cysteine as a fixed modification, monoisotopic precursor mass type, and fragmentation tolerance of 50 ppm. The AA sequence varied according to the standards analysed; where needed the initial methionine residue (myoglobin), the signal peptide (β -LG, α -S1-CN, BSA) and the pro-peptide (BSA) were removed. The fragmentation method chosen was either SID, HCD, CID, or ETD, depending on how the MS/MS data was acquired. When multiple MS/MS spectra were used including ETD data, the BY and CZ fragmentation method was selected.

[0173] Raw MS/MS files were imported into Proteome Discoverer version 2.2 (Thermo Fisher Scientific) through the Spectrum Files node and the following parameters were used in the Spectrum Selector node: use MS1 precursor with isotope pattern, lowest charge state of 2, precursor mass ranging from 500-50,000 Da, minimum peak count of 1, MS orders 1 and 2, collision energy ranging from 0-1000, full scan type. The selected

- 41 -

spectra were then deconvoluted through the Xtract node with the following parameters: S/N threshold of 3, 300-2000 m/z window, charge from 1-30 (maximum value), resolution of 60,000, and monoisotopic mass. When not specified, default parameters were used. Deconvoluted spectra (MH+) were then exported as a single Mascot Generic Format (MGF) file.

[0174] The MGF file was searched in Mascot version 2.6.1 (MatrixScience) with Top-Down searches license. A MS/MS Ion Search was performed with the NoCleave enzyme, Carbamidomethyl (C) as fixed modification and Oxidation (M), Acetyl (Protein N-term), and Phospho (ST) as variable modifications, with monoisotopic masses, 1% precursor mass tolerance, ± 50 ppm or ± 2 Da fragment mass tolerance, precursor charge of +1, 9 maximum missed cleavages, and instrument type that accounted for CID, HCD and ETD fragments (*i.e.* b-, c-, y-, and z-type ions) of up to 110 kDa. The first database searched was a fasta file containing the AA sequences of all the known variants of cow's milk most abundant proteins (all caseins, alpha-lactalbumin, beta-lactoglobulin, and BSA) along with horse's myoglobin (59 sequences in total). The decoy option was selected. The second database searched was SwissProt (all 559,228 entries, version 5) using all the entries or just the "other mammalia" taxonomy.

Analysis of LC-MS and LC-MS/MS data from cannabis samples

[0175] The RAW files were loaded and processed in the Refiner modules of Genedata Expressionist ® version 12.0.6 using the following steps and parameters: profile data cutoff of 10,000, R window of 3-99 min, m/z window of 500-1800 Da, removal of RT structures < 4 scans, removal of m/z structures < 5 points, smoothing of chromatogram using a 5 scans window and moving average estimator, spectrum smoothing using a 3 points m/z window, a chromatogram peak detection using a summation window of 15 scans, a minimum peak size of 1 min, a maximum merge distance of 10 ppm, and a curvature-based algorithm with local maximum and FWHM boundary determination, isotope clustering using a peptide isotope shaping method with charges ranging from 2-25 (maximum value) and monoisotopic masses, singleton filtering, and charges and adduct grouping using a 50 ppm mass tolerance, positive charges, and dynamic adduct list

containing protons, H₂O, K-H, and Na-H. The protein groups were used for statistical analyses.

[0176] Spectral deconvolution from 3-70 kDa was performed using manual deprecated mode and harmonic suppression deconvolution method with a 0.04 Da step, as well as curvature-based peak detection, intensity-weighted computation and inflection points to determine boundaries. This step generated LC-MS maps of protein deisotoped masses.

[0177] Group volumes were exported to the Analyst module of Genedata Expressionist to perform statistical analyses. Parameters for Principal Component Analysis (PCA) were analysis of rows, covariance matrix, 70% valid values, and row mean imputation. Parameters for Hierarchical Clustering Analysis (HCA) were clustering of columns, shown as tree, positive correlation distances, Ward linkage, 70% valid values.

Identification of cannabis proteins by Mascot

[0178] The RAW files were processed in Proteome Discoverer version 2.2 (Thermo Fisher Scientific) as detailed above for the known protein standards to create a single MGF file containing 11,250 MS/MS peak lists.

[0179] The MGF file was searched in Mascot version 2.6.1 (MatrixScience) with Top-Down searches license. A MS/MS Ion Search was performed with the NoCleave enzyme, Carbamidomethyl (C) as fixed modification and Oxidation (M), Acetyl (Protein N-term) and Phosphorylation (ST) as variable modifications, with monoisotopic masses, $\pm 1\%$ precursor mass tolerance, ± 50 ppm or ± 2 Da fragment mass tolerance, precursor charge of 1+, 9 maximum missed cleavages, and instrument type that accounted for CID, HCD and ETD fragments (*i.e.* b-, c-, y-, and z-type ions) of up to 110 kDa. The database searched was a *fasta* file previously compiled to contain all UniprotKB AA sequences from *C. sativa* and close relatives, amounting to 663 entries in total (*i.e.* 73 sequences added in 6 months). The decoy option was selected. The error tolerant option was tested as well but not pursued as search times proved much longer and number of hits diminished. The other database searched was SwissProt *viridiplantae* (39,800 sequences; version 5).

Chemicals for multiple protease strategy

[0180] All proteases were purchased from Promega: Trypsin/LysC mix (V5072, 100 µg), GluC (V1651, 50 µg), and Chymotrypsin (V106A, 25 µg). Albumin from bovine serum (BSA, A7906-10G, 98% pure) was purchased from Sigma and analysed by MS.

Protein extraction methods

[0181] The protein extraction described above at [00132] was up-scaled to prepare sufficient amount of sample to undergo various protease digestions. Briefly, 0.5 g of ground frozen powder was transferred into a 15 mL tube kept on ice pre-filled with 12 mL ice-cold 10% TCA/10 mM DTT/acetone (w/w/v). Tubes were vortexed for 1 min and left at -20°C overnight. The next day, tubes were centrifuged for 10 min at 5,000 rpm and 4°C. The supernatant was discarded, and the pellet was resuspended in 10 mL of ice-cold 10 mM DTT/acetone (w/v) by vortexing for 1 min. Tubes were left at -20°C for 2 h. The tubes were centrifuged as specified before and the supernatant discarded. This washing step of the pellets was repeated once more. The pellets were dried for 60 min under a fume hood. The dry pellets were resuspended in 2 mL of guanidine-HCl buffer (6M guanidine-HCl, 10mM DTT, 5.37 mM sodium citrate tribasic dihydrate, and 0.1 M Bis-Tris) by vortexing for 1 min, sonicating for 10 min and vortexing for another minute. Tubes were incubated at 60°C for 60 min. The tubes were centrifuged as described above and 1.8 mL of the supernatant was transferred into 2 mL microtubes. 40 µL of 1M IAA/water (w/v) solution was added to the tubes to alkylate the DTT-reduced proteins. The tubes were vortexed for 1 min and left to incubate at room temperature in the dark for 60 min.

[0182] 1.1 mL of BSA solution (2 mg/mL, Pierce) was transferred into a 2 mL microtube and 10 µL of 1 M DTT/water (w/v) solution was added. The tube was vortexed for 1 minute and incubated at 60°C for 60 min. 20 µL of 1M IAA/water (w/v) solution was added to the tube. The BSA tube was vortexed for 1 min and left to incubate at room temperature in the dark for 60 min.

- 44 -

Protein assay

[0183] Protein extracts were diluted ten times using the guanidine-HCl buffer prior to the assay. The protein concentrations were measured in triplicates using the Pierce Microplate BCA protein assay kit (ThermoFisher Scientific) following the manufacturer's instructions. The BSA solution supplied in the kit (2 mg/mL) was used as a standard.

Protein digestion

[0184] An aliquot corresponding to 100 µg of BSA or plant proteins was used for protein digestion as follows.

Digestion 1: Trypsin/LysC protease mix (T)

[0185] DTT-reduced and IAA-alkylated proteins were diluted six times using 50 mM Tris-HCl pH 8.0 to drop the resuspension buffer molarity below 1 M. Trypsin/LysC protease (Mass Spectrometry Grade, 100 µg, Promega) was carefully solubilised in 1 mL of 50 mM acetic acid and incubated at 37°C for 15 min. A 40 µL aliquot of trypsin/LysC solution was added and gently mixed with the protein extracts thus achieving a 1:25 ratio of protease:proteins. The mixture was left to incubate overnight (18 h) at 37°C in the dark.

Digestion 2: GluC (G)

[0186] DTT-reduced and IAA-alkylated proteins were diluted six times using 50 mM Ammonium bicarbonate (pH 7.8) to drop the resuspension buffer molarity below 1 M. GluC protease (Mass Spectrometry Grade, 50 µg, Promega) was carefully solubilised in 0.5 mL of ddH₂O. A 10 µL aliquot of GluC solution was added and gently mixed with the protein extracts thus achieving a 1:100 ratio of protease:proteins. The mixture was left to incubate overnight (18 h) at 37°C in the dark.

Digestion 3: Chymotrypsin (C)

[0187] DTT-reduced and IAA-alkylated proteins were diluted six times using 100 mM Tris/10mM CaCl₂ pH 8.0 to drop the resuspension buffer molarity below 1 M. Chymotrypsin protease (Sequencing Grade, 25 µg, Promega) was carefully solubilised in 0.25 mL of 1M HCl. A 10 µL aliquot of chymotrypsin solution was added and gently

- 45 -

mixed with the protein extracts thus achieving a 1:100 ratio of protease:proteins. The mixture was left to incubate overnight (18 h) at 25°C in the dark.

Sequential Digestion 1: Trypsin/LysC followed by GluC (T→G)

[0188] Digestion using trypsin/LysC was performed as described above at [00185]. The next day, a 10 µL aliquot of GluC solution (50 µg in 0.5 mL ddH₂O) was added and gently mixed with the trypsin/LysC digest. The tubes were incubated again at 37°C in the dark for 18 h.

Sequential Digestion 2: Trypsin/LysC followed by Chymotrypsin (T→C)

[0189] Digestion using trypsin/LysC was performed as described above at [00185]. The next day, a 10 µL aliquot of chymotrypsin solution (25 µg in 0.25 mL 1M HCl) was added and gently mixed with the trypsin/LysC digest. The tubes were then incubated at 25°C in the dark for 18 h.

Sequential Digestion 3: GluC followed by Chymotrypsin (G→C)

[0190] Digestion using GluC was performed as described above at [00186]. The next day, a 10 µL aliquot of chymotrypsin solution (25 µg in 0.25 mL 1M HCl) was added and gently mixed with the GluC digest. The tubes were then incubated at 25°C in the dark for 18h.

Sequential Digestion 4: Trypsin/LysC followed by GluC followed by Chymotrypsin (T→G→C)

[0191] Digestion using trypsin/LysC was performed as described above at [00185]. The next day, a 10 µL aliquot of GluC solution (50 µg in 0.5 mL ddH₂O) was added and gently mixed with the trypsin/LysC digest. The tubes were incubated again at 37°C in the dark for 18 h. The next day, a 10 µL aliquot of chymotrypsin solution (25 µg in 0.25 mL 1M HCl) was added and gently mixed with the trypsin/LysC digest. The tubes were then incubated at 25°C in the dark for 18 h.

- 46 -

Equimolar mixtures of digests (T:G, T:G, G:C, T:G:C)

[0192] In an effort to assess the efficiency of the sequential digestions (T→G, T→G, G→C, T→G→C), individual BSA digests resulting from the independent activity of trypsin/LysC, GluC and chymotrypsin were pooled together using the same volumes. Thus, the trypsin/LysC digest was pooled with the GluC digest (T:G), the trypsin/LysC digest was pooled with the chymotrypsin digest (T:C), the GluC digest was pooled with the chymotrypsin digest (G:C), and the three trypsin/Lys-, GluC and chymotrypsin were also pooled together (T:G:C).

Desalting

[0193] All of the digestion reactions were stopped by lowering the pH of the mixture using a 10% formic acid (FA) in H₂O (v/v) to a final concentration of 1% FA.

[0194] All digests were desalted using solid phase extraction (SPE) cartridges (Sep-Pak C18 1cc Vac Cartridge, 50 mg sorbent, 55-105 µm particle size, 1 mL, Waters) by gravity, followed by Speedvac evaporation.

[0195] The digest was transferred into a 100 µL glass insert placed into a glass vial. The vials were positioned into the autosampler at 4°C for immediate analyses by nLC-MS/MS.

Peptide digest analysis by nano liquid chromatography-tandem mass spectrometry (nLC-MS/MS)

[0196] The nLC-ESI-MS/MS analyses were performed on all the peptide digests in duplicate. Chromatographic separation of the peptides was performed by reverse phase (RP) using an Ultimate 3000 RSLCnano System (Dionex) online with an Elite Orbitrap hybrid ion trap-Orbitrap mass spectrometer (ThermoFisher Scientific). The parameters for nLC and MS/MS have been described in Vincent *et al.*, *supra*. A 1 µL aliquot (0.1 µg peptide) was loaded using a full loop injection mode onto a trap column (Acclaim PepMap100, 75 µm x 2 cm, C18 3 µm 100 Å, Dionex) at a 3 µL/min flow rate and switched onto a separation column (Acclaim PepMap100, 75 µm x 15 cm, C18 2 µm 100 Å, Dionex) at a 0.4 µL/min flow rate after 3 min. The column oven was set at 30°C.

- 47 -

Mobile phases for chromatographic elution were 0.1% FA in H₂O (v/v) (phase A) and 0.1% FA in ACN (v/v) (phase B). Ultraviolet (UV) trace was recorded at 215 nm for the whole duration of the nLC run. A linear gradient from 3% to 40% of ACN in 35 min was applied. Then ACN content was brought to 90% in 2 min and held constant for 5 min to wash the separation column. Finally, the ACN concentration was lowered to 3% over 0.1 min and the column reequilibrated for 5 min. On-line with the nLC system, peptides were analysed using an Orbitrap Velos hybrid ion trap-Orbitrap mass spectrometer (Thermo Scientific). Ionisation was carried out in the positive ion mode using a nanospray source. The electrospray voltage was set at 2.2 kV and the heated capillary was set at 280°C. Full MS scans were acquired in the Orbitrap Fourier Transform (FT) mass analyser over a mass range of 300 to 2000 m/z with a 60,000 resolution in profile mode. MS/MS spectra were acquired in data-dependent mode. The 20 most intense peaks with charge state ≥ 2 and a minimum signal threshold of 10,000 were fragmented in the linear ion trap using collision-induced dissociation (CID) with a normalised collision energy of 35%, 0.25 activation Q and activation time of 10 msec. The precursor isolation width was 2 m/z. Dynamic exclusion was enabled, and peaks selected for fragmentation more than once within 10 sec were excluded from selection for 30 sec. Each digest was injected twice, with first injecting all the digests (technical replicate 1) and then fully repeating the injections in the same order (technical replicate 2).

Database search for protein identification

[0197] Database searching of the .RAW files was performed in Proteome Discoverer (PD) 1.4 using SEQUEST algorithm as described above at [00145]. The database searching parameters specified trypsin, or GluC, or chymotrypsin or their respective combinations as the digestion enzymes and allowed for up to ten missed cleavages. The precursor mass tolerance was set at 10 ppm, and fragment mass tolerance set at 0.8 Da. Peptide absolute Xcorr threshold was set at 0.4, the fragment ion cutoff was set at 0.1%, and protein relevance threshold was set at 1.5. Carbamidomethylation (C) was set as a static modification and oxidation (M), phosphorylation (STY), and N-Terminus acetylation were set as dynamic modifications. The target decoy peptide-spectrum match (PSM) validator was used to estimate false discovery rates (FDR). At the peptide level, peptide confidence value set at high was used to filter the peptide identification, and the

- 48 -

corresponding FDR on peptide level was less than 1%. At the protein level, protein grouping was enabled.

[0198] All nLC-MS/MS files are available from the stable public repository MassIVE at the following URL: <http://massive.ucsd.edu/ProteoSAFe/datasets.jsp> with the accession number MSV000084216.

Data processing and statistical analyses

nLC-MS/MS data processing

[0199] The data files obtained following nLC-MS/MS analysis were processed in the Refiner MS module of Genedata Expressionist® 12.0 with the following parameters: 1) Load from file by restricted the range from 8-45 min, 2) Metadata import, 3) Spectrum smoothing using Moving Average algorithm and a minimum of 5 points, 4) RT structure removal using a minimum of 3 scans, 5) m/z grid using an adaptative grid method with a scan count of 10 and a 10% smoothing, 6) chromatogram RT alignment with a pairwise alignment based tree, a maximum shift of 50 scans and no gap penalty, 7) chromatogram peak detection using a 10 scan summation window, a 0.1 min minimum peak size, 0.04 Da maximum merge distance, a boundaries merge strategy, a 20% gap/peak ratio, a curvature-based algorithm, intensity-weighted and using inflection points to determine boundaries, 8) MS/MS consolidation, 9) Proteome Discoverer Import accepting only top-ranked database matches and no decoy results, 10) Peak Annotation, 11) Export Analyst using peak volumes.

[0200] A Peptide Mapping activity for BSA digest samples was also performed using the mature AA sequence of the protein (P02769|25-607) following step 8 (MS/MS consolidation) as follows: 12) Selection of the relevant protease digests, 13) Peptide Mapping using the following parameters: 10 ppm mass tolerance, ESI-CID/HCD instrument, 0.8 Da fragment tolerance, min fragment score of 30, top-ranked only, discard mass-only matches, enzymes varied according to the protease(s) used, 6 max missed cleavages, min peptide length of 3, fixed Carbamidomethyl (C) modification, and variable Oxidation (M) modification.

- 49 -

Statistical analyses

[0201] Statistical analyses were performed using the Analyst module of Genedata Expressionist® 12.0 where columns denote plant samples and rows denote digest peptides. Principal Component Analyses (PCA) were performed on rows using a covariance matrix with 40% valid values and row mean as imputation. A linear model performed on rows and testing the digestion type. Partial Least Square (PLS) analyses were run on the most significant rows resulting from the linear model. PLS response was the digestion type with three latent factors, 50% valid values and row mean as imputation. Hierarchical clustering analysis (HCA) was performed on columns using positive correlation and Ward linkage method. Histograms were generated by exporting number of peaks, number of MS/MS spectra, masses of the identified peptides to Microsoft Excel 2016 (Office 365) spreadsheet.

- 50 -

Example 1 – Intact protein analysis

[0202] This experiment aimed to optimise protein extraction from mature reproductive tissues of medicinal cannabis. A total of six protein extractions were tested with methods varying in their precipitation steps with the use of either acetone or ethanol as solvents, as well as changing in their final pellet resuspension step with the use of urea- or guanidine-HCL-based buffers. The six methods were applied to liquid N₂ ground apical buds. Trichomes were also isolated from apical buds. Because of the small amount of trichome recovered, only the single step extraction methods 1 and 2 were attempted. Extractions were performed in triplicates. Extraction efficiency was assessed both by intact protein proteomics and bottom-up proteomics each performed in duplicates. Rigorous method comparisons were then drawn by applying statistical analyses on protein and peptide abundances, linked with protein identification results.

[0203] The intact proteins of the 18 apical bud extracts and the 6 trichome extracts were separated by UPLC and analysed by ESI-MS in duplicates. LC-MS profiles are complex with many peaks both retention time (RT) in min and m/z axes, particularly between 5-35 min and 500-1300 m/z. Prominent proteins eluted late (25-35 min), probably due to high hydrophobicity, and within low m/z ranges (600-900 m/z), therefore bearing more positive charges. Outside this area, many proteins eluting between 5 and 25 min were resolved in samples processed using extraction methods 2, 4 and 6, irrespective of tissue types (apical buds or trichomes). Protein extracts from apical buds and trichomes overall generated 26,892 intact protein LC-MS peaks (ions), which were then clustered into 5,408 isotopic clusters, which were in turn grouped into 571 proteins of up to 11 charge states. The volumes of all the peaks comprised into a group were summed and the sum was used as a proxy for the amounts of the intact proteins. Statistical analyses were performed on the summed volumes of the 571 protein groups.

[0204] A Principal Component (PC) Analysis (PCA) was performed to verify whether the different extraction methods impacted protein LC-MS quantitative data. A plot of PC1 (60.7% variance) against PC2 (32.9% variance) clearly separates urea-based methods from guanidine-HCl-based methods (Figure 1). Each of the six methods are well defined and do

- 51 -

not cluster together. Extraction methods 3-6, which include an initial precipitation step, are further isolated.

[0205] Table 2 indicates the concentration of the protein extracts as well as the number of protein groups quantified in Genedata expressionist. Extraction method 1 yields the greatest protein concentrations: 6.6 mg/mL in apical buds and 3.5 mg/mL in trichomes, followed by extraction methods 2, 4, 6, 3 and 5. Overall, 571 proteins were quantified and the extraction methods recovering most intact proteins in apical buds are methods 2 (335 ± 15), 4 (314 ± 16) and 6 (264 ± 18). In our experiment, method 1 yielding the highest protein concentrations did not equate larger numbers of proteins resolved by LC-MS. Perhaps *C. sativa* proteins recovered by method 1 are not compatible with our downstream analytical techniques (LC-MS). In trichomes, the method yielding the highest number of intact proteins is extraction method 2 (249 ± 45). Extraction methods 2, 4, and 6 all conclude by a resuspension step in a guanidine-HCl buffer, which consequently is the buffer we recommend for intact protein analysis.

[0206] These data demonstrate that suspension of cannabis-derived proteins in a solution comprising a charged chaotropic agent is effective for preparing cannabis plant material for top-down proteomic analysis.

Table 2: Proteins quantified by top-down proteomics.

Tissue	Extraction number	Extraction method	Extraction code	Protein concentration (mg/mL) Average	Protein concentration (mg/mL) SD	Number of proteins Average	Number of proteins Percent	Number of proteins SD	Number of proteins CV
apical bud	extraction 1	Urea	AB1	6.58	0.89	254	44.51	12	4.80
apical bud	extraction 2	Gnd-HCl	AB2	3.50	0.99	335	58.58	15	4.47
apical bud	extraction 3	TCA-A/urea	AB3	0.63	0.15	247	43.23	21	8.69
apical bud	extraction 4	TCA-A/Gnd-HCl	AB4	1.50	0.28	314	54.90	16	5.13
apical bud	extraction 5	TCA-E/urea	AB5	0.60	0.11	201	35.11	5	2.64
apical bud	extraction 6	TCA-E/Gnd-HCl	AB6	0.76	0.48	264	46.18	18	6.84
trichome	extraction 1	Urea	T1	3.67	0.39	170	29.83	5	2.97
trichome	extraction 2	Gnd-HCl	T2	2.28	1.17	249	43.61	45	18.12
TOTAL						571			

- 53 -

[0207] As far as we know, this is the first time a gel-free intact protein analysis is presented. The old-fashioned technique 2-DE separates intact proteins based first on their isoelectric point and second on their molecular weight (MW). Because it is time-consuming, labour-intensive, and of low throughput, 2-DE has now been superseded by liquid-based techniques, such as LC-MS. In the present study we have chosen to separate intact proteins of medicinal cannabis based on their hydrophobicity using RP-LC and a C8 stationary phase online with a high-resolution mass analyser which separates ionised intact proteins based on their mass-to-charge ratio (m/z).

Example 2 - Tryptic peptides analysis

[0208] The 25 tryptic digests of medicinal cannabis extracts and BSA sample were separated by nLC and analysed by ESI-MS/MS in duplicates. BSA was used as a control for the digestion with the mixture of endoproteases, trypsin and Lys-C, cleaving arginine (R) and lysine (K) residues. BSA was successfully identified with overall 88 peptides covering 75.1% of the total sequence, indicating that both protein digestions and nLC-MS/MS analyses were efficient.

[0209] nLC-MS/MS profiles are very complex with altogether 105,249 LC-MS peaks (peptide ions) clustered into 43,972 isotopic clusters, with up to 11,540 MS/MS events. If we consider apical bud patterns only, guanidine-HCl-based extraction methods (2, 4, and 6) generate a lot more peaks than urea-based methods (1, 3, and 5). As far as trichomes are concerned, extraction methods 1 and 2 yield comparable patterns, albeit with less LC-MS peaks than those of apical buds.

[0210] The volumes of all the peaks comprised into a cluster were summed and the sum was used as a proxy for the amounts of the tryptic peptides. PCA were performed on the summed volumes of the 43,972 peptide clusters. A biplot of PC 1 against PC 2 illustrates the separation of guanidine-HCl based-methods from urea-based methods along PC 1 (65.2% variance), and the distinction between acetone (method 4) and ethanol (method 6) precipitations along PC 2 (11.6% variance) (Figure 2).

[0211] Table 3 indicates the number of peptides identified with high score ($X_{corr} > 1.5$) by SEQUEST algorithm and matching one of the 590 AA sequences we retrieved

- 54 -

from *C. sativa* and closely related species for the database search. Overall, 488 peptides were identified and the extraction methods yielding the greatest number of database hits in apical buds were methods 4 (435 ± 9), 6 (429 ± 6) and 2 (356 ± 20). In trichomes, the method yielding the highest number of identified peptides was extraction method 2 (102 ± 23). Similar to our conclusions from intact protein analyses, we also recommend guanidine-HCl-based extraction methods (2, 4, and 6) for trypsin digestion followed by shotgun proteomics.

[0212] Accordingly, these data demonstrate that suspension of cannabis-derived proteins in a solution comprising a charged chaotropic agent is effective for preparing cannabis plant material for bottom-up proteomic analysis.

Table 3: Peptides identified with by bottom-up proteomics.

Tissue	Extraction number	Extraction method	Extraction code	Number of hits Average	Number of hits Percent	Number of hits SD	Number of hits CV
apical bud	extraction 1	Urea	AB1	211	43.24	34	16.09
apical bud	extraction 2	Gnd-HCl	AB2	356	72.88	20	5.51
apical bud	extraction 3	TCA-A/urea	AB3	265	54.23	55	20.70
apical bud	extraction 4	TCA-A/Gnd-HCl	AB4	435	89.07	9	2.09
apical bud	extraction 5	TCA-E/urea	AB5	41	8.33	15	35.71
apical bud	extraction 6	TCA-E/Gnd-HCl	AB6	429	87.91	6	1.33
trichome	extraction 1	Urea	T1	97	19.88	22	22.27
trichome	extraction 2	Gnd-HCl	T2	102	20.83	23	22.78
TOTAL				488			

- 56 -

[0213] In an attempt to further compare the extraction methods with each other, Venn diagrams were produced on the 488 identified peptides (Figure 3).

[0214] If we start with the trichomes and compare the simplest methods, extraction methods 1 and 2 which only involve a single resuspension step of the frozen ground plant powder into a protein-friendly buffer, we observe similar identification success 35.7% (174 out of 488 peptides) for T1 and 32.4% (158 peptides) for T2 and little overlap (16.0%; 78 peptides) between the two. Therefore, both methods are complementary (Figure 4A). If we compare trichomes and apical buds, an overlap of 27.7% (135 peptides) is observed with extraction method 1 (urea-based buffer) while 32.0% (156 peptides) of database hits are shared between both tissues when extraction method 2 (guanidine-HCl) is employed (Figure 4A). Whilst both outcomes are comparable, we would thus advice employing method 2 when handling cannabis trichomes. If we now turn our attention to just apical buds, we can see that about half of the identified peptides are common between methods 1 and 2 (AB1-AB2, 246 peptides; 50.4%). Guanidine-HCL-based methods (AB2, AB4, and AB6) share a majority of hits (77.5%; 378 peptides) whereas urea-based methods (AB1, AB3, and AB5) only share 11.5% (56) of identified peptides (Figure 4B). This indicates that guanidine-HCl-based methods not only yield more identified peptides but also more consistently. Interestingly, the two most different methods (AB3 and AB6 employing different precipitant solvents and different resuspension buffers) share 80.9% (395) of the identified peptides (Figure 4B), suggesting that the initial precipitation step would make the subsequent resuspension step more homogenous, irrespective of the buffer used. All the 254 peptides identified from trichomes were also identified in apical buds (Figure 4C). Therefore, in our hands protein extraction from trichome did not yield unique protein identification. This might be explained by the fact that due to limited sample recovery only two extraction methods were tested on trichomes.

- 57 -

Example 3 - Proteins identified by bottom-up proteomics

[0215] Table 4 lists the 160 protein accessions from the 488 peptides identified from cannabis mature apical buds and trichomes in this study. These 160 accessions correspond to 99 protein annotations (including 56 enzymes) and 15 pathways (Table 4). Most proteins (83.1%) matched a *C. sativa* accession, 5% of the accessions came from European hop, and 11.8% of the accessions came from *Boehmeria nivea*, all of them annotated as small auxin up-regulated (SAUR) proteins.

Table 4: Proteins identified in medicinal cannabis apical buds and trichomes.

Protein annotation	Abbreviation	Uniprot Accession or Patent	Species	Length (AA)	No. of peptides	EC No.	Function (CC)	Pathway
Small auxin up regulated protein	SAUR03	A0A172J1X8	Boehmeria nivea	93	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR20	A0A172J1Z7	Boehmeria nivea	147	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR23	A0A172J212	Boehmeria nivea	99	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR24	A0A172J211	Boehmeria nivea	102	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR28	A0A172J206	Boehmeria nivea	108	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR30	A0A172J210	Boehmeria nivea	100	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR31	A0A172J276	Boehmeria nivea	152	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR40	A0A172J219	Boehmeria nivea	105	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR44	A0A172J227	Boehmeria nivea	152	4		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR48	A0A172J226	Boehmeria nivea	133	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR54	A0A172J237	Boehmeria nivea	118	5		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR55	A0A172J229	Boehmeria nivea	97	3		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR58	A0A172J236	Boehmeria nivea	97	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR59	A0A172J243	Boehmeria nivea	106	5		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR60	A0A172J238	Boehmeria nivea	105	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR70	A0A172J249	Boehmeria nivea	183	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR71	A0A172J2A4	Boehmeria nivea	183	1		response to auxin	Phytohormone response

Protein annotation	Abbreviation	Uniprot Accession or Patent	Species	Length (AA)	No. of peptides	EC No.	Function (CC)	Pathway
Small auxin up regulated protein	SAUR51	A0A172J290	Boehmeria nivea	97	1		response to auxin	Phytohormone response
Small auxin up regulated protein	SAUR52	A0A172J241	Boehmeria nivea	149	1		response to auxin	Phytohormone response
Cannabidiolic acid synthase	CBDAS	A6P6V9	Cannabis sativa	544	8	1.21.3.8	oxidative cyclization of CBGA, producing CBDA	Cannabinoid biosynthesis
Geranylpyrophosphate:olivetolate geranyltransferase	GOT	WO 2011/017798 A1	Cannabis sativa	395	4		alkylation of OLA with geranyldiphosphate to form CBGA	Cannabinoid biosynthesis
Olivetolic acid cyclase	OAC	I1V0C9	Cannabis sativa	545	1	4.4.1.26	functions in concert with OLS/TKS to form OLA	Cannabinoid biosynthesis
Olivetolic acid cyclase	OAC	I6WU39	Cannabis sativa	101	5	4.4.1.26	functions in concert with OLS/TKS to form OLA	Cannabinoid biosynthesis
3,5,7-trioxododecanoyl-CoA synthase	OLS	B1Q2B6	Cannabis sativa	385	7	2.3.1.206	olivetol biosynthesis	Cannabinoid biosynthesis
Tetrahydrocannabinolic acid synthase	THCAS	A0A0H3UZT7	Cannabis sativa	325	1	1.21.3.7	oxidative cyclization of CBGA, producing THCA	Cannabinoid biosynthesis
Tetrahydrocannabinolic acid synthase	THCAS	Q33DP7	Cannabis sativa	545	1	1.21.3.7	oxidative cyclization of CBGA, producing THCA	Cannabinoid biosynthesis
Tetrahydrocannabinolic acid synthase	THCAS	Q8GTB6	Cannabis sativa	545	4	1.21.3.7	oxidative cyclization of CBGA, producing THCA	Cannabinoid biosynthesis
Putative kinesin heavy chain	kin	Q5TIP9	Cannabis sativa	145	1		microtubule-based movement	Cytoskeleton
Betv1-like protein	Betv1	I6XT51	Cannabis sativa	161	38			Defence response
ATP synthase subunit alpha	atp1	A0A0M5M1Z3	Cannabis sativa	509	12		Produces ATP from ADP	Energy metabolism
ATP synthase subunit alpha	atp1	E5DK51	Cannabis sativa	349	1		Produces ATP from ADP	Energy metabolism
ATP synthase subunit 4	atp4	A0A0M4S8F3	Cannabis sativa	198	7		Produces ATP from ADP	Energy metabolism
ATP synthase subunit alpha	atpA	A0A0C5ARX6	Cannabis sativa	507	9		Produces ATP from ADP	Energy metabolism
ATP synthase subunit beta	atpB	F8TR83	Cannabis sativa	413	1	3.6.3.14	Produces ATP from ADP	Energy metabolism
ATP synthase CF1 epsilon subunit	atpE	A0A0C5AUH9	Cannabis sativa	133	1		Produces ATP from ADP	Energy metabolism
ATP synthase subunit beta, chloroplastic	atpF	A0A0C5AUUE9	Cannabis sativa	189	2		Component of the F(0) channel	Energy metabolism
NADH-ubiquinone oxidoreductase chain 1	nad1	A0A0M4S8G1	Cannabis sativa	324	1	1.6.5.3		Energy metabolism
NADH-ubiquinone oxidoreductase chain 5	nad5	A0A0M4RVP1	Cannabis sativa	669	1	1.6.5.3		Energy metabolism

Protein annotation	Abbreviation	Uniprot Accession or Patent	Species	Length (AA)	No. of peptides	EC No.	Function (CC)	Pathway
NADH dehydrogenase subunit 7	nad7	A0A0M4S7M8	Cannabis sativa	394	1			Energy metabolism
NADH dehydrogenase subunit 9	nad9	A0A0M4R4N3	Cannabis sativa	190	2			Energy metabolism
NADH dehydrogenase subunit 7	nadh7	A0A0X8GLG5	Cannabis sativa	394	1			Energy metabolism
NADH-quinone oxidoreductase subunit H	ndhA	A0A0C5APZ2	Cannabis sativa	363	1	1.6.5.11	NDH-1 shuttles electrons from NADH to quinones	Energy metabolism
NADH-quinone oxidoreductase subunit N	ndhB	A0A0C5B2K5	Cannabis sativa	510	1	1.6.5.11	NDH-1 shuttles electrons from NADH to quinones	Energy metabolism
NADH-quinone oxidoreductase subunit K	ndhE	A0A0C5AUJ8	Cannabis sativa	101	4	1.6.5.11	NDH-1 shuttles electrons from NADH to quinones	Energy metabolism
NADH-quinone oxidoreductase subunit C	ndhJ	A0A0C5B2I2	Cannabis sativa	158	2	1.6.5.11	NDH-1 shuttles electrons from NADH to quinones	Energy metabolism
1-deoxy-D-xylulose-5-phosphate reductoisomerase	DXR	A0A1V0QSG8	Cannabis sativa	472	2		Converts 2-C-methyl-D-erythritol 4P into 1-deoxy-D-xylulose 5P	Isoprenoid biosynthesis
Transferase FPPS1	FPPS1	A0A1V0QSH0	Cannabis sativa	341	1			Isoprenoid biosynthesis
Transferase FPPS2	FPPS2	A0A1V0QSH7	Cannabis sativa	340	3			Isoprenoid biosynthesis
Transferase GPPS large subunit	GPPS	A0A1V0QSH4	Cannabis sativa	393	2			Isoprenoid biosynthesis
Transferase GPPS small subunit	GPPS	A0A1V0QSG9	Cannabis sativa	326	1			Isoprenoid biosynthesis
Transferase GPPS small subunit2	GPPS	A0A1V0QSI1	Cannabis sativa	278	1			Isoprenoid biosynthesis
4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase	HDR	A0A1V0QSH9	Cannabis sativa	408	6		Converts (E)-4-hydroxy-3-methylbut-2-en-1-yl-2P into isopentenyl-2P	Isoprenoid biosynthesis
Isopentenyl-diphosphate delta-isomerase	IDI	A0A1V0QSG5	Cannabis sativa	304	7		Converts isopentenyl diphosphate into dimethylallyl diphosphate	Isoprenoid biosynthesis
Mevalonate kinase	MK	A0A1V0QSI0	Cannabis sativa	416	3	2.7.1.36	Converts (R)-mevalonate into (R)-5-phosphomevalonate	Isoprenoid biosynthesis
Diphosphomevalonate decarboxylase	MPDC	A0A1V0QSG4	Cannabis sativa	455	4			Isoprenoid biosynthesis

Protein annotation	Abbreviation	Uniprot Accession or Patent	Species	Length (AA)	No. of peptides	EC No.	Function (CC)	Pathway
Phosphomevalonate kinase	PMK	A0A1V0QSH8	Cannabis sativa	486	4		Converts (R)-5-phosphomevalonate into (R)-5-diphosphomevalonate	Isoprenoid biosynthesis
Non-specific lipid-transfer protein	ltp	P86838	Cannabis sativa	20	3		transfer lipids across membranes	Lipid biosynthesis
Non-specific lipid-transfer protein	ltp	W0U0V5	Cannabis sativa	91	9		transfer lipids across membranes	Lipid biosynthesis
4-coumarate:CoA ligase	4CL	A0A142EGJ1	Cannabis sativa	544	1	6.2.1.12	forms 4-coumaroyl-CoA from 4-coumarate	Phenylpropanoid biosynthesis
4-coumarate:CoA ligase	4CL	V5KXG5	Cannabis sativa	550	3	6.2.1.12	forms 4-coumaroyl-CoA from 4-coumarate	Phenylpropanoid biosynthesis
Phenylalanine ammonia-lyase	PAL	V5KWZ6	Cannabis sativa	707	4	4.3.1.24	Catalyses L-phenylalanine = trans-cinnamate + ammonia	Phenylpropanoid biosynthesis
NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic	ndhF	A0A0C5AUJ6	Cannabis sativa	755	1	1.6.5.-	NDH shuttles electrons from NAD(P)H:plastoquinone to quinones	Photosynthesis
Photosystem I P700 chlorophyll a apoprotein A1	psaA	A0A0U2DTB0	Cannabis sativa	750	2	1.97.1.12	bind P700, the primary electron donor of PSI	Photosynthesis
Photosystem I P700 chlorophyll a apoprotein A2	psaB	A0A0C5APY0	Cannabis sativa	734	2	1.97.1.12	bind P700, the primary electron donor of PSI	Photosynthesis
Photosystem I iron-sulfur center	psaC	A0A0C5AS17	Cannabis sativa	81	10	1.97.1.12	assembly of the PSI complex	Photosynthesis
Photosystem II CP47 reaction center protein	psbB	A9XV91	Cannabis sativa	488	1		binds chlorophyll in PSII	Photosynthesis
Ribulose biphosphate carboxylase large chain	rbcL	A0A0B4SX31	Cannabis sativa	312	15	4.1.1.39	carboxylation of D-ribulose 1,5-bisphosphate	Photosynthesis
Small ubiquitin-related modifier	smt3	Q5TIQ0	Cannabis sativa	76	2		response to auxin	Phytohormone response
Cytochrome c biogenesis FC	ccmFc	A0A0M4RVN1	Cannabis sativa	447	1		Mitochondrial electron carrier protein	Respiration
Cytochrome c biogenesis FN	ccmFn	A0A0M3UM18	Cannabis sativa	575	2		Mitochondrial electron carrier protein	Respiration

Protein annotation	Abbreviation	Uniprot Accession or Patent	Species	Length (AA)	No. of peptides	EC No.	Function (CC)	Pathway
Cytochrome c biogenesis protein CcsA	ccsA	A0A0C5B2L0	Cannabis sativa	320	1		biogenesis of c-type cytochromes	Respiration
Cytochrome c	cytC	P00053	Cannabis sativa	111	2		Mitochondrial electron carrier protein	Respiration
7S vicilin-like protein	Cs7S	A0A219D1T7	Cannabis sativa	493	2		nutrient reservoir activity	Storage
Edestin 1	ede1D	A0A090CXP5	Cannabis sativa	511	1		Seed storage protein	Storage
4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	CMK	A0A1V0QSI2	Cannabis sativa	408	4		Adds 2-phosphate to 4-CDP-2-C-methyl-D-erythritol	Terpenoid biosynthesis
1-deoxy-D-xylulose-5-phosphate synthase	DXPS1	A0A1V0QSH6	Cannabis sativa	730	2		Converts D-glyceraldehyde 3P into 1-deoxy-D-xylulose 5P	Terpenoid biosynthesis
1-deoxy-D-xylulose-5-phosphate synthase	DXS2	A0A1V0QSH5	Cannabis sativa	606	5		Converts D-glyceraldehyde 3P into 1-deoxy-D-xylulose 5P	Terpenoid biosynthesis
4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	HDS	A0A1V0QSG3	Cannabis sativa	748	3		Converts (E)-4-hydroxy-3-methylbut-2-en-1-yl-2P into 2-C-methyl-D-erythritol 2,4-cyclo-2P	Terpenoid biosynthesis
3-hydroxy-3-methylglutaryl coenzyme A reductase	hmgR	A0A1V0QSF5	Cannabis sativa	588	5	1.1.1.34	synthesizes (R)-mevalonate from acetyl-CoA	Terpenoid biosynthesis
3-hydroxy-3-methylglutaryl coenzyme A reductase	hmgR	A0A1V0QSG7	Cannabis sativa	572	2	1.1.1.34	synthesizes (R)-mevalonate from acetyl-CoA	Terpenoid biosynthesis
Terpene synthase	TPS	A0A1V0QSF2	Cannabis sativa	567	1		formation of cyclic terpenes through the cyclization of linear terpenes	Terpenoid biosynthesis
Terpene synthase	TPS	A0A1V0QSF3	Cannabis sativa	551	3		formation of cyclic terpenes through the cyclization of linear terpenes	Terpenoid biosynthesis
Terpene synthase	TPS	A0A1V0QSF4	Cannabis sativa	613	1		formation of cyclic terpenes through the cyclization of linear terpenes	Terpenoid biosynthesis

Protein annotation	Abbreviation	Uniprot Accession or Patent	Species	Length (AA)	No. of peptides	EC No.	Function (CC)	Pathway
Terpene synthase	TPS	A0A1V0QSF6	Cannabis sativa	551	1		formation of cyclic terpenes through the cyclization of linear terpenes	Terpenoid biosynthesis
Terpene synthase	TPS	A0A1V0QSF8	Cannabis sativa	629	2		formation of cyclic terpenes through the cyclization of linear terpenes	Terpenoid biosynthesis
Terpene synthase	TPS	A0A1V0QSF9	Cannabis sativa	624	2		formation of cyclic terpenes through the cyclization of linear terpenes	Terpenoid biosynthesis
Terpene synthase	TPS	A0A1V0QSG0	Cannabis sativa	573	1		formation of cyclic terpenes through the cyclization of linear terpenes	Terpenoid biosynthesis
Terpene synthase	TPS	A0A1V0QSG1	Cannabis sativa	640	1		formation of cyclic terpenes through the cyclization of linear terpenes	Terpenoid biosynthesis
Terpene synthase	TPS	A0A1V0QSG6	Cannabis sativa	556	3		formation of cyclic terpenes through the cyclization of linear terpenes	Terpenoid biosynthesis
Terpene synthase	TPS	A0A1V0QSH1	Cannabis sativa	594	1		formation of cyclic terpenes through the cyclization of linear terpenes	Terpenoid biosynthesis
(-)-limonene synthase, chloroplastic	TPS1	A7IZZ1	Cannabis sativa	622	2	4.2.3.16	monoterpene (C10) olefins biosynthesis	Terpenoid biosynthesis
Maturase K	matK	A0A1V0IS32	Cannabis sativa	509	1		assists in splicing its own and other chloroplast group II intron	Transcription
Maturase K	matK	Q95BY0	Cannabis sativa	507	2		assists in splicing its own and other chloroplast group II intron	Transcription
Maturase R	matR	A0A0M5M254	Cannabis sativa	651	1		assists in splicing introns	Transcription

Protein annotation	Abbreviation	Uniprot Accession or Patent	Species	Length (AA)	No. of peptides	EC No.	Function (CC)	Pathway
DNA-directed RNA polymerase subunit beta	rpoB	A0A0C5ARQ8	Cannabis sativa	1070	3	2.7.7.6	transcription of DNA into RNA	Transcription
DNA-directed RNA polymerase subunit beta	rpoB	A0A0C5ARX9	Cannabis sativa	1393	4	2.7.7.6	transcription of DNA into RNA	Transcription
DNA-directed RNA polymerase subunit beta	rpoB	A0A0U2H5U7	Cannabis sativa	1070	1	2.7.7.6	transcription of DNA into RNA	Transcription
DNA-directed RNA polymerase subunit beta	rpoC1	A0A0C5AUF5	Cannabis sativa	683	6	2.7.7.6	transcription of DNA into RNA	Transcription
DNA-directed RNA polymerase subunit beta	rpoC2	A0A0H3W6G1	Cannabis sativa	1389	1	2.7.7.6	transcription of DNA into RNA	Transcription
DNA-directed RNA polymerase subunit beta	rpoC2	A0A0X8GKF1	Cannabis sativa	1391	1	2.7.7.6	transcription of DNA into RNA	Transcription
DNA-directed RNA polymerase subunit beta	rpoC2	A0A1V0IS28	Cannabis sativa	1393	1	2.7.7.7	transcription of DNA into RNA	Transcription
Ribosomal protein L14	rpl14	A0A0C5AS10	Cannabis sativa	122	2		assembly of the ribosome	Translation
50S ribosomal protein L16, chloroplast	rpl16	A0A0C5AUJ2	Cannabis sativa	119	2		assembly of the 50S ribosomal subunit	Translation
Ribosomal protein L2	rpl2	A0A0M3ULW5	Cannabis sativa	337	2		assembly of the ribosome	Translation
50S ribosomal protein L20	rpl20	A0A0C5B2J3	Cannabis sativa	120	1		Binds directly to 23S rRNA to assemble the 50S ribosomal subunit	Translation
Ribosomal protein S11	rps11	A0A0C5ART4	Cannabis sativa	138	1		assembly of the ribosome	Translation
30S ribosomal protein S12, chloroplast	rps12	A0A0C5APY5	Cannabis sativa	132	1		translational accuracy	Translation
30S ribosomal protein S12, chloroplast	rps12	A0A0C5B2L8	Cannabis sativa	125	1		translational accuracy	Translation
Ribosomal protein S13	rps13	A0A0M5M201	Cannabis sativa	116	1		assembly of the ribosome	Translation
Ribosomal protein S19	rps19	A0A0M3ULW7	Cannabis sativa	94	1		assembly of the ribosome	Translation
Ribosomal protein S2	rps2	A0A0C5APX8	Cannabis sativa	236	1		assembly of the ribosome	Translation
30S ribosomal protein S3, chloroplast	rps3	A0A0C5ART6	Cannabis sativa	155	3		assembly of the 30S ribosomal subunit	Translation
Ribosomal protein S3	rps3	A0A0M3UM22	Cannabis sativa	548	1		assembly of the ribosome	Translation
Ribosomal protein S3	rps3	A0A110BC84	Cannabis sativa	548	1		assembly of the ribosome	Translation
Ribosomal protein S4	rps4	A0A0M4RG21	Cannabis sativa	352	1		assembly of the ribosome	Translation
Ribosomal protein S7	rps7	A0A0C5ARU3	Cannabis sativa	155	2		assembly of the ribosome	Translation
Ribosomal protein S7	rps7	A0A0M4R6T5	Cannabis sativa	148	1		assembly of the ribosome	Translation

Protein annotation	Abbreviation	Uniprot Accession or Patent	Species	Length (AA)	No. of peptides	EC No.	Function (CC)	Pathway
Protein TIC 214	ycf1	A0A0C5AS14	Cannabis sativa	356	2		protein precursor import into chloroplasts	Translation
Protein TIC 214	ycf1	A0A0H3W815	Cannabis sativa	1878	21		protein precursor import into chloroplasts	Translation
Acyl-activating enzyme 1	aae1	H9A1V3	Cannabis sativa	720	1			Unknown
Acyl-activating enzyme 10	aae10	H9A1W2	Cannabis sativa	564	1			Unknown
Acyl-activating enzyme 12	aae12	H9A8L1	Cannabis sativa	757	2			Unknown
Acyl-activating enzyme 13	aae13	H9A8L2	Cannabis sativa	715	3			Unknown
Acyl-activating enzyme 2	aae2	H9A1V4	Cannabis sativa	662	3			Unknown
Acyl-activating enzyme 3	aae3	H9A1V5	Cannabis sativa	543	7			Unknown
Acyl-activating enzyme 4	aae4	H9A1V6	Cannabis sativa	723	3			Unknown
Acyl-activating enzyme 5	aae5	H9A1V7	Cannabis sativa	575	1			Unknown
Acyl-activating enzyme 6	aae6	H9A1V8	Cannabis sativa	569	1			Unknown
Acyl-activating enzyme 8	aae8	H9A1W0	Cannabis sativa	526	3			Unknown
Cannabidiolic acid synthase-like 2	CBDAS-like 2	A6P6W1	Cannabis sativa	545	1		Has no cannabidiolic acid synthase activity	Unknown
Putative LOV domain-containing protein	LOV	A0A126WVX7	Cannabis sativa	664	8			Unknown
Putative LOV domain-containing protein	LOV	A0A126WVX8	Cannabis sativa	1063	7			Unknown
Putative LOV domain-containing protein	LOV	A0A126WZD3	Cannabis sativa	574	1			Unknown
Putative LOV domain-containing protein	LOV	A0A126X0M1	Cannabis sativa	725	4			Unknown
Putative LOV domain-containing protein	LOV	A0A126X1H2	Cannabis sativa	910	6			Unknown
Putative LysM domain containing receptor kinase	lyk2	U6EFF4	Cannabis sativa	599	1			Unknown
Uncharacterized protein	unknown	A0A1V0IS79	Cannabis sativa	1525	2			Unknown
Uncharacterized protein	unknown	L0N5C8	Cannabis sativa	543	1			Unknown
Protein Ycf2	ycf2	A0A0C5APZ4	Cannabis sativa	2302	9		ATPase of unknown function	Unknown
Protein translocase subunit	secA	A0A0N9ZJA6	Cannabis sativa' phytoplasm	158	7		Binds ATP	Translation
ATP synthase subunit beta, chloroplastic	atpB	A0A0U2DTE2	Cannabis sativa subsp. sativa	498	20	3.6.3.14	Produces ATP from ADP	Energy metabolism

Protein annotation	Abbreviation	Uniprot Accession or Patent	Species	Length (AA)	No. of peptides	EC No.	Function (CC)	Pathway
Acetyl-coenzyme A carboxylase subunit beta, chloroplast	accD	A0A0U2DTG7	Cannabis sativa subsp. sativa	497	3	2.1.3.15	acetyl coenzyme A carboxylase complex	Lipid biosynthesis
NAD(P)H-quinone oxidoreductase subunit K, chloroplast	ndhK	A0A0U2DTF9	Cannabis sativa subsp. sativa	226	1	1.6.5.-	NDH shuttles electrons from NAD(P)H:plastoquinone to quinones	Photosynthesis
Cytochrome f	petA	A0A0U2DW83	Cannabis sativa subsp. sativa	320	1		mediates electron transfer between PSII and PSI	Photosynthesis
Photosystem II protein D1	psbA	A0A0U2DTE4	Cannabis sativa subsp. sativa	353	2	1.10.3.9	assembly of the PSII complex	Photosynthesis
Photosystem II CP43 reaction center protein	psbC	A0A0U2DTE2	Cannabis sativa subsp. sativa	473	5		core complex of PSII	Photosynthesis
Photosystem II D2 protein	psbD	A0A0U2DVP6	Cannabis sativa subsp. sativa	353	3	1.10.3.9	assembly of the PSII complex	Photosynthesis
Cytochrome b559 subunit alpha	psbE	A0A0U2DTH9	Cannabis sativa subsp. sativa	83	2		reaction center of PSII	Photosynthesis
Ribulose biphosphate carboxylase large chain	rbcL	A0A0U2DW50	Cannabis sativa subsp. sativa	475	13	4.1.1.39	carboxylation of D-ribulose 1,5-bisphosphate	Photosynthesis
Photosystem I assembly protein Ycf4	ycf4	A0A0U2DVM4	Cannabis sativa subsp. sativa	184	1		assembly of the PSI complex	Photosynthesis
30S ribosomal protein S14, chloroplast	rps14	A0A0U2DTL4	Cannabis sativa subsp. sativa	100	2		Binds 16S rRNA, required for the assembly of 30S particles	Translation
30S ribosomal protein S15, chloroplast	rps15	A0A0U2DW79	Cannabis sativa subsp. sativa	90	1		assembly of the 30S ribosomal subunit	Translation
ATP synthase subunit beta, chloroplast	atpB	A0A0U2H0U7	Humulus lupulus	498	2	3.6.3.14	Produces ATP from ADP	Energy metabolism
ATP synthase subunit beta, chloroplast	atpB	A0A0U2H587	Humulus lupulus	191	1		Component of the F(0) channel	Energy metabolism
NAD(P)H-quinone oxidoreductase subunit I, chloroplast	ndhI	A0A0U2GY49	Humulus lupulus	171	2	1.6.5.-	NDH shuttles electrons from NAD(P)H:plastoquinone to quinones	Photosynthesis
DNA-directed RNA polymerase subunit beta	rpoC2	A0A0U2H146	Humulus lupulus	1398	1	2.7.7.6	transcription of DNA into RNA	Transcription

Protein annotation	Abbreviation	Uniprot Accession or Patent	Species	Length (AA)	No. of peptides	EC No.	Function (CC)	Pathway
50S ribosomal protein L20, chloroplastic	rpl20	A0A0U2H0V8	Humulus lupulus	120	1		Binds directly to 23S rRNA to assemble the 50S ribosomal subunit	Translation
30S ribosomal protein S4, chloroplastic	rps4	A0A0U2H5A0	Humulus lupulus	202	1		binds directly to 16S rRNA to assemble the 30S subunit	Translation
30S ribosomal protein S8, chloroplastic	rps8	A0A0U2GZU5	Humulus lupulus	134	2		binds directly to 16S rRNA to assemble the 30S subunit	Translation
Protein Ycf2	ycf2	A0A0U2H6B6	Humulus lupulus	2287	1		ATPase of unknown function	Unknown

- 68 -

[0216] The frequency of protein for each pathway in apical buds and trichomes is illustrated in pie charts (Figure 4).

[0217] For buds, most proteins belong to the cannabis secondary metabolism (24% in apical buds and 27% in trichomes), which encompasses the biosynthesis of phenylpropanoids, lipid, isoprenoids, terpenoids, and cannabinoids. Cannabinoid biosynthesis (5.6% in buds and 7.1% in trichomes) and terpenoid biosynthesis (6.8% in buds and 7.5% in trichomes) are a significant portion of this classification, with many terpene synthases (TPS, Table 4). We have identified two major enzymes involved in monolignol biosynthesis: phenylalanine ammonia-lyase (PAL) and 4-coumarate:CoA ligase (4CL) (Table 4); with three accessions the phenylpropanoid pathway only contributes to 1.9% of the identification results.

[0218] The second most prominent category is energy metabolism (28% in buds and 24% in trichomes), comprising photosynthesis and respiration. The third major category is gene expression metabolism (22% in buds and 26% in trichomes) which includes transcriptional and translational mechanisms. A significant portion of protein accessions remain of unknown function (13.4% in apical buds and 12.3% in trichomes). The pattern in the trichomes is very similar to that of apical buds although there is an enrichment of cannabinoid biosynthetic proteins (7.1% compared to 5.6%) and terpenoid biosynthetic proteins (7.5% to 6.8%).

[0219] We retrieved all the entries referenced under the keyword “*Cannabis sativa*” in UniprotKB and produced a histogram of their distribution per year of creation; most entries (81%) were created in 2015-2017, with only 10 created in 2018 (Figure 5). Therefore, whilst ever-increasing, the number of sequences from *C. sativa* publicly available in Uniprot is far from sufficient, and the proteomics community still must rely on information from unrelated plants species, such as *Arabidopsis*, and rice, to identify cannabis proteins.

Example 4 - Enzymes involved in phytocannabinoid pathway

[0220] To validate the extraction methods, we focused on the cannabis-specific pathway that attracts most of the interest in the medicinal cannabis industry, namely the

- 69 -

biosynthesis of phytocannabinoids. In our bottom-up results, five enzymes involved in phytocannabinoid biosynthesis and whose functions were described in the introduction were identified: 3,5,7-trioxododecanoyl-CoA synthase (OLS) identified with 7 peptides (19% coverage), olivetolic acid cyclase (OAC) identified with 6 peptides (13% coverage), geranyl-pyrophosphate-olivetolic acid geranyltransferase (GOT) identified with 5 peptides (17% coverage), delta9-tetrahydrocannabinolic acid synthase (THCAS) identified with 6 peptides (15 % coverage), and cannabidiolic acid synthase (CBDAS) identified with 8 peptides (17% coverage). The steps these enzymes catalyse are summarised in Figure 6A.

[0221] The two-dimensional hierarchical clustering analysis (2-D HCA) presented in Figure 6B clusters guanidine-HCl-based samples away from the urea-based samples, in particular, methods 3 and 5. Peptides do not cluster based on the protein they belong to. The greatest majority of the peptides (24, 84%) are more abundant in samples prepared using extraction methods 4 and 6. Both methods apply a TCA/solvent precipitation step followed by resuspension in a guanidine-HCl buffer. Consequently, this is the protein extraction method we recommend in order to recover and analyse the phytocannabinoid-related enzymes using a bottom-up proteomics strategy.

[0222] As more genomes are released, the identification of additional genes in the biosynthetic pathways is likely. Already THCAS and CBDAS gene clusters have been identified where the genes are highly homologous. The function of all these genes is yet to be confirmed and proteomics methods will be useful to identify which of genes are translated at high efficiency in different cannabis strains. In designing medicinal cannabis strains for specific therapeutic requirements, either by genomic assisted breeding techniques (especially genomic selection) or through genome editing this protein expression information will be critical to optimise cannabinoid and terpene biosynthesis.

Discussion

[0223] Six different extraction methods were assessed to analyse proteins from medicinal cannabis apical buds and trichomes. This is the first-time protein extraction is optimised from cannabis reproductive organs, and the guanidine-HCl buffer employed here has never been used before on *C. sativa* samples. Based on the number of intact proteins

- 70 -

quantified and the number of peptides identified it is evident that guanidine-HCl-based methods (2, 4, and 6) are best suited to recover proteins from medicinal cannabis buds and preceding this with a precipitation step in TCA/acetone (AB4) or TCA/ethanol (AB6), ensures optimum trypsin digestion followed by MS. The method is equally applicable to trichomes and buds and the trichomes display and will be instrumental in the production of designer medicinal cannabis strains.

Example 5 – Optimisation of manual top-down proteomics analysis

[0224] The known protein standards tested are myoglobin (Myo), β -lactoglobulin (β -LG), α -S1-casein (α -S1-CN) and bovine serum albumin (BSA) which vary not only in their AA sequence, their MW, but also the number of disulfide bridges and post-translational modifications (PTMs) they present. Only mature AA sequences, *i.e.* not including initial methionine residues and signal peptides, are used for sequencing annotations. Myoglobin (P68083., 153 AAs) can carry a phosphoserine on its third residue, β -lactoglobulin (P02754, 162 AAs) has two disulfide bonds, α -S1-casein (P02662, 199 AAs) is constitutively phosphorylated with up to nine phosphoserines, and BSA (P02769, 583 AAs) contains 35 disulfide bonds as well as various PTMs, most of which are phosphorylation sites. Oxidation of methionine residues of protein standards was encountered, possibly resulting from vortexing during the sample preparation. Precursors of oxidized proteoforms is purposefully disregarded in the manual annotation step, however, it is included as a dynamic modification for the Mascot search.

[0225] Tandem MS data from infused known protein standards fragmented using SID, ETD, CID and HCD were processed either manually in order to include SID data which are not considered as genuine MS/MS data, or automatically on *bona fide* MS/MS data only to test whether an automated workflow would successfully reproduce manual searches, and therefore could be applied to unknown proteins from cannabis samples. For manual curation, not all the MS/MS data produced was used, only that corresponding to the major isoforms. For instance, an oxidised proteoform of myoglobin was found but ignored for the manual annotation step which proved very labour-intensive and time-consuming.

- 71 -

[0226] Figure 7 displays spectra from myoglobin acquired following SID, ETD, CID, and HCD where increased energy was applied. No fragmentation is observed at SID 15V. Fragmentation of the most abundant ions of lower m/z starts to occur at SID 45V (not shown), is evident at SID 60V, and complete at SID 100V (Figure 7A).

[0227] Whilst MS/MS spectra of the most abundant multiply-charged ions were obtained as attested in Table 5, only two charge states, 942.68 m/z ($z=+18$) and 1211.79 m/z ($z=+14$), are exemplified in Figure 7B and 7C, respectively. Applying ETD for increasingly longer periods, from 5 to 25 ms, results in greater protein dissociations. As ETD fragmentation improves, fragments mass range extends from intermediate to high m/z values (Figure 7B). Less fragmentation is observed when ETD is applied for 5 ms (356 and 143 deisotoped fragments for 942.68 m/z and 1211.79 m/z , respectively), than when ETD is sustained for longer activation times (Table 5).

[0228] Maximum number of fragments are reached with 20 ms for 942.68 m/z (516 deisotoped fragments) and 15 ms from 1211.79 m/z (455 deisotoped fragments) (Table 5).

Table 5. Number of spectral MS/MS fragments for each protein standard

Myoglobin										
	m/z	All	848.51	893.22	942.68	1211.79	1304.93			
	Z	NA	20	19	18	14	13			
	RI(%)	NA	100	98	96	38	24			
MS/MS mode	NCE									Mean
SID	15	171								171
SID	60	725								725
SID	100	656								656
CID	30		210	174	194	241	180			200
CID	35		255	180	233	369	389			285
CID	40		223	176	243	389	411			288
CID	45		226	219	227	385	383			288
CID	50		233	227	209	402	368			288
ETD	5		220	229	356	143	79			205
ETD	10		66	172	470	392	282			276
ETD	15		120	190	504	455	273			308
ETD	20		135	457	516	411	309			366
ETD	25		89	431	468	365	263			323
HCD	10		102	71	116	60	42			78
HCD	15		146	148	175	105	118			138
HCD	20		250	244	280	252	262			258
HCD	25		253	301	511	529	499			419
HCD	30		303	260	376	462	572			395
Min		171	66	71	116	60	42			
Max		656	303	457	516	529	572			
Mean		517	189	232	325	331	295			274

b-LG		m/z	All	972.19	1026.15	1091.4	1232.84			
		Z	NA	19	18	17	15			
		RI(%)	NA	46	74	80	100			
	MS/MS mode	NCE						Mean		
	SID	15	543					543		
	SID	60	2160					2160		
	SID	100	3882					3882		
	CID	30		336	344	397	481	390		
	CID	35		392	412	507	529	460		
	CID	40		333	397	474	571	444		
	CID	45		358	439	511	531	460		
	CID	50		343	387	440	544	429		
	ETD	5		379	220		160	253		
	ETD	10		375	271		456	367		
	ETD	15		325	137		433	298		
	ETD	20		412	170		431	338		
	ETD	25		242	102		443	262		
	HCD	10		155	230	252	119	189		
	HCD	15		395	469	608	517	497		
	HCD	20		504	588	815	664	643		
	HCD	25		310	449	634	737	533		
	HCD	30		298	350	443	419	378		
		Min		543	155	102	252	119		
		Max		3882	504	588	815	737		
		Mean		2195	344	331	508	469	413	
a-SI-CN		m/z	All	1139.6	1193.38	1319.14	1480.59			

BSA	Z	NA	21	20	18	17	16	
	RI(%)	NA	94	100	70	52	36	
	MS/MS mode	NCE						Mean
	SID		414					414
	SID		728					728
	SID		891					891
	CID		159	166		51		125
	CID		455	460		247		387
	CID		401	466		259		375
	CID		455	389		254		366
	CID		432	375		259		356
	ETD	5		111	97			104
	ETD	10		424	302			363
	ETD	15		352	224			288
	ETD	20		292	209			251
	ETD	25		193	145			169
	HCD	10		112	120	51	46	82
	HCD	15		660	702	721	472	639
	HCD	20		660	651	586	464	590
	HCD	25		431	519	544	459	488
	HCD	30		289	301	256	251	274
	Min		414	112	111	51	46	
	Max		891	660	702	721	259	472
	Mean		678	406	368	314	214	338
		m/z	All	953.93	994.98	1061.5	118.08	
		Z	NA	72	69	65	59	

MS/MS mode	RI(%)	NA	72	76	68	44	Mean
SID	15						
SID	60	84					84
SID	100	436					436
CID	30			0	0	0	0
CID	35			182	203	109	165
CID	40			150	177	96	141
CID	45			153	196	101	150
CID	50			157	223	125	168
ETD	5		0		0		0
ETD	10		161		359		260
ETD	15		58		409		234
ETD	20		124		352		238
ETD	25		58		277		168
HCD	10		0	0			0
HCD	15		232	196			214
HCD	20		238	227			233
HCD	25		113	121			117
HCD	30		85	87			86
Min		84	0	0	0	0	
Max		436	238	227	409	125	
Mean		260	107	127	220	86	145

- 76 -

[0229] Increasing the energy of CID mode from 35 to 50 eV has less impact on fragmentation as can be visually assessed on Figure 7B and 7C and in Table 5, with more constant numbers of fragments generated, albeit still increasing with the energy levels applied. As CID fragmentation intensifies, more ions of low m/z appear (Figure 7B). The least number of fragments are obtained at CID 35 eV (194 and 241 deisotoped fragments for 942.68 m/z and 1211.79 m/z , respectively) and maximum numbers are reached at CID 50 eV with 209 and 402 fragments for 942.68 m/z and 1211.79 m/z , respectively (Table 5). Compiling all CID fragment masses together in Prosight Lite program yields a myoglobin sequence coverage of 44%. Similar to ETD, fragmentation resulting from HCD mode is enhanced as more energy is applied, from 10 to 30 eV. This is clearly visible on Figure 7B and 7C, with only a handful of fragments observed at HCD 10-15 eV, and fragmentation fully developing at HCD 20 eV and above. As HCD fragmentation improves, the mass range of the ions visibly extends (Figure 7B and 7C). Only 116 and 60 deisotoped fragments were detected at HCD 10 eV from 942.68 m/z and 1211.79 m/z , respectively, with number of fragments peaking at HCD 25 eV to 511 and 529 for 942.68 m/z and 1211.79 m/z , respectively (Table 5). Compiling all HCD fragment masses together in Prosight Lite program yielded a myoglobin sequence coverage of 57%. The outcome of fragmentation is much less dependent on a particular collisional value for CID than for HCD. Furthermore, while CID and HCD spectra are very similar, HCD achieves optimal fragmentation at lower energy levels.

[0230] Different precursors of the same protein (*i.e.* different charge states) require different energy level for optimum fragmentation (Table 5). Furthermore, targeting a lower charge state shifts the fragment masses to the right of the mass range, towards high m/z values (Figure 7C). Row averages of fragments across all five charge states of myoglobin (+20, +19, +18, +14, +13) highlight that a minimum energy level must be reached for any meaningful protein dissociation to occur (Table 5). As far as myoglobin is concerned, these values are 60 eV for SID, 25 eV for HCD, 20 ms for ETD, and 40-50 eV for CID, sorted in decreasing order. Column averages of fragments across all MS/MS modes indicate that some precursors are more amenable to fragmentation than others, with charge states +18 (942.68 m/z) and +14 (1211.79 m/z) on average generating most fragments (325 and 331,

- 77 -

respectively, Table 5). This suggests that parent ions displaying both high m/z (low charge state) and high intensity should be favoured for top-down sequencing experiments.

[0231] All the deconvoluted and deisotoped masses obtained by applying increasing energy levels of SID, CID, HCD and ETD were submitted to ProSight Lite and searched against the AA sequence of myoglobin, without the initial methionine which gets processed out during the maturation step. All the resulting matching b-, c-, y-, and z-type ions are reported into Table 6 and plotted according to their position along the mature AA sequence of myoglobin (153 AA).

Table 6. Number of matching ions in Prosight Lite program (tolerance of 50 ppm) for each protein standard

	MS/MS mode	m/z	All	848.51	893.22	942.68	1211.79	1304.93	
Myoglobin	Z		NA	20	19	18	14	13	
	RI(%)		NA	100	98	96	38	24	
	NCE								Mean
	SID	15	1						1
	SID	60	19						19
	SID	100	20						20
	CID	30		10	4	10	27	13	13
	CID	35		12	8	12	42	41	23
	CID	40		11	8	14	44	40	23
	CID	45		10	9	14	39	44	23
	CID	50		19	12	14	36	44	25
	ETD	5		25	6	17	5	2	11
	ETD	10		17	24	36	24	21	24
	ETD	15		28	17	45	29	20	28
	ETD	20		40	45	57	36	21	40
	ETD	25		28	48	53	26	19	35
	HCD	10		2	3	2	1	1	2
	HCD	15		4	2	5	2	4	3
	HCD	20		9	11	22	12	7	12
	HCD	25		17	11	33	48	55	33
	HCD	30		17	11	22	52	47	30
b-LG	Min		1	2	2	2	1	1	2
	Max		20	40	48	57	52	55	45
	Mean		13	17	15	24	28	25	20
	Length of seq (AA)		153	153	153	153	153	153	153
	% Max		13.1	26.1	31.4	37.3	34.0	35.9	30
	m/z		All	972.19	1026.15	1091.4	1232.84		
	Z		NA	19	18	17	15		
	RI(%)		NA	46	74	80	100		
	NCE								Mean
	SID	15	2						2
	SID	60	27						27
	SID	100	66						66
	CID	30		11	11	11	23	14	14
	CID	35		17	18	24	23	21	21
	CID	40		20	19	23	21	21	21
	CID	45		20	20	26	23	22	22

	CID	50		21	17	18	22	20
	ETD	5		8	4		4	5
	ETD	10		20	9		8	12
	ETD	15		14	9		12	12
	ETD	20		20	14		13	16
	ETD	25		20	11		19	17
	HCD	10		1	6	5	3	4
	HCD	15		14	28	34	17	23
	HCD	20		19	24	29	27	25
	HCD	25		15	22	28	27	23
	HCD	30		21	20	26	21	22
	Min		2	1	4	5	3	3
	Max		66	21	28	29	23	33
	Mean		32	16	15	22	18	21
	Length of seq (AA)		162	162	162	162	162	162
a-15-b	% Max		40.7	13.0	17.3	17.9	14.2	21
	m/z		All	1139.6	1193.38	1319.14	1480.59	
	Z		NA	21	20	18	17	16
	RI(%)		NA	94	100	70	52	36
	MS/MS mode	NCE						Mean
	SID	15	1					1
	SID	60	3					3
	SID	100	7					7
	CID	30		4	2		6	4
	CID	35		7	10		12	10
	CID	40		8	9		12	10
	CID	45		7	10		9	9
	CID	50		17	6		15	13
	ETD	5			3	0		2
	ETD	10			23	13		18
	ETD	15			25	15		20
	ETD	20			24	19		22
	ETD	25			25	18		22
	HCD	10		1	2	1	1	1
	HCD	15		24	32	30	28	29
	HCD	20		37	41	35	33	37
	HCD	25		43	37	39	39	40
	HCD	30		37	36	38	38	37
	Min		1	1	2	0	6	2
	Max		7	43	41	39	15	31

BSA	Mean	4	19	19	19	23	11	28	17
	Length of seq (AA)	199	199	199	199	199	199	199	199
	% Max	3.5	21.6	20.6	19.6	19.6	7.5	19.6	15
	m/z	All	953.93	994.98	1061.5	118.08			
	Z	NA	72	69	65	59			
	RI(%)	NA	72	76	68	44			
	MS/MS mode	NCE							Mean
	SID	15							
	SID	60							1
	SID	100							4
	CID	30		0	0	0	0		0
	CID	35		4	4	6	4		5
	CID	40		5	5	5	2		4
	CID	45		5	5	5	3		4
	CID	50		1	6	6	7		5
	ETD	5	0		0	0			0
	ETD	10	6		4				5
	ETD	15	4		8	8			6
	ETD	20	8		4	4			6
	ETD	25	7		8	8			8
	HCD	10	0	0					0
	HCD	15	9	3					6
	HCD	20	13	11					12
	HCD	25	11	12					12
	HCD	30	9	11					10
	Min	1	0	0	0	0	0		0
	Max	4	13	12	8	8	7		9
	Mean	2	7	5	5	5	3		4
	Length of seq (AA)	583	583	583	583	583	583		583
	% Max	0.7	2.2	2.1	1.4	1.4	1.2		2

- 81 -

[0232] Because different ions of the same protein underwent different types of fragmentation at varying energy levels, the data is quite redundant, with many dots depicted at a particular AA position (Figure 8A).

[0233] Mostly darker colours are represented, confirming that higher energy levels produced meaningful data. Figure 8B corresponds to the summation of the number of matched ions per MS/MS mode, irrespective of the energy applied. It shows that some parts of the sequence are highly amenable to specific dissociation modes. For instance, ETD is more suited for N-terminus and the central part of the protein, while CID and HCD help sequence the C-terminus. CID generates predominantly low yields N- and C-terminal fragments from intact proteins. SID was only effective on the N-terminus of myoglobin.

[0234] Figure 8C represents a summation of the number of matched ions at each AA position, irrespective of the MS/MS mode or the energy applied. Because less dots are displayed, the areas of myoglobin that resisted fragmentation under our conditions become more visible. Myoglobin N-terminus is well covered up to position 99, albeit with some interruptions, whereas the C-terminus is only covered up to the last 10 AAs. The region spanning AAs 100 to 140 of myoglobin is only partially sequenced

[0235] ProSight Lite output confirmed that both N- and C-termini of myoglobin sequence are well covered, with many AAs identified from b-, c-, y-, and z-types of ions (Figure 8D). Some AAs were could only be fragmented once, either using ETD or HCD. Therefore, resorting to multiple MS/MS modes is essential to maximise top-down sequencing. Overall, 83% inter-residues cleavages were annotated, accounting for 73% (111/153 AAs) sequence coverage of myoglobin (Figure 8D). Figure 8C summarizes top-down sequencing efficiency for myoglobin in these experiments. It varies according to the charge state and the dissociation type.

- 82 -

[0236] The commercial standards used in this study contain mixtures of protein isoforms. Deconvolution of full scan FTMS1 (Figure 9A) supplied accurate masses for β -lactoglobulin, α -S1-casein and average masses for BSA with an error < 50 ppm, which assisted in the determination of which protein isoforms underwent MS/MS analysis and which sequence to use for ProSight Lite annotation.

[0237] Precursors from allelic variant A of β -lactoglobulin and allelic variant B of α -S1-casein with eight phosphorylation were selected for fragmentation. Examples of SID, ETD, CID, and HCD spectra for each protein are shown in Figure 9A. Theoretical charge state distributions for proteins showed that the absolute number of charges that precursors carry and the relative width of the charge state distribution both increased as protein mass augmented. In this study, high numbers of microscans were used to perform spectral averaging in order to increase S/N but the trade-off is a longer duty cycle and acquisition time, which restricts throughput.

[0238] The number of deconvoluted, deisotoped fragments of all protein standards are listed in Table 5. As previously observed for myoglobin, fragmentation efficiency assessed on the number of fragments generated depends on the charge state of the precursor, the MS/MS mode, and the energy applied, albeit in a protein-specific fashion. For instance, abundant parents of lower charge states yielded numerous fragments in the case of β -lactoglobulin ($z=+17$, 508 fragments on average) and BSA ($z=+68$, 220 fragments on average), whereas abundant precursor of high charge state yielded numerous fragments in the case of α -S1-casein ($z=+21$, 406 fragments on average). If we look at which MS/MS mode and which energy level produced the greatest number of fragments on average across all charge states, we find that the ranking for β -lactoglobulin is SID 100 V > HCD 20 eV > CID 35-45 eV > ETD 10 ms. The ranking for α -S1-casein is SID 100 V > HCD 15 eV >

- 83 -

CID 35 eV > ETD 10 ms. The ranking for BSA is SID 100 V > ETD 10 ms > HCD 20 eV > CID 50 eV.

[0239] A plethora of fragments does not necessary translate into high AA sequence coverage as can be seen when Tables 5 and 6, similarly arranged, are compared. The phenomenon of “overfragmentation” is predicted to result from secondary dissociation of the initial daughter ions when normalized collision energies are enhanced. Whilst noticeable for all MS/MS modes tested, the best evidence of this applied to SID fragmentation with at best only 3% (26/656 for myoglobin) of the fragments being annotated in ProSight Lite. Its efficacy in top-down sequencing varies greatly among the proteins studied here, accounting for as little as 1% coverage of BSA sequence, 4% coverage of α -S1-casein sequence, up to 13% for myoglobin and an impressive 41% for β -lactoglobulin (Table 6).

[0240] When true MS/MS data resulting from ETD, CID, HCD experiments are considered, high number of fragments are a requisite for proper top-down sequencing, yet it is not the MS/MS spectra with the maximum number of peaks that yields the greatest number of matched ions in ProSight Lite (Tables 5 and 6). For instance, in the case of β -lactoglobulin precursor 1091.4 m/z undergoing HCD fragmentation, 815 fragments were obtained with 20 eV which accounted for 29 matched ions, and 608 fragments were obtained with 15 eV which accounted for 34 matched ions. In another example, looking at α -S1-casein precursor 1139.6 m/z undergoing CID fragmentations, 35 eV created 455 fragments with only 7 being annotated in Prosight Lite, while 435 fragments obtained with 50 eV led to 17 matches. Compiling all fragmentation data obtained for each protein and submitting them to Prosight Lite program gave the maximum sequence coverage achieved in this study: 56% for β -lactoglobulin, 41% for α -S1-casein and 6% for BSA (Figure 9B).

- 84 -

[0241] These data demonstrate that for known proteins of different MWs, sequence coverage varies according to the protein itself, its size (Figure 10) and intrinsic properties, the abundance and charge state of the precursor ion, the MS/MS mode, and the level of energy applied. Therefore, not many general rules can be surmised apart from the fact that the more MS/MS data, the greater the sequence coverage. A key factor though is the signal intensity, the higher S/N the better the fragmentation pattern (data not shown). Generally speaking and under the optimised conditions, medium to high energy levels tend to improve sequence annotation.

Example 6 - Optimisation of automatic top-down proteomics analysis

[0242] An automated workflow was developed using Proteome Discovered to export a Mascot Generic File (MGF) containing 371 MS/MS peak lists which was submitted to Mascot algorithm. The parameters bearing the greatest impact on the results were tested, namely the database, the type of dynamic modifications and the fragment tolerance. The search results are summarised in Table 7. Mascot outcome was then compared to the manual curation described above. The immediate advantage of automation is the speed at which all the data is processed, not accounting for database search times which can be significant (days if the error-tolerant option is selected in mascot program). Another advantage is that the search runs in the background, freeing up time to perform other tasks. Automation also greatly limits the potential for man-made errors.

Table 7. Summary of Mascot results for standards and cannabis samples using various databases, dynamic modifications, and fragment tolerance.

Mascot job #	Sample	DB	Taxonomy	# entries	# residues	Static mods.	Dynamic mods.	Frag. toler.	Decoy or Error	Duration			Total # MS2 spectra	# unassign MS/MS spectra	# MS2 spectra matched	% MS2 spectra matched	# unique proteins
										(s)	(min)	(h)					
19018	Stand.	HM	all	59	10,517	carbamidome thyl C	Protein N-term acetyl, oxidation M, phospho ST	50 ppm	decoy	118	2.0	0.03	371	266	105	28	4
19037	Stand.	HM	all	59	10,517	carbamidome thyl C	Protein N-term acetyl, oxidation M, phospho ST	2 Da	decoy	189	3.2	0.05	371	49	322	87	13
19020	Stand.	SP	all	559228	200,905,86 ₉	carbamidome thyl C	oxidation M, phospho ST	50 ppm	decoy	25923 ₆	4320.6	72.01	371	325	46	12	1
19040	Stand.	SP	all	559228	200,905,86 ₉	carbamidome thyl C	oxidation M, phospho ST	2 Da	decoy	14514 ₄	2419.1	40.32	371	258	113	30	1
19052	Stand.	SP	other mammalia	13186		carbamidome thyl C	Protein N-term acetyl, oxidation M, phospho ST	50 ppm	decoy	17651	294.2	4.90	371	309	62	17	1
19047	Stand.	SP	other mammalia	13186		carbamidome thyl C	Protein N-term acetyl, oxidation M, phospho ST	2 Da	decoy	11549	192.5	3.21	371	235	136	37	3
19031	Canna.	UP	all	663	221,206	carbamidome thyl C	Protein N-term acetyl, oxidation M	50 ppm	error	88377	1473.0	24.55	11250	11040	210	2	12
19030	Canna.	UP	all	663	221,206	carbamidome thyl C	Protein N-term acetyl, oxidation M	50 ppm	decoy	29	0.5	0.01	11250	11037	213	2	20
19048	Canna.	UP	all	663	221,206	carbamidome thyl C	Protein N-term acetyl, oxidation M	2 Da	decoy	150	2.5	0.04	11250	10895	355	3	36
19050	Canna.	UP	all	663	221,206	carbamidome thyl C	Protein N-term acetyl, oxidation M, phospho ST	50 ppm	decoy	6308	105.1	1.75	11250	11063	187	2	21
19049	Canna.	UP	all	663	221,206	carbamidome thyl C	Protein N-term acetyl, oxidation M, phospho ST	2 Da	decoy	6195	103.3	1.72	11250	10660	590	5	61
19051	Canna.	UP	all	663	221,206	carbamidome thyl C	none	50 ppm	decoy	12	0.2	0.00	11250	11036	214	2	20
19043	Canna.	UP	all	663	221,206	carbamidome thyl C	none	2 Da	decoy	18	0.3	0.01	11250	10959	291	3	24
19042	Canna.	SP	all	559228	200,905,86 ₉	carbamidome thyl C	none	2 Da	decoy	883	14.7	0.25	11250	10252	998	9	94

Masco job #	Sample	DB	Taxonomy	# entries	# residues	Static mods.	Dynamic mods.	Frag. toler.	Decoy or Error	Duration			Total # MS2 spectra	# unassign MS/MS spectra	# MS2 spectra matched	% MS2 spectra matched	# unique proteins
										(s)	(min)	(h)					
19044	Canna.	SP	viridiplanta e	39800		carbamidome thyl C	none	2 Da	decoy	233	3.9	0.06	11250	10069	1181	10	80
19045	Canna.	SP	viridiplanta e	39800		carbamidome thyl C	Protein N-term acetyl, oxidation M	2 Da	decoy	1685	28.1	0.47	11250	9898	1352	12	141
19046	Canna.	SP	viridiplanta e	39800		carbamidome thyl C	Protein N-term acetyl, oxidation M, phospho ST	2 Da	decoy	19237 6	3206.3	53.44	11250	9387	1863	17	274

- 87 -

[0243] A 'homemade' database of 59 *fasta* sequences comprising horse myoglobin, all known allelic variants of bovine caseins, and the most abundant bovine whey proteins (α -lactalbumin, β -lactoglobulin, bovine serum albumin) was searched on our local Mascot server using a ± 50 ppm fragment tolerance. The Mascot output is reported in as a list of proteins and proteoforms in Tables 8 and 9, respectively as well as exemplified in Figure 12A. Four accessions are listed, based on 105 (28%) MS/MS spectra matched, correctly identifying myoglobin, α -S1-casein variant B and β -lactoglobulin, albeit not the correct allelic variant. Based on accurate mass and accounting for carbamidomethylation sites, variant A of β -lactoglobulin was expected and Mascot identified variants E and F instead which differ at five AA positions, due to insufficient sequence coverage. Bovine serum albumin was not identified. Myoglobin achieves the highest score (3782), with 97 MS/MS spectra yielding annotations, 82% of them being redundant, which is expected as our data is on purpose highly repetitive. Unmodified myoglobin was the most frequently identified (41%), as it was the most abundant proteoform in the spectra. Oxidised proteoforms were also identified, in combination or not with phosphorylated and acetylated proteoforms. Six MS/MS spectra led to the correct identification of α -S1-casein B with a score of 123. Several proteoforms are listed, all of them oxidized and bearing from 6 to 13 phosphorylations. Mascot scores for β -lactoglobulin were below the ion score threshold (<27), indicative of low sequence homology. If the fragment tolerance is increased to ± 2 Da, 13 proteins are identified from 322 (87%) MS/MS spectra matches (Tables 8 and 9). Search times presented are in the order of minutes.

Table 8. List of proteins identified from standard samples using Mascot algorithm and either a homemade or SwissProt database

Job no.	DB	Taxonomy	PTM	Frag. tol.	Family	M	DB	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI
19018	HM	all	AOP	50 ppm	1	1	TDS_milk-protein-variants-sequences	P68082	3782	16941	97	97	1	1	2.94
19018	HM	all	AOP	50 ppm	2	1	TDS_milk-protein-variants-sequences	P02662	123	22960	6	6	1	1	1.16
19018	HM	all	AOP	50 ppm	3	1	TDS_milk-protein-variants-sequences	P02754	21	18531	1	1	1	1	0.17
19018	HM	all	AOP	50 ppm	4	1	TDS_milk-protein-variants-sequences	P02754	17	18472	1	1	1	1	0.17
19037	HM	all	AOP	2 Da	1	1	TDS_milk-protein-variants-sequences	P68082	12740	16941	131	131	1	1	5.59
19037	HM	all	AOP	2 Da	2	1	TDS_milk-protein-variants-sequences	P02662	628	22960	22	22	1	1	5
19037	HM	all	AOP	2 Da	3	1	TDS_milk-protein-variants-sequences	P02662	407	22888	13	13	1	1	2.18
19037	HM	all	AOP	2 Da	4	1	TDS_milk-protein-variants-sequences	P02754	395	18482	35	35	1	1	3.13
19037	HM	all	AOP	2 Da	5	1	TDS_milk-protein-variants-sequences	P02662	359	22987	10	10	1	1	1.79
19037	HM	all	AOP	2 Da	6	1	TDS_milk-protein-variants-sequences	P02662	332	22990	18	18	1	1	6.76
19037	HM	all	AOP	2 Da	7	1	TDS_milk-protein-variants-sequences	P02754	330	18472	30	30	1	1	2.03
19037	HM	all	AOP	2 Da	7	2	TDS_milk-protein-variants-sequences	P02754	72	18564	5	5	1	1	0.37
19037	HM	all	AOP	2 Da	8	1	TDS_milk-protein-variants-sequences	P02754	292	18500	25	25	1	1	2.01
19037	HM	all	AOP	2 Da	9	1	TDS_milk-protein-variants-sequences	P02754	117	18554	10	10	1	1	0.88
19037	HM	all	AOP	2 Da	10	1	TDS_milk-protein-variants-sequences	P02754	98	18531	9	9	1	1	0.88
19037	HM	all	AOP	2 Da	11	1	TDS_milk-protein-variants-sequences	P02754	75	18555	7	7	1	1	0.88
19037	HM	all	AOP	2 Da	12	1	TDS_milk-protein-variants-sequences	P02754	50	18641	3	3	1	1	0.17
19037	HM	all	AOP	2 Da	13	1	TDS_milk-protein-variants-sequences	P02754	41	18571	4	4	1	1	0.6
19020	SP	all	OP	50 ppm	1	1	SwissProt	MYG EQUUBU	1456	17072	46	46	2	2	2.91
19040	SP	all	OP	2 Da	1	1	SwissProt	MYG EQUUBU	8764	17072	113	113	2	2	4.49
19052	SP	other mammalia	AOP	50 ppm	1	1	SwissProt	MYG EQUUBU	2119	17072	62	62	2	2	6.72
19047	SP	other mammalia	AOP	2 Da	1	1	SwissProt	MYG EQUUBU	10298	17072	134	134	2	2	11.87
19047	SP	other mammalia	AOP	2 Da	2	1	SwissProt	NU6M TACAC	46	18085	1	1	1	1	0.18
19047	SP	other mammalia	AOP	2 Da	3	1	SwissProt	NU6M HIPAM	34	18642	1	1	1	1	0.17

Legend: HM, homemade database; SP, SwissProt database; A, Protein N-term acetylation; O, oxidation (M); P, phosphorylation.

Table 9. List of proteoforms identified from standard samples using Mascot algorithms and either a homemade or SwissProt database.

Job no.	Description	Score	Mass	Matches	Seqs	emPAI	Query	Dupes	Observed	Mrtc(prot)	Mrtc(alc)	%	M	Score	Expect	Rank	SEQ ID
19018	myoglobin (P68082)	3782	16941	97	1	2.94	35	3	16947.0184	16946.0112	17036.9261	-0.5336	0	66	2.60E-07	1	1
19018	myoglobin (P68082)	3782	16941	97	1	2.94	48	4	16948.0746	16947.0673	17036.9261	-0.5274	0	148	1.70E-15	1	2
19018	myoglobin (P68082)	3782	16941	97	1	2.94	62		16949.0282	16948.021	17116.8924	-0.9866	0	13	0.049	1	3
19018	myoglobin (P68082)	3782	16941	97	1	2.94	63		16949.0282	16948.021	17116.8924	-0.9866	0	15	0.029	1	4
19018	myoglobin (P68082)	3782	16941	97	1	2.94	64		16949.0395	16948.0322	17116.8924	-0.9865	0	32	0.0007	1	5
19018	myoglobin (P68082)	3782	16941	97	1	2.94	66	4	16949.0395	16948.0322	17116.8924	-0.9865	0	39	0.00014	1	6
19018	myoglobin (P68082)	3782	16941	97	1	2.94	71		16949.0502	16948.0429	17036.9261	-0.5217	0	103	5.00E-11	1	7
19018	myoglobin (P68082)	3782	16941	97	1	2.94	72		16949.0502	16948.0429	17116.8924	-0.9864	0	50	9.30E-06	1	8
19018	myoglobin (P68082)	3782	16941	97	1	2.94	74		16949.0738	16948.0665	17078.9367	-0.7663	0	18	0.017	1	9
19018	myoglobin (P68082)	3782	16941	97	1	2.94	133	17	16951.0397	16950.0324	16956.9598	-0.0409	0	122	5.80E-13	1	10
19018	myoglobin (P68082)	3782	16941	97	1	2.94	143	40	16951.0512	16950.044	16940.9649	0.0536	0	143	5.30E-15	1	11
19018	myoglobin (P68082)	3782	16941	97	1	2.94	147	11	16952.0406	16951.0333	16956.9598	-0.035	0	92	6.60E-10	1	12
19018	myoglobin (P68082)	3782	16941	97	1	2.94	165		16953.0819	16952.0746	16998.9704	-0.2759	0	53	5.20E-06	1	13
19018	myoglobin (P68082)	3782	16941	97	1	2.94	188	1	17008.0223	17007.0151	17020.9312	-0.0818	0	172	6.50E-18	1	14
19018	aS1CN B (P02662)	123	22960	6	1	1.16	301		23673.3328	23672.3256	23456.2738	0.9211	0	59	7.00E-05	1	15
19018	aS1CN B (P02662)	123	22960	6	1	1.16	306		23673.426	23672.4187	23872.1004	-0.8365	0	55	0.00019	1	16
19018	aS1CN B (P02662)	123	22960	6	1	1.16	308		23673.426	23672.4187	23616.2065	0.238	0	31	0.043	1	17
19018	aS1CN B (P02662)	123	22960	6	1	1.16	313		23729.3675	23728.3602	23936.0718	-0.8678	0	47	0.0012	1	18
19018	aS1CN B (P02662)	123	22960	6	1	1.16	348		23846.4878	23845.4805	24016.0381	-0.7102	0	42	0.0051	1	19
19018	aS1CN B (P02662)	123	22960	6	1	1.16	353		23848.4692	23847.4619	23632.2014	0.9109	0	41	0.0056	2	20
19018	BLG E (P02754)	21	18531	1	1	0.17	236		18452.5792	18451.5719	18610.5071	-0.854	0	21	0.043	1	21
19018	BLG F (P02754)	17	18472	1	1	0.17	195		18394.4984	18393.4911	18488.4786	-0.5138	0	17	0.046	1	22
19037	myoglobin (P68082)	12740	16941	131	1	5.59	47	6	16948.0746	16947.0673	17036.9261	-0.5274	0	229	1.30E-23	1	23
19037	myoglobin (P68082)	12740	16941	131	1	5.59	48	2	16948.0746	16947.0673	17036.9261	-0.5274	0	245	3.50E-25	1	24
19037	myoglobin (P68082)	12740	16941	131	1	5.59	53		16948.1149	16947.1076	17062.9418	-0.6789	0	243	5.00E-25	1	25
19037	myoglobin (P68082)	12740	16941	131	1	5.59	57		16949.0234	16948.0161	17116.8924	-0.9866	0	22	0.0069	1	26
19037	myoglobin (P68082)	12740	16941	131	1	5.59	59		16949.0282	16948.021	17078.9367	-0.7665	0	23	0.0051	1	27
19037	myoglobin (P68082)	12740	16941	131	1	5.59	66	2	16949.0395	16948.0322	17036.9261	-0.5218	0	155	2.90E-16	1	28
19037	myoglobin (P68082)	12740	16941	131	1	5.59	69		16949.0502	16948.0429	17036.9261	-0.5217	0	142	6.20E-15	1	29
19037	myoglobin (P68082)	12740	16941	131	1	5.59	72	1	16949.0502	16948.0429	17036.9261	-0.5217	0	168	1.60E-17	1	30
19037	myoglobin (P68082)	12740	16941	131	1	5.59	73		16949.0502	16948.0429	17020.9312	-0.4282	0	140	9.60E-15	1	31
19037	myoglobin (P68082)	12740	16941	131	1	5.59	76		16949.0738	16948.0665	17116.8924	-0.9863	0	35	0.00033	1	32
19037	myoglobin (P68082)	12740	16941	131	1	5.59	80		16950.0213	16949.014	17078.9367	-0.7607	0	67	1.80E-07	1	33
19037	myoglobin (P68082)	12740	16941	131	1	5.59	85		16950.063	16949.0557	17052.921	-0.6091	0	23	0.0052	1	34
19037	myoglobin (P68082)	12740	16941	131	1	5.59	96		16950.0707	16949.0635	17036.9261	-0.5157	0	27	0.002	1	35
19037	myoglobin (P68082)	12740	16941	131	1	5.59	97		16950.0707	16949.0635	17036.9261	-0.5157	0	30	0.0011	1	36
19037	myoglobin (P68082)	12740	16941	131	1	5.59	106		16950.1168	16949.1095	17100.8975	-0.8876	0	41	7.80E-05	1	37

Job no.	Description	Score	Mass	Matches	Seqs	embAI	Query	Dupes	Observed	Mt(expt)	Mt(scale)	%	M	Score	Expect	Rank	SEQ ID
19037	myoglobin (P68082)	12740	16941	131	1	5.59	107		16950.1168	16949.1095	16998.9704	-0.2933	0	66	2.30E-07	1	38
19037	myoglobin (P68082)	12740	16941	131	1	5.59	113	37	16950.999	16949.9917	16956.9598	-0.0411	0	202	5.60E-21	1	39
19037	myoglobin (P68082)	12740	16941	131	1	5.59	116		16951.0228	16950.0155	17052.921	-0.6034	0	63	5.30E-07	1	40
19037	myoglobin (P68082)	12740	16941	131	1	5.59	117		16951.0228	16950.0155	17036.9261	-0.5101	0	18	0.016	1	41
19037	myoglobin (P68082)	12740	16941	131	1	5.59	118		16951.0228	16950.0155	17094.9316	-0.8477	0	68	1.70E-07	1	42
19037	myoglobin (P68082)	12740	16941	131	1	5.59	120		16951.0229	16950.0156	17094.9316	-0.8477	0	58	1.60E-06	1	43
19037	myoglobin (P68082)	12740	16941	131	1	5.59	127		16951.0272	16950.0199	17100.8975	-0.8823	0	18	0.014	1	44
19037	myoglobin (P68082)	12740	16941	131	1	5.59	133	2	16951.0397	16950.0324	17020.9312	-0.4165	0	212	5.90E-22	1	45
19037	myoglobin (P68082)	12740	16941	131	1	5.59	138		16951.0491	16950.0418	17100.8975	-0.8822	0	164	4.10E-17	1	46
19037	myoglobin (P68082)	12740	16941	131	1	5.59	140		16951.0512	16950.044	17052.921	-0.6033	0	14	0.044	1	47
19037	myoglobin (P68082)	12740	16941	131	1	5.59	146		16952.0406	16951.0333	17036.9261	-0.5042	0	16	0.026	1	48
19037	myoglobin (P68082)	12740	16941	131	1	5.59	148	21	16952.0406	16951.0333	16940.9649	0.0594	0	285	3.40E-29	1	49
19037	myoglobin (P68082)	12740	16941	131	1	5.59	162		16952.0964	16951.0891	17062.9418	-0.6555	0	40	9.00E-05	1	50
19037	myoglobin (P68082)	12740	16941	131	1	5.59	163		16952.0964	16951.0891	17116.8924	-0.9687	0	14	0.043	1	51
19037	myoglobin (P68082)	12740	16941	131	1	5.59	187	28	17008.0223	17007.0151	16956.9598	0.2952	0	276	2.50E-28	1	52
19037	myoglobin (P68082)	12740	16941	131	1	5.59	188		17008.0223	17007.0151	17116.8924	-0.6419	0	253	5.60E-26	1	53
19037	as1CN B (P02662)	628	22960	22	1	5	296		23672.2825	23671.2753	23824.1239	-0.6416	0	43	0.0025	3	54
19037	as1CN B (P02662)	628	22960	22	1	5	301		23673.3328	23672.3256	23472.2688	0.8523	0	107	1.10E-09	1	55
19037	as1CN B (P02662)	628	22960	22	1	5	303		23673.3328	23672.3256	23712.1677	-0.168	0	36	0.015	1	56
19037	as1CN B (P02662)	628	22960	22	1	5	306		23673.426	23672.4187	23872.1004	-0.8365	0	108	7.90E-10	1	57
19037	as1CN B (P02662)	628	22960	22	1	5	308		23673.426	23672.4187	23616.2065	0.238	0	57	0.00011	3	58
19037	as1CN B (P02662)	628	22960	22	1	5	313	2	23729.3675	23728.3602	23856.1055	-0.5355	0	102	4.20E-09	1	59
19037	as1CN B (P02662)	628	22960	22	1	5	314		23729.3675	23728.3602	23872.1004	-0.6021	0	41	0.0045	4	60
19037	as1CN B (P02662)	628	22960	22	1	5	316		23729.3675	23728.3602	23712.1677	0.0683	0	46	0.0016	1	61
19037	as1CN B (P02662)	628	22960	22	1	5	323		23788.3773	23787.37	23728.1626	0.2495	0	35	0.024	3	62
19037	as1CN B (P02662)	628	22960	22	1	5	348		23846.4878	23845.4805	24032.033	-0.7763	0	74	2.90E-06	1	63
19037	as1CN B (P02662)	628	22960	22	1	5	350		23846.4878	23845.4805	23664.1912	0.7661	0	50	0.00077	1	64
19037	as1CN B (P02662)	628	22960	22	1	5	351	1	23846.4878	23845.4805	23856.1055	-0.0445	0	46	0.0019	1	65
19037	as1CN B (P02662)	628	22960	22	1	5	353		23848.4692	23847.4619	23808.129	0.1652	0	74	2.90E-06	7	66
19037	as1CN B (P02662)	628	22960	22	1	5	355		23848.4692	23847.4619	24032.033	-0.768	0	42	0.0049	1	67
19037	as1CN B (P02662)	628	22960	22	1	5	363		23910.537	23909.5298	23824.1239	0.3585	0	40	0.0075	6	68
19037	as1CN B (P02662)	628	22960	22	1	5	364		23910.537	23909.5298	23744.1576	0.6965	0	41	0.0065	5	69
19037	as1CN B (P02662)	628	22960	22	1	5	366		23910.537	23909.5298	24143.9892	-0.9711	0	58	0.00011	3	70
19037	as1CN B (P02662)	628	22960	22	1	5	369		23910.567	23909.5597	23904.0902	0.0229	0	56	0.0002	1	71
19037	as1CN B (P02662)	628	22960	22	1	5	370		23910.567	23909.5597	23818.1497	0.3838	0	38	0.011	2	72
19037	as1CN E (P02662)	407	22888	13	1	2.18	306		23673.426	23672.4187	23736.1442	-0.2685	0	104	2.40E-09	2	73
19037	as1CN E (P02662)	407	22888	13	1	2.18	313		23729.3675	23728.3602	23576.2116	0.6453	0	99	7.70E-09	4	74
19037	as1CN E (P02662)	407	22888	13	1	2.18	323		23788.3773	23787.37	23656.1779	0.5546	0	37	0.013	1	75
19037	as1CN E (P02662)	407	22888	13	1	2.18	343		23846.462	23845.4547	23752.1391	0.3929	0	32	0.048	3	76

Job no.	Description	Score	Mass	Matches	Seqs	embAI	Query	Dupes	Observed	Mt(expt)	Mt(scale)	%	M	Score	Expect	Rank	SEQ ID
19037	aS1CN E (P02662)	407	22888	13	1	2.18	348		23846.4878	23845.4805	23752.1391	0.393	0	73	3.40E-06	2	77
19037	aS1CN E (P02662)	407	22888	13	1	2.18	350		23846.4878	23845.4805	23624.1881	0.9367	0	48	0.0013	2	78
19037	aS1CN E (P02662)	407	22888	13	1	2.18	351		23846.4878	23845.4805	24024.0197	-0.7432	0	45	0.0021	2	79
19037	aS1CN E (P02662)	407	22888	13	1	2.18	353		23848.4692	23847.4619	23672.1728	0.7405	0	75	2.20E-06	2	80
19037	aS1CN E (P02662)	407	22888	13	1	2.18	356		23848.4692	23847.4619	23784.1207	0.2663	0	36	0.019	7	81
19037	aS1CN E (P02662)	407	22888	13	1	2.18	363		23910.537	23909.5298	24119.9809	-0.8725	0	42	0.0052	3	82
19037	aS1CN E (P02662)	407	22888	13	1	2.18	364		23910.537	23909.5298	23784.1207	0.5273	0	41	0.0058	4	83
19037	aS1CN E (P02662)	407	22888	13	1	2.18	366		23910.537	23909.5298	23752.1391	0.6626	0	59	8.60E-05	1	84
19037	aS1CN E (P02662)	407	22888	13	1	2.18	368		23910.567	23909.5597	24119.9809	-0.8724	0	87	1.60E-07	3	85
19037	bLG I (P02754)	395	18482	35	1	3.13	190	2	18392.5387	18391.5315	18498.4994	-0.5783	0	32	0.0013	1	86
19037	bLG I (P02754)	395	18482	35	1	3.13	192		18392.5387	18391.5315	18514.4943	-0.6641	0	20	0.019	2	87
19037	bLG I (P02754)	395	18482	35	1	3.13	193		18392.5387	18391.5315	18498.4994	-0.5783	0	18	0.033	3	88
19037	bLG I (P02754)	395	18482	35	1	3.13	212	1	18422.5717	18421.5644	18578.4657	-0.8445	0	41	0.00031	1	89
19037	bLG I (P02754)	395	18482	35	1	3.13	228	2	18450.559	18449.5517	18514.4943	-0.3508	0	48	7.80E-05	1	90
19037	bLG I (P02754)	395	18482	35	1	3.13	236	1	18452.5792	18451.5719	18578.4657	-0.683	0	35	0.0017	10	91
19037	bLG I (P02754)	395	18482	35	1	3.13	239		18452.5792	18451.5719	18562.4708	-0.5974	0	34	0.002	9	92
19037	bLG I (P02754)	395	18482	35	1	3.13	242		18475.5423	18474.535	18658.432	-0.9856	0	36	0.0018	3	93
19037	bLG I (P02754)	395	18482	35	1	3.13	244		18475.5423	18474.535	18658.432	-0.9856	0	32	0.0042	1	94
19037	bLG I (P02754)	395	18482	35	1	3.13	246		18476.5099	18475.5026	18578.4657	-0.5542	0	39	0.0087	1	95
19037	bLG I (P02754)	395	18482	35	1	3.13	248		18476.5099	18475.5026	18594.4606	-0.6397	0	34	0.003	6	96
19037	bLG I (P02754)	395	18482	35	1	3.13	249	1	18476.5099	18475.5026	18578.4657	-0.5542	0	42	0.0004	1	97
19037	bLG I (P02754)	395	18482	35	1	3.13	251		18477.6176	18476.6103	18578.4657	-0.5482	0	39	0.00093	1	98
19037	bLG I (P02754)	395	18482	35	1	3.13	254		18477.6176	18476.6103	18578.4657	-0.5482	0	28	0.012	5	99
19037	bLG I (P02754)	395	18482	35	1	3.13	258		18478.5355	18477.5282	18642.4371	-0.8846	0	23	0.037	6	100
19037	bLG I (P02754)	395	18482	35	1	3.13	261	1	18478.5709	18477.5636	18594.4606	-0.6287	0	30	0.0079	1	101
19037	bLG I (P02754)	395	18482	35	1	3.13	266		18478.6278	18477.6205	18658.432	-0.9691	0	32	0.0047	1	102
19037	bLG I (P02754)	395	18482	35	1	3.13	268		18478.6278	18477.6205	18658.432	-0.9691	0	30	0.0066	2	103
19037	bLG I (P02754)	395	18482	35	1	3.13	269		18478.6278	18477.6205	18578.4657	-0.5428	0	31	0.0052	1	104
19037	bLG I (P02754)	395	18482	35	1	3.13	274		18479.5647	18478.5574	18594.4606	-0.6233	0	34	0.0025	1	105
19037	bLG I (P02754)	395	18482	35	1	3.13	281		18533.656	18532.6488	18674.4269	-0.7592	0	34	0.0041	1	106
19037	bLG I (P02754)	395	18482	35	1	3.13	282		18533.656	18532.6488	18674.4269	-0.7592	0	24	0.043	4	107
19037	bLG I (P02754)	395	18482	35	1	3.13	284		18533.656	18532.6488	18610.4555	-0.4181	0	27	0.022	5	108
19037	bLG I (P02754)	395	18482	35	1	3.13	287		18535.632	18534.6247	18610.4555	-0.4075	0	26	0.029	4	109
19037	bLG I (P02754)	395	18482	35	1	3.13	293		18536.5494	18535.5421	18578.4657	-0.231	0	33	0.005	4	110
19037	bLG I (P02754)	395	18482	35	1	3.13	294		18536.5494	18535.5421	18578.4657	-0.231	0	30	0.01	4	111
19037	aS1CN F (P02662)	359	22987	10	1	1.79	296		23672.2825	23671.2753	23674.2484	-0.0126	0	45	0.0017	1	112
19037	aS1CN F (P02662)	359	22987	10	1	1.79	301	1	23673.3328	23672.3256	23802.1912	-0.5456	0	102	3.80E-09	5	113
19037	aS1CN F (P02662)	359	22987	10	1	1.79	307		23673.426	23672.4187	23460.365	0.9039	0	39	0.0066	3	114
19037	aS1CN F (P02662)	359	22987	10	1	1.79	313		23729.3675	23728.3602	23882.1575	-0.644	0	97	1.20E-08	6	115

Job no.	Description	Score	Mass	Matches	Seqs	embAI	Query	Dupes	Observed	Mit(expt)	Mit(cale)	%	M	Score	Expect	Rank	SEQ ID
19037	aS1CN F (P02662)	359	22987	10	1	1.79	323		23788.3773	23787.37	24010.1086	-0.9277	0	34	0.027	10	116
19037	aS1CN F (P02662)	359	22987	10	1	1.79	350		23846.4878	23845.4805	24058.0851	-0.8837	0	73	3.70E-06	3	117
19037	aS1CN F (P02662)	359	22987	10	1	1.79	350		23846.4878	23845.4805	24026.0952	-0.7517	0	47	0.0015	4	118
19037	aS1CN F (P02662)	359	22987	10	1	1.79	353		23848.4692	23847.4619	23754.2147	0.3926	0	75	2.30E-06	4	119
19037	aS1CN F (P02662)	359	22987	10	1	1.79	370		23910.567	23909.5597	23754.2147	0.654	0	35	0.026	7	120
19037	aS1CN D (P02662)	332	22990	18	1	6.76	296		23672.2825	23671.2753	23678.2069	-0.0293	0	42	0.0036	6	121
19037	aS1CN D (P02662)	332	22990	18	1	6.76	302	1	23673.3328	23672.3256	23566.2507	0.4501	0	53	0.00025	1	122
19037	aS1CN D (P02662)	332	22990	18	1	6.76	307		23673.426	23672.4187	23688.2276	-0.0667	0	40	0.0058	1	123
19037	aS1CN D (P02662)	332	22990	18	1	6.76	308		23673.426	23672.4187	23598.2406	0.3143	0	61	4.30E-05	1	124
19037	aS1CN D (P02662)	332	22990	18	1	6.76	309		23673.426	23672.4187	23646.2171	0.1108	0	48	0.0008	1	125
19037	aS1CN D (P02662)	332	22990	18	1	6.76	316		23729.3675	23728.3602	23582.2457	0.6196	0	42	0.0042	6	126
19037	aS1CN D (P02662)	332	22990	18	1	6.76	326		23788.3773	23787.37	23998.0722	-0.878	0	38	0.01	1	127
19037	aS1CN D (P02662)	332	22990	18	1	6.76	343		23846.462	23845.4547	23710.1967	0.5705	0	34	0.031	1	128
19037	aS1CN D (P02662)	332	22990	18	1	6.76	348		23846.4878	23845.4805	23614.2355	0.9793	0	72	4.20E-06	4	129
19037	aS1CN D (P02662)	332	22990	18	1	6.76	350		23846.4878	23845.4805	23630.2304	0.9109	0	43	0.0035	7	130
19037	aS1CN D (P02662)	332	22990	18	1	6.76	353		23848.4692	23847.4619	23854.1345	-0.028	0	76	1.90E-06	1	131
19037	aS1CN D (P02662)	332	22990	18	1	6.76	356		23848.4692	23847.4619	23806.1497	0.1735	0	36	0.017	6	132
19037	aS1CN D (P02662)	332	22990	18	1	6.76	363		23910.537	23909.5298	24094.0334	-0.7658	0	45	0.0026	1	133
19037	aS1CN D (P02662)	332	22990	18	1	6.76	364		23910.537	23909.5298	23710.1967	0.8407	0	45	0.0021	1	134
19037	aS1CN D (P02662)	332	22990	18	1	6.76	365		23910.537	23909.5298	24126.015	-0.8973	0	37	0.015	1	135
19037	aS1CN D (P02662)	332	22990	18	1	6.76	369		23910.567	23909.5597	23838.1395	0.2996	0	50	0.00078	4	136
19037	aS1CN D (P02662)	332	22990	18	1	6.76	370		23910.567	23909.5597	23934.1008	-0.1025	0	40	0.0083	1	137
19037	BLG F/C (P02754)	330	18472	30	1	2.03	190		18392.5387	18391.5315	18552.45	-0.8674	0	28	0.003	2	138
19037	BLG F/C (P02754)	330	18472	30	1	2.03	196		18394.4984	18393.4911	18568.4449	-0.9422	0	21	0.015	5	139
19037	BLG F/C (P02754)	330	18472	30	1	2.03	201	1	18394.5584	18393.5511	18568.4449	-0.9419	0	36	0.00056	1	140
19037	BLG F/C (P02754)	330	18472	30	1	2.03	206		18416.4322	18415.4249	18584.4399	-0.9094	0	35	0.00099	2	141
19037	BLG F/C (P02754)	330	18472	30	1	2.03	209		18419.4725	18418.4653	18488.4786	-0.3787	0	21	0.027	2	142
19037	BLG F/C (P02754)	330	18472	30	1	2.03	218	2	18449.5008	18448.4935	18568.4449	-0.646	0	31	0.0036	1	143
19037	BLG F/C (P02754)	330	18472	30	1	2.03	231		18451.5042	18450.4969	18600.4348	-0.8061	0	22	0.032	1	144
19037	BLG F/C (P02754)	330	18472	30	1	2.03	242	1	18475.5423	18474.535	18568.4449	-0.5058	0	37	0.0013	1	145
19037	BLG F/C (P02754)	330	18472	30	1	2.03	246		18476.5099	18475.5026	18584.4399	-0.5862	0	37	0.0014	4	146
19037	BLG F/C (P02754)	330	18472	30	1	2.03	248		18476.5099	18475.5026	18659.4871	-0.986	0	39	0.00082	1	147
19037	BLG F/C (P02754)	330	18472	30	1	2.03	257		18478.5355	18477.5282	18568.4449	-0.4896	0	24	0.027	1	148
19037	BLG F/C (P02754)	330	18472	30	1	2.03	258		18478.5355	18477.5282	18579.5208	-0.549	0	22	0.05	8	149
19037	BLG F/C (P02754)	330	18472	30	1	2.03	262		18478.5709	18477.5636	18648.4113	-0.9162	0	26	0.017	1	150
19037	BLG F/C (P02754)	330	18472	30	1	2.03	268		18478.6278	18477.6205	18648.4113	-0.9158	0	31	0.0053	1	151
19037	BLG F/C (P02754)	330	18472	30	1	2.03	271		18479.5647	18478.5574	18584.4399	-0.5697	0	46	0.00018	1	152
19037	BLG F/C (P02754)	330	18472	30	1	2.03	274		18479.5647	18478.5574	18659.4871	-0.9696	0	30	0.0071	5	153
19037	BLG F/C (P02754)	330	18472	30	1	2.03	281	1	18533.656	18532.6488	18648.4113	-0.6208	0	31	0.0085	5	154

Job no.	Description	Score	Mass	Matches	Seqs	emb/PI	Query	Dupes	Observed	Mit(expt)	Mit(cale)	%	M	Score	Expect	Rank	SEQ ID
19037	blG F/C (P02754)	330	18472	30	1	2.03	284		18533.656	18532.6488	18648.4113	-0.6208	0	31	0.0084	1	155
19037	blG F/C (P02754)	330	18472	30	1	2.03	286	1	18535.632	18534.6247	18664.4062	-0.6953	0	38	0.0019	1	156
19037	blG F/C (P02754)	330	18472	30	1	2.03	288	1	18535.632	18534.6247	18664.4062	-0.6953	0	46	0.00029	1	157
19037	blG F/C (P02754)	330	18472	30	1	2.03	289		18535.632	18534.6247	18664.4062	-0.6953	0	30	0.012	1	158
19037	blG F/C (P02754)	330	18472	30	1	2.03	292		18536.5494	18535.5421	18568.4449	-0.1772	0	47	0.0002	1	159
19037	blG F/C (P02754)	330	18472	30	1	2.03	293		18536.5494	18535.5421	18664.4062	-0.6904	0	35	0.0037	3	160
19037	blG F/C (P02754)	330	18472	30	1	2.03	294	1	18536.5494	18535.5421	18664.4062	-0.6904	0	38	0.0017	1	161
19037	blG G (P02754)	292	18500	25	1	2.01	195		18394.4984	18393.4911	18516.4558	-0.6641	0	19	0.026	3	162
19037	blG G (P02754)	292	18500	25	1	2.01	197	1	18394.4984	18393.4911	18532.4507	-0.7498	0	28	0.0036	1	163
19037	blG G (P02754)	292	18500	25	1	2.01	206		18416.4322	18415.4249	18596.4221	-0.9733	0	36	0.00076	1	164
19037	blG G (P02754)	292	18500	25	1	2.01	227		18450.559	18449.5517	18612.417	-0.875	0	22	0.03	3	165
19037	blG G (P02754)	292	18500	25	1	2.01	236		18452.5792	18451.5719	18612.417	-0.8642	0	39	0.00067	1	166
19037	blG G (P02754)	292	18500	25	1	2.01	239		18452.5792	18451.5719	18596.4221	-0.7789	0	37	0.001	4	167
19037	blG G (P02754)	292	18500	25	1	2.01	241		18475.5423	18474.535	18628.4119	-0.826	0	24	0.028	1	168
19037	blG G (P02754)	292	18500	25	1	2.01	245		18476.5099	18475.5026	18612.417	-0.7356	0	27	0.014	3	169
19037	blG G (P02754)	292	18500	25	1	2.01	246		18476.5099	18475.5026	18580.4272	-0.5647	0	37	0.0015	7	170
19037	blG G (P02754)	292	18500	25	1	2.01	247		18476.5099	18475.5026	18612.417	-0.7356	0	39	0.00081	1	171
19037	blG G (P02754)	292	18500	25	1	2.01	248		18476.5099	18475.5026	18612.417	-0.7356	0	39	0.00087	2	172
19037	blG G (P02754)	292	18500	25	1	2.01	254		18477.6176	18476.6103	18628.4119	-0.8149	0	30	0.0074	4	173
19037	blG G (P02754)	292	18500	25	1	2.01	264		18478.5709	18477.5636	18612.417	-0.7245	0	25	0.022	4	174
19037	blG G (P02754)	292	18500	25	1	2.01	271		18479.5647	18478.5574	18628.4119	-0.8044	0	42	0.00046	8	175
19037	blG G (P02754)	292	18500	25	1	2.01	272	1	18479.5647	18478.5574	18612.417	-0.7192	0	39	0.00093	1	176
19037	blG G (P02754)	292	18500	25	1	2.01	281		18533.656	18532.6488	18676.3884	-0.7696	0	34	0.0045	2	177
19037	blG G (P02754)	292	18500	25	1	2.01	282		18533.656	18532.6488	18596.4221	-0.3429	0	25	0.033	1	178
19037	blG G (P02754)	292	18500	25	1	2.01	284		18533.656	18532.6488	18628.4119	-0.5141	0	28	0.016	3	179
19037	blG G (P02754)	292	18500	25	1	2.01	286		18535.632	18534.6247	18596.4221	-0.3323	0	32	0.0069	3	180
19037	blG G (P02754)	292	18500	25	1	2.01	288	1	18535.632	18534.6247	18612.417	-0.418	0	39	0.0015	7	181
19037	blG G (P02754)	292	18500	25	1	2.01	289		18535.632	18534.6247	18596.4221	-0.3323	0	25	0.031	10	182
19037	blG G (P02754)	292	18500	25	1	2.01	291		18536.5494	18535.5421	18676.3884	-0.7541	0	26	0.03	4	183
19037	blG G (P02754)	292	18500	25	1	2.01	292		18536.5494	18535.5421	18676.3884	-0.7541	0	46	0.00025	2	184
19037	blG D (P02754)	117	18554	10	1	0.88	228		18450.559	18449.5517	18553.5416	-0.5605	0	40	0.00056	8	185
19037	blG D (P02754)	117	18554	11	2	1.88	236		18452.5792	18451.5719	18633.5079	-0.9764	0	39	0.00069	7	186
19037	blG D (P02754)	117	18554	12	3	2.88	238		18452.5792	18451.5719	18633.5079	-0.9764	0	34	0.0021	5	187
19037	blG D (P02754)	117	18554	13	4	3.88	244		18475.5423	18474.535	18649.5028	-0.9382	0	26	0.016	2	188
19037	blG D (P02754)	117	18554	14	5	4.88	251		18477.6176	18476.6103	18649.5028	-0.9271	0	34	0.003	3	189
19037	blG D (P02754)	117	18554	15	6	5.88	254		18477.6176	18476.6103	18569.5365	-0.5004	0	26	0.016	6	190
19037	blG D (P02754)	117	18554	16	7	6.88	257		18478.5355	18477.5282	18649.5028	-0.9221	0	24	0.027	2	191
19037	blG D (P02754)	117	18554	17	8	7.88	258		18478.5355	18477.5282	18649.5028	-0.9221	0	27	0.015	1	192
19037	blG D (P02754)	117	18554	18	9	8.88	278		18482.6285	18481.6212	18649.5028	-0.9002	0	27	0.016	1	193

Job no.	Description	Score	Mass	Matches	Seqs	embAI	Query	Dupes	Observed	Mt(expt)	Mt(scale)	%	M	Score	Expect	Rank	SEQ ID
19037	BLG D (P02754)	117	18554	19	10	9.88	289	1	18535.632	18534.6247	18633.5079	-0.5307	0	29	0.014	3	194
19037	BLG E (P02754)	98	18531	9	1	0.88	192		18392.5387	18391.5315	18562.5307	-0.9212	0	27	0.0037	1	195
19037	BLG E (P02754)	98	18531	9	1	0.88	237	1	18452.5792	18451.5719	18546.5357	-0.512	0	32	0.0061	5	196
19037	BLG E (P02754)	98	18531	9	1	0.88	239	1	18452.5792	18451.5719	18562.5307	-0.5978	0	39	0.00061	1	197
19037	BLG E (P02754)	98	18531	9	1	0.88	247	1	18476.5099	18475.5026	18610.5071	-0.7254	0	33	0.0036	8	198
19037	BLG E (P02754)	98	18531	9	1	0.88	272		18479.5647	18478.5574	18626.5021	-0.7943	0	30	0.0068	10	199
19037	BLG E (P02754)	98	18531	9	1	0.88	287		18535.632	18534.6247	18626.5021	-0.4933	0	25	0.036	6	200
19037	BLG B (P02754)	75	18555	7	1	0.88	193		18392.5387	18391.5315	18570.5205	-0.9638	0	20	0.021	1	201
19037	BLG B (P02754)	75	18555	7	1	0.88	228		18450.559	18449.5517	18554.5256	-0.5658	0	42	0.00036	2	202
19037	BLG B (P02754)	75	18555	7	1	0.88	245		18476.5099	18475.5026	18634.4919	-0.8532	0	28	0.011	1	203
19037	BLG B (P02754)	75	18555	7	1	0.88	258		18478.5355	18477.5282	18650.4868	-0.9274	0	23	0.034	4	204
19037	BLG B (P02754)	75	18555	7	1	0.88	261		18478.5709	18477.5636	18650.4868	-0.9272	0	23	0.035	4	205
19037	BLG B (P02754)	75	18555	7	1	0.88	279		18482.6285	18481.6212	18650.4868	-0.9054	0	23	0.033	1	206
19037	BLG B (P02754)	75	18555	7	1	0.88	293		18536.5494	18535.5421	18650.4868	-0.6163	0	39	0.0015	1	207
19037	BLG A (P02754)	50	18641	3	1	0.17	254	1	18477.6176	18476.6103	18656.5573	-0.9645	0	36	0.0016	1	208
19037	BLG A (P02754)	50	18641	3	1	0.17	287		18535.632	18534.6247	18656.5573	-0.6536	0	24	0.039	8	209
19037	BLG J (P02754)	41	18571	4	1	0.6	227		18450.559	18449.5517	18602.5467	-0.8224	0	26	0.014	1	210
19037	BLG J (P02754)	41	18571	4	1	0.6	284		18533.656	18532.6488	18682.513	-0.8022	0	27	0.02	4	211
19037	BLG J (P02754)	41	18571	4	1	0.6	286		18535.632	18534.6247	18682.513	-0.7916	0	28	0.017	10	212
19037	BLG J (P02754)	41	18571	4	1	0.6	289		18535.632	18534.6247	18666.5181	-0.7066	0	26	0.025	8	213
19020	MYG EQUUB	1456	17072	46	2	2.91	35	1	16947.0184	16946.0112	17036.9261	-0.5336	0	66	0.0065	1	214
19020	MYG EQUUB	1456	17072	46	2	2.91	48	1	16948.0746	16947.0673	17036.9261	-0.5274	0	148	4.30E-11	1	215
19020	MYG EQUUB	1456	17072	46	2	2.91	53	2	16948.1149	16947.1076	17088.0003	-0.8245	0	151	2.00E-11	1	216
19020	MYG EQUUB	1456	17072	46	2	2.91	67		16949.0395	16948.0322	17020.9312	-0.4283	0	58	0.043	1	217
19020	MYG EQUUB	1456	17072	46	2	2.91	71		16949.0502	16948.0429	17036.9261	-0.5217	0	103	1.20E-06	1	218
19020	MYG EQUUB	1456	17072	46	2	2.91	105		16950.1168	16949.1095	17072.0054	-0.7199	0	22	0.017	1	219
19020	MYG EQUUB	1456	17072	46	2	2.91	133	2	16951.0397	16950.0324	16956.9598	-0.0409	0	122	1.40E-08	1	220
19020	MYG EQUUB	1456	17072	46	2	2.91	137	1	16951.0491	16950.0418	17088.0003	-0.8073	0	70	0.0025	1	221
19020	MYG EQUUB	1456	17072	46	2	2.91	138		16951.0491	16950.0418	17100.8975	-0.8822	0	128	4.10E-09	1	222
19020	MYG EQUUB	1456	17072	46	2	2.91	143	18	16951.0512	16950.044	16940.9649	0.0536	0	143	1.30E-10	1	223
19020	MYG EQUUB	1456	17072	46	2	2.91	147	6	16952.0406	16951.0333	16956.9598	-0.035	0	92	1.60E-05	1	224
19020	MYG EQUUB	1456	17072	46	2	2.91	180	1	16968.0376	16967.0303	17088.0003	-0.7079	0	94	2.30E-06	1	225
19020	MYG EQUUB	1456	17072	46	2	2.91	188		17008.0223	17007.0151	17020.9312	-0.0818	0	172	1.60E-13	1	226
19040	MYG EQUUB	8764	17072	113	2	4.49	47	3	16948.0746	16947.0673	17036.9261	-0.5274	0	229	3.10E-19	1	227
19040	MYG EQUUB	8764	17072	113	2	4.49	48	2	16948.0746	16947.0673	17036.9261	-0.5274	0	245	8.60E-21	1	228
19040	MYG EQUUB	8764	17072	113	2	4.49	53		16948.1149	16947.1076	17036.9261	-0.5272	0	236	6.00E-20	1	229
19040	MYG EQUUB	8764	17072	113	2	4.49	61	3	16949.0282	16948.021	17103.9952	-0.9119	0	67	0.0046	1	230
19040	MYG EQUUB	8764	17072	113	2	4.49	66	2	16949.0395	16948.0322	17036.9261	-0.5218	0	155	7.20E-12	1	231
19040	MYG EQUUB	8764	17072	113	2	4.49	69		16949.0502	16948.0429	17036.9261	-0.5217	0	142	1.50E-10	1	232

Job no.	Description	Score	Mass	Matches	Seqs	embAI	Query	Dupes	Observed	Mtr(expt)	Mtr(scale)	%	M	Score	Expect	Rank	SEQ ID
19040	MYG EQUUBU	8764	17072	113	2	4.49	72		16949.0502	16948.0429	17036.9261	-0.5217	0	168	4.00E-13	1	233
19040	MYG EQUUBU	8764	17072	113	2	4.49	73		16949.0502	16948.0429	17020.9312	-0.4282	0	140	2.40E-10	1	234
19040	MYG EQUUBU	8764	17072	113	2	4.49	100	2	16950.078	16949.0707	17088.0003	-0.813	0	116	6.30E-08	1	235
19040	MYG EQUUBU	8764	17072	113	2	4.49	113	24	16950.999	16949.9917	16956.9598	-0.0411	0	202	1.40E-16	1	236
19040	MYG EQUUBU	8764	17072	113	2	4.49	116		16951.0228	16950.0155	17052.921	-0.6034	0	63	0.013	1	237
19040	MYG EQUUBU	8764	17072	113	2	4.49	118		16951.0228	16950.0155	17052.921	-0.6034	0	61	0.019	1	238
19040	MYG EQUUBU	8764	17072	113	2	4.49	133		16951.0397	16950.0324	17020.9312	-0.4165	0	212	1.50E-17	1	239
19040	MYG EQUUBU	8764	17072	113	2	4.49	138		16951.0491	16950.0418	17100.8975	-0.8822	0	164	1.00E-12	1	240
19040	MYG EQUUBU	8764	17072	113	2	4.49	148	14	16952.0406	16951.0333	16940.9649	0.0594	0	285	8.40E-25	1	241
19040	MYG EQUUBU	8764	17072	113	2	4.49	156	3	16952.0839	16951.0766	17088.0003	-0.8013	0	80	0.00027	1	242
19040	MYG EQUUBU	8764	17072	113	2	4.49	165	1	16953.0819	16952.0746	17088.0003	-0.7954	0	165	8.30E-13	1	243
19040	MYG EQUUBU	8764	17072	113	2	4.49	173		16965.0545	16964.0472	17116.8924	-0.8929	0	101	1.90E-06	6	244
19040	MYG EQUUBU	8764	17072	113	2	4.49	187	20	17008.0223	17007.0151	16956.9598	0.2952	0	276	6.10E-24	1	245
19040	MYG EQUUBU	8764	17072	113	2	4.49	188		17008.0223	17007.0151	17116.8924	-0.6419	0	253	1.40E-21	1	246
19052	MYG EQUUBU	2119	17072	62	2	6.72	35	1	16947.0184	16946.0112	17036.9261	-0.5336	0	66	0.00042	1	247
19052	MYG EQUUBU	2119	17072	62	2	6.72	48	1	16948.0746	16947.0673	17036.9261	-0.5274	0	148	2.80E-12	1	248
19052	MYG EQUUBU	2119	17072	62	2	6.72	53	1	16948.1149	16947.1076	17088.0003	-0.8245	0	151	1.30E-12	1	249
19052	MYG EQUUBU	2119	17072	62	2	6.72	67		16949.0395	16948.0322	17020.9312	-0.4283	0	58	0.0027	1	250
19052	MYG EQUUBU	2119	17072	62	2	6.72	69	2	16949.0502	16948.0429	17033.9952	-0.9118	0	54	0.0066	1	251
19052	MYG EQUUBU	2119	17072	62	2	6.72	71		16949.0502	16948.0429	17036.9261	-0.5217	0	103	7.90E-08	1	252
19052	MYG EQUUBU	2119	17072	62	2	6.72	72		16949.0502	16948.0429	17116.8924	-0.9864	0	50	0.015	1	253
19052	MYG EQUUBU	2119	17072	62	2	6.72	105		16950.1168	16949.1095	17072.0054	-0.7199	0	22	0.017	1	254
19052	MYG EQUUBU	2119	17072	62	2	6.72	133	5	16951.0397	16950.0324	16956.9598	-0.0409	0	122	9.10E-10	1	255
19052	MYG EQUUBU	2119	17072	62	2	6.72	137		16951.0491	16950.0418	17088.0003	-0.8073	0	70	0.00016	1	256
19052	MYG EQUUBU	2119	17072	62	2	6.72	138		16951.0491	16950.0418	17100.8975	-0.8822	0	128	2.60E-10	1	257
19052	MYG EQUUBU	2119	17072	62	2	6.72	143	22	16951.0512	16950.044	16940.9649	0.0536	0	143	8.30E-12	1	258
19052	MYG EQUUBU	2119	17072	62	2	6.72	147	6	16952.0406	16951.0333	16956.9598	-0.035	0	92	1.00E-06	1	259
19052	MYG EQUUBU	2119	17072	62	2	6.72	180	1	16968.0376	16967.0303	17088.0003	-0.7079	0	94	6.70E-07	1	260
19052	MYG EQUUBU	2119	17072	62	2	6.72	188		17008.0223	17007.0151	17020.9312	-0.0818	0	172	1.00E-14	1	261
19047	MYG EQUUBU	10298	17072	134	2	11.87	47	4	16948.0746	16947.0673	17036.9261	-0.5274	0	229	2.00E-20	1	262
19047	MYG EQUUBU	10298	17072	134	2	11.87	48	2	16948.0746	16947.0673	17036.9261	-0.5274	0	245	5.50E-22	1	263
19047	MYG EQUUBU	10298	17072	134	2	11.87	53		16948.1149	16947.1076	17062.9418	-0.6789	0	243	7.80E-22	1	264
19047	MYG EQUUBU	10298	17072	134	2	11.87	66	2	16949.0395	16948.0322	17036.9261	-0.5218	0	155	4.60E-13	1	265
19047	MYG EQUUBU	10298	17072	134	2	11.87	69		16949.0502	16948.0429	17036.9261	-0.5217	0	142	9.70E-12	1	266
19047	MYG EQUUBU	10298	17072	134	2	11.87	72		16949.0502	16948.0429	17036.9261	-0.5217	0	168	2.50E-14	1	267
19047	MYG EQUUBU	10298	17072	134	2	11.87	73		16949.0502	16948.0429	17020.9312	-0.4282	0	140	1.50E-11	1	268
19047	MYG EQUUBU	10298	17072	134	2	11.87	100	3	16950.078	16949.0707	17088.0003	-0.813	0	116	4.00E-09	1	269
19047	MYG EQUUBU	10298	17072	134	2	11.87	113	25	16950.999	16949.9917	16956.9598	-0.0411	0	202	8.90E-18	1	270
19047	MYG EQUUBU	10298	17072	134	2	11.87	116		16951.0228	16950.0155	17052.921	-0.6034	0	63	0.00084	1	271

WO 2020/124128

PCT/AU2019/051228

- 96 -

Job no.	Description	Score	Mass	Matches	Seqs	embAI	Query	Dupes	Observed	Mt(expt)	Mt(scale)	%	M	Score	Expect	Rank	SEQ ID
19047	MYG EQUUBU	10298	17072	134	2	11.87	118		16951.0228	16950.0155	17094.9316	-0.8477	0	68	0.00026	1	272
19047	MYG EQUUBU	10298	17072	134	2	11.87	133	1	16951.0397	16950.0324	17020.9312	-0.4165	0	212	9.40E-19	1	273
19047	MYG EQUUBU	10298	17072	134	2	11.87	137		16951.0491	16950.0418	17114.0159	-0.9581	0	141	1.30E-11	1	274
19047	MYG EQUUBU	10298	17072	134	2	11.87	138		16951.0491	16950.0418	17100.8975	-0.8822	0	164	6.50E-14	1	275
19047	MYG EQUUBU	10298	17072	134	2	11.87	148	15	16952.0406	16951.0333	16940.9649	0.0594	0	285	5.40E-26	1	276
19047	MYG EQUUBU	10298	17072	134	2	11.87	156	3	16952.0839	16951.0766	17088.0003	-0.8013	0	80	1.70E-05	1	277
19047	MYG EQUUBU	10298	17072	134	2	11.87	165	3	16953.0819	16952.0746	17088.0003	-0.7954	0	165	5.30E-14	1	278
19047	MYG EQUUBU	10298	17072	134	2	11.87	166	1	16953.0819	16952.0746	17072.0054	-0.7025	0	217	3.00E-19	1	279
19047	MYG EQUUBU	10298	17072	134	2	11.87	173		16965.0545	16964.0472	17116.8924	-0.8929	0	101	1.20E-07	6	280
19047	MYG EQUUBU	10298	17072	134	2	11.87	187	24	17008.0223	17007.0151	16956.9598	0.2952	0	276	3.90E-25	1	281
19047	MYG EQUUBU	10298	17072	134	2	11.87	188		17008.0223	17007.0151	17116.8924	-0.6419	0	253	8.90E-23	1	282
19047	NU6M_TACAC	46	18085	1	1	0.18	294		18536.5494	18535.5421	18577.8376	-0.2277	0	46	0.042	1	283
19047	NU6M_HIPAM	34	18642	1	1	0.17	267		18478.6278	18477.6205	18654.5484	-0.9484	0	34	0.039	1	284

- 97 -

[0244] All the entries of Swissprot database (559,228 sequences) were also searched with a ± 50 ppm fragment tolerance. The Mascot search result is reported in Table 8 and Figure 12. Not only was the search much longer than with our smaller more targeted homemade database lasting 3 days, but also only myoglobin could be identified, based on a total of 46 (12%) MS/MS spectra (71% redundancy) yielding a protein score of 1,456. As observed with the 'homemade' database described at [0185], above, the unmodified isoform was the most frequently identified (39%), the other proteoforms comprised oxidation and/or phosphorylation sites (Table 9). Raising the MS/MS tolerance to 2 Da did not increase the list of protein identified but adjusted the score to 8,764 with 113 (30%) matches. Limiting Swissprot taxonomy to "other mammalia" adjusted myoglobin scores to 17,072 with 62 (17%) matches and 10,298 with 136 (37%) matches, respectively applying ± 50 ppm and ± 2 Da fragment tolerance. While this reduces search times to hours, it results in the identification of a protein we do not expect in our known protein samples, NADH-ubiquinone oxidoreductase (Tables 8 and 9). As the commercial standards we used are not pure, it is possible that this protein is genuinely present in the sample. In any case, these data indicated that increasing the search space by choosing a database with more entries and selecting more dynamic modifications lengthens the time needed to complete the search (Table 7), without necessarily yielding more relevant identities (Table 8).

Example 7 – Proteins identified by top-down proteomics

[0245] Protein extracts from cannabis mature buds were concentrated by evaporation to maximise signal intensity. The chromatographic separation of intact denatured proteins was optimised from 15 to 40% of mobile phase B for 87 min. ETD, CID and HCD was applied in succession with three levels of energy so called "Low" (ETD 5 ms, CID 35 eV, HCD 19 eV), "Mid" (ETD 10 ms, CID 42 eV, HCD 23 eV) and "High" (ETD 15 ms, CID 50 eV, HCD 27 eV).

- 98 -

[0246] Three cannabis extracts (bud 1 to 3) were run using LC-MS in duplicate and using LC-MS/MS in triplicate with high reproducibility (Figure 12). Total ion chromatograms (TIC) were very similar across technical replicates, as well as among biological replicates 2 and 3 (Figure 12A); sample bud 1 differed slightly mostly due to lower signal intensities during the first half of the LC run. LC-MS patterns are very similar, generally differing in peak intensities across biological replicates (Figure 12B) as the number of protein groups was consistent with small standard deviation (SD) values (470 ± 17 groups) (Table 10).

Table 10. Statistics on cannabis proteins analysed by LC-MS and LC-MS/MS obtained from Genedata Refiner analysis.

Tech. Rep.	Bud 1	Bud 2	Bud 3	Mean	SD
Replicate 1	442	483	483	469	19
Replicate 2	474	486	453	471	14
Mean	458	485	468		
SD	16	2	15		

[0247] Maps of deconvoluted masses were also highly comparable, with the greatest majority of proteins (93%) being smaller than 20 kD (Figure 12C and Figure 13); a zoom-in confirms the lesser intensity of bud 1 pattern (Figure 12D). Increasing the chromatographic separation from 60 to 120 min and using HPLC column packed with a C4 rather than a C8 stationary phase. This results in better utilisation of the 500-2000 m/z range (503-1799 m/z), enhanced dynamic range (from 10^4 to 10^8 , *i.e.* 4 orders of magnitude), increased numbers of multiply-charged ions, and overall superior and more reproducible LC-MS profiles.

- 99 -

[0248] The triplicated LC-MS/MS patterns are also very similar as exemplified in bud 1 (Figure 12E). Table 11 lists the number of MS/MS spectra per sample (1160 to 1220 MS/MS spectra on average) and method (1178 to 1189 MS/MS spectra on average); SD values were very small and comparable across samples (± 8 to 11) and methods (± 22 to 31), indicative of high reproducibility. The reproducibility of the LC-MS and LC-MS/MS analyses was statistically assessed (Figure 14). Both PCA and HCA clearly separate the bud 1 sample from the other two biological samples, and on the LC-MS data from LC-MS/MS data. Technical replicates clustered together.

Table 11. Number of MS/MS spectra collected across each “Low”, “Mid”, and “High” MS/MS method.

Method	Bud 1	Bud 2	Bud 3	Mean	SD
“Low”	1157	1169	1208	1178	22
“Mid”	1173	1193	1226	1197	22
“High”	1149	1192	1225	1189	31
Mean	1160	1185	1220		
SD	10	11	8		

The most abundant multiply charged precursors were selected for MS/MS experiments (Table 12).

- 100 -

Table 12. Statistics on parent ions from cannabis proteins analysed by LC-MS/MS.

Charge state	No. of precursors	Min. m/z	Max. m/z	Min. Mass (Da)	Max. Mass (Da)	No. of MS/MS events
2	34	714.18	1500.37	1426.36	2998.73	63
3	8	848.75	1176.15	2543.23	3525.44	32
4	45	714.08	1380.06	2852.31	5516.21	143
5	39	803.49	1325.52	4012.42	6622.58	120
6	43	775.62	1458.49	4647.67	8744.89	109
7	61	747.77	1534.29	5227.35	10732.96	222
8	86	787.70	1429.84	6293.52	11430.63	341
9	69	700.41	1564.79	6294.62	14074.01	262
10	48	756.92	1729.69	7559.16	17286.78	195
11	32	726.96	1338.87	7985.51	14716.50	113
12	30	710.98	1338.68	8519.65	16052.07	99
13	32	762.47	1256.51	9898.99	16321.52	114
14	36	732.89	1318.67	10246.31	18447.31	125
15	32	738.60	1099.47	11063.95	16433.03	109
16	29	708.10	1153.96	11269.49	18447.30	105
17	29	737.28	1129.03	12516.63	19176.39	86
18	27	754.89	1163.66	13569.88	20927.81	96
19	37	715.21	1135.96	13569.85	21564.03	124
20	38	710.24	1240.59	14184.59	24791.58	126
21	34	723.89	1185.04	15180.59	24864.66	106
22	28	701.95	1155.10	15420.70	25390.00	92
23	14	711.74	1104.83	16346.79	25387.98	31
24	8	746.08	1036.99	17881.77	24863.64	18
25	3	745.98	992.59	18624.23	24789.59	3

- 101 -

[0249] Overall, precursor charge states ranged from +2 to +25, parent ions from 700.4 to 1729.7 m/z, and their accurate masses span 1.4 to 25.4 kDa. Inherent to MS, the greater the charge state, the greater the mass of cannabis proteins (Figure 15A). The most abundant precursors comprised 4 to 10 charges and their accurate masses range from 2.8 to 17.3 kDa. Therefore, this type of analysis predominantly favours small proteins from cannabis buds. Another factor determining precursor selection pertains to protein abundance, emulated by base peak intensity in the mass spectrometer. In particular, for a proteins larger than 20 kDa to undergo MS/MS, its base peak intensity must exceed 2,000 counts (Figure 15B).

[0250] The last factor determining precursor selection relates to protein hydrophobicity which affects the chromatographic elution. Figure 15C demonstrates that proteins larger than 20 kD were eluted after 75 min of reverse phase separation, indicating that these proteins were more hydrophobic than proteins of smaller size. Therefore, for highly hydrophobic proteins, the separation method prior to the MS analysis needs to be refined using a different type of stationary phase and/or different mobile phases and gradients.

[0251] A total of 11,250 MS/MS peak lists were searched against the UniprotKB *C. sativa* database (663 entries) using Mascot algorithm, a fragment tolerance of ± 50 ppm or ± 2 Da, and validating the results using a decoy or an error tolerant method (Table 7). With a ± 50 ppm fragment tolerance, Protein N-term acetylation and Met oxidation set as dynamic modifications and an error tolerant method, 12 proteins were identified (210 (2%) matches) with 11,040 (98%) MS/MS spectra remaining unassigned and a search time of over 24 h. Using the same parameters but changing error tolerance to decoy brings the number of accessions identified to 21 from 213 (2%) matched MS/MS spectra and a very fast search time of 29 s (Table 13). Excessive stringency in Mascot algorithm could justify the low number of database hits. Rising the fragment tolerance to ± 2 Da, listed 36 proteins based on 355 (3%) assigned MS/MS spectra with a search time of 2.5 min. With a ± 50 ppm

- 102 -

fragment tolerance, Protein N-term acetylation, Met oxidation, phosphorylations of Ser and Tyr residues set as dynamic modifications and a decoy method, the number of unique protein identified was 21 (187 matches) after almost 2 h search. Lifting the fragment tolerance to ± 2 Da as well as the number of hits (61 proteins, 590 (5%) MS/MS spectra assigned). Forsaking dynamic modifications reduced search times and yielded 20 and 24 identities using ± 50 ppm and ± 2 Da fragment tolerance, respectively (Tables 7 and 14).

Table 13 List of cannabis proteins identified by top-down proteomics using Mascot algorithm, *C. sativa* UniprotKB database and ± 50 ppm fragment tolerance.

Member	Accession	Score	Mass (Da)	No. of matches	No. of sequences	emPAI	Description	Species	Proteoforms	BUP ¹
1	A0A0C5ARS8	2265	9367	37	1	0.83	Cytochrome b559 subunit alpha	Cannabis sativa	Unmodified, Acetyl	yes
1	A0A0C5AS17	1664	9545	39	1	1.43	Photosystem I iron-sulfur center	Cannabis sativa	Unmodified, 1 and 2 Oxidations	yes
1	A0A0U2DTK8	1555	3815	25	1	13.87	Photosystem II reaction center protein T	C. sativa subsp. sativa	Unmodified	no
1	A0A0C5B2J7	1348	7645	12	1	1.06	Photosystem II reaction center protein H	Cannabis sativa	Unmodified, Oxidation	no
1	A0A0U2GZT5	902	9381	21	1	0.35	Cytochrome b559 subunit alpha	Humulus lupulus	Unmodified	yes
1	A0A0C5APX7	292	4165	9	1	5.31	Photosystem II reaction center protein I	Cannabis sativa	Unmodified, Acetyl, Oxidation	no
1	A0A0C5ARQ5	272	7985	12	1	1.84	ATP synthase CF0 C subunit	Cannabis sativa	Unmodified, Oxidation	no
1	A0A0U2H3S7	182	11833	5	1	0.62	30S ribosomal protein S14, chloroplastic	Humulus lupulus	Unmodified, Oxidation	yes
1	A0A0C5AU12	182	4421	17	1	0.8	Cytochrome b559 subunit beta	Cannabis sativa	Unmodified	no
1	I6WU39	162	11994	9	1	0.61	Olivetolic acid cyclase	Cannabis sativa	Unmodified, Acetyl	yes
1	A0A0H3W6G0	123	10414	5	1	0.72	Ribosomal protein S16	Cannabis sativa	Unmodified, Oxidation	no
1	I6XT51	113	17597	7	2	1.28	Betv1-like protein	Cannabis sativa	Unmodified, Acetyl, Oxidation	yes
2	A0A0U2DTC8	111	10380	4	1	0.72	30S ribosomal protein S16, chloroplastic	C. sativa subsp. sativa	Unmodified	no
1	A0A0C5APY3	79	4128	2	1	0.87	Photosystem II reaction center protein J	Cannabis sativa	Acetyl	no
1	A0A0C5AU15	72	7910	1	1	0.42	Ribosomal protein L33	Cannabis sativa	Unmodified	no
1	A0A0C5AUH9	62	14696	1	1	0.22	ATP synthase CF1 epsilon subunit	Cannabis sativa	Acetyl	yes
1	A0A0C5APY4	27	4167	1	1	0.85	Cytochrome b6-f complex subunit 5	Cannabis sativa	Unmodified	no
1	W0U0V5	26	9489	2	1	0.35	Non-specific lipid-transfer protein	Cannabis sativa	Unmodified	yes
1	A0A0H3W8G1	25	4494	2	1	0.8	Photosystem II reaction center protein L	Cannabis sativa	Unmodified	no
1	A0A0H3W844	24	17504	1	1	0.18	Cytochrome b6-f complex subunit 4	Cannabis sativa	Unmodified	no
1	A0A0C5AS04	15	4770	1	1	0.74	Photosystem I reaction center subunit IX	Cannabis sativa	Acetyl, Oxidation	no

¹ BUP, protein identified by bottom-up proteomics in Table 4.

Table 14 List of proteins identified from medicinal cannabis protein samples using Mascot algorithm and UniProtKB and SwissProt C. sativa databases

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19031	C. sativa and relatives	AO	50 ppm	error	1	1	tr A0A0C5ARS8 A0A0C5ARS8_CANSA	2174	9367	39	16	2	2	n.a.	Cannabis sativa
19031	C. sativa and relatives	AO	50 ppm	error	2	1	tr A0A0C5AS17 A0A0C5AS17_CANSA	1649	9545	43	4	2	1	n.a.	Cannabis sativa
19031	C. sativa and relatives	AO	50 ppm	error	3	1	tr A0A0C5B2J7 A0A0C5B2J7_CANSA	1348	7645	16	5	1	1	n.a.	Cannabis sativa
19031	C. sativa and relatives	AO	50 ppm	error	4	1	tr A0A0U2GZT5 A0A0U2GZT5_HUMLU	902	9381	31	5	1	1	n.a.	Humulus lupulus
19031	C. sativa and relatives	AO	50 ppm	error	5	1	tr A0A0U2DTK8 A0A0U2DTK8_CANSA	448	3815	33	2	2	1	n.a.	Cannabis sativa subsp. sativa
19031	C. sativa and relatives	AO	50 ppm	error	6	1	tr A0A0C5ARQ5 A0A0C5ARQ5_CANSA	167	7985	32	2	2	1	n.a.	Cannabis sativa
19031	C. sativa and relatives	AO	50 ppm	error	7	1	sp G6WU39JOL AC_CANSA	162	1199	26	1	2	1	n.a.	Cannabis sativa
19031	C. sativa and relatives	AO	50 ppm	error	8	1	tr A0A0C5APX7 A0A0C5APX7_CANSA	127	4165	15	1	2	1	n.a.	Cannabis sativa
19031	C. sativa and relatives	AO	50 ppm	error	9	1	tr A0A0U2DTC8 A0A0U2DTC8_CANSA	111	1038	7	1	1	1	n.a.	Cannabis sativa subsp. sativa
19031	C. sativa and relatives	AO	50 ppm	error	10	1	tr A0A0C5APY3 A0A0C5APY3_CANSA	79	4128	2	1	1	1	n.a.	Cannabis sativa
19031	C. sativa and relatives	AO	50 ppm	error	11	1	tr A0A0U2HI59 A0A0U2HI59_HUMLU	54	1469	3	1	2	1	n.a.	Humulus lupulus
19031	C. sativa and relatives	AO	50 ppm	error	12	1	tr A0A0H3W8G1 A0A0H3W8G1_CANSA	25	4494	2	1	1	1	n.a.	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	1	1	tr A0A0C5ARS8 A0A0C5ARS8_CANSA	2265	9367	37	37	1	1	0.83	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	2	1	tr A0A0C5AS17 A0A0C5AS17_CANSA	1664	9545	39	39	1	1	1.43	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	3	1	tr A0A0U2DTK8 A0A0U2DTK8_CANSA	1555	3815	25	25	1	1	13.87	Cannabis sativa subsp. sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	4	1	tr A0A0C5B2J7 A0A0C5B2J7_CANSA	1348	7645	12	12	1	1	1.06	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	5	1	tr A0A0U2GZT5 A0A0U2GZT5_HUMLU	902	9381	21	21	1	1	0.35	Humulus lupulus
19030	C. sativa and relatives	AO	50 ppm	decoy	6	1	tr A0A0C5APX7 A0A0C5APX7_CANSA	292	4165	9	9	1	1	5.31	Cannabis sativa

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19030	C. sativa and relatives	AO	50 ppm	decoy	7	1	tr A0A0C5ARQ5 A0A0C5ARQ5 CANSA	272	7985	12	12	1	1	1.84	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	8	1	tr A0A0U2H3S7 A0A0U2H3S7 HUMLU	182	11833	5	5	1	1	0.62	Humulus lupulus
19030	C. sativa and relatives	AO	50 ppm	decoy	9	1	tr A0A0C5AUJ2 A0A0C5AUJ2 CANSA	182	4421	17	17	1	1	0.8	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	10	1	tr A0A0H3W6G0 A0A0H3W6G0 CANSA	162	11994	9	9	1	1	0.61	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	11	1	tr A0A0U2DTC8 A0A0U2DTC8 CANSA	123	10414	5	5	1	1	0.72	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	11	2	tr A0A0U2DTC8 A0A0U2DTC8 CANSA	111	10380	4	4	1	1	0.72	Cannabis sativa subsp. sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	12	1	tr A0A0C5APY3 A0A0C5APY3 CANSA	113	17597	7	7	2	2	1.28	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	13	1	tr A0A0C5AUJ5 A0A0C5AUJ5 CANSA	79	4128	2	2	1	1	0.87	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	14	1	tr A0A0C5AUH9 A0A0C5AUH9 CANSA	72	7910	1	1	1	1	0.42	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	15	1	tr A0A0C5APY4 A0A0C5APY4 CANSA	62	14696	1	1	1	1	0.22	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	16	1	tr A0A0C5W8G1 A0A0H3W8G1 CANSA	27	4167	1	1	1	1	0.85	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	17	1	tr A0A0C5W8G1 A0A0H3W8G1 CANSA	26	9489	2	2	1	1	0.35	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	18	1	tr A0A0C5W8G1 A0A0H3W8G1 CANSA	25	4494	2	2	1	1	0.8	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	19	1	tr A0A0C5W8G1 A0A0H3W8G1 CANSA	24	17504	1	1	1	1	0.18	Cannabis sativa
19030	C. sativa and relatives	AO	50 ppm	decoy	20	1	tr A0A0C5W8G1 A0A0H3W8G1 CANSA	15	4770	1	1	1	1	0.74	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	1	1	tr A0A0C5AS17 A0A0C5AS17 CANSA	3341	9545	53	53	1	1	1.43	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	2	1	tr A0A0C5ARS8 A0A0C5ARS8 CANSA	3243	9367	43	43	2	2	1.47	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	3	1	tr A0A0C5B2J7 A0A0C5B2J7 CANSA	2046	7645	23	23	2	2	11.61	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	4	1	tr A0A0U2DTC8 A0A0U2DTC8 CANSA	1983	3815	29	29	1	1	13.87	Cannabis sativa subsp. sativa
19048	C. sativa and relatives	AO	2 Da	decoy	5	1	tr A0A0C5W8G1 A0A0H3W8G1 CANSA	1227	17597	46	46	2	2	3.42	Cannabis sativa

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19048	C. sativa and relatives	AO	2 Da	decoy	6	1	tr A0A0C5ARQ5 A0A0C5ARQ5_CANSA	618	7985	17	17	1	1	4.7	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	7	1	tr W0U0V5W0U0V5_CANSA	477	9489	17	17	1	1	0.82	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	8	1	sp I6WU39 OLIA_CANSA	445	1199	19	19	1	1	1.05	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	9	1	tr A0A0U2H3S7 A0A0U2H3S7_HUMLU	418	1183	10	10	2	2	1.06	Humulus lupulus
19048	C. sativa and relatives	AO	2 Da	decoy	10	1	tr A0A0C5APX7 A0A0C5APX7_CANSA	333	4165	9	9	1	1	0.85	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	11	1	tr A0A0U2H3Q7 A0A0U2H3Q7_HUMLU	293	1046	5	5	2	2	0.72	Humulus lupulus
19048	C. sativa and relatives	AO	2 Da	decoy	12	1	tr A0A0H3W6G0 A0A0H3W6G0_CANSA	272	1041	7	7	1	1	0.72	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	13	1	tr A0A0C5B2H7 A0A0C5B2H7_CANSA	266	1182	4	4	1	1	0.62	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	14	1	tr A0A0C5AU12 A0A0C5AU12_CANSA	262	4421	19	19	1	1	0.8	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	15	1	tr A0A0C5AUH9 A0A0C5AUH9_CANSA	240	1469	6	6	2	2	1.68	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	16	1	tr A0A0U2DTC8 A0A0U2DTC8_CANSA	239	1038	7	7	1	1	0.72	Cannabis sativa subsp. sativa
19048	C. sativa and relatives	AO	2 Da	decoy	17	1	tr A0A0C5AU15 A0A0C5AU15_CANSA	137	7910	1	1	1	1	0.42	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	18	1	tr A0A0C5APY3 A0A0C5APY3_CANSA	114	4128	2	2	1	1	0.87	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	19	1	tr A0A172J205 A0A172J205_B_OENI	86	1001	11	11	2	2	6.26	Boehmeria nivea
19048	C. sativa and relatives	AO	2 Da	decoy	20	1	tr A0A0H3W844 A0A0H3W844_CANSA	57	1750	1	1	1	1	0.18	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	21	1	tr A0A0C5AS04 A0A0C5AS04_CANSA	54	4770	5	5	1	1	2.02	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	22	1	tr A0A0C5APY7 A0A0C5APY7_CANSA	45	1551	1	1	1	1	0.21	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	23	1	tr A0A0H3W8G1 A0A0H3W8G1_CANSA	33	4494	3	3	1	1	0.8	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	24	1	tr A0A172J223 A0A172J223_B_OENI	31	1132	2	2	1	1	0.66	Boehmeria nivea
19048	C. sativa and relatives	AO	2 Da	decoy	25	1	tr A0A3G3NDF5 A0A3G3NDF5_CANSA	29	9475	2	2	1	1	0.35	Cannabis sativa

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19048	C. sativa and relatives	AO	2 Da	decoy	26	1	tr A0A0C5APY4 A0A0C5APY4_CANSA	28	4167	1	1	1	1	0.85	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	27	1	tr A0A172J276 A0A172J276_BOENI	27	17456	1	1	1	1	0.18	Boehmeria nivea
19048	C. sativa and relatives	AO	2 Da	decoy	28	1	tr A0A172J254 A0A172J254_BOENI	27	12135	1	1	1	1	0.27	Boehmeria nivea
19048	C. sativa and relatives	AO	2 Da	decoy	29	1	tr A0A0U2H2X0 A0A0U2H2X0_HUMLU	22	15282	1	1	1	1	0.21	Humulus lupulus
19048	C. sativa and relatives	AO	2 Da	decoy	30	1	tr A0A172J266 A0A172J266_BOENI	22	9630	1	1	1	1	0.34	Boehmeria nivea
19048	C. sativa and relatives	AO	2 Da	decoy	31	1	tr A0A0Y0U203 A0A0Y0U203_CANSA	19	3386	3	3	1	1	3.3	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	32	1	tr Q5TIQ0Q5 TIQ0_CANSA	16	8785	1	1	1	1	0.38	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	33	1	tr A0A172J200 A0A172J200_BOENI	16	16123	1	1	1	1	0.2	Boehmeria nivea
19048	C. sativa and relatives	AO	2 Da	decoy	34	1	tr A0A0C5B2J2 A0A0C5B2J2_CANSA	15	3299	1	1	1	1	1.11	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	35	1	tr A0A1W2KS3 A0A1W2KS3_1_CANSA	15	8525	1	1	1	1	0.39	Cannabis sativa
19048	C. sativa and relatives	AO	2 Da	decoy	36	1	tr A0A1U9VXL5 A0A1U9VXL_5_CANSA	14	4711	1	1	1	1	0.76	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	1	1	tr A0A0C5ARS8 A0A0C5ARS8_CANSA	2166	9367	35	35	1	1	2.35	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	2	1	tr A0A0C5B2J7 A0A0C5B2J7_CANSA	1547	7645	14	14	1	1	3.26	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	3	1	tr A0A0C5AS17 A0A0C5AS17_CANSA	1499	9545	37	37	1	1	1.43	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	4	1	tr A0A0U2DTK8 A0A0U2DTK_8_CANSA	1459	3815	25	25	1	1	13.87	Cannabis sativa subsp. sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	5	1	tr A0A0C5AU12 A0A0C5AU12_CANSA	676	4421	20	20	1	1	2.24	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	6	1	tr A0A0C5APX7 A0A0C5APX7_CANSA	279	4165	8	8	2	2	20.57	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	7	1	tr A0A0C5ARQ5 A0A0C5ARQ_5_CANSA	223	7985	10	10	2	2	4.7	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	8	1	sp G6WU39 OLAC_CANSA	156	11994	10	10	1	1	1.6	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	9	1	tr A0A0U2H3S7 A0A0U2H3S7_HUMLU	140	11833	5	5	1	1	0.62	Humulus lupulus

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19050	C. sativa and relatives	AOP	50 ppm	decoy	10	1	tr A0A0H3W6G0 A0A0H3W6G0 CANSA	112	10414	3	3	1	1	0.72	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	11	1	tr A0A0U2DTC8 A0A0U2DTC8 CANSA	111	10380	3	3	1	1	0.72	Cannabis sativa subsp. sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	12	1	tr A0A0C5APY3 A0A0C5APY3 CANSA	74	4128	2	2	1	1	0.87	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	13	1	tr A0A0C5AU15 A0A0C5AU15 CANSA	72	7910	1	1	1	1	0.42	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	14	1	tr A0A0C5AU15 A0A0C5AU15 CANSA	68	17597	3	3	1	1	0.39	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	15	1	tr A0A0C5AUH9 A0A0C5AUH9 CANSA	62	14696	1	1	1	1	0.22	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	16	1	tr W0U0V5W0U0V5 CANSA	34	9489	3	3	1	1	0.82	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	17	1	tr A0A0C5AS00 A0A0C5AS00 CANSA	30	4008	2	2	1	1	2.62	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	18	1	tr A0A0C5APY4 A0A0C5APY4 CANSA	27	4167	1	1	1	1	0.85	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	19	1	tr A0A0H3W8G1 A0A0H3W8G1 CANSA	25	4494	2	2	1	1	0.8	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	20	1	tr A0A0H3W844 A0A0H3W844 CANSA	24	17504	1	1	1	1	0.18	Cannabis sativa
19050	C. sativa and relatives	AOP	50 ppm	decoy	21	1	tr A0A0C5AS04 A0A0C5AS04 CANSA	15	4770	1	1	1	1	0.74	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	1	1	tr A0A0C5ARS8 A0A0C5ARS8 CANSA	3186	9367	44	44	2	2	3.53	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	2	1	tr A0A0C5AS17 A0A0C5AS17 CANSA	3158	9545	53	53	1	1	2.26	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	3	1	tr A0A0C5B2J7 A0A0C5B2J7 CANSA	2468	7645	43	43	2	2	5937.4	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	4	1	tr A0A0U2DTC8 A0A0U2DTC8 CANSA	2057	3815	33	33	2	2	111.64	Cannabis sativa subsp. sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	5	1	tr A0A0C5ARQ5 A0A0C5ARQ5 CANSA	1902	7985	34	34	2	2	91.46	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	6	1	tr A0A0U2GZT5 A0A0U2GZT5 HUMLU	1831	9381	29	29	2	2	9.91	Humulus lupulus
19049	C. sativa and relatives	AOP	2 Da	decoy	7	1	tr A0A0C5AU12 A0A0C5AU12 CANSA	1314	4421	23	23	1	1	2.24	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	8	1	tr A0A0C5AU12 A0A0C5AU12 CANSA	986	17597	36	36	2	2	5.15	Cannabis sativa

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19049	C. sativa and relatives	AOP	2 Da	decoy	9	1	tr W0U0V5 W0U0V5_CANSA	896	9489	39	39	1	1	3.45	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	10	1	tr A0A0C5APX7 A0A0C5APX7_CANSA	691	4165	16	16	1	1	5.31	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	11	1	tr A0A0U2DTC8 A0A0U2DTC8_CANSA	382	10380	7	7	1	1	0.31	Cannabis sativa subsp. sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	12	1	tr A0A0U2H3S7 A0A0U2H3S7_CANSA	379	11994	13	13	1	1	1.6	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	13	1	tr A0A0C5AS04 A0A0C5AS04_CANSA	285	4770	10	10	2	2	2.02	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	14	1	tr A0A0U2H3S7 A0A0U2H3S7_HUMLU	278	11833	5	5	1	1	1.06	Humulus lupulus
19049	C. sativa and relatives	AOP	2 Da	decoy	15	1	tr A0A0C5AUH9 A0A0C5AUH9_CANSA	229	14696	7	7	2	2	2.27	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	16	1	tr A0A0C5B2H7 A0A0C5B2H7_CANSA	224	11823	4	4	1	1	0.62	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	17	1	tr A0A0C5AS00 A0A0C5AS00_CANSA	217	4008	17	17	2	2	46.41	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	18	1	tr A0A0C5APY3 A0A0C5APY3_CANSA	195	4128	18	18	1	1	11.35	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	19	1	tr A0A0U2H1S9 A0A0U2H1S9_HUMLU	167	14695	4	4	2	2	0.81	Humulus lupulus
19049	C. sativa and relatives	AOP	2 Da	decoy	20	1	tr A0A0U2H3Q7 A0A0U2H3Q7_HUMLU	161	10464	2	2	1	1	0.31	Humulus lupulus
19049	C. sativa and relatives	AOP	2 Da	decoy	21	1	tr A0A172J1Y7 A0A172J1Y7_B_OENI	160	9893	28	28	2	2	406.84	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	22	1	tr A0A0C5AUJ5 A0A0C5AUJ5_CANSA	137	7910	1	1	1	1	0.42	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	23	1	tr A0A0M4QY14 A0A0M4QY14_CANSA	88	11151	9	9	2	2	5.03	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	24	1	tr A0A0H3W8G1 A0A0H3W8G1_CANSA	78	4494	13	13	2	2	4.83	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	25	1	tr A0A0H3W8B6 A0A0H3W8B6_CANSA	78	15404	2	2	1	1	0.46	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	26	1	tr A0A0H3W844 A0A0H3W844_CANSA	77	17504	2	2	2	2	0.39	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	27	1	tr A0A172J205 A0A172J205_B_OENI	73	10012	8	8	2	2	6.26	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	28	1	tr R47F6 R47F6_CANSA	63	13263	4	4	1	1	0.55	Cannabis sativa

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19049	C. sativa and relatives	AOP	2 Da	decoy	29	1	tr A0A3G3NDF5 A0A3G3NDF5_CANSA	60	9475	3	3	1	1	0.82	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	30	1	tr A0A0M3ULW1 A0A0M3ULW1_CANSA	60	13819	9	9	2	2	5.59	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	31	1	tr A0A0C5AS02 A0A0C5AS02_CANSA	53	4464	5	5	1	1	0.8	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	32	1	tr A0A0C5ARS1 A0A0C5ARS1_CANSA	46	6493	8	8	2	2	4.45	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	33	1	tr A0A0C5APY7 A0A0C5APY7_CANSA	45	15516	1	1	1	1	0.21	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	34	1	tr A0A172J1X8 A0A172J1X8_BOENI	42	10484	1	1	1	1	0.31	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	35	1	tr A0A172J290 A0A172J290_BOENI	41	10804	1	1	1	1	0.3	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	36	1	tr A0A172J266 A0A172J266_BOENI	41	9630	6	6	2	2	3.31	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	37	1	tr A0A172J222 A0A172J222_BOENI	40	10864	2	2	1	1	0.69	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	38	1	tr A0A172J232 A0A172J232_BOENI	39	10863	1	1	1	1	0.3	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	39	1	tr A0A0Y0UZ03 A0A0Y0UZ03_CANSA	39	3386	10	10	2	2	339.69	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	40	1	tr A0A3G3NDF7 A0A3G3NDF7_CANSA	37	9406	2	2	1	1	0.82	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	41	1	tr A0A172J230 A0A172J230_BOENI	36	11172	1	1	1	1	0.29	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	42	1	tr A0A172J220 A0A172J220_BOENI	34	10824	1	1	1	1	0.3	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	43	1	tr A0A172J239 A0A172J239_BOENI	34	11040	1	1	1	1	0.3	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	44	1	tr A0A0C5ART4 A0A0C5ART4_CANSA	34	15045	1	1	1	1	0.21	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	45	1	tr A0A3R5T0F7 A0A3R5T0F7_CANSA	33	13331	1	1	1	1	0.24	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	46	1	tr A0A172J1X4 A0A172J1X4_BOENI	33	10628	2	2	1	1	0.31	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	47	1	tr A0A0C5APY8 A0A0C5APY8_CANSA	32	10505	1	1	1	1	0.31	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	48	1	tr A0A0C5AUJ2 A0A0C5AUJ2_CANSA	31	13360	2	2	1	1	0.54	Cannabis sativa

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19049	C. sativa and relatives	AOP	2 Da	decoy	49	1	tr A0A172J1Y0 A0A172J1Y0_B OENI	31	1456 3	1	1	1	1	0.22	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	50	1	tr A0A172J237 A0A172J237_B OENI	30	1368 3	1	1	1	1	0.24	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	51	1	tr A0A172J213 A0A172J213_B OENI	30	1242 2	1	1	1	1	0.26	Boehmeria nivea
19049	C. sativa and relatives	AOP	2 Da	decoy	52	1	tr A0A0C5APY4 A0A0C5APY4 _CANSA	28	4167	1	1	1	1	0.85	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	53	1	tr A0A0U2DTJ2 A0A0U2DTJ2_ CANSA	28	4719	3	3	2	2	4.24	Cannabis sativa subsp. sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	54	1	tr Q5TIQ0 Q5TIQ0_CANSA	28	8785	3	3	1	1	1.61	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	55	1	tr B5AFH3 B5AFH3_CANSA	27	5014	7	7	1	1	13.21	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	56	1	tr Q5TIP7 Q5TIP7_CANSA	27	7198	2	2	2	2	1.15	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	57	1	tr A0A1U9VXK6 A0A1U9VXK 6_CANSA	23	4162	2	2	1	1	2.51	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	58	1	tr A9XV94 A9XV94_CANSA	20	2760	1	1	1	1	1.38	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	59	1	tr A0A0C5B2J2 A0A0C5B2J2_ CANSA	19	3299	2	2	1	1	3.47	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	60	1	tr A0A0C5B2G1 A0A0C5B2G1 _CANSA	19	3168	2	2	1	1	3.66	Cannabis sativa
19049	C. sativa and relatives	AOP	2 Da	decoy	61	1	tr Q5TIP6 Q5TIP6_CANSA	18	8111	1	1	1	1	0.41	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	1	1	tr A0A0C5ARS8 A0A0C5ARS8 CANSA	2260	9367	37	37	2	2	0.83	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	2	1	tr A0A0C5AS17 A0A0C5AS17_ CANSA	1696	9545	42	42	1	1	0.34	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	3	1	tr A0A0U2DTK8 A0A0U2DTK 8_CANSA	1326	3815	18	18	1	1	0.96	Cannabis sativa subsp. sativa
19051	C. sativa and relatives	none	50 ppm	decoy	4	1	tr A0A0C5B2J7 A0A0C5B2J7_ CANSA	1285	7645	12	12	1	1	0.44	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	5	1	tr A0A0U2GZT5 A0A0U2GZT5 HUMLU	905	9381	21	21	1	1	0.35	Humulus lupulus
19051	C. sativa and relatives	none	50 ppm	decoy	6	1	tr A0A0C5APX7 A0A0C5APX7 CANSA	291	4165	8	8	1	1	0.85	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	7	1	tr A0A0C5ARQ5 A0A0C5ARQ 5_CANSA	250	7985	11	11	1	1	0.42	Cannabis sativa

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19051	C. sativa and relatives	none	50 ppm	decoy	8	1	sp I6WU39 OLAC_CANSA	191	1199 ₄	13	13	1	1	0.27	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	9	1	tr A0A0C5AUJ2 A0A0C5AUJ2_CANSA	182	4421	17	17	1	1	0.8	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	10	1	tr A0A0H3W6G0 A0A0H3W6G0_CANSA	152	1041 ₄	5	5	1	1	0.31	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	11	1	tr A0A0U2H3S7 A0A0U2H3S7_HUMLU	144	1183 ₃	4	4	1	1	0.27	Humulus lupulus
19051	C. sativa and relatives	none	50 ppm	decoy	12	1	tr A0A0U2DTC8 A0A0U2DTC8_CANSA	132	1038 ₀	5	5	1	1	0.31	Cannabis sativa subsp. sativa
19051	C. sativa and relatives	none	50 ppm	decoy	13	1	tr I6XT51 I6XT51_CANSA	125	1759 ₇	10	10	2	2	0.39	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	14	1	tr A0A0C5AUJ5 A0A0C5AUJ5_CANSA	72	7910	1	1	1	1	0.42	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	15	1	tr A0A0C5AUH9 A0A0C5AUH9_CANSA	51	1469 ₆	3	3	2	2	0.48	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	16	1	tr W0U0V5 W0U0V5_CANSA	29	9489	2	2	1	1	0.35	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	17	1	tr A0A0C5APY4 A0A0C5APY4_CANSA	27	4167	1	1	1	1	0.85	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	18	1	tr A0A0H3W8G1 A0A0H3W8G1_CANSA	25	4494	2	2	1	1	0.8	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	19	1	tr A0A0H3W844 A0A0H3W844_CANSA	24	1750 ₄	1	1	1	1	0.18	Cannabis sativa
19051	C. sativa and relatives	none	50 ppm	decoy	20	1	tr A0A0C5AS04 A0A0C5AS04_CANSA	14	4770	1	1	1	1	0.74	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	1	1	tr A0A0C5AS17 A0A0C5AS17_CANSA	3384	9545	53	53	1	1	0.34	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	2	1	tr A0A0C5ARS8 A0A0C5ARS8_CANSA	3236	9367	43	43	2	2	0.83	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	3	1	tr A0A0C5B2J7 A0A0C5B2J7_CANSA	1996	7645	16	16	1	1	0.44	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	4	1	tr A0A0U2DTC8 A0A0U2DTC8_CANSA	1606	3815	18	18	1	1	0.96	Cannabis sativa subsp. sativa
19043	C. sativa and relatives	none	2 Da	decoy	5	1	tr I6XT51 I6XT51_CANSA	959	1759 ₇	36	36	2	2	0.39	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	6	1	tr W0U0V5 W0U0V5_CANSA	521	9489	20	20	1	1	0.35	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	7	1	sp I6WU39 OLAC_CANSA	464	1199 ₄	18	18	2	2	0.61	Cannabis sativa

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19043	C. sativa and relatives	none	2 Da	decoy	8	1	tr A0A0C5ARQ5 A0A0C5ARQ5 CANSA	449	7985	15	15	1	1	0.42	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	9	1	tr A0A0U2H3S7 A0A0U2H3S7 HUMLU	344	1183	8	8	2	2	0.62	Humulus lupulus
19043	C. sativa and relatives	none	2 Da	decoy	10	1	tr A0A0H3W6G0 A0A0H3W6G0 CANSA	310	1041	8	8	1	1	0.31	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	11	1	tr A0A0C5APX7 A0A0C5APX7 CANSA	294	4165	8	8	1	1	0.85	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	12	1	tr A0A0C5AUJ2 A0A0C5AUJ2 CANSA	262	4421	19	19	1	1	0.8	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	13	1	tr A0A0U2DTC8 A0A0U2DTC8 CANSA	243	1038	7	7	1	1	0.31	Cannabis sativa subsp. sativa
19043	C. sativa and relatives	none	2 Da	decoy	14	1	tr A0A0C5B2H7 A0A0C5B2H7 CANSA	208	1182	4	4	1	1	0.27	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	15	1	tr A0A0C5AUH9 A0A0C5AUH9 CANSA	149	1469	4	4	2	2	0.48	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	16	1	tr A0A0C5AUJ5 A0A0C5AUJ5 CANSA	137	7910	1	1	1	1	0.42	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	17	1	tr A0A0H3W844 A0A0H3W844 CANSA	62	1750	2	2	1	1	0.18	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	18	1	tr A0A0H3W8G1 A0A0H3W8G1 CANSA	33	4494	3	3	1	1	0.8	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	19	1	tr A0A0C5APY7 A0A0C5APY7 CANSA	32	1551	1	1	1	1	0.21	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	20	1	tr A0A0C5APY4 A0A0C5APY4 CANSA	28	4167	1	1	1	1	0.85	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	21	1	tr A0A0C5AS04 A0A0C5AS04 CANSA	18	4770	3	3	1	1	0.74	Cannabis sativa
19043	C. sativa and relatives	none	2 Da	decoy	22	1	tr A0A172J269 A0A172J269_B OENI	17	1150	1	1	1	1	0.28	Boehmeria nivea
19043	C. sativa and relatives	none	2 Da	decoy	23	1	tr A0A172J229 A0A172J229_B OENI	15	1074	1	1	1	1	0.3	Boehmeria nivea
19043	C. sativa and relatives	none	2 Da	decoy	24	1	tr A0A1U9VXP2 A0A1U9VXP2 CANSA	14	1396	1	1	1	1	0.23	Cannabis sativa

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	embAI	Species
19042	all	none	2 Da	decoy	1	1	H42_WHEAT	21948	11460	159	159	2		0.65	Triticum aestivum
19042	all	none	2 Da	decoy	2	1	H4_CAPAN	4176	11418	77	77	2	2	0.65	Capsicum annuum
19042	all	none	2 Da	decoy	3	1	UBIQ_AVESA	2508	8520	26	26	1	1	0.39	Avena sativa
19042	all	none	2 Da	decoy	4	1	PSAC_AETCO	2359	9545	42	42	1	1	0.34	Aethionema cordifolium
19042	all	none	2 Da	decoy	5	1	PSBF_EPHSI	2249	4507	23	23	1	1	0.78	Ephedra sinica
19042	all	none	2 Da	decoy	6	1	PSAC_PHAHO	1938	9561	34	34	1	1	0.34	Phalaenopsis aphrodite subsp. formosana
19042	all	none	2 Da	decoy	7	1	ATPH_CYCTA	1710	7995	20	20	1	1	0.42	Cycas taitungensis
19042	all	none	2 Da	decoy	8	1	PSBE_AMBTC	1608	9381	21	21	1	1	0.35	Amborella trichopoda
19042	all	none	2 Da	decoy	9	1	PSBT_PELHO	1460	3831	25	25	1	1	0.93	Pelargonium hortorum
19042	all	none	2 Da	decoy	10	1	UBIQ_COPCO	1421	8536	25	25	1	1	0.39	Coprinellus congregatus
19042	all	none	2 Da	decoy	11	1	PSBT_ALLTE	1419	3815	18	18	1	1	0.96	Allium textile
19042	all	none	2 Da	decoy	12	1	H32_ENCICAL	1364	15344	55	55	1	1	0.21	Encephalartos altensteinii
19042	all	none	2 Da	decoy	13	1	PSBT_PIPCE	1249	3833	25	25	1	1	0.93	Piper cenocladum
19042	all	none	2 Da	decoy	14	1	PSBE_CITSI	979	9380	18	18	1	1	0.35	Citrus sinensis
19042	all	none	2 Da	decoy	14	2	PSBE_MESCR	673	9353	22	22	1	1	0.35	Mesembryanthemum crystallinum
19042	all	none	2 Da	decoy	15	1	H33_TRIPS	862	15360	37	37	1	1	0.21	Trichinella pseudospiralis
19042	all	none	2 Da	decoy	16	1	PSBE_AGRST	742	9439	19	19	1	1	0.35	Agrostis stolonifera
19042	all	none	2 Da	decoy	17	1	H3_VOICCA	740	15358	43	43	2	2	0.46	Volvox carteri
19042	all	none	2 Da	decoy	18	1	PSAC_SPIOL	695	9531	21	21	1	1	0.34	Spinacia oleracea
19042	all	none	2 Da	decoy	19	1	RL23_ARATH	588	15188	14	14	2	2	0.46	Arabidopsis thaliana
19042	all	none	2 Da	decoy	20	1	PSBF_AGARO	546	4481	24	24	1	1	0.8	Agathis robusta
19042	all	none	2 Da	decoy	21	1	RL371_ORYSJ	415	10464	6	6	1	1	0.31	Oryza sativa subsp. japonica
19042	all	none	2 Da	decoy	22	1	H31_CHLRE	397	15344	26	26	1	1	0.21	Chlamydomonas reinhardtii
19042	all	none	2 Da	decoy	23	1	RL37A_GOSH	360	10435	6	6	1	1	0.31	Gossypium hirsutum
19042	all	none	2 Da	decoy	24	1	RL391_ARAT	353	6412	7	7	1	1	0.53	Arabidopsis thaliana
19042	all	none	2 Da	decoy	25	1	RR14_NICSY	348	11850	5	5	1	1	0.27	Nicotiana sylvestris
19042	all	none	2 Da	decoy	26	1	OLIAC_CANS	299	11994	12	12	2	2	0.61	Cannabis sativa
19042	all	none	2 Da	decoy	27	1	PSBL_CRYJA	234	4164	5	5	1	1	0.85	Cryptomeria japonica
19042	all	none	2 Da	decoy	28	1	RS28_OSTOS	220	7500	7	7	2	2	1.08	Ostertagia ostertagi

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19042	all	none	2 Da	decoy	29	1	PSAC_DRIGR	217	9529	12	12	1	1	0.34	<i>Drimys granadensis</i>
19042	all	none	2 Da	decoy	30	1	RR14_SOLBU	203	11866	4	4	1	1	0.27	<i>Solanum bulbocastanum</i>
19042	all	none	2 Da	decoy	31	1	H332_CAEEL	173	15408	15	15	1	1	0.21	<i>Caenorhabditis elegans</i>
19042	all	none	2 Da	decoy	32	1	RL38_SOLJC	162	8192	10	10	1	1	0.4	<i>Solanum lycopersicum</i>
19042	all	none	2 Da	decoy	33	1	H32_CICIN	153	15425	15	15	1	1	0.21	<i>Cichorium intybus</i>
19042	all	none	2 Da	decoy	34	1	H32_MEDSA	150	15332	15	15	2	2	0.46	<i>Medicago sativa</i>
19042	all	none	2 Da	decoy	35	1	H3LI_ARATH	143	15406	13	13	1	1	0.21	<i>Arabidopsis thaliana</i>
19042	all	none	2 Da	decoy	36	1	PLAS_MERPE	123	10536	6	6	1	1	0.31	<i>Mercurialis perennis</i>
19042	all	none	2 Da	decoy	37	1	RS30_ARATH	122	6883	2	2	1	1	0.49	<i>Arabidopsis thaliana</i>
19042	all	none	2 Da	decoy	38	1	PSBL_LEPVR	101	4180	5	5	1	1	0.85	<i>Lepidium virginicum</i>
19042	all	none	2 Da	decoy	39	1	PSAI_LEMMI	94	4782	4	4	1	1	0.74	<i>Lemna minor</i>
19042	all	none	2 Da	decoy	40	1	H2A3_ORYSI	74	13909	4	4	1	1	0.23	<i>Oryza sativa subsp. indica</i>
19042	all	none	2 Da	decoy	41	1	PETD_ATRBE	57	17504	1	1	1	1	0.18	<i>Atropa belladonna</i>
19042	all	none	2 Da	decoy	42	1	H2B8_ARATH	57	15215	3	3	1	1	0.21	<i>Arabidopsis thaliana</i>
19042	all	none	2 Da	decoy	43	1	GRP1_ARATH	50	25070	3	3	1	1	0.12	<i>Arabidopsis thaliana</i>
19042	all	none	2 Da	decoy	44	1	EX7S_BEUC1	47	9351	1	1	1	1	0.35	<i>Boutenbergia cavernae</i> (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)
19042	all	none	2 Da	decoy	45	1	TATAO_HAL VD	46	9577	2	2	1	1	0.34	<i>Haloflex volcanii</i> (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2)
19042	all	none	2 Da	decoy	46	1	H3C_CAIMO	45	15535	1	1	1	1	0.21	<i>Cairnia moschata</i>
19042	all	none	2 Da	decoy	47	1	RR16_MORIN	45	10496	3	3	1	1	0.31	<i>Morus indica</i>
19042	all	none	2 Da	decoy	48	1	PLAS_LACSA	43	10410	2	2	1	1	0.31	<i>Lactuca sativa</i>
19042	all	none	2 Da	decoy	49	1	HSL32_DICDI	41	8984	1	1	1	1	0.37	<i>Dictyostelium discoideum</i>
19042	all	none	2 Da	decoy	50	1	H2A2_ORYSI	40	13968	2	2	1	1	0.23	<i>Oryza sativa subsp. indica</i>
19042	all	none	2 Da	decoy	51	1	RL342_ARAT H	40	13699	1	1	1	1	0.24	<i>Arabidopsis thaliana</i>
19042	all	none	2 Da	decoy	52	1	ATPL_LACPL	40	7163	1	1	1	1	0.47	<i>Lactobacillus plantarum</i> (strain ATCC BAA-793 / NCIMB 8826 / WCFS1)
19042	all	none	2 Da	decoy	53	1	ATPL_ILYTA	39	8790	1	1	1	1	0.38	<i>Ilyobacter tartaricus</i>
19042	all	none	2 Da	decoy	54	1	CX6B3_ARAT H	37	9474	1	1	1	1	0.35	<i>Arabidopsis thaliana</i>
19042	all	none	2 Da	decoy	55	1	CRCB1_CORD I	37	9997	1	1	1	1	0.33	<i>Corynebacterium diphtheriae</i> (strain ATCC 700971 / NCTC 13129 /

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
															Biotype gravis)
19042	all	none	2 Da	decoy	56	1	ACYP_MANS M	36	10120	1	1	1	1	0.32	Mannheimia succiniciproducens (strain MBEL55E)
19042	all	none	2 Da	decoy	57	1	UBIQ_HELAN	36	8667	3	3	1	1	0.38	Helianthus annuus
19042	all	none	2 Da	decoy	58	1	RL30_LUPLU	35	12553	1	1	1	1	0.26	Lupinus luteus
19042	all	none	2 Da	decoy	59	1	RL13_PSEHT	34	15934	3	3	1	1	0.2	Pseudoalteromonas haloplanktis (strain TAC 125)
19042	all	none	2 Da	decoy	60	1	GRP2_ORYSI	33	14873	3	3	1	1	0.21	Oryza sativa subsp. indica
19042	all	none	2 Da	decoy	61	1	Y2513_ANAV T	33	9665	1	1	1	1	0.34	Anabaena variabilis (strain ATCC 29413 / PCC 7937)
19042	all	none	2 Da	decoy	62	1	MOAC_SALA R	33	17590	1	1	1	1	0.18	Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980)
19042	all	none	2 Da	decoy	63	1	PSAJ_OSTTA	33	4727	2	2	1	1	0.74	Ostreococcus tauri
19042	all	none	2 Da	decoy	64	1	HSL39_DICDI	32	9177	2	2	1	1	0.36	Dictyostelium discoideum
19042	all	none	2 Da	decoy	65	1	RBR1_CANAL	32	9524	1	1	1	1	0.34	Candida albicans (strain SC5314 / ATCC MYA-2876)
19042	all	none	2 Da	decoy	66	1	GBG_YARLI	32	12673	1	1	1	1	0.25	Yarrowia lipolytica (strain CLIB 122 / E 150)
19042	all	none	2 Da	decoy	67	1	OLF9_APIJI	32	9346	1	1	1	1	0.35	Apis mellifera ligustica
19042	all	none	2 Da	decoy	68	1	UBL1_SCHPO	31	8713	1	1	1	1	0.38	Schizosaccharomyces pombe (strain 972 / ATCC 24843)
19042	all	none	2 Da	decoy	69	1	CWP2_YEAST	29	8905	1	1	1	1	0.37	Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
19042	all	none	2 Da	decoy	70	1	HEM3_DICCH	29	9973	1	1	1	1	0.33	Dickeya chrysanthemi
19042	all	none	2 Da	decoy	71	1	PSBX_GUITH	29	4168	1	1	1	1	0.85	Guillardia theta
19042	all	none	2 Da	decoy	72	1	COCA_CONC L	28	9556	1	1	1	1	0.34	Californiconus californicus
19042	all	none	2 Da	decoy	73	1	PETG_CUSEX	28	4181	1	1	1	1	0.85	Cuscuta exaltata
19042	all	none	2 Da	decoy	74	1	R15A1_ARAT H	27	14852	1	1	1	1	0.21	Arabidopsis thaliana
19042	all	none	2 Da	decoy	75	1	PSAJ_AMBIC	27	4774	1	1	1	1	0.74	Amborella trichopoda
19042	all	none	2 Da	decoy	76	1	H2B10_ARAT H	27	15723	1	1	1	1	0.2	Arabidopsis thaliana
19042	all	none	2 Da	decoy	77	1	PSBJ_AGRST	27	4114	1	1	1	1	0.87	Agrostis stolonifera
19042	all	none	2 Da	decoy	78	1	ANP4_PSEAM R35A3_ARAT H	26	7211	1	1	1	1	0.47	Pseudopleuronectes americanus
19042	all	none	2 Da	decoy	79	1	H	26	12965	1	1	1	1	0.25	Arabidopsis thaliana

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	empAI	Species
19042	all	none	2 Da	decoy	80	1	H2B1_ARATH	26	16392	1	1	1	1	0.19	Arabidopsis thaliana
19042	all	none	2 Da	decoy	81	1	RS12_AC1PL	25	9242	1	1	1	1	0.36	Actinobacillus pleuropneumoniae
19042	all	none	2 Da	decoy	82	1	RL34_LEUCK	25	5317	1	1	1	1	0.65	Leuconostoc citreum (strain KM20)
19042	all	none	2 Da	decoy	83	1	U512A_DICDI	25	9492	1	1	1	1	0.34	Dictyostelium discoideum
															Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)
19042	all	none	2 Da	decoy	84	1	PPNP_AERHH	25	10561	1	1	1	1	0.31	Takifugu rubripes
19042	all	none	2 Da	decoy	85	1	ANFB_TAKR	25	14907	1	1	1	1	0.21	Bacillus subtilis (strain 168)
19042	all	none	2 Da	decoy	86	1	YWZA_BACS	24	8289	1	1	1	1	0.4	Shewanella frigidimarina (strain NCIMB 400)
19042	all	none	2 Da	decoy	87	1	RL15_SHEFN	24	14989	1	1	1	1	0.21	Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JRI1)
19042	all	none	2 Da	decoy	88	1	HIS2_METMJ	24	10776	1	1	1	1	0.3	Shewanella ballica (strain OS223)
19042	all	none	2 Da	decoy	89	1	MOAC_SHEB	23	17353	1	1	1	1	0.18	Euphorbia esula
19042	all	none	2 Da	decoy	90	1	RL35_EUPES	22	14405	1	1	1	1	0.22	Vitis sp.
19042	all	none	2 Da	decoy	91	1	NLTP3_VITXS	22	9733	1	1	1	1	0.34	Nitrobacter winogradskyi (strain ATCC 25391 / DSM 10237 / CIP 104748 / NCIMB 11846 / Nb-255)
															Aeromonas salmonicida (strain A449)
19042	all	none	2 Da	decoy	92	1	SLYX_NITWN	20	8037	1	1	1	1	0.42	Frankia sp. (strain EAN1 pec)
19042	all	none	2 Da	decoy	93	1	RL13_AERS4	20	15799	1	1	1	1	0.2	
19042	all	none	2 Da	decoy	94	1	NUOK_FRAS	20	10763	1	1	1	1	0.3	

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19044	viridiplantae	none	2 Da	decoy	1	1	H42_WHEAT	2408 ⁷	11460	182	182	2	2	0.65	Triticum aestivum
19044	viridiplantae	none	2 Da	decoy	1	2	H4_CAPAN	5384	11418	93	93	2	2	0.65	Capsicum annuum
19044	viridiplantae	none	2 Da	decoy	2	1	UBIQ_AVESA	2884	8520	27	27	1	1	0.39	Avena sativa
19044	viridiplantae	none	2 Da	decoy	3	1	PSAC_AETCO	2788	9545	46	46	1	1	0.34	Aethionema cordifolium
19044	viridiplantae	none	2 Da	decoy	4	1	PSBF_EPHSI	2335	4507	23	23	1	1	0.78	Ephedra sinica
19044	viridiplantae	none	2 Da	decoy	5	1	PSAC_PHAEO	2286	9561	38	38	1	1	0.34	Phalaenopsis aphrodite subsp. formosana
19044	viridiplantae	none	2 Da	decoy	6	1	H32_ENCAL	2015	15344	63	63	1	1	0.21	Encephalartos altensteinii
19044	viridiplantae	none	2 Da	decoy	7	1	ATPH_CYCTA	1880	7995	23	23	1	1	0.42	Cycas taitungensis
19044	viridiplantae	none	2 Da	decoy	8	1	PSBE_AMBTC	1858	9381	27	27	1	1	0.35	Amborella trichopoda
19044	viridiplantae	none	2 Da	decoy	8	2	PSBE_MESCR	903	9353	24	24	1	1	0.35	Mesembryanthemum crystallinum
19044	viridiplantae	none	2 Da	decoy	9	1	PSBT_PELHO	1571	3831	27	27	1	1	0.93	Pelargonium hortorum
19044	viridiplantae	none	2 Da	decoy	10	1	PSBT_ALLTE	1487	3815	18	18	1	1	0.96	Allium textile
19044	viridiplantae	none	2 Da	decoy	11	1	PSBT_PIPCE	1352	3833	25	25	1	1	0.93	Piper cenocladum
19044	viridiplantae	none	2 Da	decoy	12	1	H3_VOLCA	1314	15358	61	61	2	2	0.46	Volvox carteri
19044	viridiplantae	none	2 Da	decoy	12	2	H31_CHLRE	875	15344	51	51	1	1	0.21	Chlamydomonas reinhardtii
19044	viridiplantae	none	2 Da	decoy	12	3	H32_MEDSA	517	15332	45	45	2	2	0.46	Medicago sativa
19044	viridiplantae	none	2 Da	decoy	13	1	PSBE_AGRST	950	9439	20	20	1	1	0.35	Agrostis stolonifera
19044	viridiplantae	none	2 Da	decoy	14	1	PSAC_SPIOL	932	9531	29	29	1	1	0.34	Spinacia oleracea
19044	viridiplantae	none	2 Da	decoy	15	1	PSAC_CUSRE	764	9545	31	31	1	1	0.34	Cuscuta reflexa
19044	viridiplantae	none	2 Da	decoy	16	1	RL23_ARATH	657	15188	15	15	2	2	0.46	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	17	1	PSBF_AGARO	636	4481	24	24	1	1	0.8	Agathis robusta
19044	viridiplantae	none	2 Da	decoy	18	1	H33_ARATH	295	15454	26	26	2	2	0.46	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	19	1	H32_CICIN	495	15425	38	38	1	1	0.21	Cichorium intybus
19044	viridiplantae	none	2 Da	decoy	20	1	RL371_ORYSJ	480	10464	6	6	1	1	0.31	Oryza sativa subsp. japonica
19044	viridiplantae	none	2 Da	decoy	21	1	RL391_ARATH	430	6412	8	8	1	1	0.53	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	22	1	RL37A_GOSHI	425	10435	6	6	1	1	0.31	Gossypium hirsutum
19044	viridiplantae	none	2 Da	decoy	23	1	RL14_NICSY	404	11850	6	6	1	1	0.27	Nicotiana sylvestris
19044	viridiplantae	none	2 Da	decoy	24	1	OL1AC_CANSA	370	11994	14	14	2	2	0.61	Cannabis sativa
19044	viridiplantae	none	2 Da	decoy	25	1	PSAC_DRIGR	348	9529	17	17	1	1	0.34	Drimys granadensis
19044	viridiplantae	none	2 Da	decoy	26	1	RL38_SOLLC	285	8192	14	14	1	1	0.4	Solanum lycopersicum
19044	viridiplantae	none	2 Da	decoy	27	1	PSBL_CYCTA	251	4198	7	7	1	1	0.85	Cycas taitungensis
19044	viridiplantae	none	2 Da	decoy	28	1	RL14_SOLBU	245	11866	4	4	1	1	0.27	Solanum bulbocastanum
19044	viridiplantae	none	2 Da	decoy	29	1	ATPH_CRYJA	229	8015	7	7	1	1	0.42	Cryptomeria japonica
19044	viridiplantae	none	2 Da	decoy	30	1	PLAS_MERPE	219	10536	21	21	1	1	0.31	Mercurialis perennis
19044	viridiplantae	none	2 Da	decoy	31	1	RS30_ARATH	133	6883	3	3	1	1	0.49	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	32	1	PSAJ_LEMMI	122	4782	7	7	1	1	0.74	Lemna minor
19044	viridiplantae	none	2 Da	decoy	33	1	PSBL_LEPVR	113	4180	5	5	1	1	0.85	Lepidium virginicum
19044	viridiplantae	none	2 Da	decoy	34	1	H2A3_ORYSJ	104	13909	5	5	1	1	0.23	Oryza sativa subsp. indica

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19044	viridiplantae	none	2 Da	decoy	35	1	PLAS_LACSA	89	10410	11	11	1	1	0.31	Lactuca sativa
19044	viridiplantae	none	2 Da	decoy	36	1	H2B8_ARATH	77	15215	3	3	1	1	0.21	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	37	1	GRP2_ORYSI	71	14873	8	8	2	2	0.48	Oryza sativa subsp. indica
19044	viridiplantae	none	2 Da	decoy	38	1	GRP1_ARATH	65	25070	8	8	1	1	0.12	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	39	1	RR16_MORIN	64	10496	5	5	1	1	0.31	Morus indica
19044	viridiplantae	none	2 Da	decoy	40	1	H2A2_ORYSI	58	13968	3	3	1	1	0.23	Oryza sativa subsp. indica
19044	viridiplantae	none	2 Da	decoy	41	1	PE1D_ATRBE	57	17504	1	1	1	1	0.18	Atropa belladonna
19044	viridiplantae	none	2 Da	decoy	42	1	RL30_LUPLU	51	12553	3	3	1	1	0.26	Lupinus luteus
19044	viridiplantae	none	2 Da	decoy	43	1	PSA1_OSTTA	44	4727	4	4	1	1	0.74	Ostreococcus tauri
19044	viridiplantae	none	2 Da	decoy	44	1	UBIQ_HELAN	42	8667	3	3	1	1	0.38	Helianthus annuus
19044	viridiplantae	none	2 Da	decoy	45	1	RL342_ARATH	40	13699	1	1	1	1	0.24	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	46	1	R35A3_ARATH	39	12965	3	3	1	1	0.25	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	47	1	PLAS2_TOBAC	38	10409	5	5	1	1	0.31	Nicotiana tabacum
19044	viridiplantae	none	2 Da	decoy	48	1	CX6B3_ARATH	37	9474	1	1	1	1	0.35	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	49	1	BCP1_ARATH	33	11329	1	1	1	1	0.29	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	50	1	RK33_MORIN	31	7939	1	1	1	1	0.42	Morus indica
19044	viridiplantae	none	2 Da	decoy	51	1	RL35_EUPES	29	14405	2	2	2	2	0.49	Euphorbia esula
19044	viridiplantae	none	2 Da	decoy	52	1	RL271_ARATH	29	15632	1	1	1	1	0.2	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	53	1	PE1G_CUSEX	28	4181	1	1	1	1	0.85	Cuscuta exaltata
19044	viridiplantae	none	2 Da	decoy	54	1	R15A1_ARATH	27	14852	1	1	1	1	0.21	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	55	1	PSAJ_AMBTC	27	4774	1	1	1	1	0.74	Amborella trichopoda
19044	viridiplantae	none	2 Da	decoy	56	1	H2B10_ARATH	27	15723	1	1	1	1	0.2	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	57	1	PSBL_AGRST	27	4114	1	1	1	1	0.87	Agrostis stolonifera
19044	viridiplantae	none	2 Da	decoy	58	1	PEP7_ARATH	26	9395	1	1	1	1	0.35	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	59	1	PSAM_ZYGCR	26	3484	2	2	1	1	1.07	Zygnema circumcarinatum
19044	viridiplantae	none	2 Da	decoy	60	1	H2B1_ARATH	26	16392	1	1	1	1	0.19	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	61	1	H2B_GOSHI	25	16077	1	1	1	1	0.2	Gossypium hirsutum
19044	viridiplantae	none	2 Da	decoy	62	1	PSBL_AMBTC	25	4134	1	1	1	1	0.87	Amborella trichopoda
19044	viridiplantae	none	2 Da	decoy	63	1	PSBL_MARPO	25	4476	1	1	1	1	0.8	Marchantia polymorpha
19044	viridiplantae	none	2 Da	decoy	64	1	NDUA5_SOLTU	25	4071	2	2	1	1	0.87	Solanum tuberosum
19044	viridiplantae	none	2 Da	decoy	65	1	PSBL_ACOCL	25	4494	1	1	1	1	0.8	Acorus calamus
19044	viridiplantae	none	2 Da	decoy	66	1	PSBE_PANGI	24	9445	1	1	1	1	0.35	Panax ginseng
19044	viridiplantae	none	2 Da	decoy	67	1	NLTP3_VITIS	22	9733	1	1	1	1	0.34	Vitis sp.
19044	viridiplantae	none	2 Da	decoy	68	1	DPM2_ARATH	22	9050	1	1	1	1	0.36	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	69	1	RLF17_ARATH	22	8657	1	1	1	1	0.38	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	70	1	RS252_ARATH	21	12062	1	1	1	1	0.27	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	71	1	M1210_ARATH	20	11580	1	1	1	1	0.28	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	72	1	DPM3_ARATH	20	9918	1	1	1	1	0.33	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	73	1	ACBP1_ORYSI	19	10137	2	2	1	1	0.32	Oryza sativa subsp. japonica

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	empAI	Species
19044	viridiplantae	none	2 Da	decoy	74	1	PSBH_LACSA	19	7738	1	1	1	1	0.43	Lactuca sativa
19044	viridiplantae	none	2 Da	decoy	75	1	GASA7_ARATH	18	12058	1	1	1	1	0.27	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	76	1	M7_LILHE	18	9576	1	1	1	1	0.34	Lilium henryi
19044	viridiplantae	none	2 Da	decoy	77	1	PSBK_VITV1	17	7095	1	1	1	1	0.47	Vitis vinifera
19044	viridiplantae	none	2 Da	decoy	78	1	ATP9_ARATH	16	8930	1	1	1	1	0.37	Arabidopsis thaliana
19044	viridiplantae	none	2 Da	decoy	79	1	EAI_MAIZE	16	9635	1	1	1	1	0.34	Zea mays
19044	viridiplantae	none	2 Da	decoy	80	1	H2A2_PEA	16	15695	1	1	1	1	0.2	Pisum sativum
19045	viridiplantae	AO	2 Da	decoy	1	1	H4_ARATH	3181	11402	239	239	2	2	8.46	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	2	1	H4_CHLRE	1269	11450	113	113	2	2	0.65	Chlamydomonas reinhardtii
19045	viridiplantae	AO	2 Da	decoy	3	1	PSBF_AGARO	3132	4481	29	29	1	1	0.8	Agathis robusta
19045	viridiplantae	AO	2 Da	decoy	4	1	PSBF_PINKO	2822	4465	25	25	1	1	2.24	Pinus koraiensis
19045	viridiplantae	AO	2 Da	decoy	5	1	UBIQ_AVESA	2738	8520	27	27	1	1	0.92	Avena sativa
19045	viridiplantae	AO	2 Da	decoy	6	1	PSBF_MARPO	2603	4465	26	26	1	1	0.8	Marchantia polymorpha
19045	viridiplantae	AO	2 Da	decoy	7	1	PSAC_AETCO	2538	9545	43	43	1	1	0.81	Aethionema cordifolium
19045	viridiplantae	AO	2 Da	decoy	8	1	H32_ENCAL	2507	15344	61	61	1	1	0.46	Encephalartos altensteinii
19045	viridiplantae	AO	2 Da	decoy	9	1	PSAC_SPIOL	2084	9531	40	40	1	1	1.43	Spinacia oleracea
19045	viridiplantae	AO	2 Da	decoy	10	1	H3_VOLCA	1969	15558	55	55	2	2	0.76	Volvox carteri
19045	viridiplantae	AO	2 Da	decoy	11	1	ATPH_ARAHI	1906	7971	20	20	1	1	0.42	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	12	1	ATPH_CYCTA	1760	7995	20	20	1	1	1.01	Cycas taiungensis
19045	viridiplantae	AO	2 Da	decoy	13	1	PSBE_AMBTC	1694	9381	24	24	1	1	0.82	Amborella trichopoda
19045	viridiplantae	AO	2 Da	decoy	14	1	ATPH_CERDE	1670	8001	19	19	1	1	0.42	Ceratophyllum demersum
19045	viridiplantae	AO	2 Da	decoy	15	1	PSBT_ALLTE	1651	3815	25	25	1	1	13.87	Allium textile
19045	viridiplantae	AO	2 Da	decoy	16	1	PSBT_PELHO	1434	3831	26	26	1	1	12.94	Pelargonium hortorum
19045	viridiplantae	AO	2 Da	decoy	17	1	PSAC_DRIGR	1381	9529	32	32	1	1	0.81	Drimys granadensis
19045	viridiplantae	AO	2 Da	decoy	18	1	PSBT_PIPCE	1263	3833	25	25	1	1	12.94	Piper cenocladum
19045	viridiplantae	AO	2 Da	decoy	19	1	H31_CHLRE	1184	15344	41	41	1	1	0.46	Chlamydomonas reinhardtii
19045	viridiplantae	AO	2 Da	decoy	20	1	RL391_ARATH	1124	6412	13	13	1	1	1.33	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	21	1	H32_ARATH	880	15316	36	36	2	2	1.13	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	22	1	PSBE_AGRST	756	9439	18	18	1	1	0.35	Agrostis stolonifera
19045	viridiplantae	AO	2 Da	decoy	23	1	RL23_ARATH	736	15188	29	29	2	2	2.79	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	24	1	H32_MEDSA	697	15332	32	32	2	2	3.54	Medicago sativa
19045	viridiplantae	AO	2 Da	decoy	25	1	ATPH_AGRST	688	7969	13	13	1	1	0.42	Agrostis stolonifera
19045	viridiplantae	AO	2 Da	decoy	26	1	PSBE_MESCR	612	9353	18	18	1	1	0.35	Mesembryanthemum crystallinum
19045	viridiplantae	AO	2 Da	decoy	27	1	RL371_ORYSJ	473	10463	6	6	1	1	0.72	Oryza sativa subsp. japonica
19045	viridiplantae	AO	2 Da	decoy	28	1	RL37A_GOSHI	390	10435	6	6	1	1	0.31	Gossypium hirsutum
19045	viridiplantae	AO	2 Da	decoy	29	1	PLAS_MERPE	387	10536	23	23	1	1	1.94	Mercurialis perennis
19045	viridiplantae	AO	2 Da	decoy	30	1	RL14_NICSY	366	11850	5	5	1	1	0.27	Nicotiana sylvestris
19045	viridiplantae	AO	2 Da	decoy	31	1	OLIAC_CANSA	334	11994	11	11	1	1	0.61	Cannabis sativa

Job no.	Taxonomy	PTMs	fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	empAI	Species
19045	viridiplantae	AO	2 Da	decoy	32	1	RS28_MAIZE	332	7463	10	10	1	1	3.43	Zea mays
19045	viridiplantae	AO	2 Da	decoy	33	1	H3L1_ARATH	321	15406	16	16	2	2	1.12	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	34	1	PSBI_CRYJA	248	4164	5	5	1	1	0.85	Cryptomeria japonica
19045	viridiplantae	AO	2 Da	decoy	35	1	PSBI_CVCTA	245	4198	7	7	1	1	5.31	Cycas taitungensis
19045	viridiplantae	AO	2 Da	decoy	36	1	RRI4_SOILBU	221	11866	4	4	1	1	0.27	Solanum bulbocastanum
19045	viridiplantae	AO	2 Da	decoy	37	1	RL38_SOLLIC	216	8192	12	12	1	1	0.97	Solanum lycopersicum
19045	viridiplantae	AO	2 Da	decoy	38	1	PSBI_PINKO	195	4134	2	2	1	1	0.87	Pinus koraiensis
19045	viridiplantae	AO	2 Da	decoy	39	1	H33_ARATH	182	15454	10	10	1	1	0.46	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	40	1	RS30_ARATH	124	6883	2	2	1	1	0.49	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	41	1	RL30_EUPES	116	12505	8	8	1	1	0.26	Euphorbia esula
19045	viridiplantae	AO	2 Da	decoy	42	1	ATPH_PEA	113	8027	6	6	1	1	1.01	Pisum sativum
19045	viridiplantae	AO	2 Da	decoy	43	1	H32_LILLO	109	15318	5	5	1	1	0.21	Lilium longiflorum
19045	viridiplantae	AO	2 Da	decoy	44	1	PSBI_AETCO	99	4128	2	2	1	1	0.87	Aethionema cordifolium
19045	viridiplantae	AO	2 Da	decoy	45	1	PSAI_LEMMI	98	4782	6	6	1	1	2.02	Lemna minor
19045	viridiplantae	AO	2 Da	decoy	46	1	H2A3_ORYSI	93	13909	4	4	1	1	0.52	Oryza sativa subsp. indica
19045	viridiplantae	AO	2 Da	decoy	47	1	PSBI_ARATH	91	4114	2	2	1	1	0.87	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	48	1	RL373_ARATH	87	10993	4	4	1	1	0.3	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	49	1	H32_CICIN	77	15425	3	3	1	1	0.46	Cichorium intybus
19045	viridiplantae	AO	2 Da	decoy	50	1	GRP1_ARATH	74	25070	9	9	2	2	0.42	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	51	1	PSK2_ARATH	73	9906	1	1	1	1	0.33	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	52	1	RR16_MORIN	68	10496	3	3	1	1	0.31	Morus indica
19045	viridiplantae	AO	2 Da	decoy	53	1	RS242_ARATH	67	15467	4	4	1	1	0.46	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	54	1	H2B8_ARATH	66	15215	2	2	1	1	0.21	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	55	1	PSAC_PINTH	66	9515	4	4	1	1	0.81	Pinus thunbergii
19045	viridiplantae	AO	2 Da	decoy	56	1	PSAI_CHLAT	59	4746	5	5	1	1	0.74	Chlorokybus atmophyticus
19045	viridiplantae	AO	2 Da	decoy	57	1	GRP2_ORYSI	58	14873	4	4	2	2	0.79	Oryza sativa subsp. indica
19045	viridiplantae	AO	2 Da	decoy	58	1	PSBH_COFAR	58	7742	2	2	1	1	0.43	Coffea arabica
19045	viridiplantae	AO	2 Da	decoy	59	1	PEID_ATRBE	57	17504	1	1	1	1	0.18	Atropa belladonna
19045	viridiplantae	AO	2 Da	decoy	60	1	PLAS_CAPBU	55	10434	1	1	1	1	0.31	Capsella bursa-pastoris
19045	viridiplantae	AO	2 Da	decoy	61	1	RL30_LUPLU	54	12553	2	2	1	1	0.26	Lupinus luteus
19045	viridiplantae	AO	2 Da	decoy	62	1	EAI_MAIZE	54	9635	2	2	1	1	0.79	Zea mays
19045	viridiplantae	AO	2 Da	decoy	63	1	KRP6_ORYSI	54	9383	4	4	1	1	0.82	Oryza sativa subsp. japonica
19045	viridiplantae	AO	2 Da	decoy	64	1	H2A2_ORYSI	52	13968	3	3	1	1	0.51	Oryza sativa subsp. indica
19045	viridiplantae	AO	2 Da	decoy	65	1	RTS_ORYSI	48	8851	5	5	1	1	0.88	Oryza sativa subsp. japonica
19045	viridiplantae	AO	2 Da	decoy	66	1	ATP9_OENBI	48	7584	2	2	1	1	1.08	Oenothera biennis
19045	viridiplantae	AO	2 Da	decoy	67	1	H3L3_ARATH	47	15450	1	1	1	1	0.21	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	68	1	EMPL_ORYSI	45	10159	1	1	1	1	0.32	Oryza sativa subsp. japonica
19045	viridiplantae	AO	2 Da	decoy	69	1	PSBH_NYMAL	45	7708	1	1	1	1	0.44	Nymphaea alba
19045	viridiplantae	AO	2 Da	decoy	70	1	RS142_MAIZE	44	16310	1	1	1	1	0.19	Zea mays

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19045	viridiplantae	AO	2 Da	decoy	71	1	RLF36_ARATH	44	7637	3	3	2	2	1.06	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	72	1	PSAL_HORVU	44	4005	2	2	1	1	0.9	Hordeum vulgare
19045	viridiplantae	AO	2 Da	decoy	73	1	PSBI_ANTAG	42	4221	1	1	1	1	0.85	Anthoceros angustus
19045	viridiplantae	AO	2 Da	decoy	74	1	ATP9_MARPO	41	7529	2	2	1	1	1.08	Marchantia polymorpha
19045	viridiplantae	AO	2 Da	decoy	75	1	ACBP1_ORYSJ	41	10137	2	2	1	1	0.32	Oryza sativa subsp. japonica
19045	viridiplantae	AO	2 Da	decoy	76	1	RR8_MESVI	41	14869	2	2	1	1	0.21	Mesostigma viride
19045	viridiplantae	AO	2 Da	decoy	77	1	PROFW_OLEEU	40	14590	1	1	1	1	0.22	Olea europaea
19045	viridiplantae	AO	2 Da	decoy	78	1	RL342_ARATH	40	13699	1	1	1	1	0.24	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	79	1	GRC14_ORYSJ	39	11420	1	1	1	1	0.28	Oryza sativa subsp. japonica
19045	viridiplantae	AO	2 Da	decoy	80	1	PROF4_ARATH	39	14654	1	1	1	1	0.22	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	81	1	GRXS3_ORYSJ	38	13912	1	1	1	1	0.23	Oryza sativa subsp. japonica
19045	viridiplantae	AO	2 Da	decoy	82	1	ACBP_BRANA	38	10165	2	2	2	2	0.74	Brassica napus
19045	viridiplantae	AO	2 Da	decoy	83	1	TIM13_ARATH	38	9634	1	1	1	1	0.34	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	84	1	RLF28_ARATH	38	9669	2	2	1	1	0.79	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	85	1	PSBH_HORVU	38	7796	1	1	1	1	0.43	Hordeum vulgare
19045	viridiplantae	AO	2 Da	decoy	86	1	PETG_PLAOC	38	4153	1	1	1	1	0.87	Platanus occidentalis
19045	viridiplantae	AO	2 Da	decoy	87	1	PST2_PETHY	38	11481	1	1	1	1	0.28	Petunia hybrida
19045	viridiplantae	AO	2 Da	decoy	88	1	H2B10_ARATH	38	15723	2	2	2	2	0.45	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	89	1	H2B1_ARATH	37	16392	1	1	1	1	0.19	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	90	1	ATP9_PEA	37	7500	3	3	1	1	1.08	Pisum sativum
19045	viridiplantae	AO	2 Da	decoy	91	1	CX6B3_ARATH	37	9474	1	1	1	1	0.35	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	92	1	PST2_ARATH	37	11192	1	1	1	1	0.29	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	93	1	PFD5_ARATH	37	16457	1	1	1	1	0.19	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	94	1	RR11_PHAVU	37	15183	1	1	1	1	0.21	Phaseolus vulgaris
19045	viridiplantae	AO	2 Da	decoy	95	1	H2B9_ARATH	36	14535	1	1	1	1	0.22	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	96	1	RK16_OENAM	36	9935	1	1	1	1	0.33	Oenothera ammobila
19045	viridiplantae	AO	2 Da	decoy	97	1	COPT3_ARATH	36	16387	1	1	1	1	0.19	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	98	1	PLAS_PHYPA	35	17205	1	1	1	1	0.18	Physcomitrella patens subsp. patens
19045	viridiplantae	AO	2 Da	decoy	99	1	PSBK_CHLVU	35	4677	1	1	1	1	0.76	Chlorella vulgaris
19045	viridiplantae	AO	2 Da	decoy	100	1	NLTP3_HORVU	35	12189	1	1	1	1	0.26	Hordeum vulgare
19045	viridiplantae	AO	2 Da	decoy	101	1	PSBH_PHAEO	34	7695	1	1	1	1	0.44	Phalaenopsis aphrodite subsp. formosana
19045	viridiplantae	AO	2 Da	decoy	102	1	AGP12_ARATH	34	6085	1	1	1	1	0.56	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	103	1	PSAL_MARPO	34	4015	2	2	1	1	0.9	Marchantia polymorpha
19045	viridiplantae	AO	2 Da	decoy	104	1	GRC10_ORYSJ	34	11339	1	1	1	1	0.29	Oryza sativa subsp. japonica
19045	viridiplantae	AO	2 Da	decoy	105	1	EM3_WHEAT	34	9981	1	1	1	1	0.33	Triticum aestivum
19045	viridiplantae	AO	2 Da	decoy	106	1	ACBP_RICCO	34	10045	1	1	1	1	0.33	Ricinus communis
19045	viridiplantae	AO	2 Da	decoy	107	1	LGB2_MEDTR	33	15742	1	1	1	1	0.2	Medicago truncatula
19045	viridiplantae	AO	2 Da	decoy	108	1	DEF97_ARATH	33	9593	1	1	1	1	0.34	Arabidopsis thaliana

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19045	viridiplantae	AO	2 Da	decoy	109	1	PSAL_WELMI	32	4081	1	1	1	1	0.87	Welwitschia mirabilis
19045	viridiplantae	AO	2 Da	decoy	110	1	TOM91_ARATH	32	9990	1	1	1	1	0.33	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	111	1	RK33_MORIN	32	7939	1	1	1	1	0.42	Morus indica
19045	viridiplantae	AO	2 Da	decoy	112	1	R35A3_ARATH	31	12965	1	1	1	1	0.25	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	113	1	POLC3_CHEAL	31	9546	1	1	1	1	0.34	Chenopodium album
19045	viridiplantae	AO	2 Da	decoy	114	1	RR19_OEDCA	31	10462	1	1	1	1	0.31	Oedogonium cardiacum
19045	viridiplantae	AO	2 Da	decoy	115	1	POLC4_BETPN	31	9442	1	1	1	1	0.35	Beulia pendula
19045	viridiplantae	AO	2 Da	decoy	116	1	CML4_ORYSJ	30	17379	1	1	1	1	0.18	Oryza sativa subsp. japonica
19045	viridiplantae	AO	2 Da	decoy	117	1	IC12_HORVU	30	9375	1	1	1	1	0.35	Hordeum vulgare
19045	viridiplantae	AO	2 Da	decoy	118	1	MT2_MUSAC	29	8525	1	1	1	1	0.39	Musa acuminata
19045	viridiplantae	AO	2 Da	decoy	119	1	APEP2_ORYSJ	29	5798	1	1	1	1	0.6	Oryza sativa subsp. japonica
19045	viridiplantae	AO	2 Da	decoy	120	1	UBIQ_HELAN	29	8667	1	1	1	1	0.38	Helianthus annuus
19045	viridiplantae	AO	2 Da	decoy	121	1	CH60_SOLJU	29	4237	1	1	1	1	0.85	Solanum tuberosum
19045	viridiplantae	AO	2 Da	decoy	122	1	PSBH_PIPE	29	7750	1	1	1	1	0.43	Piper cenocladum
19045	viridiplantae	AO	2 Da	decoy	123	1	PSBH_MAIZE	29	7782	1	1	1	1	0.43	Zea mays
19045	viridiplantae	AO	2 Da	decoy	124	1	GRS13_ARATH	29	16469	1	1	1	1	0.19	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	125	1	ATP9_PETHY	29	7558	3	3	2	2	2.01	Petunia hybrida
19045	viridiplantae	AO	2 Da	decoy	126	1	CYCK_PETHY	28	8620	1	1	1	1	0.38	Petunia hybrida
19045	viridiplantae	AO	2 Da	decoy	127	1	PSBK_STIHE	28	5189	1	1	1	1	0.67	Stigeoclonium helveticum
19045	viridiplantae	AO	2 Da	decoy	128	1	PSAJ_AMBTC	27	4774	1	1	1	1	0.74	Amborella trichopoda
19045	viridiplantae	AO	2 Da	decoy	129	1	RK16_GOSHI	27	15408	1	1	1	1	0.21	Gossypium hirsutum
19045	viridiplantae	AO	2 Da	decoy	130	1	RS192_ARATH	27	15864	1	1	1	1	0.2	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	131	1	IC1A_HORVU	27	8877	1	1	1	1	0.37	Hordeum vulgare
19045	viridiplantae	AO	2 Da	decoy	132	1	PS5_PINST	25	4312	1	1	1	1	0.82	Pinus strobus
19045	viridiplantae	AO	2 Da	decoy	133	1	DEF84_ARATH	25	9899	1	1	1	1	0.33	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	134	1	RK14_VIGUN	23	5224	1	1	1	1	0.67	Vigna unguiculata
19045	viridiplantae	AO	2 Da	decoy	135	1	GRP3_POPEU	22	5214	2	2	1	1	0.67	Populus euphratica
19045	viridiplantae	AO	2 Da	decoy	136	1	SMAP1_ARATH	22	6937	1	1	1	1	0.49	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	137	1	DPM2_ARATH	22	9050	1	1	1	1	0.36	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	138	1	PSBJ_WHEAT	21	4048	1	1	1	1	0.9	Triticum aestivum
19045	viridiplantae	AO	2 Da	decoy	139	1	LSM5_ARATH	21	9709	1	1	1	1	0.34	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	140	1	AGP15_ARATH	20	5845	1	1	1	1	0.58	Arabidopsis thaliana
19045	viridiplantae	AO	2 Da	decoy	141	1	ALFC_PINST	20	7251	1	1	1	1	0.47	Pinus strobus
19046	viridiplantae	AOP	2 Da	decoy	1	1	H4_ARATH	2816	11402	208	208	2	2	8.46	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	2	1	H42_WHEAT	2144	11460	143	143	1	1	6.37	Triticum aestivum
19046	viridiplantae	AOP	2 Da	decoy	3	1	H4_CAPAN	8894	11418	86	86	2	2	2.48	Capsicum annuum
19046	viridiplantae	AOP	2 Da	decoy	4	1	H4_CHIRE	6116	11450	49	49	1	1	0.28	Chlamydomonas reinhardtii
19046	viridiplantae	AOP	2 Da	decoy	5	1	UBIQ_AVESA	2941	8520	37	37	2	2	12.72	Avena sativa

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	empAI	Species
19046	viridiplantae	AOP	2 Da	decoy	6	1	PSBF_AGARO	2936	4481	29	29	1	1	0.8	Agathis robusta
19046	viridiplantae	AOP	2 Da	decoy	7	1	PSBF_PINKO	2628	4465	22	22	1	1	0.8	Pinus koraiensis
19046	viridiplantae	AOP	2 Da	decoy	8	1	PSBF_MARPO	2434	4465	24	24	1	1	0.8	Marchantia polymorpha
19046	viridiplantae	AOP	2 Da	decoy	9	1	PSAC_HELAN	2191	9545	39	39	1	1	1.43	Helianthus annuus
19046	viridiplantae	AOP	2 Da	decoy	10	1	H32_ENCAL	1905	15344	53	53	1	1	1.13	Encephalartos altensteinii
19046	viridiplantae	AOP	2 Da	decoy	11	1	ATPH_ARAHI	1777	7971	22	22	1	1	3.03	Arabis hirsuta
19046	viridiplantae	AOP	2 Da	decoy	12	1	ATPH_CYCTA	1633	7995	19	19	1	1	1.84	Cycas taitungensis
19046	viridiplantae	AOP	2 Da	decoy	13	1	PSAC_SPIOL	1620	9531	33	33	1	1	2.26	Spinacia oleracea
19046	viridiplantae	AOP	2 Da	decoy	14	1	PSBT_ALLTE	1557	3815	26	26	2	2	56.36	Allium textile
19046	viridiplantae	AOP	2 Da	decoy	15	1	ATPH_ACOAM	1550	7985	16	16	1	1	0.42	Acorus americanus
19046	viridiplantae	AOP	2 Da	decoy	16	1	ATPH_CERDE	1530	8001	17	17	1	1	1.84	Ceratophyllum demersum
19046	viridiplantae	AOP	2 Da	decoy	17	1	PSBE_AMBTC	1512	9381	19	19	1	1	0.82	Amborella trichopoda
19046	viridiplantae	AOP	2 Da	decoy	18	1	PSBT_PIPCE	1352	3833	26	26	2	2	25.93	Piper cenocladum
19046	viridiplantae	AOP	2 Da	decoy	19	1	H3_VOLCA	1342	15358	37	37	2	2	1.13	Volvox carteri
19046	viridiplantae	AOP	2 Da	decoy	20	1	ATPH_IPOPU	1157	7986	13	13	2	2	1.01	Ipomoea purpurea
19046	viridiplantae	AOP	2 Da	decoy	21	1	PSBT_PELHO	1141	3831	24	24	2	2	25.93	Pelargonium hortorum
19046	viridiplantae	AOP	2 Da	decoy	22	1	RL391_ARATH	1025	6412	12	12	1	1	1.33	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	23	1	PSBE_CITSI	797	9380	15	15	1	1	0.82	Citrus sinensis
19046	viridiplantae	AOP	2 Da	decoy	24	1	RS28_MAIZE	705	7463	11	11	1	1	0.45	Zea mays
19046	viridiplantae	AOP	2 Da	decoy	25	1	UBIQ_WHEAT	602	8648	10	10	1	1	0.91	Triticum aestivum
19046	viridiplantae	AOP	2 Da	decoy	26	1	UBIQ_HELAN	582	8667	10	10	1	1	2.65	Helianthus annuus
19046	viridiplantae	AOP	2 Da	decoy	27	1	H32_MEDSA	513	15332	21	21	2	2	1.58	Medicago sativa
19046	viridiplantae	AOP	2 Da	decoy	28	1	PSBL_ACOAM	497	4165	10	10	1	1	5.31	Acorus americanus
19046	viridiplantae	AOP	2 Da	decoy	29	1	RL23_ARATH	466	15188	16	16	2	2	1.59	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	30	1	RL371_ORYSJ	461	10464	6	6	1	1	1.97	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	31	1	PSAC_DRIGR	428	9529	11	11	1	1	1.43	Drimys granadensis
19046	viridiplantae	AOP	2 Da	decoy	32	1	GRP2_ORYSI	424	14873	52	52	2	2	613.3	Oryza sativa subsp. indica
19046	viridiplantae	AOP	2 Da	decoy	33	1	RS281_ARATH	404	7366	10	10	1	1	2.1	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	34	1	ATPH_AGRST	385	7969	10	10	1	1	1.84	Agrostis stolonifera
19046	viridiplantae	AOP	2 Da	decoy	35	1	RR14_SOLBU	380	11866	4	4	1	1	0.27	Solanum bulbocastanum
19046	viridiplantae	AOP	2 Da	decoy	36	1	RTS_ORYSI	345	9078	38	38	2	2	655.08	Oryza sativa subsp. indica
19046	viridiplantae	AOP	2 Da	decoy	37	1	H32_ARATH	272	15316	10	10	1	1	0.76	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	38	1	PSAC_ACOCL	269	9419	7	7	1	1	0.35	Acorus calamus
19046	viridiplantae	AOP	2 Da	decoy	39	1	PLAS_SOLITU	254	10381	13	13	1	1	1.26	Solanum tuberosum
19046	viridiplantae	AOP	2 Da	decoy	40	1	RTS_ORYSI	250	8851	28	28	2	2	761.23	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	41	1	OLAC_CANSA	250	11994	9	9	1	1	1.05	Cannabis sativa
19046	viridiplantae	AOP	2 Da	decoy	42	1	ATPH_ATRBE	241	8031	7	7	2	2	3.03	Atropa belladonna
19046	viridiplantae	AOP	2 Da	decoy	43	1	RL30_LUPLU	233	12553	5	5	1	1	0.58	Lupinus luteus
19046	viridiplantae	AOP	2 Da	decoy	44	1	PSAL_ZYGCR	230	3967	11	11	2	2	12.1	Zygnema circumcarinatum

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	empAI	Species
19046	viridiplantae	AOP	2 Da	decoy	45	1	LE25_SOLLC	230	9253	26	26	2	2	178.85	Solanum lycopersicum
19046	viridiplantae	AOP	2 Da	decoy	46	1	PSAL LOTJA	216	3813	9	9	1	1	13.87	Lotus japonicus
19046	viridiplantae	AOP	2 Da	decoy	47	1	TGD5_ ARATH	210	9282	20	20	2	2	91.82	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	48	1	RL37A_GOSHI	194	10435	3	3	1	1	0.31	Gossypium hirsutum
19046	viridiplantae	AOP	2 Da	decoy	49	1	H3L1_ ARATH	190	15406	7	7	1	1	0.21	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	50	1	PSBE_MESCR	189	9353	6	6	1	1	0.83	Mesembryanthemum crystallinum
19046	viridiplantae	AOP	2 Da	decoy	51	1	PLAS_MERPE	186	10536	9	9	1	1	0.71	Mercurialis perennis
19046	viridiplantae	AOP	2 Da	decoy	52	1	PSBE_OSTTA	159	9220	4	4	1	1	0.84	Ostreococcus tauri
19046	viridiplantae	AOP	2 Da	decoy	53	1	RL38_SOLLC	140	8192	8	8	1	1	0.97	Solanum lycopersicum
19046	viridiplantae	AOP	2 Da	decoy	54	1	SC61B_CHLRE	138	9183	14	14	2	2	52.01	Chlamydomonas reinhardtii
19046	viridiplantae	AOP	2 Da	decoy	55	1	EAI_MAIZE	128	9635	10	10	2	2	17.61	Zea mays
19046	viridiplantae	AOP	2 Da	decoy	56	1	DEF97_ ARATH	124	9593	7	7	2	2	3.38	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	57	1	RS30_ ARATH	115	6883	3	3	1	1	1.22	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	58	1	SC61B_ ARATH	114	8211	12	12	2	2	57.84	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	59	1	IF5A_SENVE	109	17483	1	1	1	1	0.18	Senecio vernalis
19046	viridiplantae	AOP	2 Da	decoy	60	1	ATP9_BETVU	105	9001	9	9	2	2	5.52	Beta vulgaris
19046	viridiplantae	AOP	2 Da	decoy	61	1	ALFC_PINST	103	7251	9	9	6	6	30.21	Pinus strobus
19046	viridiplantae	AOP	2 Da	decoy	62	1	H2A3_ORYSI	102	13909	3	3	1	1	0.52	Oryza sativa subsp. indica
19046	viridiplantae	AOP	2 Da	decoy	63	1	PSBI_LEPVR	98	4180	4	4	1	1	2.42	Lepidium virginicum
19046	viridiplantae	AOP	2 Da	decoy	64	1	PSAK_CHLRE	98	11194	4	4	1	1	1.14	Chlamydomonas reinhardtii
19046	viridiplantae	AOP	2 Da	decoy	65	1	H2B11_ORYSI	96	15357	5	5	2	2	1.13	Oryza sativa subsp. indica
19046	viridiplantae	AOP	2 Da	decoy	66	1	ACBP_RICCO	95	10045	9	9	1	1	4.47	Ricinus communis
19046	viridiplantae	AOP	2 Da	decoy	67	1	PSBI_AETCO	93	4128	2	2	1	1	0.87	Aethionema cordifolium
19046	viridiplantae	AOP	2 Da	decoy	68	1	SP112_ ARATH	93	10875	6	6	2	2	1.85	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	69	1	ACBP2_ORYSI	91	10242	4	4	1	1	0.32	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	70	1	AMP_AMARE	89	9374	8	8	2	2	10.21	Amaranthus retroflexus
19046	viridiplantae	AOP	2 Da	decoy	71	1	PSBJ_GNEPA	88	4142	2	2	2	2	2.51	Gnetum parvifolium
19046	viridiplantae	AOP	2 Da	decoy	72	1	MT2C_ORYSI	87	8932	8	8	2	2	8.13	Oryza sativa subsp. indica
19046	viridiplantae	AOP	2 Da	decoy	73	1	H32_LILLO	86	15318	2	2	1	1	0.21	Lilium longiflorum
19046	viridiplantae	AOP	2 Da	decoy	74	1	MFS18_MAIZE	86	12527	4	4	2	2	1.5	Zea mays
19046	viridiplantae	AOP	2 Da	decoy	75	1	H2A2_ORYSI	85	13968	3	3	1	1	0.51	Oryza sativa subsp. indica
19046	viridiplantae	AOP	2 Da	decoy	76	1	PSBJ_ ARATH	85	4114	2	2	1	1	0.87	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	77	1	ATPH_CHLAT	84	8059	3	3	1	1	1.81	Chlorokybus atrophycicus
19046	viridiplantae	AOP	2 Da	decoy	78	1	HSBP_ ARATH	84	9341	7	7	2	2	7.28	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	79	1	MT4A_ ARATH	83	9254	3	3	2	2	1.5	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	80	1	ATP5E_IPOBA	81	8037	4	4	1	1	1.01	Ipomoea batatas
19046	viridiplantae	AOP	2 Da	decoy	81	1	GRP1_ORYSI	79	13830	6	6	1	1	1.83	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	82	1	PLAS_CAPBU	79	10434	3	3	1	1	0.31	Capsella bursa-pastoris
19046	viridiplantae	AOP	2 Da	decoy	83	1	SAU19_ ARATH	74	9789	3	3	2	2	0.78	Arabidopsis thaliana

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19046	viridiplantae	AOP	2 Da	decoy	84	1	DLDH_SOLTU	74	3910	10	10	7	7	193.23	Solanum tuberosum
19046	viridiplantae	AOP	2 Da	decoy	85	1	PSBI_JASNU	73	4293	2	2	1	1	0.82	Jasminum nudiflorum
19046	viridiplantae	AOP	2 Da	decoy	86	1	PSK2_ARATH	73	9906	1	1	1	1	0.33	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	87	1	H2B9_ARATH	73	14535	3	3	2	2	0.82	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	88	1	RS242_ARATH	73	15467	4	4	1	1	0.76	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	89	1	RL272_ARATH	72	15719	1	1	1	1	0.2	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	90	1	PSAI_LEMMI	71	4782	2	2	1	1	2.02	Lemna minor
19046	viridiplantae	AOP	2 Da	decoy	91	1	RUXG_MEDSA	71	8912	4	4	2	2	2.54	Medicago sativa
19046	viridiplantae	AOP	2 Da	decoy	92	1	PSAI_MORIN	71	4008	4	4	2	2	5.89	Morus indica
19046	viridiplantae	AOP	2 Da	decoy	93	1	GRP1_ORYSI	70	13528	5	5	2	2	1.9	Oryza sativa subsp. indica
19046	viridiplantae	AOP	2 Da	decoy	94	1	PROCK_OLEEU	70	14182	3	3	1	1	0.5	Olea europaea
19046	viridiplantae	AOP	2 Da	decoy	95	1	PSAI_CALFG	70	3935	6	6	1	1	12.94	Calycanthus floridus var. glaucus
19046	viridiplantae	AOP	2 Da	decoy	96	1	DURL1_ARATH	70	11150	3	3	2	2	1.16	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	97	1	PSAI_ACOGR	69	3931	3	3	1	1	0.93	Acorus gramineus
19046	viridiplantae	AOP	2 Da	decoy	98	1	FER_SOLLY	69	10668	2	2	1	1	0.31	Solanum lyratum
19046	viridiplantae	AOP	2 Da	decoy	99	1	GRXS1_ARATH	68	11232	5	5	2	2	2.57	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	100	1	MT2A_ARATH	67	8955	5	5	1	1	3.77	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	101	1	PSK5_ORYSI	67	11150	5	5	2	2	1.16	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	102	1	PSAI_PHAAO	67	3975	6	6	1	1	5.89	Phalaenopsis aphrodite subsp. formosana
19046	viridiplantae	AOP	2 Da	decoy	103	1	NLTPA_RICCO	66	9763	3	3	1	1	0.78	Ricinus communis
19046	viridiplantae	AOP	2 Da	decoy	104	1	PE1D_GOSBA	66	17538	1	1	1	1	0.18	Gossypium barbadense
19046	viridiplantae	AOP	2 Da	decoy	105	1	GLRX_VERFO	65	11292	4	4	2	2	1.74	Vernicia fordii
19046	viridiplantae	AOP	2 Da	decoy	106	1	ATPH_STIHE	65	8172	5	5	1	1	4.46	Stigeocolonium helveticum
19046	viridiplantae	AOP	2 Da	decoy	107	1	RS241_ARATH	65	15363	2	2	1	1	0.21	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	108	1	PSAI_HORVU	64	4005	2	2	1	1	2.62	Hordeum vulgare
19046	viridiplantae	AOP	2 Da	decoy	109	1	DEF85_ARATH	64	9014	2	2	1	1	0.87	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	110	1	RL30_EUPES	63	12505	2	2	1	1	0.58	Euphorbia esula
19046	viridiplantae	AOP	2 Da	decoy	111	1	ATPH_ANEMIR	63	7895	2	2	1	1	1.02	Aneura mirabilis
19046	viridiplantae	AOP	2 Da	decoy	112	1	WIR1A_WHEAT	62	8679	3	3	2	2	1.64	Triticum aestivum
19046	viridiplantae	AOP	2 Da	decoy	113	1	BCP1_BRACM	62	11283	2	2	1	1	0.66	Brassica campestris
19046	viridiplantae	AOP	2 Da	decoy	114	1	LEA2_ARATH	61	9821	2	2	1	1	0.34	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	115	1	AGP1_ARATH	61	12630	2	2	1	1	0.57	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	116	1	GRP5_ARATH	61	13709	3	3	2	2	0.87	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	117	1	RR16_MORIN	60	10496	1	1	1	1	0.31	Morus indica
19046	viridiplantae	AOP	2 Da	decoy	118	1	ATP9_PEA	60	7500	3	3	1	1	1.08	Pisum sativum
19046	viridiplantae	AOP	2 Da	decoy	119	1	ATP9_HELAN	60	8262	4	4	2	2	2.89	Helianthus annuus
19046	viridiplantae	AOP	2 Da	decoy	120	1	NU41C_CHLAT	59	11139	1	1	1	1	0.29	Chlorokybus atmophyticus
19046	viridiplantae	AOP	2 Da	decoy	121	1	MT2B_SOLLC	59	9046	2	2	1	1	0.87	Solanum lycopersicum

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	empAI	Species
19046	viridiplantae	AOP	2 Da	decoy	122	1	AGP4_ARATH	59	12795	3	3	2	2	0.96	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	123	1	PSBH_STIHE	59	8853	5	5	2	2	3.86	Stigeoclonium helveticum
19046	viridiplantae	AOP	2 Da	decoy	124	1	GRS10_ARATH	59	11220	2	2	2	2	0.66	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	125	1	RL271_ARATH	59	15632	2	2	2	2	0.45	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	126	1	PSAJ_ACOCL	59	4744	2	2	1	1	0.74	Acorus calamus
19046	viridiplantae	AOP	2 Da	decoy	127	1	RLA2A_MAIZE	58	11470	1	1	1	1	0.28	Zea mays
19046	viridiplantae	AOP	2 Da	decoy	128	1	NO93_SOYBN	57	10941	1	1	1	1	0.3	Glycine max
19046	viridiplantae	AOP	2 Da	decoy	129	1	H2B8_ARATH	57	15215	1	1	1	1	0.21	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	130	1	IF5A2_MEDSA	57	17502	1	1	1	1	0.18	Medicago sativa
19046	viridiplantae	AOP	2 Da	decoy	131	1	PLAS_LACSA	57	10410	3	3	1	1	0.72	Lactuca sativa
19046	viridiplantae	AOP	2 Da	decoy	132	1	AGP15_ARATH	56	5845	3	3	2	2	2.97	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	133	1	PCEP6_ARATH	56	11215	1	1	1	1	0.29	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	134	1	PSAC_PINTH	55	9515	2	2	1	1	0.81	Pinus thunbergii
19046	viridiplantae	AOP	2 Da	decoy	135	1	NDUA2_ARATH	55	11015	1	1	1	1	0.3	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	136	1	PROFE_OLEEU	55	14558	1	1	1	1	0.22	Olea europaea
19046	viridiplantae	AOP	2 Da	decoy	137	1	PSAJ_CHLSC	55	4726	3	3	2	2	2.02	Chloranthus spicatus
19046	viridiplantae	AOP	2 Da	decoy	138	1	PSBH_ARATH	55	7697	2	2	1	1	0.44	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	139	1	LIRP1_ORYSJ	55	13537	1	1	1	1	0.24	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	140	1	MOC2A_MAIZE	55	9444	3	3	1	1	0.82	Zea mays
19046	viridiplantae	AOP	2 Da	decoy	141	1	CB21_PEA	55	24369	2	2	1	1	0.27	Pisum sativum
19046	viridiplantae	AOP	2 Da	decoy	142	1	H2B7_ARATH	54	15902	1	1	1	1	0.2	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	143	1	PSBH_TETOB	54	9136	7	7	2	2	5.38	Tetrademus obliquus
19046	viridiplantae	AOP	2 Da	decoy	144	1	IL13_ORYSJ	54	10002	2	2	1	1	0.76	Oryza sativa subsp. indica
19046	viridiplantae	AOP	2 Da	decoy	145	1	RS142_MAIZE	54	16310	1	1	1	1	0.19	Zea mays
19046	viridiplantae	AOP	2 Da	decoy	146	1	PSBH_DAUCA	54	7734	2	2	1	1	1.04	Daucus carota
19046	viridiplantae	AOP	2 Da	decoy	147	1	MT2_BRARP	54	8901	1	1	1	1	0.37	Brassica rapa subsp. pekinensis
19046	viridiplantae	AOP	2 Da	decoy	148	1	PROF9_PHLPR	53	14208	1	1	1	1	0.23	Phleum pratense
19046	viridiplantae	AOP	2 Da	decoy	149	1	CSPL8_ORYSJ	53	17105	1	1	1	1	0.19	Oryza sativa subsp. indica
19046	viridiplantae	AOP	2 Da	decoy	150	1	SDH32_ORYSJ	53	13854	1	1	1	1	0.23	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	151	1	FER_GLEJA	53	10511	1	1	1	1	0.31	Gleichenia japonica
19046	viridiplantae	AOP	2 Da	decoy	152	1	EM1_WHEAT	52	9957	3	3	1	1	1.34	Triticum aestivum
19046	viridiplantae	AOP	2 Da	decoy	153	1	SAU21_ARATH	52	9671	1	1	1	1	0.34	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	154	1	ATP9_MARPO	52	7529	2	2	1	1	1.08	Marchantia polymorpha
19046	viridiplantae	AOP	2 Da	decoy	155	1	PROCI_OLEEU	52	14300	1	1	1	1	0.22	Olea europaea
19046	viridiplantae	AOP	2 Da	decoy	156	1	PSBL_CEDDE	52	4464	2	2	1	1	0.8	Cedrus deodara
19046	viridiplantae	AOP	2 Da	decoy	157	1	PROF2_CORAV	52	14266	1	1	1	1	0.22	Corylus avellana
19046	viridiplantae	AOP	2 Da	decoy	158	1	RL36_DAUCA	51	12300	1	1	1	1	0.26	Daucus carota
19046	viridiplantae	AOP	2 Da	decoy	159	1	POLC7_CYNDA	51	8852	1	1	1	1	0.37	Cynodon dactylon
19046	viridiplantae	AOP	2 Da	decoy	160	1	OP164_ARATH	51	14347	1	1	1	1	0.22	Arabidopsis thaliana

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	emPAI	Species
19046	viridiplantae	AOP	2 Da	decoy	161	1	PSBL_TUPAK	51	4080	1	1	1	1	0.87	Tupia akina
19046	viridiplantae	AOP	2 Da	decoy	162	1	PSBW_ARATH	51	13726	1	1	1	1	0.23	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	163	1	HRD11_ARATH	51	10789	1	1	1	1	0.3	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	164	1	EPFL2_ARATH	51	14651	1	1	1	1	0.22	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	165	1	CM129_ARATH	50	9042	1	1	1	1	0.37	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	166	1	ICIA_HORVU	50	8877	1	1	1	1	0.37	Hordeum vulgare
19046	viridiplantae	AOP	2 Da	decoy	167	1	PSBH_COFAR	50	7742	1	1	1	1	0.43	Coffea arabica
19046	viridiplantae	AOP	2 Da	decoy	168	1	LE19_GOSHI	50	11065	2	2	1	1	0.67	Gossypium hirsutum
19046	viridiplantae	AOP	2 Da	decoy	169	1	PST2_ARATH	50	11192	2	2	2	2	0.66	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	170	1	PROF3_PHLPR	50	14269	1	1	1	1	0.22	Phleum pratense
19046	viridiplantae	AOP	2 Da	decoy	171	1	KIC_ARATH	50	15329	1	1	1	1	0.21	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	172	1	PE1D_ATRBE	50	17504	1	1	1	1	0.18	Atropa belladonna
19046	viridiplantae	AOP	2 Da	decoy	173	1	PROFI_LILLO	50	14176	2	2	1	1	0.5	Lilium longiflorum
19046	viridiplantae	AOP	2 Da	decoy	174	1	PROCB_OLEEU	50	14143	1	1	1	1	0.23	Olea europaea
19046	viridiplantae	AOP	2 Da	decoy	175	1	ATPE_LACSA	50	14604	1	1	1	1	0.22	Lactuca sativa
19046	viridiplantae	AOP	2 Da	decoy	176	1	TOM92_ARATH	50	10372	2	2	1	1	0.73	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	177	1	PSBI_AMBIC	50	4134	2	2	1	1	2.51	Amborella trichopoda
19046	viridiplantae	AOP	2 Da	decoy	178	1	GRP10_BRANA	49	16351	1	1	1	1	0.19	Brassica napus
19046	viridiplantae	AOP	2 Da	decoy	179	1	PE1M_CHLRE	49	10105	2	2	2	2	0.75	Chlamydomonas reinhardtii
19046	viridiplantae	AOP	2 Da	decoy	180	1	ACPI_CASGL	49	14514	1	1	1	1	0.22	Casuarina glauca
19046	viridiplantae	AOP	2 Da	decoy	181	1	PSBL_HUPLU	49	4476	3	3	1	1	2.24	Huperzia lucidula
19046	viridiplantae	AOP	2 Da	decoy	182	1	PROAW_OLEEU	49	14608	1	1	1	1	0.22	Olea europaea
19046	viridiplantae	AOP	2 Da	decoy	183	1	PSBI_OENEH	49	4112	3	3	1	1	2.51	Oenothera elata subsp. hookeri
19046	viridiplantae	AOP	2 Da	decoy	184	1	PSBH_TUPAK	49	8425	3	3	2	2	1.7	Tupia akina
19046	viridiplantae	AOP	2 Da	decoy	185	1	RLA25_ARATH	49	11752	2	2	2	2	0.63	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	186	1	SODC_BRAOC	49	15276	1	1	1	1	0.21	Brassica oleracea var. capitata
19046	viridiplantae	AOP	2 Da	decoy	187	1	PROCE_OLEEU	48	14199	1	1	1	1	0.23	Olea europaea
19046	viridiplantae	AOP	2 Da	decoy	188	1	NLT22_PARJU	48	14553	1	1	1	1	0.22	Parietaria judaica
19046	viridiplantae	AOP	2 Da	decoy	189	1	PIP2_ARATH	48	9027	2	2	2	2	0.87	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	190	1	ACBP_FRIAG	48	9798	2	2	1	1	0.34	Fritillaria agrestis
19046	viridiplantae	AOP	2 Da	decoy	191	1	RL373_ARATH	48	10993	2	2	1	1	0.3	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	192	1	MT2_MUSAC	48	8525	1	1	1	1	0.39	Musa acuminata
19046	viridiplantae	AOP	2 Da	decoy	193	1	TIM8_ARATH	48	8972	3	3	1	1	0.87	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	194	1	FB41_ARATH	48	7337	1	1	1	1	0.46	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	195	1	MT21A_ORYSJ	47	9457	1	1	1	1	0.35	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	196	1	PROF_PYRGO	47	14169	2	2	1	1	0.5	Pyrus communis
19046	viridiplantae	AOP	2 Da	decoy	197	1	TT141_ARATH	47	11989	1	1	1	1	0.27	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	198	1	PSAK_SPIOL	47	3056	3	3	3	3	9.77	Spinacia oleracea
19046	viridiplantae	AOP	2 Da	decoy	199	1	PSBI_MESVI	47	4301	1	1	1	1	0.82	Mesostigma viride

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/ error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	empAI	Species
19046	viridiplantae	AOP	2 Da	decoy	200	1	CYC6_BRYMA	46	9395	1	1	1	1	0.35	Bryopsis maxima
19046	viridiplantae	AOP	2 Da	decoy	201	1	CYC4_CHACT	46	8653	1	1	1	1	0.38	Chassalia chartacea
19046	viridiplantae	AOP	2 Da	decoy	202	1	DEF10_ARATH	46	8169	1	1	1	1	0.4	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	203	1	LSM5_ARATH	46	9709	1	1	1	1	0.34	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	204	1	PSBJ_EUCGG	46	4158	2	2	1	1	0.87	Eucalyptus globulus subsp. globulus
19046	viridiplantae	AOP	2 Da	decoy	205	1	FER_SCEQU	46	10506	1	1	1	1	0.31	Scenedesmus quadricauda
19046	viridiplantae	AOP	2 Da	decoy	206	1	ATP9_PETSP	46	7789	3	3	1	1	1.92	Petunia sp.
19046	viridiplantae	AOP	2 Da	decoy	207	1	BOLA2_ARATH	45	10425	1	1	1	1	0.31	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	208	1	GRC13_ORYSJ	45	11580	1	1	1	1	0.28	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	209	1	PSK6_ARATH	45	9457	1	1	1	1	0.35	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	210	1	ATPH_PEA	45	8027	1	1	1	1	0.42	Pisum sativum
19046	viridiplantae	AOP	2 Da	decoy	211	1	TOM72_ARATH	45	8357	2	2	1	1	0.96	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	212	1	PSAC_TUPAK	45	9239	1	1	1	1	0.36	Tupella akineta
19046	viridiplantae	AOP	2 Da	decoy	213	1	EMP1_ORYSJ	45	10159	1	1	1	1	0.32	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	214	1	POLC7_PHLPR	45	8728	1	1	1	1	0.38	Phleum pratense
19046	viridiplantae	AOP	2 Da	decoy	215	1	PSBH_MARPO	44	7923	1	1	1	1	0.42	Marchantia polymorpha
19046	viridiplantae	AOP	2 Da	decoy	216	1	DEF73_ARATH	44	8321	1	1	1	1	0.4	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	217	1	LSM6B_ARATH	44	9779	1	1	1	1	0.34	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	218	1	DEF83_ARATH	44	9953	1	1	1	1	0.33	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	219	1	TT143_ARATH	44	12056	1	1	1	1	0.27	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	220	1	PSBH_PHAAO	44	7695	1	1	1	1	0.44	Phalaenopsis aphrodite subsp. formosana
19046	viridiplantae	AOP	2 Da	decoy	221	1	PSBH_SPIMX	44	8337	1	1	1	1	0.4	Spirogyra maxima
19046	viridiplantae	AOP	2 Da	decoy	222	1	RK14_OENAM	44	8278	1	1	1	1	0.4	Oenothera ammobila
19046	viridiplantae	AOP	2 Da	decoy	223	1	PAPF_PHYAM	44	7141	2	2	1	1	1.17	Phytolacca americana
19046	viridiplantae	AOP	2 Da	decoy	224	1	PSAC_ZYGCR	43	9319	1	1	1	1	0.35	Zygnema circumcarinatum
19046	viridiplantae	AOP	2 Da	decoy	225	1	PSBH_CALFG	43	7732	1	1	1	1	0.43	Calycanthus floridus var. glaucus
19046	viridiplantae	AOP	2 Da	decoy	226	1	PSBJ_CHLRE	43	4287	4	4	1	1	2.32	Chlamydomonas reinhardtii
19046	viridiplantae	AOP	2 Da	decoy	227	1	PSAK_CUCSA	43	3584	1	1	1	1	1.03	Cucumis sativus
19046	viridiplantae	AOP	2 Da	decoy	228	1	TIM13_ORYSJ	43	9158	2	2	1	1	0.84	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	229	1	ATPH_CICAR	43	8057	1	1	1	1	0.41	Cicer arietinum
19046	viridiplantae	AOP	2 Da	decoy	230	1	NU5C_PSEMZ	42	3049	2	2	1	1	4.11	Pseudotsuga menziesii
19046	viridiplantae	AOP	2 Da	decoy	231	1	ATP9_PETHY	42	7558	3	3	2	2	2.01	Petunia hybrida
19046	viridiplantae	AOP	2 Da	decoy	232	1	PSBJ_AETGR	42	4086	2	2	1	1	2.51	Aethionema grandiflorum
19046	viridiplantae	AOP	2 Da	decoy	233	1	DF208_ARATH	42	8874	1	1	1	1	0.37	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	234	1	PSBH_DRIGR	42	7814	1	1	1	1	0.43	Drimys granadensis
19046	viridiplantae	AOP	2 Da	decoy	235	1	PSBH_CHAVU	42	8440	1	1	1	1	0.39	Chara vulgaris
19046	viridiplantae	AOP	2 Da	decoy	236	1	PSBH_HELAN	42	7725	1	1	1	1	0.43	Helianthus annuus
19046	viridiplantae	AOP	2 Da	decoy	237	1	R35A1_ARATH	42	12897	1	1	1	1	0.25	Arabidopsis thaliana

Job no.	Taxonomy	PTMs	Fragment tolerance	decoy/error	Family	M	Accession	Score	Mass	Matches	Match (sig)	Seqs	Seq (sig)	empAI	Species
19046	viridiplantae	AOP	2 Da	decoy	238	1	DF117_ARATH	42	8957	1	1	1	1	0.37	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	239	1	PSBM_PINTH	41	3868	1	1	1	1	0.93	Pinus thunbergii
19046	viridiplantae	AOP	2 Da	decoy	240	1	AGP14_ARATH	41	6358	1	1	1	1	0.54	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	241	1	MT2A_ORYSJ	41	8644	1	1	1	1	0.38	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	242	1	PSBL_ADICA	41	4460	1	1	1	1	0.8	Adiantum capillus-veneris
19046	viridiplantae	AOP	2 Da	decoy	243	1	EC1_WHEAT	41	8676	1	1	1	1	0.38	Triticum aestivum
19046	viridiplantae	AOP	2 Da	decoy	244	1	PSBJ_CYCTA	40	4146	1	1	1	1	0.87	Cycas taitungensis
19046	viridiplantae	AOP	2 Da	decoy	245	1	ATPH_OEDCA	39	8175	1	1	1	1	0.4	Oedogonium cardiacum
19046	viridiplantae	AOP	2 Da	decoy	246	1	AGP24_ARATH	39	7104	2	2	1	1	1.17	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	247	1	PSBH_PSINU	39	8133	1	1	1	1	0.41	Psilotum nudum
19046	viridiplantae	AOP	2 Da	decoy	248	1	ATP9_BRANA	39	7472	2	2	1	1	1.1	Brassica napus
19046	viridiplantae	AOP	2 Da	decoy	249	1	PSBJ_AGRST	39	4114	1	1	1	1	0.87	Agrostis stolonifera
19046	viridiplantae	AOP	2 Da	decoy	250	1	PSBL_ANTMA	39	4467	1	1	1	1	0.8	Antirrhinum majus
19046	viridiplantae	AOP	2 Da	decoy	251	1	AGP41_ARATH	39	6570	1	1	1	1	0.52	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	252	1	PSBJ_HORIU	38	4084	2	2	1	1	0.87	Hordeum jubatum
19046	viridiplantae	AOP	2 Da	decoy	253	1	PSBJ_WHEAT	38	4048	1	1	1	1	0.9	Triticum aestivum
19046	viridiplantae	AOP	2 Da	decoy	254	1	PSBZ_ACOGR	38	6537	1	1	1	1	0.52	Acorus gramineus
19046	viridiplantae	AOP	2 Da	decoy	255	1	PSBJ_PSINU	38	4133	1	1	1	1	0.87	Psilotum nudum
19046	viridiplantae	AOP	2 Da	decoy	256	1	NDUA5_SOLTU	38	4071	1	1	1	1	0.87	Solanum tuberosum
19046	viridiplantae	AOP	2 Da	decoy	257	1	PE1G_PLAOC	38	4153	1	1	1	1	0.87	Platanus occidentalis
19046	viridiplantae	AOP	2 Da	decoy	258	1	PSAL_CHLVU	38	3947	2	2	2	2	2.62	Chlorella vulgaris
19046	viridiplantae	AOP	2 Da	decoy	259	1	PSBJ_CUSEX	37	4172	1	1	1	1	0.85	Cuscuta exaltata
19046	viridiplantae	AOP	2 Da	decoy	260	1	PSBZ_PINTH	37	6442	1	1	1	1	0.53	Pinus thunbergii
19046	viridiplantae	AOP	2 Da	decoy	261	1	NFD6_ARATH	37	10558	1	1	1	1	0.31	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	262	1	PETN_CHLRE	36	3782	1	1	1	1	0.96	Chlamydomonas reinhardtii
19046	viridiplantae	AOP	2 Da	decoy	263	1	ACBP1_ORYSJ	35	10137	1	1	1	1	0.32	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	264	1	GRP1_PETHY	34	28873	1	1	1	1	0.11	Petunia hybrida
19046	viridiplantae	AOP	2 Da	decoy	265	1	PSBN_CALFL	34	4673	1	1	1	1	0.76	Calycanthus floridus
19046	viridiplantae	AOP	2 Da	decoy	266	1	AGP12_ARATH	34	6085	1	1	1	1	0.56	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	267	1	PSAC_PHYPA	33	9279	1	1	1	1	0.35	Physcomitrella patens subsp. patens
19046	viridiplantae	AOP	2 Da	decoy	268	1	NLTP3_VITXS	31	9733	1	1	1	1	0.34	Vitis sp.
19046	viridiplantae	AOP	2 Da	decoy	269	1	Y3974_ARATH	31	9603	1	1	1	1	0.34	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	270	1	F26G_SOLTU	31	6762	1	1	1	1	0.5	Solanum torvum
19046	viridiplantae	AOP	2 Da	decoy	271	1	DEF43_ARATH	30	9112	1	1	1	1	0.36	Arabidopsis thaliana
19046	viridiplantae	AOP	2 Da	decoy	272	1	APEP2_ORYSJ	29	5798	1	1	1	1	0.6	Oryza sativa subsp. japonica
19046	viridiplantae	AOP	2 Da	decoy	273	1	NLTP_RAPSA	26	4537	1	1	1	1	0.78	Raphanus sativus
19046	viridiplantae	AOP	2 Da	decoy	274	1	HSP90_POPEU	25	5122	1	1	1	1	0.68	Populus euphratica

- 131 -

[0252] Swissprot was also searched using the least stringent fragment tolerance (± 2 Da) and a decoy method. Without any dynamic modification set, searching the whole taxonomy yielded 94 accessions with 998 (9%) MS/MS matches, while searching only *viridiplantae* taxonomy (39,800 entries) yielded 80 hits (1181 (10%) matches). Searching *viridiplantae* taxonomy and setting Protein N-term acetylation and Met oxidation as dynamic modifications listed 141 accessions (1352 (12%) matches). Finally, by searching *viridiplantae* taxonomy but adding phosphorylations of Ser and Tyr residues as dynamic modification generated 274 accessions (1863 (17%) matches). The latter search lasted the longest (53 h) (Tables 7 and 14). Therefore, while the list of proteins extended when using a bigger database in conjunction with more relaxed mass tolerances, confidence in the identified proteins was relatively low. Accordingly, the search results obtain from the uniprotKB data, with a stringent fragment tolerance (± 50 ppm) (Table 13), was selected to continue this study.

[0253] The masses of the 21 identified proteins range from 4.1 kD to 17.6 kD. Thirteen accessions had a Mascot score above 100, and 16 accessions were identified using more than one MS/MS spectrum (Tables 13 and 15). No missed cleavage was found ($M > 0$), possibly explaining the low number of identified proteins.

Table 15. List of proteoforms identified from protein standards samples using Mascot algorithm with 50 ppm fragment tolerance and UniProtKB *C.sativa* database

Job no.	Description	Accession	Score	Mass	Matches	Seq s	emPA I	Query	Dupes	Observed	Mr (exp)	Mr (calc)	%	M	Score	Expect	Rank	U	SEQ ID:
19030	Cytochrome b559 subunit alpha	A0A0C5ARS8_CA NSA	2265	9367	37	1	0.83	3456	34	9237.666	9236.658	9235.647	0.011	0	197	1.90E-20	1	U	285
19030	Cytochrome b559 subunit alpha	A0A0C5ARS8_CA NSA	2265	9367	37	1	0.83	3543	1	9278.672	9277.665	9277.657	0.000	0	31	0.00072	1	U	286
19030	Photosystem I iron-sulfur center	A0A0C5AS17_CA NSA	1664	9545	39	1	1.43	3918		9416.363	9415.356	9446.328	-0.328	0	20	0.018	1	U	287
19030	Photosystem I iron-sulfur center	A0A0C5AS17_CA NSA	1664	9545	39	1	1.43	3925	26	9416.378	9415.371	9414.338	0.011	0	170	1.80E-17	1	U	288
19030	Photosystem I iron-sulfur center	A0A0C5AS17_CA NSA	1664	9545	39	1	1.43	3970	10	9416.458	9415.451	9430.333	-0.158	0	150	2.10E-15	1	U	289
19030	Photosystem II reaction center protein T	A0A0U2DTK8_CA NSA	1555	3815	25	1	13.87	198	10	3844.163	3843.156	3815.150	0.734	0	138	1.70E-14	1	U	290
19030	Photosystem II reaction center protein H	A0A0C5B2J7_CA NSA	1348	7645	12	1	1.06	1878	8	7515.975	7514.968	7529.904	-0.198	0	188	1.70E-19	1	U	291
19030	Photosystem II reaction center protein H	A0A0C5B2J7_CA NSA	1348	7645	12	1	1.06	1886	2	7516.017	7515.010	7513.909	0.015	0	239	1.30E-24	1	U	292
19030	Cytochrome b559 subunit alpha	A0A0U2GZT5_HU MLU	902	9381	21	1	0.35	3456	20	9237.666	9236.658	9249.662	-0.141	0	91	7.70E-10	3	U	293
19030	Photosystem II reaction center protein I	A0A0C5APX7_CA NSA	292	4165	9	1	5.31	547	2	4194.221	4193.214	4165.212	0.672	0	89	2.20E-09	1	U	294
19030	Photosystem II reaction center protein I	A0A0C5APX7_CA NSA	292	4165	9	1	5.31	550	4	4194.248	4193.240	4223.217	-0.710	0	79	2.30E-08	1	U	295
19030	ATP synthase CF0 C subunit	A0A0C5ARQ5_CA NSA	272	7985	12	1	1.84	2264	5	8015.408	8014.400	8043.399	-0.361	0	49	1.40E-05	1	U	296
19030	ATP synthase CF0 C subunit	A0A0C5ARQ5_CA NSA	272	7985	12	1	1.84	2273	3	8015.472	8014.464	7985.393	0.364	0	54	5.00E-06	1	U	297
19030	ATP synthase CF0 C subunit	A0A0C5ARQ5_CA NSA	272	7985	12	1	1.84	2332	1	8031.495	8030.488	8001.388	0.364	0	53	6.00E-06	1	U	298
19030	30S ribosomal protein S14, chloroplastic	A0A0U2H3A0A0U 2H3S7_HUMMLU	182	11833	5	1	0.62	6673	2	11721.470	11720.463	11702.389	0.154	0	68	4.10E-07	1	U	299

Job no.	Description	Accession	Score	Mass	Matches	Seq s	emPA I	Query	Dupes	Observed	Mr (exp)	Mr (calc)	%	M	Score	Expect	Rank	U	SEQ ID:
19030	30S ribosomal protein S14, chloroplastic	A0A0U2H3S7_HU MLU	182	11833	5	1	0.62	6681	1	11721.561	11720.554	11718.384	0.019	0	55	8.20E-06	1	U	300
19030	Cytochrome b559 subunit beta	A0A0C5AU12_CA NSA	182	4421	17	1	0.8	740	16	4393.373	4392.365	4421.355	-0.656	0	31	0.00073	1	U	301
19030	Olivetolic acid cyclase	OLLAC_CANSA	162	11994	9	1	0.61	6725	7	11869.288	11868.280	11863.163	0.043	0	54	1.90E-05	1	U	302
19030	Olivetolic acid cyclase	OLLAC_CANSA	162	11994	9	1	0.61	6795		11910.306	11909.299	11905.174	0.035	0	54	1.90E-05	1	U	303
19030	Ribosomal protein S16	A0A0H3W6G0_C ANSA	123	10414	5	1	0.72	5400	1	10442.950	10441.942	10379.805	0.599	0	70	6.10E-07	1	U	304
19030	Ribosomal protein S16	A0A0H3W6G0_C ANSA	123	10414	5	1	0.72	5402		10442.953	10441.946	10429.784	0.117	0	29	0.0084	1	U	305
19030	Ribosomal protein S16	A0A0H3W6G0_C ANSA	123	10414	5	1	0.72	5405	3	10444.951	10443.943	10413.789	0.290	0	63	3.30E-06	1	U	306
19030	Betv1-like protein	I6XT51_CANSA	113	17597	7	2	1.28	10077	1	17491.194	17490.187	17466.018	0.138	0	46	0.00017	1	U	307
19030	Betv1-like protein	I6XT51_CANSA	113	17597	7	2	1.28	10081		17491.212	17490.205	17613.053	-0.698	0	29	0.0017	1	U	308
19030	Betv1-like protein	I6XT51_CANSA	113	17597	7	2	1.28	10082		17491.212	17490.205	17597.058	-0.607	0	29	0.0021	1	U	309
19030	Betv1-like protein	I6XT51_CANSA	113	17597	7	2	1.28	10100	1	17492.208	17491.201	17508.028	-0.096	0	27	0.0032	4	U	310
19030	Photosystem II reaction center protein J	A0A0C5APY3_CA NSA	79	4128	2	1	0.87	553	1	4194.259	4193.252	4170.248	0.552	0	66	4.30E-07	1	U	311
19030	Ribosomal protein L33	A0A0C5AU15_CA NSA	72	7910	1	1	0.42	2163		7781.137	7780.129	7779.095	0.013	0	72	7.20E-08	1	U	312
19030	ATP synthase CF1 epsilon subunit	A0A0C5AUH9_CA ANSA	62	14696	1	1	0.22	8145		14615.867	14614.860	14622.683	-0.054	0	62	3.20E-06	1	U	313
19030	Cytochrome b6-f complex subunit 5	A0A0C5APY4_CA NSA	27	4167	1	1	0.85	559		4196.345	4195.338	4167.321	0.672	0	27	0.0034	1	U	314
19030	Non-specific lipid-transfer protein	W0U0V5_CANSA	26	9489	2	1	0.35	4269	1	9563.825	9562.817	9488.689	0.781	0	25	0.0078	1	U	315
19030	Photosystem II reaction center protein L	A0A0H3W8G1_CA ANSA	25	4494	2	1	0.8	686	1	4364.282	4363.275	4363.232	0.001	0	24	0.0044	1	U	316
19030	Cytochrome b6-f	A0A0H3W844_CA	24	17504	1	1	0.18	10025		17382.498	17381.491	17373.464	0.046	0	24	0.0067	1	U	317

- 134 -

Job no.	Description	Accession	Score	Mass	Matches	Seqs	emPA	Query	Dupes	Observed	Mr (exp)	Mr (calc)	%	M	Score	Expect	Rank	U	SEQ ID:
	complex subunit 4	NSA																	
19030	Photosystem I reaction center subunit IX	A0A0C5AS04_CA NSA	15	4770	1	1	0.74	1002		4814.619	4813.612	4827.612	-0.290	0	15	0.035	1	U	318

- 135 -

[0254] Two of the 20 proteins match hits from hop (*Humulus lupulus*), with one hit (cytochrome b559 subunit alpha) identified in both *C. sativa* (accession A0A0C5ARS8, highest score of 2265, Figure 16) and *H. lupulus* species (accession A0A0U2GZT5, score of 902). The other protein from *H. lupulus* was chloroplastic 30S ribosomal protein S14. Overall, 18 accessions were unmodified proteoforms, six with one oxidation, one with 2 oxidations, and seven that display a N-terminus acetylation.

[0255] Comparing the list of cannabis intact proteins identified by a top-down approach to that of trypsin-digested proteins identified by bottom-up proteomics described above, 7 proteins overlap and 13 proteins are novel (Table 13).

[0256] Most identified proteins (12/20, 60%) are involved in photosynthesis (subunits of cytochromes and photosystems I and II), then in protein translation (4 ribosomal proteins, 20%). Also identified are two ATP synthases, a non-specific lipid-transfer protein, and Betv1-like protein. Only one protein belongs to the phytocannabinoid biosynthesis, olivetolic acid cyclase (I6WU39, OAC), also identified by bottom-up proteomics (Table 4). With a Mascot score of 162, OAC is identified both as an unmodified proteoform and an acetylated proteoform (Table 13).

[0257] Consistent with the data obtained from the protein standards, fragmentation efficiency of cannabis intact proteins depends on the charge state of the parent ion, on the type of MS/MS mode, and on the level of energy applied. We are illustrating this using the protein exhibiting the second highest Mascot score (1664), Photosystem I iron-sulfur center (PS I Fe-S center, accession A0A0C5AS17) identified with 39 MS/MS spectra. Fragmentation efficiency is assessed using ProSight Lite program by the percentage of inter-residue cleavages achieved. MS/MS spectra differ in the number of peaks and their distribution along the mass range (Figures 17A and B).

- 136 -

[0258] The optimum dissociation of a precursor ion with high charge state (857.31 m/z, $z=+11$) is achieved with ETD at “Mid” energy, whereas a precursor ion of comparable intensity but with lower charge state (1178.55 m/z, $z=+8$) responds better to CID and HCD at “Low” and “High” energy levels, respectively. All MS/MS data considered, fragmenting 857.31 m/z and 1178.55 m/z parent ions yields 70% and 65% inter-residue cleavages, respectively, and 82% all together (Figure 17C). In order to maximise AA sequence coverage, it is essential to multiply the MS/MS conditions on as many precursor ions as possible. This of course limits the total number of different proteins analysed in a top-down approach. Coupling this strategy with an extended separation run should alleviate this drawback.

Example 8 – Optimisation of multiple protease strategy for the preparation of samples for bottom-up and middle-down proteomics

[0259] In this experiment, a trypsin/LysC mixture, GluC and chymotrypsin were applied on their own or in combination, either sequentially in a serial digestion fashion, or by pooling individual digests together. The analytical method was first tested on BSA and then applied to complex plant samples. The experimental design is schematised in Figure 18.

[0260] BSA was used as a positive control in the experiment as it is often used as the gold standard for shotgun proteomics. BSA is a monomeric protein particularly amenable to trypsin digestion. Many laboratories determine the sequence coverage of BSA tryptic digest in order to rapidly evaluate instrument performance because it is sensitive to method settings in both MS1 and MS2 acquisition modes. Beside the trypsin/LysC mixture (T), we tested two other proteases, GluC (G) and chymotrypsin (C), either independently or applied sequentially (denoted by an arrow or $\rightarrow$) as follows: trypsin/LysC followed by GluC (T $\rightarrow$ G), trypsin/LysC followed by chymotrypsin (T $\rightarrow$ C), GluC followed by chymotrypsin

- 137 -

(G→C), and trypsin/LysC followed by GluC followed by chymotrypsin (T→G→C). We also pooled equal volumes of the individual digests (denoted by a colon or :) as follows: trypsin/LysC with GluC (T:G), trypsin/LysC with chymotrypsin (T:C), GluC with chymotrypsin (G:C), and trypsin/LysC with GluC and chymotrypsin (T:G:C).

[0261] Each BSA digest underwent nLC-MS/MS analysis in which each duty cycle comprised a full MS scan was followed by CID MS/MS events of the 20 most abundant parent ions above a 10,000 counts threshold. Figure 19 displays the LC-MS profiles corresponding to one replicate of each BSA digest.

[0262] The peptides elute from 9 to 39 min corresponding to 9-39% ACN gradient, respectively and span m/z values from 300 to 1600. Visually, LC-MS patterns from samples subject to digestion with trypsin/LysC (T) and GluC followed by chymotrypsin (G→C) are relatively less complex than the other digests. Technical duplicates of the BSA digests yield MS and MS/MS spectra of high reproducibility as can be seen in Table 16.

Table 16. Number of MS peaks, MS/MS spectra and MS/MS spectra annotated with SEQUEST for each BSA digest.

1. MS										2. all MS/MS										3. SEQUEST annotated MS/MS										% MS annotated ^c	
Sample	Protease mix	Rep 1	Rep 2	Mean	SD	% CV	Rep 1	Rep 2	Mean	SD	Percent	Rep 1	Rep 2	Mean	SD																
BSA	T	83678	83056	83367	440	0.5	9769	9325	9547	314	11	2133	1875	2004	182																
BSA	G	91922	98895	95409	3487	3.7	9081	9628	9355	387	10	929	1363	1146	307																
BSA	C	92116	90303	91210	907	1.0	10327	9792	10060	378	11	1358	1267	1313	64																
BSA	T->G	89648	83107	86378	3271	3.8	11311	9698	10505	1141	12	2178	1978	2078	141																
BSA	T:G	84347	87462	85905	1558	1.8	8605	9720	9163	788	11	2141	2332	2237	135																
BSA	T->C	87203	79616	83410	3794	4.5	10944	8810	9877	1509	12	1864	1549	1707	223																
BSA	T:C	90847	92736	91792	945	1.0	10245	10115	10180	92	11	2428	1931	2180	351																
BSA	G->C	77085	82055	79570	2485	3.1	6450	5163	5807	910	7	1103	475	789	444																
BSA	G:C	99001	100001	99501	500	0.5	9980	9847	9914	94	10	1169	1065	1117	74																
BSA	T->G->C	88919	84798	86859	2061	2.4	9880	6137	8009	2647	9	1485	1005	1245	339																
BSA	T:G:C	91975	89420	90698	1278	1.4	10201	9503	9852	494	11	1015	1616	1316	425																
BSA	mean	88795	88314	88554	1884	2	9708	8885	9297	796	10	1618	1496	1557	244																
BSA	SD	5707	6752	5811	1218	1	1317	1648	1333	756	1	544	531	501	136																
	min	77085	79616	79570	440	1	6450	5163	5807	92	7	929	475	789	64																
	max	99001	100001	99501	3794	5	11311	10115	10505	2647	12	2428	2332	2237	444																

^athese percentages were obtained by dividing the mean of the number of MS/MS events by the mean of the number of MS peaks; ^bthese percentages were obtained by dividing the mean of the number of annotated MS/MS spectra by the mean of the number of MS/MS event; ^cthese percentages were obtained by dividing the mean of the number of annotated MS/MS spectra by the mean of the number of MS peaks.

[0263] All LC-MS patterns are highly complex. The number of MS peaks vary from 77,085 (G→C rep 1) to 100,001 (G:C rep 2) across all patterns and SDs range from 440 (T) to 3,794 (T→C) with coefficient of variations (%CVs) always lower than 5%, even though a full set of eleven digest combinations (Figure 18) was run first (technical replicate 1), and then fully repeated in the same order (technical replicate 2) with no randomisation applied. The number of MS/MS events ranges from 5,163 (6%, G→C rep 2) to 11,311 (13% T→G rep 1), which amounts to 10% of all the MS peaks on average (Table 16). The number of MS/MS events per sample is determined by the duration of the run (50 min) and the duty cycle (3 sec) which in turn is controlled by the resolution (60,000), number of microscans (2) and number of MS/MS per cycle (20). In our experiment, a 50 min run allows for 1,000 cycles and 20,000 MS/MS events. Proteotypic peptides elute for 30 min, thus allowing for a maximum of 12,000 MS/MS scans. With an average number of 9,297 MS/MS spectra obtained (Table 16), 77% of the potential is thus achieved. Duty cycles can be shortened by lowering the resolving power of the instrument, minimising the number of microscans and diminishing the number of MS/MS events. The MS/MS data was searched against a database containing the BSA sequence using SEQUEST algorithm for protein identification purpose. Of all the MS/MS spectra generated in this study, between 475 (9%, G→C rep 2) and 2,428 (24%, T:C rep 1) are successfully annotated as BSA peptides (Table 16). On average, 17% of the MS/MS spectra yield positive database hits, which amounts to an average of 1.8% of MS peaks. Trypsin/LysC yields 68 unique BSA peptides, GluC yields 79 unique BSA peptides, and chymotrypsin yields 104 unique BSA peptides. BSA was identified with 51 unique peptides obtained using trypsin on its own; therefore, the mixture trypsin/LysC further enhances the digestion of BSA. The percentages of Table 16 are presented as a histogram in Figure 20. The proportion of MS peaks fragmented by MS/MS remains constant across BSA digests, oscillating around $10 \pm 3\%$ (light grey bars). The

- 140 -

proportions of MS/MS spectra annotated in SEQUEST (*i.e.* successful hits) however show more variation across proteases (black bars). Higher percentages are reached when trypsin/LysC is employed on its own or in combination with GluC and/or chymotrypsin (Figure 20). This is expected as BSA is amenable to trypsin digestion and often used as shotgun proteomics standard.

[0264] BSA (P02769) mature primary sequence contains 583 amino acids (AA), from position 25 to 607; the signal peptide (position 1 to 18) and propeptide (position 19 to 24) are excised during processing. In theory, BSA should favourably respond to each protease as it contains plethora of the AAs targeted during the digestion step. Figure 20A indicates the AA composition of BSA. Targets of chymotrypsin (L, F, Y, and W) account for 19% of BSA sequence, targets of GluC (E and D) represent 17% of the sequence, and targets of trypsin/LysC (K, R) make 14% of the total AA composition of BSA. As these percentages are similar, the difference in the numbers of MS/MS spectra successfully matched by SEQUEST from one protease to another cannot be attributed to digestion site predominance. When we compare these predicted percentages to those observed in our study based on unique peptides (Figure 21B), all the targeted AAs indeed undergo cleavage. The predicted rate always exceeds the observed one, but only moderately for W, Y, E, K, and R residues (less than 1.5% difference). However, F, L, and in particular D residues present an observed cleavage rate that is much lower than the predicted one (Figure 21B). GluC efficiently cleaves E residues, but misses most of D residues, even though the digestion step is performed under slightly alkaline conditions (pH = 7.8) optimal for GluC activity as recommended by the manufacturer.

[0265] The number of successfully annotated MS/MS events to that of MS peaks, fluctuated from 1.0% (G->C) to 2.6% (T:C) (Table 16 and dark grey bars in Figure 19).

- 141 -

[0266] Together, these data demonstrate that LC-MS/MS data from BSA digests are very reproducible.

[0267] The statistical tests performed and the BSA sequence information as well as a visual assessment of BSA sequencing success for each combination of enzymes is provided by Figure 22.

[0268] PCA shows that technical duplicates group together (Figure 22A). BSA samples arising from enzymatic digestion using chymotrypsin in combination or not with GluC separate from the rest, particularly tryptic digests, along PC 2 explaining 17.5% of the variance. HCA confirms PCA results and further indicates that samples treated with trypsin/LysC (T) and GluC (G) on their own or pooled (T:C) form one cluster (cluster 4, Figure 21B). The closest cluster (cluster 3) comprises all the samples subject to sequential digestions (represented by an arrow $\rightarrow$), except for digests resulting from the consecutive actions of GluC and chymotrypsin (G $\rightarrow$ C) which constitute a cluster on their own (cluster 1). The last cluster (cluster 2) groups chymotryptic samples with the remaining pooled digests (represented by a colon). The fact that clusters 1-3 contains samples treated with chymotrypsin (except for T $\rightarrow$ G) suggests that this protease produces peptides with unique properties, which affect the down-stream analytical process. These data confirm that chymotrypsin acts in an orthogonal fashion to trypsin.

[0269] Based on the 589 unique peptides identified in this study, we generated a BSA sequence alignment map (Figure 22C) and coverage histogram (Figure 22D). All digests considered, BSA sequence is at least 70% covered (G->C), up to 97% (T:G) (Figure 22D), with an average of 87% coverage. Despite this almost complete coverage, the seven AA-long area positioned between residues 214 and 220 (ASSARQR) resist digestion, even though R residues targeted by trypsin/LysC are present (Figure 22C). Other areas resisting cleavage were common across different digests (*e.g.*, position 162-171, LYEIARRHPY,

- 142 -

shared between C, T→C, G→C, and T→G→C) or unique to a particular digest (*e.g.*, position 268-275, CCHGDLLE, in G:C) (Figure 22C). Comparison of digests obtained using a unique enzyme demonstrate excellent BSA sequence coverage: 91.3% for trypsin/LysC, 93.1% for GluC, and 90.2% for chymotrypsin (Figure 22D).

[0270] We compared digests obtained using multiple enzymes and compare sequential digestions (→) with pooled digests (:), and observed better alignment and coverage when individual digests are combined than when proteases are added. For instance, T→C digests covers 81% of the BSA sequence while T:C digest reach 91% coverage (Figure 22D); the 10% difference represents 56 AAs. This is better exemplified when the three proteases are used together, with a 75% coverage in T→G→C samples and 94% coverage in T:G:C samples (Figure 22D); the 19% difference representing 111 AAs.

[0271] The masses of identified peptides ranged from 688 to 6,412 Da, with an average of $1,758 \pm 753$ Da (Figure 22E), containing 5-54 AA residues. GluC is the enzyme that generates the longest peptides with an average of $2,342 \pm 1052$ Da, followed by trypsin/LysC (2053 ± 1000 Da), the mixture GluC/chymotrypsin (G:C, 2008 ± 765), and chymotrypsin (1989 ± 901 Da). GluC on its own produces peptides large enough to undertake MDP analyses. The smallest peptides result from the sequential actions of GluC and chymotrypsin (G→C, 1541 ± 511 Da), trypsin/LysC and chymotrypsin (T→C, 1481 ± 567 Da), and all three proteases (T→G→C, 1295 ± 348 Da). This confirms that adding multiple proteases to a sample enhances protein cleavage. BSA peptides contain up to six miscleavages, with the majority (59%) presenting 1-3 miscleavages (Figure 22F). The different digestion conditions peak at different miscleavages as can be seen in Figure 23. For instance, the greatest number of tryptic and chymotryptic peptides exhibit one miscleavage while GluC-released peptides containing three miscleavages are the most numerous.

The longest peptide

- 143 -

(VSRSLGKVGTRCCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTKCCTE, 6.4 kDa) released from the action of GluC contains eight charges, and six miscleavages; it has a SpScore of 1,572 and a Xcorr of 4.14. Where trypsin is used to perform the enzymatic digestion of the protein extracts, the maximum number of missed cleavages is typically set to two. However, these data demonstrate that a significant proportion of BSA peptides (47%) contain more than two miscleavages (35% of BSA tryptic peptides).

[0272] Together, these data demonstrate that BSA is highly amenable to enzymatic digestion by trypsin/LysC, GluC and chymotrypsin. Pooling the individual digests does not affect the LC-MS/MS analysis as attested by the high sequencing coverage. Using multiple proteases consecutively yields relatively lower sequence coverage of BSA.

Example 9 – Application of a multiple protease strategy for the preparation of medicinal cannabis samples for shotgun proteomics

[0273] LC-MS patterns are very complex with cannabis peptides eluting from 9-39 min (9-39% ACN gradient) exhibiting m/z values spanning from 300 to 1,700 (Figure 24).

[0274] Statistical analyses were carried out on volumes of the 27,635 peptides identified in this study. Multivariate analyses (PCA, PLS, HCA) were performed as well as a linear model which isolated 3,349 peptides significantly responding to the digestion type. The PCA projection plot of PC1 and PC2 using all identified peptides shows that samples are grouped by digestion type, with biological triplicates closely clustering together but technical duplicates separating out as they were run at two independent times (Figure 25A), which can be resolved by randomizing the LC injection order.

[0275] PC1 explains 35% of the total variance and separates samples that include digestion with trypsin/LysC on the right-hand side away from the samples which do not on the left-hand side. PC2 explains 11.3% of the variance and discriminates samples on the

- 144 -

basis of their treatment with or without chymotrypsin (Figure 25A). Peptide mass is the determining factor behind the sample grouping across PC1 x PC2 as can be seen on the PCA loading plot which illustrates that samples treated with GluC generate the longest peptides (> 5 kDa, Figure 25B). A PLS analysis was performed using the 3,349 peptides that were most significantly differentially expressed across the seven digestion types. This supervised statistical process defined groups according to a particular experimental design, in this instance the digestion type. The score plot of the first two components indeed achieve better separation of the different digestion types, with samples treated with GluC away from all the other types (Figure 25C). One group is composed of the samples treated with trypsin/LysC on its own and combined to GluC. Another group comprises samples treated with chymotrypsin on its own and with GluC. The last group positioned in between contains samples treated with trypsin/LysC and chymotrypsin, as well as with GluC. The main peptide characteristics behind such grouping is the m/z value as illustrated on the PLS loading plot (Figure 25D). These data confirm the orthogonality of the proteases used in this experiment.

[0276] The number of MS peaks varies from 49,316 (Bud 2 T→G→C rep 2) to 118,020 (Bud 3 T→G rep 1), with an average value of $93,771 \pm 15,426$ (Table 17).

Table 17. Number of MD peaks, MS/MS spectra and MS/MS spectra annotated in SEQUEST for each medicinal cannabis digest

Biol rep	Protease mix	1. MS					2. all MS/MS					% MS/MS ^a		3. SEQUEST annotated MS/MS			% MS/MS annotated ^b		% MS annotated ^c	
		Rep 1	Rep 2	Mean	SD	% CV	Rep 1	Rep 2	Mean	SD	Percent	Rep 1	Rep 2	Mean	SD	Percent	Rep 1	Rep 2	Mean	SD
Bud 1	T	86458	115577	101018	20590	20.4	12827	11731	12279	775	12	2042	1929	1986	80	16	16	16	16	2.0
Bud 2	T	72907	113303	93105	28564	30.7	10775	11160	10968	272	12	1606	1740	1673	95	15	15	15	15	1.8
Bud 3	T	70473	112818	91646	29942	32.7	10541	10585	10563	31	12	1513	1643	1578	92	15	15	15	15	1.7
Bud 1	G	106622	84761	95692	15458	16.2	9035	8501	8768	378	9	1388	1376	1382	8	16	16	16	16	1.4
Bud 2	G	95761	88387	92074	5214	5.7	8032	7906	7969	89	9	1200	1146	1173	38	15	15	15	15	1.3
Bud 3	G	93760	91846	92803	1353	1.5	8810	8115	8463	491	9	1326	1290	1308	25	15	15	15	15	1.4
Bud 1	C	93117	95399	94258	1614	1.7	9486	8644	9065	595	10	2589	2200	2395	275	26	26	26	26	2.5
Bud 2	C	93778	92536	93157	878	0.9	8433	7788	8111	456	9	2232	1857	2045	265	25	25	25	25	2.2
Bud 3	C	97359	97813	97586	321	0.3	9508	8341	8925	825	9	2382	2098	2240	201	25	25	25	25	2.3
Bud 1	T->G	116131	113352	114742	1965	1.7	11909	11406	11658	356	10	3416	3163	3290	179	28	28	28	28	2.9
Bud 2	T->G	113690	111601	112646	1477	1.3	11511	10857	11184	462	10	3103	2904	3004	141	27	27	27	27	2.7
Bud 3	T->G	118020	115958	116989	1458	1.2	12362	11811	12087	390	10	3633	3405	3519	161	29	29	29	29	3.0
Bud 1	T->C	98125	94395	96260	2638	2.7	10963	9568	10266	986	11	4066	3434	3750	447	37	37	37	37	3.9
Bud 2	T->C	98455	97615	98035	594	0.6	10622	9090	9856	1083	10	4024	3308	3666	506	37	37	37	37	3.7
Bud 3	T->C	100667	97679	99173	2113	2.1	11238	8873	10056	1672	10	4297	3321	3809	690	38	38	38	38	3.8
Bud 1	G->C	92277	90930	91604	952	1.0	8219	7625	7922	420	9	2786	2545	2666	170	34	34	34	34	2.9
Bud 2	G->C	86056	83949	85003	1490	1.8	7160	6390	6775	544	8	2393	2190	2292	144	34	34	34	34	2.7
Bud 3	G->C	93847	89624	91736	2986	3.3	8158	7398	7778	537	8	2687	2502	2595	131	33	33	33	33	2.8
Bud 1	T->G->C	88886	56861	72874	22645	31.1	9479	4279	6879	3677	9	4117	2002	3060	1496	44	44	44	44	4.2
Bud 2	T->G->C	67123	49316	58220	12591	21.6	6835	1770	4303	3581	7	3065	824	1945	1585	45	45	45	45	3.3
Bud 3	T->G->C	84077	77062	80570	4960	6.2	7685	5570	6628	1496	8	3392	2524	2958	614	45	45	45	45	3.7
Mean		13559	17773	13095	9797	11	1743	2526	2047	992	1	991	787	836	439	10	10	10	10	1
SD		13232	17345	12779	9561	11	1701	2465	1997	968	1	967	769	816	428	10	10	10	10	1
Min		67123	49316	58220	321	0.33	6835	1770	4303	311	7.391	1200	824	1173	8.49	14.7195	14.7195	14.7195	14.7195	1.27398
Max		118020	115958	116989	29942	32.7	12827	11811	12279	3677	12.155	4297	3434	3809	1585	45.1894	45.1894	45.1894	45.1894	4.19837

^athese percentages were obtained by dividing the mean of the number of MS/MS events by the mean of the number of MS peaks; ^bthese percentages were obtained by

dividing the mean of the number of annotated MS/MS spectra by the mean of the number of MS/MS events; these percentages were obtained by dividing the mean of the number of annotated MS/MS spectra by the mean of the number of MS peaks.

- 147 -

[0277] The MS data was searched against a *C. sativa* database using SEQUEST algorithm for protein identification purpose. Of all the MS/MS spectra generated from medicinal cannabis digests, between 824 (47% of the 1,770 MS/MS spectra for Bud 2 T→G→C rep 2) and 4,297 (38% of the 11,238 MS/MS spectra for Bud 3 T→C rep 1) are successfully annotated (Table 17). On average, 29% of the MS/MS spectra yield positive database hits, which amounts to an average of 2.7% of MS1 peaks.

[0278] The percentages of Table 17 are presented as a histogram in Figure 26. As observed before for BSA samples, the proportion of MS peaks fragmented by MS/MS remains fairly constant across the medicinal cannabis digests, ranging from 7-12% as it is set by the duty cycle. The proportion of MS/MS spectra annotated in SEQUEST (*i.e.*, successful hits), however, shows even more variation across proteases than BSA, fluctuating from 15 to 45%. Higher percentages are reached when chymotrypsin is employed on its own or in combination with trypsin/LysC and/or GluC (Figure 26). In the case of medicinal cannabis protein extracts, the strategy involving sequential enzymatic digestions using two or three proteases proves very successful with high annotation rates: 28% for T→G, 34% for G→C, 37% for T→C and 45% for T→G→C (Figure 26).

[0279] A total of 22,046 unique peptides from cannabis samples are identified. This improves upon the results achieved using bottom-up proteomics based on trypsin digestion. In view of these results, it is demonstrated that proteases behave differently. For instance, the highest peptide ion scores are found among the peptides generated by trypsin/LysC, in particular when arginine residues (R) are targeted, whereas the lowest scores belong to peptides resulting from the cleavage of aspartic acid residues (D) upon the action of GluC (Figure 27A).

[0280] Ion scores average around 6.1 ± 9.6 and reach up to 148. Apart from the expected (fixed) PTMs due to the carbamidomethylation of reduced/alkylated cysteine

- 148 -

residues during sample preparation, dynamic PTMs such as oxidation, phosphorylations and N-terminus acetylations are also found. Annotated MS/MS spectra can be viewed in Figure 28. In these examples, peptides from ribulose biphosphate carboxylase large chain (RBCL) are identified with high scores from GluC, chymotrypsin and trypsin/LysC (Figure 28A). MS/MS annotation from SEQUEST in Figure 28B illustrates how each enzyme helps extend the coverage of RBCL spanning the region Tyr29 to Arg79 (YQTKDTDILAAFRVTPQPGVPPEEAGAAVA AESSTGTWTTVWTDGLTSLDR) with chymotrypsin covering residues 41-66, GluC extending the coverage to the left down to residue 29 and Trypsin/LysC extending it to the right up to residue 79. MS/MS spectra display almost complete b- and y-series ions (Figure 28B). RBCL is adorned with several dynamic PTMs, for instance oxidation of Met116 (Figure 28C) and phosphorylation of Thr173 and Tyr185 (Figure 28D).

[0281] The distribution of identified cannabis peptides according to the number of missed cleavages also reveals differences among proteases. Our method specified a maximum of ten missed cleavage sites, which is highest number allowed in Proteome Discoverer program and SEQUEST algorithm. 5% of the peptides present no missed cleavage and up to nine missed cleavages are detected in the MS/MS data (Figure 27B). The greatest numbers of peptides resulting from trypsin/LysC or GluC present two missed cleavages while the largest number of chymotrypsin-released peptides possess three missed cleavages. Average masses of cannabis peptides steadily increase with the number of enzymatic cleaving sites missed, in a similar manner for each of the proteases (Figure 27C). When we observe the minimum masses, we can see that they increase with the number of missed cleavages, very similarly across all three proteases (Figure 27D). The shortest cannabis peptide has a mass of 627.3956 Da (7 AAs, position 286-292, from Photosystem II protein D2), presents one miscleavage and arises from the action of chymotrypsin, which is the least specific of the proteases tested. When we observe the maximum masses, GluC

- 149 -

systematically produce the largest peptides, fluctuating from 9,479.692 to 10,0027.014 Da, regardless of the number of missed cleavages (Figure 27D). Trypsin/LysC and chymotrypsin display similar patterns, namely the maximum masses increase as the number of missed cleavages go from 0 to 4, and then plateau around 9.6 kDa for subsequent numbers of missed cleavages. The longest peptide has a mass of 10,0027.014 Da (88 AAs, position 57 to 144, from CBDA synthase), bears six missed cleavage sites and arise from the action of GluC which is the most specific of the proteases tested.

[0282] A total of 494 unique accessions corresponding to 229 unique proteins from *C. sativa* and close relatives were identified (Table 18).

- 150 -

Table 18. Proteins identified in medicinal cannabis mature apical buds

Protein annotation	Protein score	Number of peptides	Coverage	MW (Da)	Pathway	Seen in Table 4
3,5,7-trioxododecanoyl-CoA	2824	149	100	42585	Cannabinoid	yes
Cannabidiolic acid synthase	3403	660	100	62268	Cannabinoid	yes
Geranylpyrophosphate:olivetola	17	3	11	44514	Cannabinoid	yes
Olivetolic acid cyclase	767	40	100	12002	Cannabinoid	yes
Polyketide synthase 1	69	13	16	42507	Cannabinoid	no
Polyketide synthase 2	81	20	72	42610	Cannabinoid	no
Polyketide synthase 3	94	2	11	42571	Cannabinoid	no
Polyketide synthase 4	53	7	12	42604	Cannabinoid	no
Polyketide synthase 5	56	14	21	42571	Cannabinoid	no
Tetrahydrocannabinolic acid	10696	2204	100	62108	Cannabinoid	yes
Tetrahydrocannabinolic acid	9	3	10	10774	Cannabinoid	no
Tetrahydrocannabinolic acid	37	5	20	33101	Cannabinoid	no
Tetrahydrocannabinolic acid	77	16	89	49047	Cannabinoid	no
Cellulose synthase	878	187	99	12192	Cell wall	no
Putative kinesin heavy chain	160	41	100	15826	Cytoskeleton	yes
Betv1-like protein	2076	86	96	17608	Defence	yes
ATP synthase CF0 A subunit	292	60	100	27206	Energy	no
ATP synthase CF0 B subunit	10	3	14	21037	Energy	no
ATP synthase CF0 C subunit	58	18	54	7990	Energy	no
ATP synthase CF1 epsilon	876	44	100	14648	Energy	yes
ATP synthase epsilon chain,	4	2	39	14647	Energy	no
ATP synthase subunit 4	323	71	99	22199	Energy	yes
ATP synthase subunit 8	148	29	100	18231	Energy	no
ATP synthase subunit 9,	237	49	100	13828	Energy	no
ATP synthase subunit a	442	98	95	26500	Energy	no
ATP synthase subunit a,	39	10	47	27161	Energy	no
ATP synthase subunit alpha	7748	452	100	55324	Energy	yes
ATP synthase subunit alpha,	232	41	79	55336	Energy	no
ATP synthase subunit b,	486	71	95	21773	Energy	no
ATP synthase subunit beta	6851	276	100	53766	Energy	yes
ATP synthase subunit beta,	112	24	86	53665	Energy	yes
ATP synthase subunit c,	10	3	14	7990	Energy	no
Cytochrome b	265	53	98	44352	Energy	no
Cytochrome c	410	50	100	12044	Energy	yes
Cytochrome c biogenesis B	287	57	100	22916	Energy	no
Cytochrome c biogenesis FC	552	115	100	50562	Energy	yes
Cytochrome c biogenesis FN	597	146	98	64755	Energy	yes
Cytochrome c biogenesis protein	805	135	99	36850	Energy	yes
Cytochrome c oxidase subunit 1	872	162	99	59034	Energy	no
Cytochrome c oxidase subunit 2	253	60	100	29465	Energy	no
Cytochrome c oxidase subunit 3	326	60	98	29864	Energy	no
NADH dehydrogenase subunit	902	180	100	53480	Energy	no
NADH dehydrogenase subunit	281	52	100	11159	Energy	no
NADH dehydrogenase subunit	521	135	100	44457	Energy	yes
NADH dehydrogenase subunit	142	38	94	22667	Energy	yes
NADH-plastoquinone	36	11	60	85480	Energy	no
NADH-quinone oxidoreductase	132	24	98	13798	Energy	no
NADH-quinone oxidoreductase	591	110	100	25529	Energy	no
NADH-quinone oxidoreductase	93	20	96	18752	Energy	yes
NADH-quinone oxidoreductase	445	99	100	45497	Energy	no
NADH-quinone oxidoreductase	655	129	100	40394	Energy	yes

- 151 -

Protein annotation	Protein score	Number of peptides	Coverage	MW (Da)	Pathway	Seen in Table 4
NADH-quinone oxidoreductase	137	30	99	11276	Energy	yes
NADH-quinone oxidoreductase	1126	224	100	56578	Energy	yes
NADH-ubiquinone	772	156	99	35591	Energy	yes
NADH-ubiquinone	909	166	100	54897	Energy	no
NADH-ubiquinone	1586	301	100	74182	Energy	yes
NADH-ubiquinone	428	84	100	23568	Energy	no
Putative cytochrome c	481	107	98	27659	Energy	no
Succinate dehydrogenase	121	19	97	12122	Energy	no
Succinate dehydrogenase	196	42	100	20940	Energy	no
1-deoxy-D-xylulose-5-phosphate	754	126	100	51629	Isoprenoid	yes
2-C-methyl-D-erythritol 4-	513	92	100	35881	Isoprenoid	no
3-hydroxy-3-methylglutaryl	1411	313	100	63352	Isoprenoid	yes
3-hydroxy-3-methylglutaryl	731	145	100	50029	Isoprenoid	no
4-hydroxy-3-methylbut-2-en-1-	1737	121	100	46398	Isoprenoid	yes
Diphosphomevalonate	689	140	100	50403	Isoprenoid	yes
Isopentenyl-diphosphate delta-	869	98	100	34848	Isoprenoid	yes
Mevalonate kinase	878	162	100	44769	Isoprenoid	yes
Phosphomevalonate kinase	800	161	100	52543	Isoprenoid	yes
Transferase FPPS1	340	75	100	39266	Isoprenoid	yes
Transferase FPPS2	424	96	99	39162	Isoprenoid	yes
Transferase GPPS large subunit	606	131	100	42738	Isoprenoid	yes
Transferase GPPS small subunit	361	69	100	36249	Isoprenoid	yes
Transferase GPPS small	194	51	100	31157	Isoprenoid	yes
Acetyl-coenzyme A carboxylase	649	119	99	56437	Lipid	no
Acetyl-coenzyme A carboxylase	140	50	47	56204	Lipid	yes
Delta 12 desaturase	328	72	95	44611	Lipid	no
Delta 15 desaturase	229	48	99	46061	Lipid	no
Non-specific lipid-transfer	376	22	87	9038	Lipid	yes
4-coumarate:CoA ligase	929	189	98	60351	Phenylpropanoi	yes
Naringenin-chalcone synthase	679	101	100	42720	Phenylpropanoi	no
Phenylalanine ammonia-lyase	958	185	98	76959	Phenylpropanoi	yes
Chloroplast envelope membrane	298	62	100	27370	Photosynthesis	no
Cytochrome b559 subunit alpha	444	30	100	9387	Photosynthesis	yes
Cytochrome b559 subunit beta	52	12	100	4424	Photosynthesis	no
Cytochrome b6	382	84	100	26282	Photosynthesis	no
Cytochrome b6-f complex	443	69	100	18975	Photosynthesis	no
Cytochrome b6-f complex	60	10	81	4170	Photosynthesis	no
Cytochrome b6-f complex	122	17	100	3301	Photosynthesis	no
Cytochrome b6-f complex	147	27	100	3388	Photosynthesis	no
Cytochrome f	727	87	99	35269	Photosynthesis	yes
envelope membrane protein,	24	8	34	27332	Photosynthesis	no
NAD(P)H-quinone	1049	227	100	56235	Photosynthesis	no
NAD(P)H-quinone	172	28	75	56522	Photosynthesis	no
NAD(P)H-quinone	13	4	29	13756	Photosynthesis	no
NAD(P)H-quinone	14	5	27	11145	Photosynthesis	no
NAD(P)H-quinone	1950	414	99	86098	Photosynthesis	yes
NAD(P)H-quinone	23	8	88	19363	Photosynthesis	no
NAD(P)H-quinone	29	8	31	19977	Photosynthesis	yes
NAD(P)H-quinone	2	1	6	18723	Photosynthesis	no
NAD(P)H-quinone	32	7	26	25579	Photosynthesis	yes
NADH dehydrogenase subunit	214	48	95	19407	Photosynthesis	no
NADH-quinone oxidoreductase	150	26	100	19995	Photosynthesis	no
Photosystem I assembly protein	170	41	100	19730	Photosynthesis	no
Photosystem I assembly protein	223	50	95	21438	Photosynthesis	yes
Photosystem I iron-sulfur center	757	23	100	9038	Photosynthesis	yes

- 152 -

Protein annotation	Protein score	Number of peptides	Coverage	MW (Da)	Pathway	Seen in Table 4
Photosystem I P700 chlorophyll	820	140	100	83138	Photosynthesis	yes
Photosystem I P700 chlorophyll	860	125	100	82402	Photosynthesis	yes
Photosystem I reaction center	115	19	100	4973	Photosynthesis	no
Photosystem I reaction center	98	21	100	4011	Photosynthesis	no
Photosystem II CP43 reaction	1356	136	100	51848	Photosynthesis	yes
Photosystem II CP47 reaction	1437	119	96	56013	Photosynthesis	yes
Photosystem II phosphoprotein	11	4	100	2762	Photosynthesis	no
Photosystem II protein D1	446	68	97	38979	Photosynthesis	yes
Photosystem II protein D2	623	72	99	39580	Photosynthesis	yes
Photosystem II reaction center	258	43	100	7650	Photosynthesis	no
Photosystem II reaction center	51	12	75	4168	Photosynthesis	no
Photosystem II reaction center	49	11	90	4131	Photosynthesis	no
Photosystem II reaction center	39	8	77	6862	Photosynthesis	no
Photosystem II reaction center	84	10	100	4497	Photosynthesis	no
Photosystem II reaction center	60	11	100	3756	Photosynthesis	no
Photosystem II reaction center	103	28	100	4165	Photosynthesis	no
Photosystem II reaction center	62	13	97	6497	Photosynthesis	no
Protein PsbN	131	25	100	4722	Photosynthesis	no
Ribulose biphosphate	15356	749	99	52797	Photosynthesis	yes
Small auxin up regulated	7731	1811	100	20806	Phytohormone	yes
30S ribosomal protein S11	180	38	99	14940	Protein	no
30S ribosomal protein S12	17	5	17	13893	Protein	no
30S ribosomal protein S12,	268	65	94	14656	Protein	yes
30S ribosomal protein S14	103	21	85	11717	Protein	no
30S ribosomal protein S14,	80	11	49	11727	Protein	yes
30S ribosomal protein S15	25	8	48	10839	Protein	no
30S ribosomal protein S15,	338	44	100	10867	Protein	yes
30S ribosomal protein S16,	459	52	79	10413	Protein	no
30S ribosomal protein S18	149	32	100	12010	Protein	no
30S ribosomal protein S19	21	8	32	10543	Protein	no
30S ribosomal protein S19,	94	18	95	10511	Protein	no
30S ribosomal protein S2	220	54	100	26726	Protein	no
30S ribosomal protein S2,	17	3	11	26769	Protein	no
30S ribosomal protein S3,	371	86	96	24961	Protein	yes
30S ribosomal protein S4	305	54	96	23628	Protein	no
30S ribosomal protein S4,	86	18	89	23651	Protein	yes
30S ribosomal protein S7,	20	5	31	17403	Protein	no
30S ribosomal protein S8	524	71	100	15469	Protein	no
30S ribosomal protein S8,	113	22	49	15582	Protein	yes
50S ribosomal protein L16	42	13	19	15357	Protein	no
50S ribosomal protein L16,	182	31	100	13312	Protein	yes
50S ribosomal protein L2	65	15	23	29880	Protein	no
50S ribosomal protein L2,	507	72	94	29981	Protein	no
50S ribosomal protein L20	81	24	98	14602	Protein	yes
50S ribosomal protein L20,	7	3	13	14554	Protein	yes
50S ribosomal protein L22	192	47	100	14768	Protein	no
50S ribosomal protein L22,	69	17	99	15178	Protein	no
50S ribosomal protein L23	156	47	100	10719	Protein	no
50S ribosomal protein L32	58	18	100	6078	Protein	no
50S ribosomal protein L33	26	5	74	7687	Protein	no
50S ribosomal protein L36	33	8	84	4460	Protein	no
ATP-dependent Clp protease	326	68	99	21936	Protein	no
Protein TIC 214	2063	481	100	22545	Protein	yes
Ribosomal protein L10	232	47	90	17514	Protein	no
Ribosomal protein L14	157	26	100	13565	Protein	yes

- 153 -

Protein annotation	Protein score	Number of peptides	Coverage	MW (Da)	Pathway	Seen in Table 4
Ribosomal protein L16	214	43	100	16078	Protein	no
Ribosomal protein L2	291	79	98	37499	Protein	yes
Ribosomal protein L32	1	1	100	6078	Protein	no
Ribosomal protein L5	232	48	99	21072	Protein	no
Ribosomal protein S10	125	30	100	14102	Protein	no
Ribosomal protein S12	112	22	99	14193	Protein	yes
Ribosomal protein S13	121	21	99	13563	Protein	yes
Ribosomal protein S16	22	6	38	8530	Protein	no
Ribosomal protein S19	33	15	97	11106	Protein	yes
Ribosomal protein S3	665	165	99	63062	Protein	yes
Ribosomal protein S4	296	79	100	41622	Protein	yes
Ribosomal protein S7	386	72	97	17440	Protein	yes
Small ubiquitin-related modifier	78	11	100	8734	Protein	yes
7S vicilin-like protein	783	183	100	55890	Seed	yes
Edestin 1	276	65	100	58523	Seed	yes
Edestin 2	426	92	100	55986	Seed	no
Edestin 3	522	114	99	56080	Seed	no
(-)-limonene synthase,	1013	180	100	72385	Terpenoid	yes
(+)-alpha-pinene synthase,	706	172	100	71842	Terpenoid	no
1-deoxy-D-xylulose-5-phosphate	1918	334	100	78767	Terpenoid	yes
2-acetylphloroglucinol 4-	526	129	97	45481	Terpenoid	no
4-(cytidine 5'-diphospho)-2-C-	412	90	100	45086	Terpenoid	yes
4-hydroxy-3-methylbut-2-en-1-	2259	277	100	82920	Terpenoid	yes
Terpene synthase	6717	1432	98	75307	Terpenoid	yes
DNA-directed RNA polymerase	404	82	98	39004	Transcription	no
DNA-directed RNA polymerase	5129	1080	100	12089	Transcription	yes
Maturase K	1198	253	100	60623	Transcription	yes
Maturase R	737	164	100	72891	Transcription	yes
RNA polymerase beta subunit	27	8	92	14495	Transcription	no
RNA polymerase C	11	3	25	17867	Transcription	no
Acyl-activating enzyme 1	773	156	100	79715	Unknown	yes
Acyl-activating enzyme 10	783	157	99	61538	Unknown	yes
Acyl-activating enzyme 11	330	62	98	36708	Unknown	no
Acyl-activating enzyme 12	1070	198	100	83743	Unknown	yes
Acyl-activating enzyme 13	877	170	100	78902	Unknown	yes
Acyl-activating enzyme 14	154	32	87	80353	Unknown	no
Acyl-activating enzyme 15	924	200	100	86725	Unknown	no
Acyl-activating enzyme 2	920	177	100	74107	Unknown	yes
Acyl-activating enzyme 3	896	182	99	59500	Unknown	yes
Acyl-activating enzyme 4	970	186	100	80008	Unknown	yes
Acyl-activating enzyme 5	916	192	100	63333	Unknown	yes
Acyl-activating enzyme 6	722	159	100	62313	Unknown	yes
Acyl-activating enzyme 7	781	156	100	66590	Unknown	no
Acyl-activating enzyme 8	647	135	100	56197	Unknown	yes
Acyl-activating enzyme 9	723	150	100	61501	Unknown	no
Albumin	126	25	86	16742	Unknown	no
Cannabidiolic acid synthase-like	575	109	98	62390	Unknown	no
Cannabidiolic acid synthase-like	77	19	76	62296	Unknown	yes
Chalcone isomerase-like protein	729	155	100	23715	Unknown	no
Chalcone synthase-like protein 1	579	129	100	43175	Unknown	no
Inactive tetrahydrocannabinolic	307	55	83	61990	Unknown	no
Prenyltransferase 1	513	107	97	44500	Unknown	no
Prenyltransferase 2	241	58	87	45105	Unknown	no
Prenyltransferase 3	406	79	99	45147	Unknown	no
Prenyltransferase 4	332	88	99	44928	Unknown	no

- 154 -

Protein annotation	Protein score	Number of peptides	Coverage	MW (Da)	Pathway	Seen in Table 4
Prenyltransferase 5	540	108	98	42610	Unknown	no
Prenyltransferase 6	569	107	95	44392	Unknown	no
Prenyltransferase 7	498	99	98	44753	Unknown	no
Protein Ycf2	3168	643	99	27118	Unknown	yes
Putative calcium dependent	37	12	100	8116	Unknown	no
Putative LOV domain-	4899	1081	99	11838	Unknown	yes
Putative LysM domain	635	143	100	66028	Unknown	yes
Putative permease	64	14	100	10243	unknown	no
Putative rac-GTP binding	135	24	100	7145	unknown	no
Transport membrane protein	326	63	100	32085	Unknown	no
Uncharacterized protein	46	11	100	4657	Unknown	no
Uncharacterized protein	1	1	9	20410	Unknown	no
Uncharacterized protein	727	161	53	18318	Unknown	yes

[0283] The MW of these cannabis proteins average 38 ± 34 kDa, ranging from 2.8 kDa (Photosystem II phosphoprotein) to 271.2 kDa (Protein Ycf2). The AA sequence coverage varies from 6% (NAD(P)H-quinone oxidoreductase subunit J, chloroplastic) to 100% (108 out of 229 identities, 47%). The vast majority of the proteins (187/229, 82%) display a sequence coverage greater than 80%. These data demonstrate that using proteases asdic from trypsin, either on their own or in combination, further improves the identification of more proteins with greater confidence.

[0284] The 494 cannabis protein accessions are predominantly involved in cannabis secondary metabolism (23%), energy production (31%) including 18% of photosynthetic proteins, and gene expression (19%), in particular protein metabolism (14%) (Figure 28). Ten percent of the proteins are of unknown function, including Cannabidiolic acid synthase-like 1 and 2 which display 84% similarity with CBDA synthase. Most of the additional functions belong to the energy/photosynthesis pathway, translation mechanisms with many ribosomal proteins identified here (Table 18), as well as a plethora (14.4%, 71 out of 494 accessions) of small auxin up regulated (SAUR) proteins. More significantly, all the enzymes involved in the cannabinoid biosynthetic pathway are identified and account for 14.4% of all the accessions (Figure 29). Additional proteins from this pathway are three

- 155 -

truncated products from THCA synthase of 11, 33 and 49 kDa, as well as polyketide synthases 1 to 5 whose AA sequences show 95% similarity to that of OLS. Newly identified proteins include enzymes from the isoprenoid biosynthetic pathway: 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase, 3-hydroxy-3-methylglutaryl coenzyme A synthase and a naringenin-chalcone synthase involved in the biosynthesis of phenylpropanoids. Finally, novel elements of the terpenoid pathway include (+)-alpha-pinene synthase and 2-acylphloroglucinol 4-prenyltransferase found in the chloroplast (Table 18). Together, these data demonstrate that combining different proteases improves recovery and allows for the thorough analysis of the proteins involved in the secondary metabolism of *C. sativa* and the diverse biological mechanisms occurring in the mature buds.

[0285] Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

- 156 -

CLAIMS

1. A method of extracting cannabis-derived proteins from cannabis plant material, the method comprising:
 - (a) suspending cannabis plant material in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution; and
 - (b) separating the solution comprising the cannabis-derived proteins from residual plant material.
2. The method of claim 1, wherein the charged chaotropic agent is selected from the group consisting of guanidine isothiocyanate and guanidine hydrochloride.
3. The method of claim 2, wherein the charged chaotropic agent is guanidine hydrochloride.
4. The method of claim 3, wherein the solution comprises from about 5.5M to about 6.5M guanidine hydrochloride.
5. The method of any one of claims 1 to 4, wherein the solution further comprises a reducing agent.
6. The method of claim 5, wherein the reducing agent is dithiothreitol.
7. The method of claim 6, wherein the solution comprises from about 5mM to about 20mM dithiothreitol (DTT).
8. The method of any one of claims 1 to 7, wherein the cannabis plant material is pre-treated with an organic solvent before step (a) for a period of time to precipitate the cannabis-derived proteins.
9. The method of claim 8, wherein the organic solvent is selected from the group consisting of trichloroacetic acid (TCA)/acetone and TCA/ethanol.
10. The method of claim 9, wherein the organic solvent comprises from about 5% to about 20% TCA/acetone or from about 5% to about 20% TCA/ethanol.
11. The method of any one of claims 1 to 10, wherein the cannabis-derived proteins separated in step (b) are digested by a protease in preparation for proteomic analysis.
12. The method of claim 11, wherein the protease is selected from the group consisting of trypsin, trypsin/LysC, chymotrypsin, GluC and pepsin.

- 157 -

13. The method of claim 11, wherein the cannabis-derived proteins separated by step (b) are digested by two or more proteases.
14. The method of claim 13, wherein the cannabis-derived proteins separated by step (b) are digested by the two or more proteases sequentially.
15. The method of claim 14, wherein the cannabis-derived proteins separated by step (b) are digested by the two or more proteases simultaneously.
16. The method of any one of claims 13 to 15, wherein the protease is selected from the group consisting of trypsin, trypsin/LysC, chymotrypsin, GluC and pepsin.
17. The method of claim 16, wherein the protease is selected from the group consisting of trypsin/LysC, GluC and chymotrypsin.
18. The method of any one of claims 1 to 17, wherein the cannabis-derived proteins separated by step (b) are alkylated in preparation for proteomic analysis.
19. The method of claim 18, wherein the cannabis-derived proteins are alkylated with iodoacetamide (IAA).
20. The method of any one of claims 11 to 19, wherein the proteomic analysis is selected from the group consisting of liquid chromatography-mass spectroscopy (LC-MS), ultra-performance LC-MS (UPLC-MS), and nano liquid chromatography-tandem mass spectrometry (nLC-MS/MS).
21. The method of any one of claims 1 to 20, wherein the cannabis plant material is selected from the group consisting of leaves, stems, roots, apical buds, and trichomes, or parts thereof.
22. The method of claim 21, wherein the plant material comprises apical buds.
23. The method of claim 21 or claim 22, wherein the plant material comprises trichomes.
24. A method of extracting cannabis-derived proteins from cannabis plant material, the method comprising:
 - (a) pre-treating the cannabis plant material with an organic solvent to precipitate the cannabis-derived proteins;
 - (b) suspending the precipitated cannabis-derived proteins of (a) in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution; and

- 158 -

- (c) separating the solution comprising the cannabis-derived proteins from residual plant material.
25. A method of preparing a sample of cannabis-derived proteins from cannabis plant material for proteomic analysis, the method comprising:
- (a) pre-treating the cannabis plant material with an organic solvent to precipitate the cannabis-derived proteins;
 - (b) suspending the precipitated cannabis-derived proteins of (a) in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution;
 - (c) separating the solution comprising the cannabis-derived proteins from residual plant material; and
 - (d) digesting the solution of (c) with a protease.
26. A method of analysing a cannabis plant proteome, the method comprising:
- (a) preparing a sample of cannabis-derived proteins in accordance with method of claim 25; and
 - (b) subjecting the digested solution of step (d) to proteomic analysis.
27. The method of claim 26, wherein the proteomic analysis comprises a parameter setting the maximum number of missed cleavages to between about 2 and about 10.
28. The method of claim 27, wherein the proteomic analysis comprises a parameter setting the maximum number of missed cleavages of between about 6 and about 10.
29. A method of preparing a sample of cannabis-derived proteins from cannabis plant material for proteomic analysis, the method comprising:
- (a) pre-treating the cannabis plant material with an organic solvent to precipitate the cannabis-derived proteins;
 - (b) suspending the precipitated cannabis-derived proteins of (a) in a solution comprising a charged chaotropic agent for a period of time to allow for extraction of cannabis-derived proteins into the solution; and
 - (c) separating the solution comprising the cannabis-derived proteins from residual plant material
30. The method of claim 29, further comprising alkylating the cannabis-derived proteins separated in (c).
31. A method of analysing a cannabis plant proteome, the method comprising:

- 159 -

- (a) preparing a sample of cannabis-derived proteins in accordance with method of claim 29 or claim 30; and
- (b) subjecting the sample to proteomic analysis.

1/35

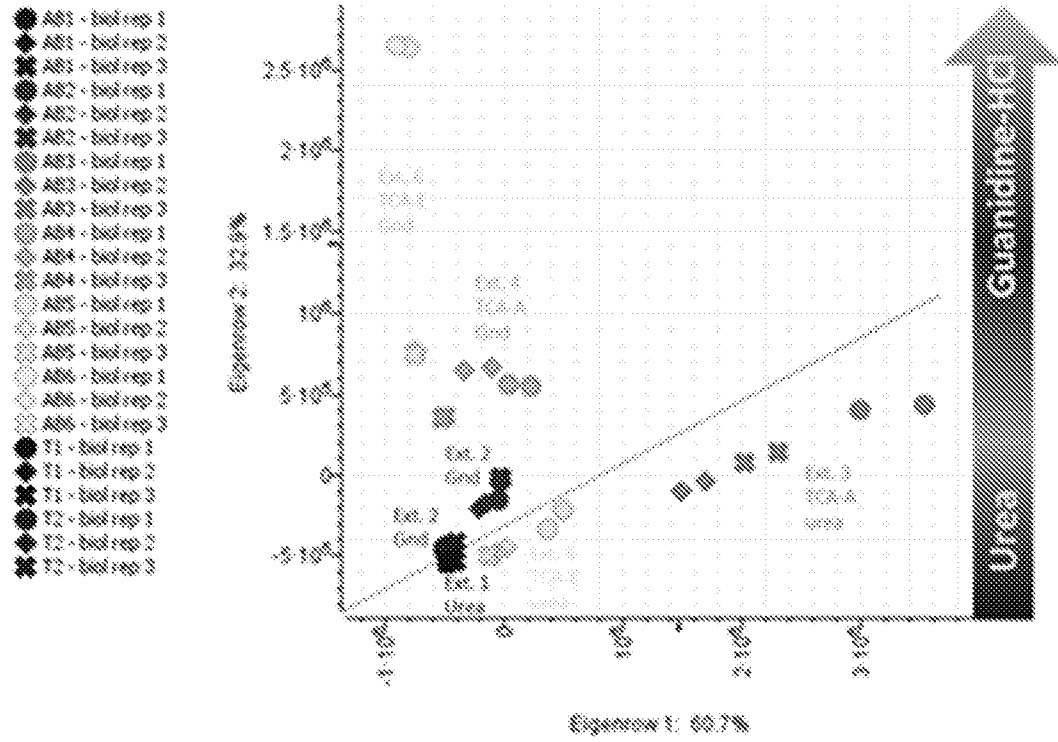
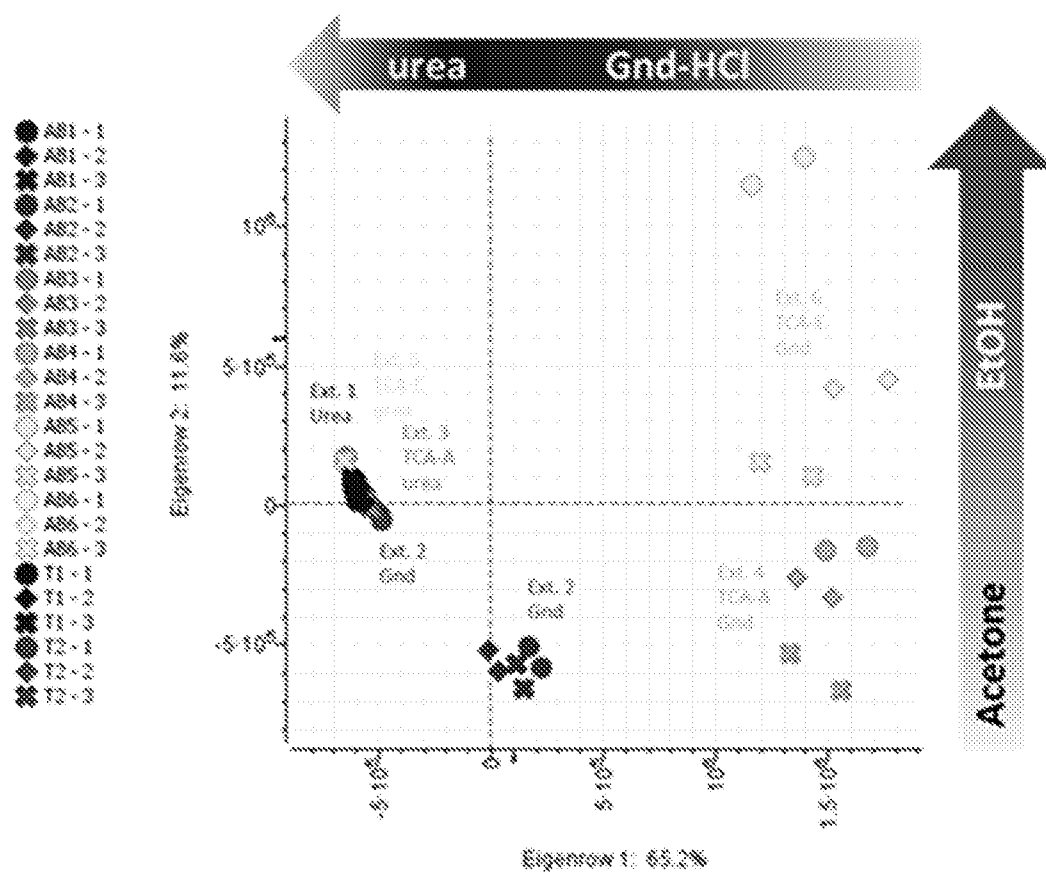
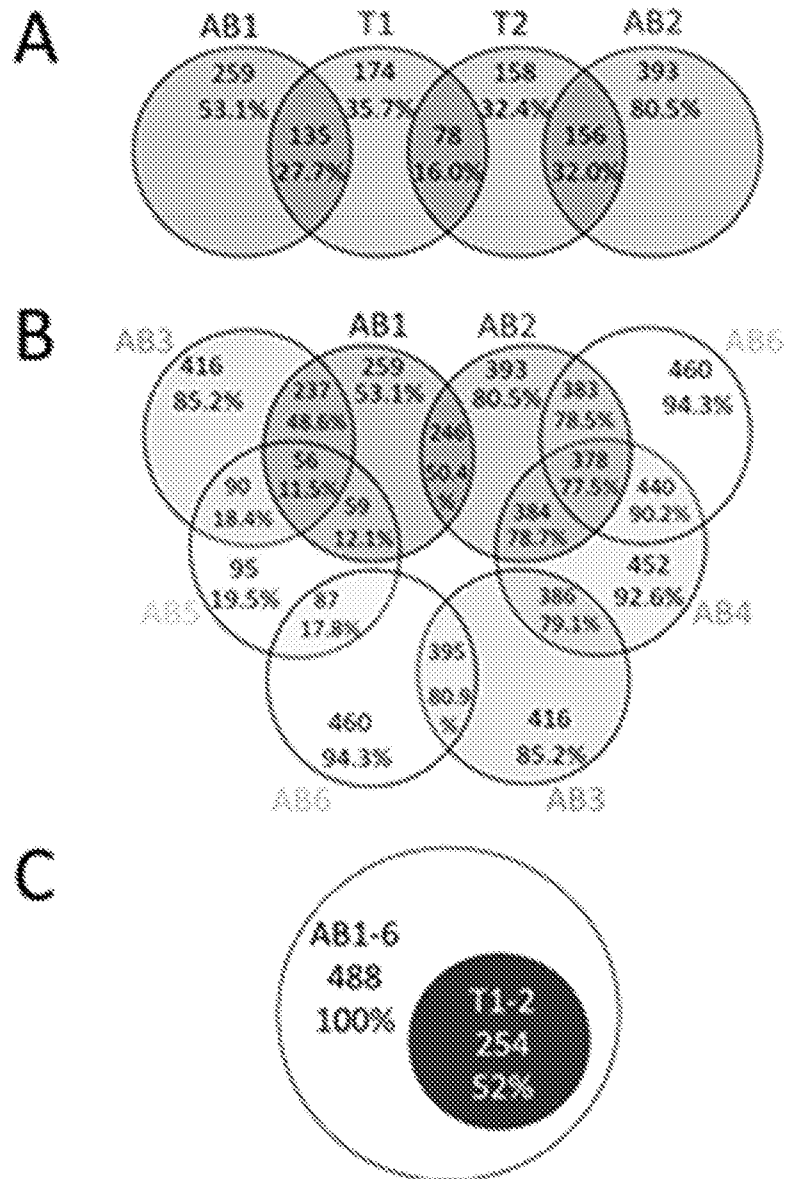
FIGURE 1

FIGURE 2

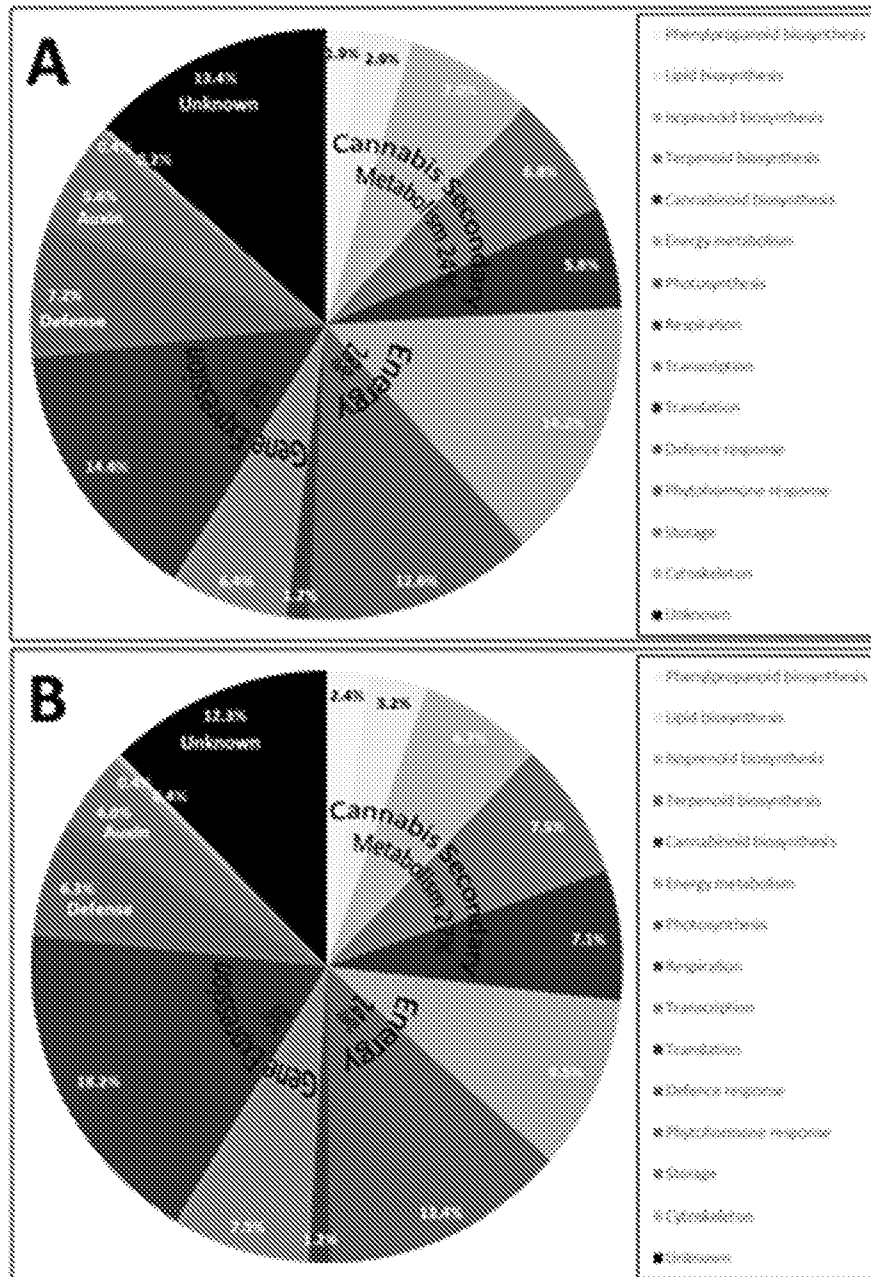


3/35

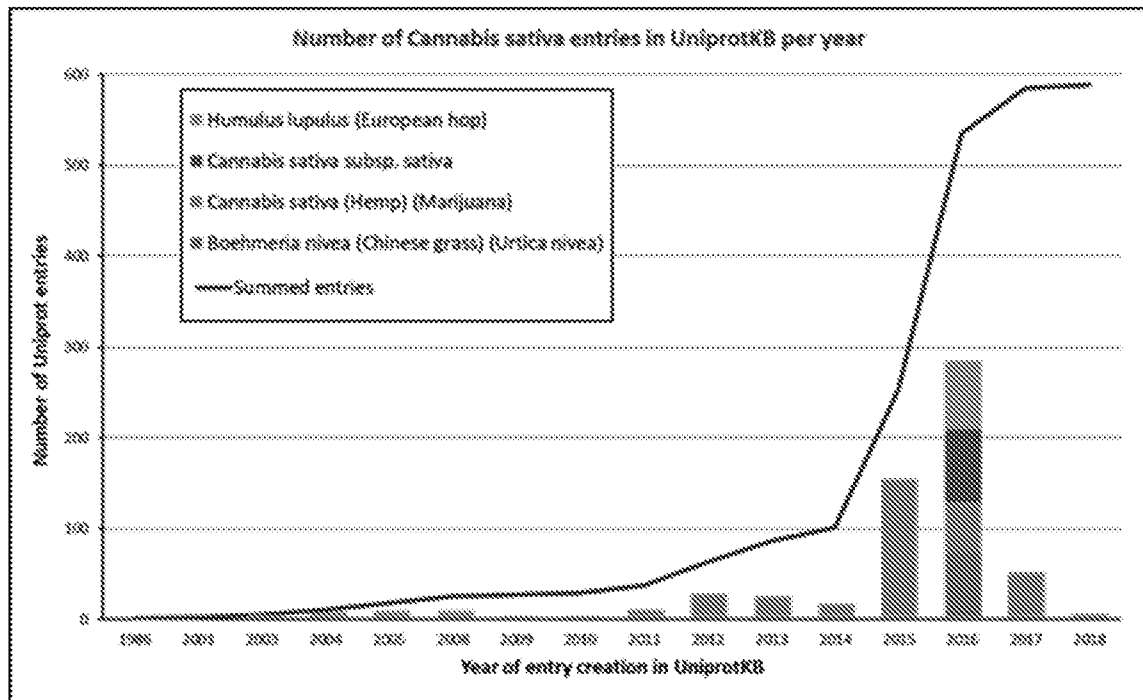
FIGURE 3

4/35

FIGURE 4

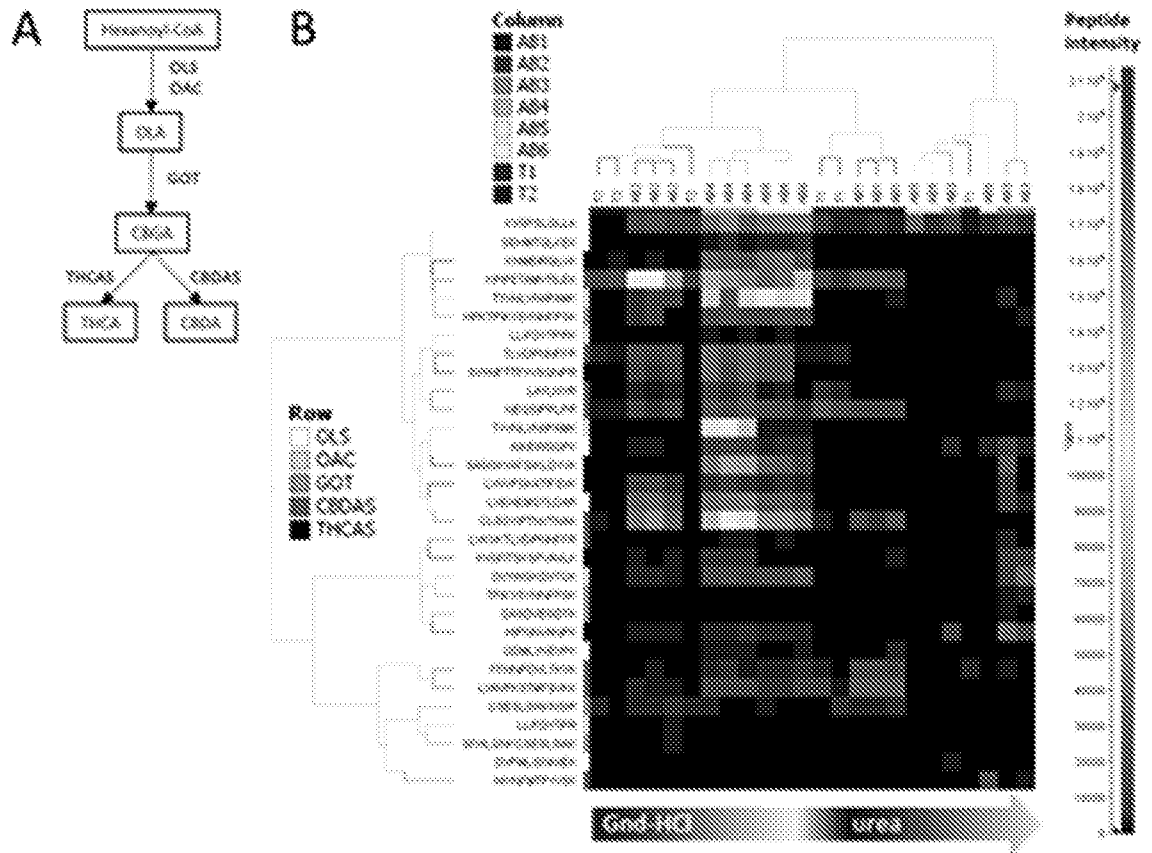


5/35

FIGURE 5

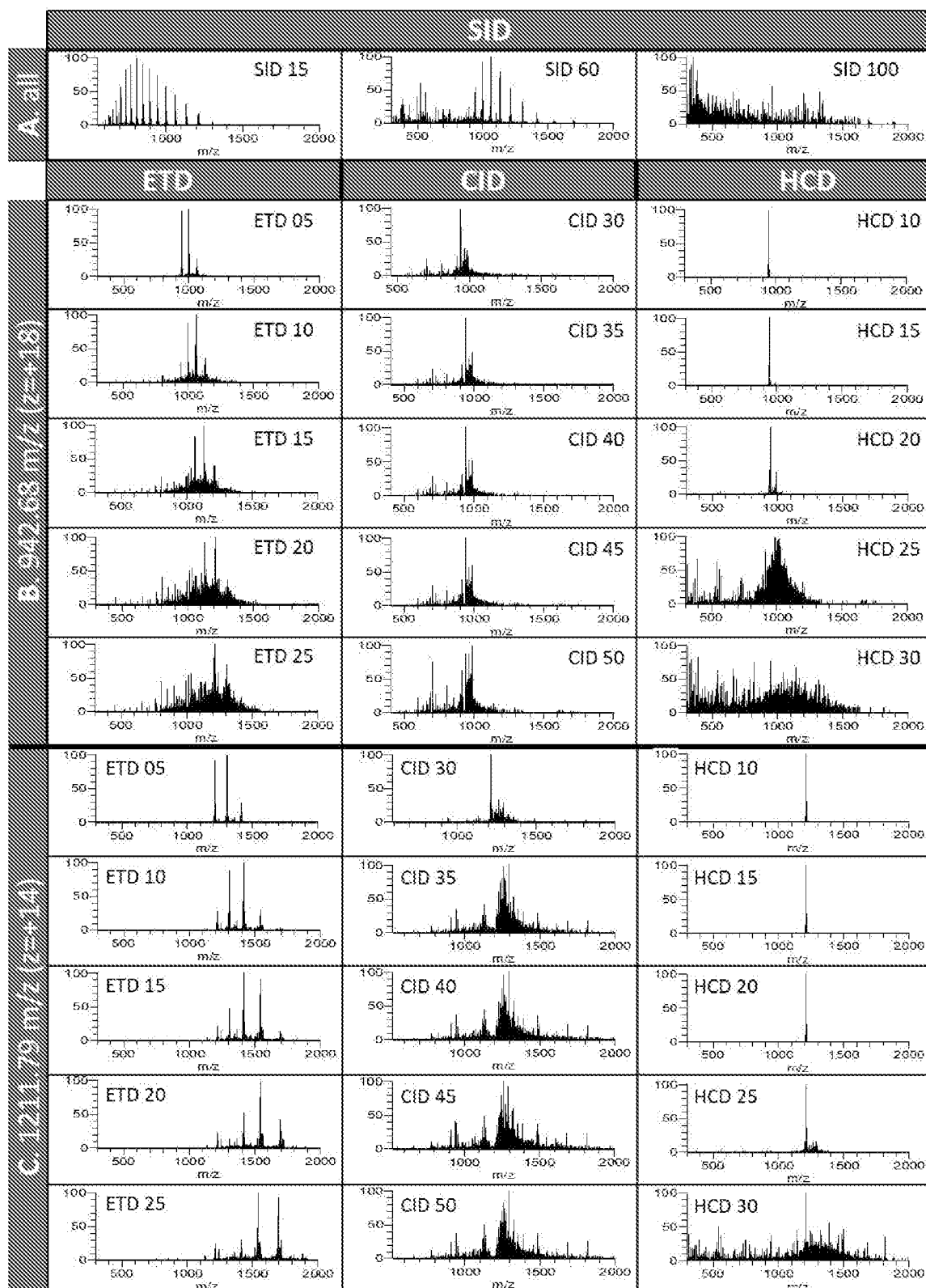
6/35

FIGURE 6



7/35

FIGURE 7



8/35

FIGURE 8

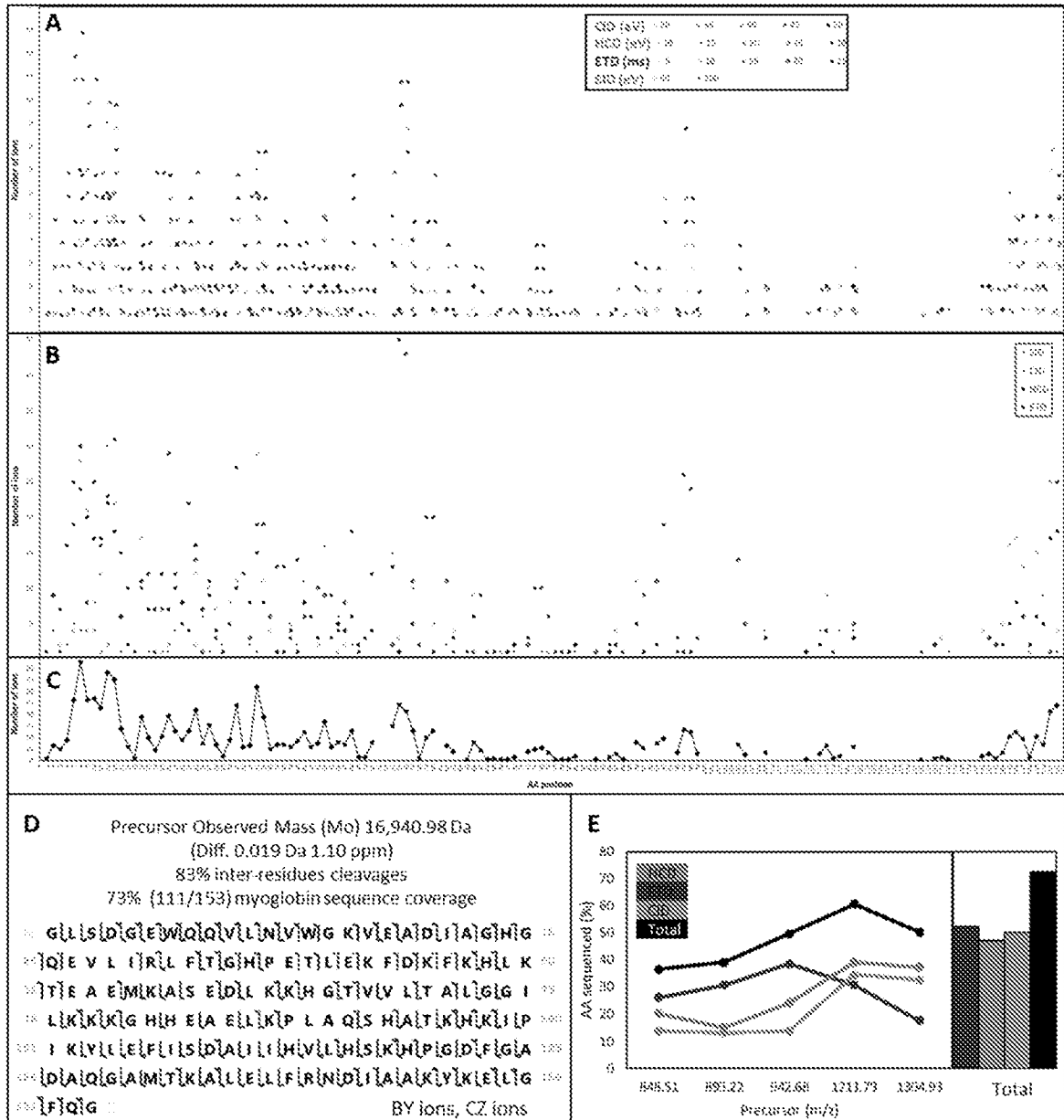
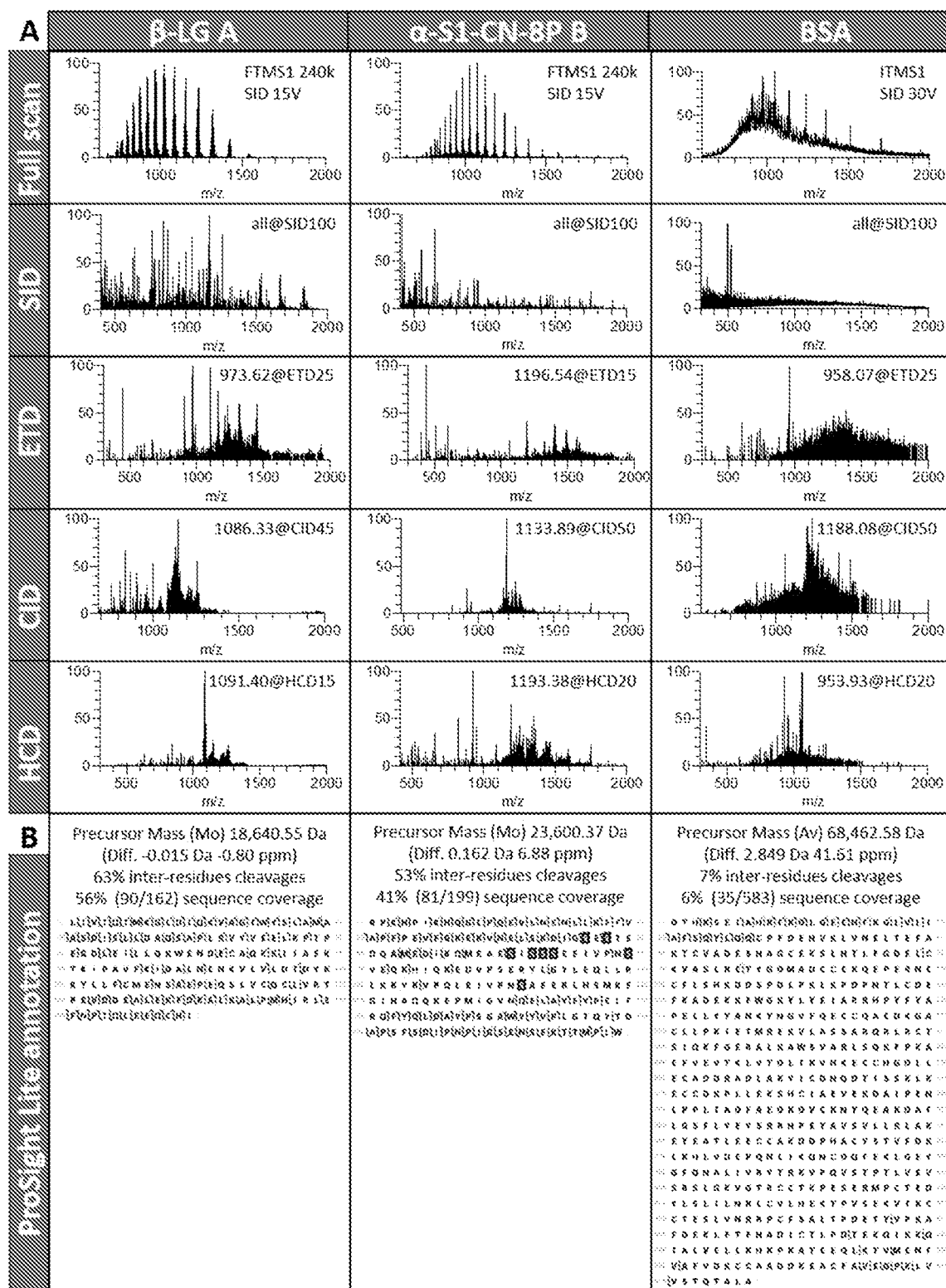
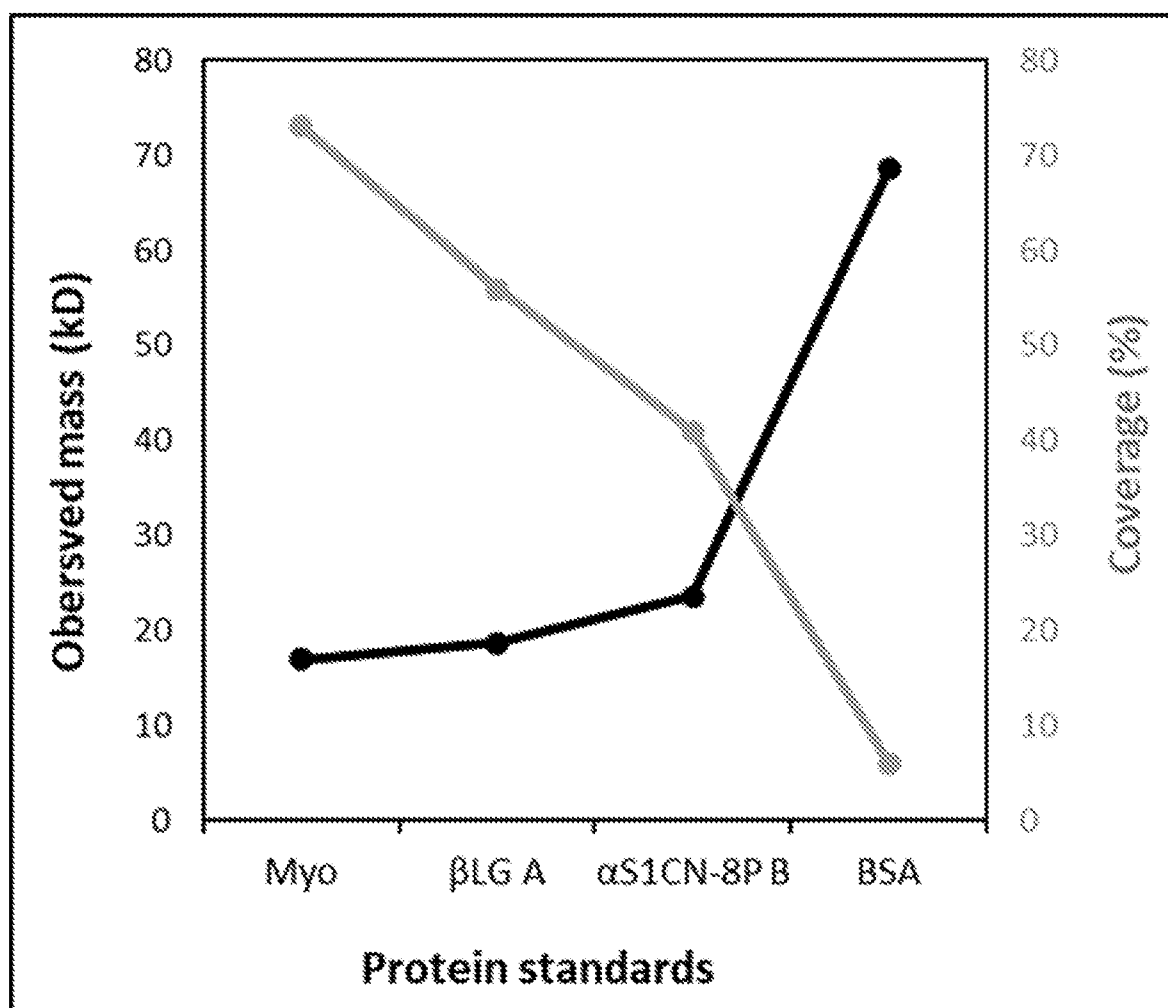


FIGURE 9

FIGURE 9

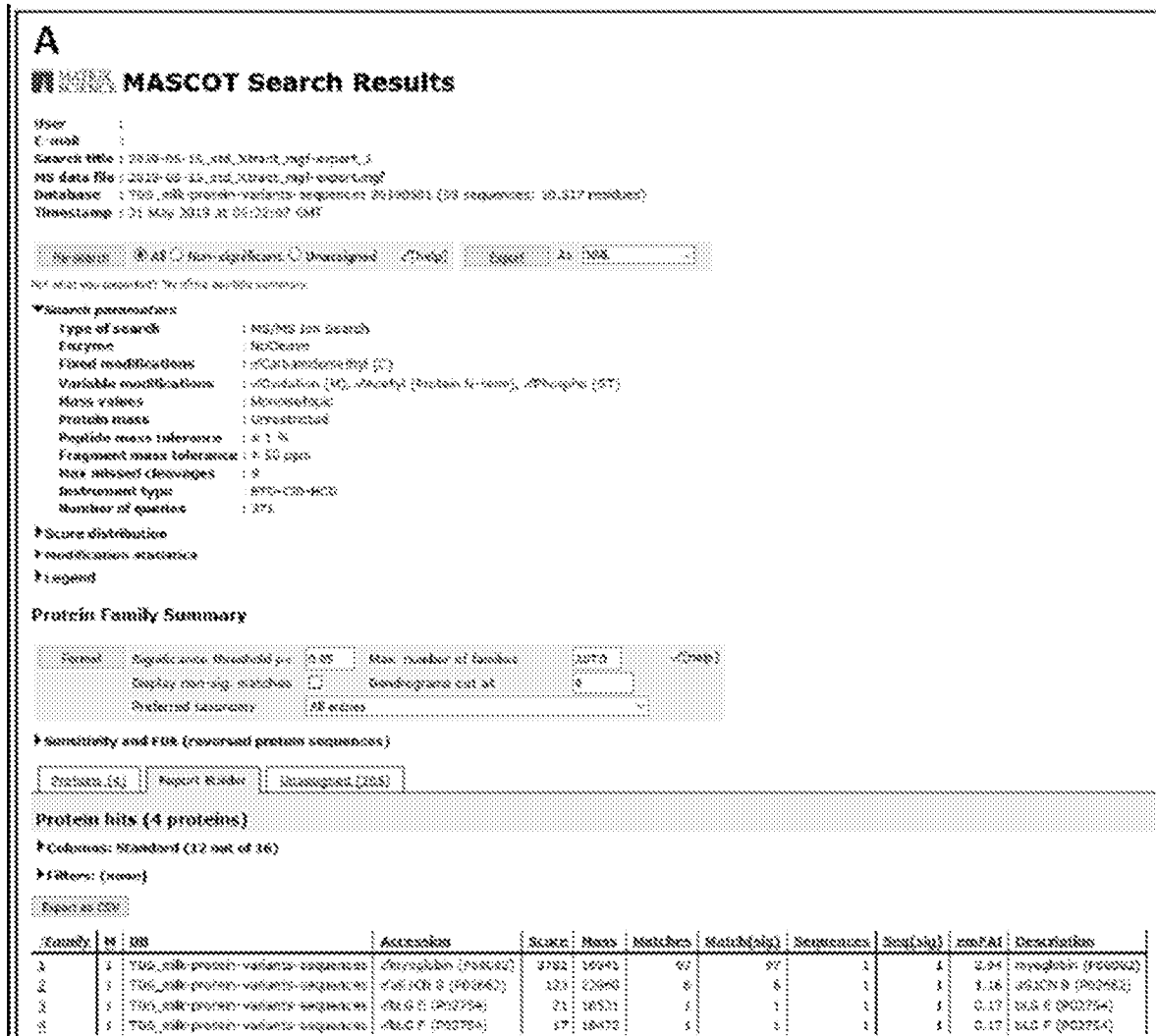


10/35

FIGURE 10

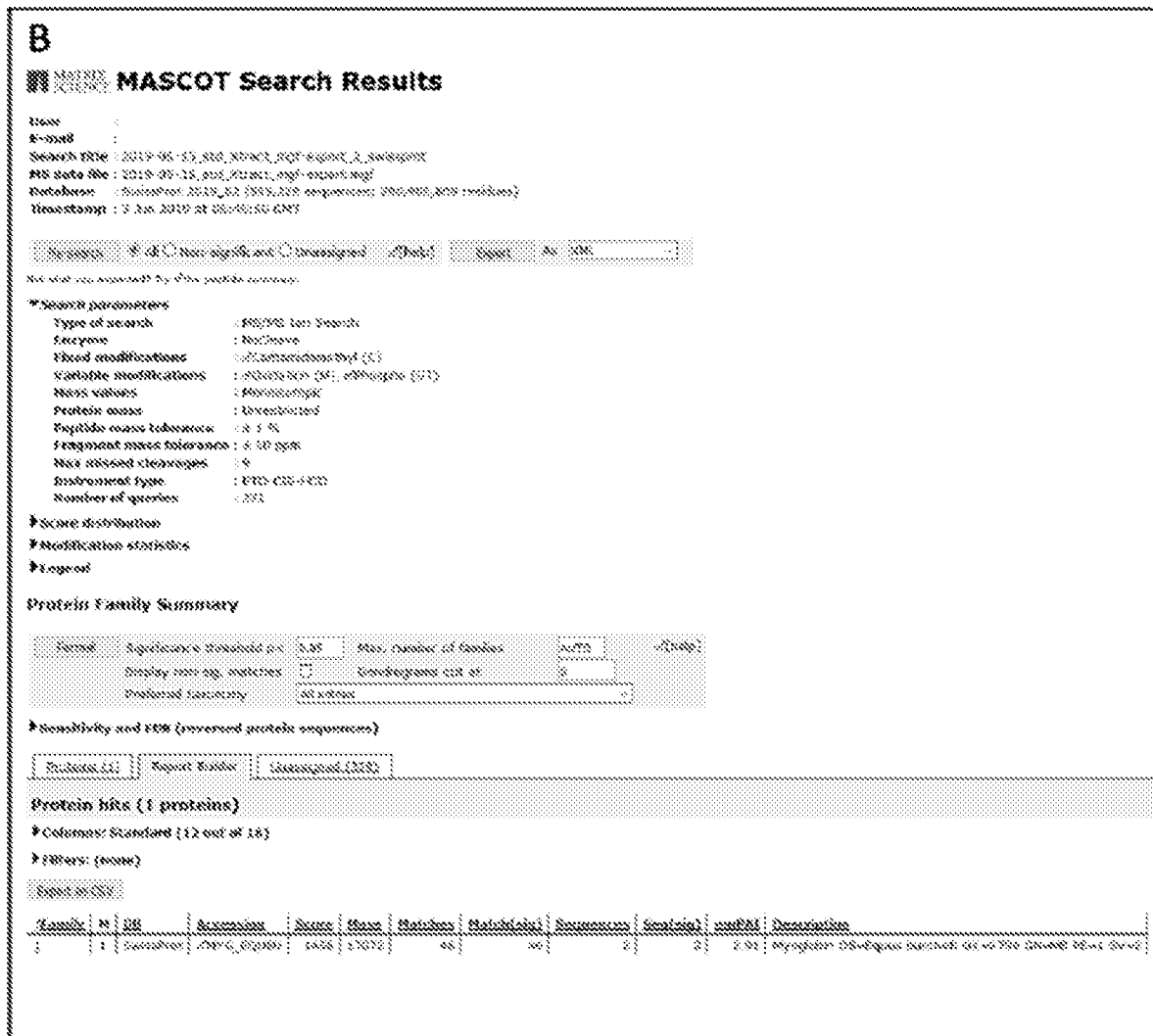
11/35

FIGURE 11



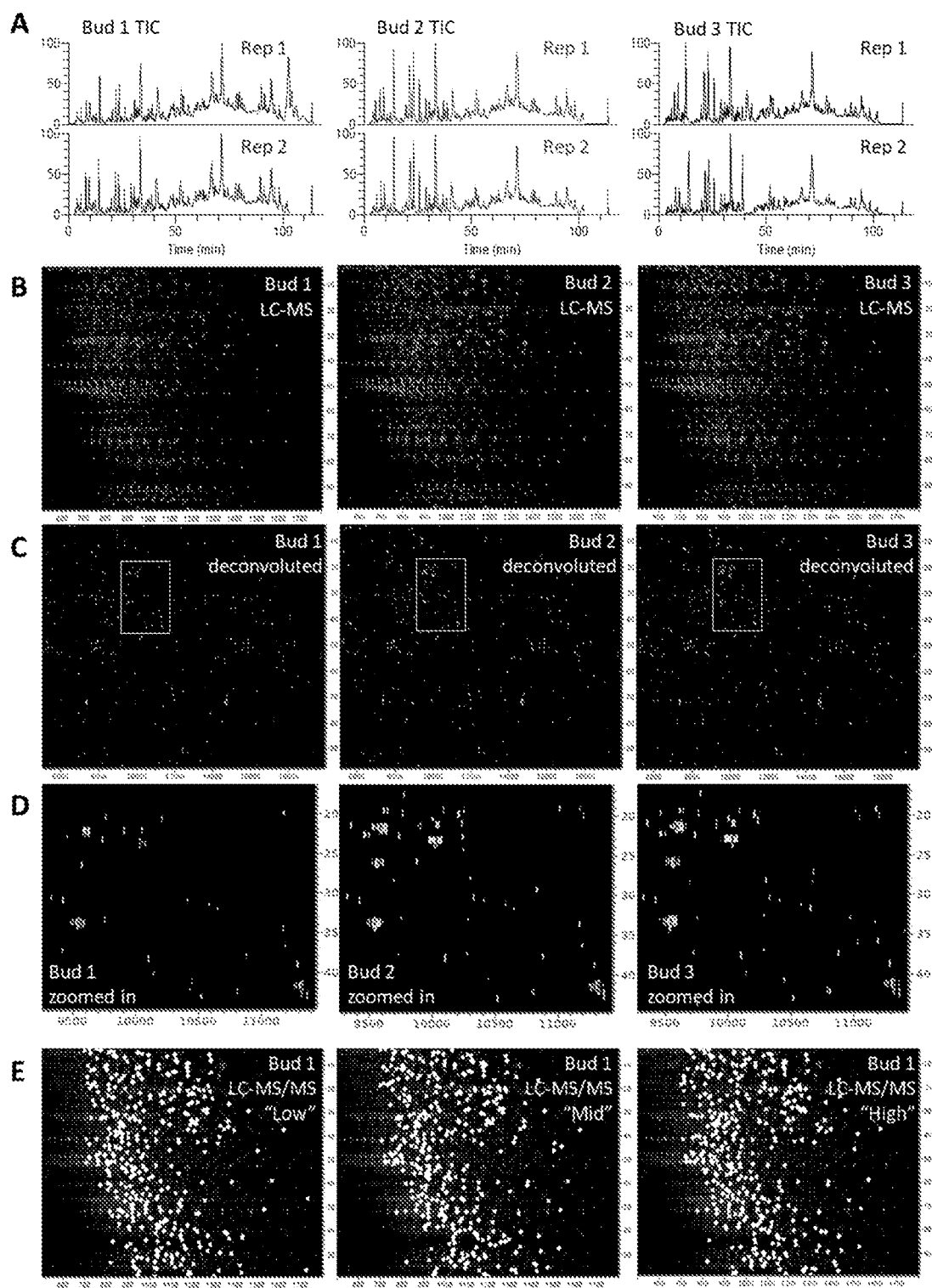
12/35

FIGURE 11 (continued)



13/35

FIGURE 12



14/35

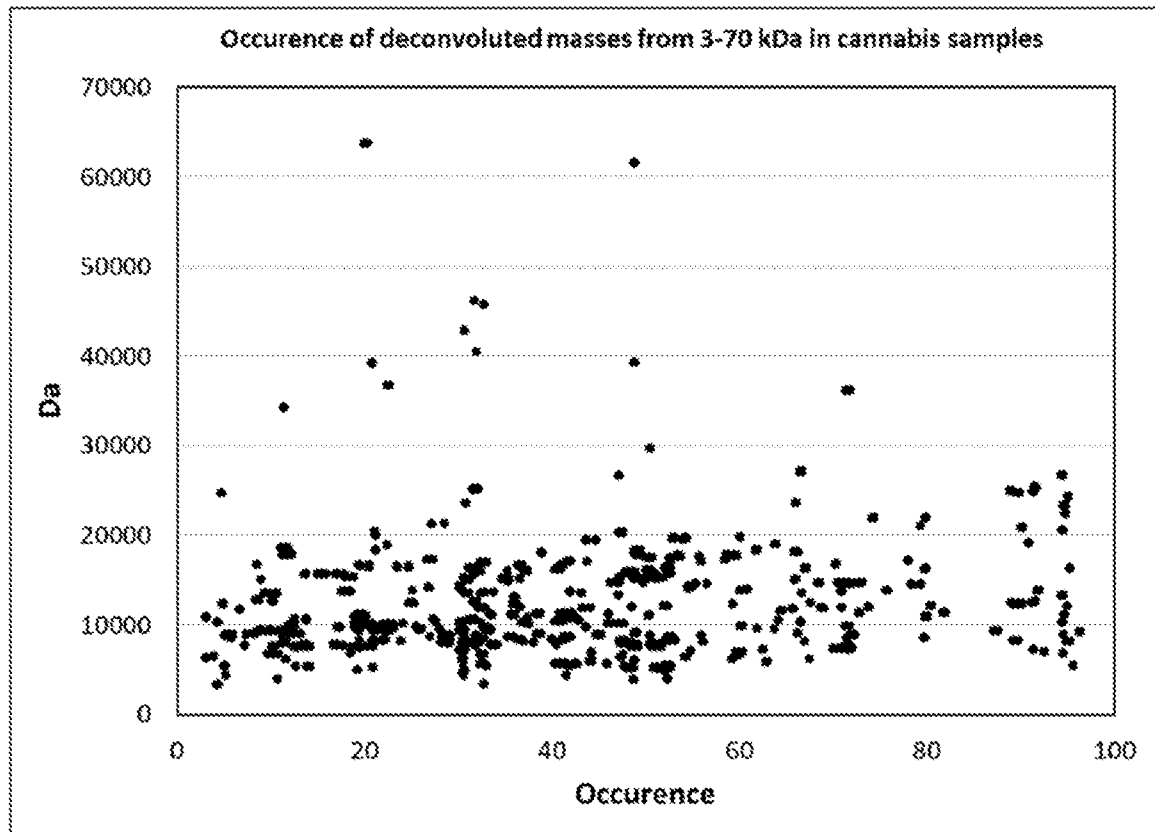
FIGURE 13

FIGURE 14

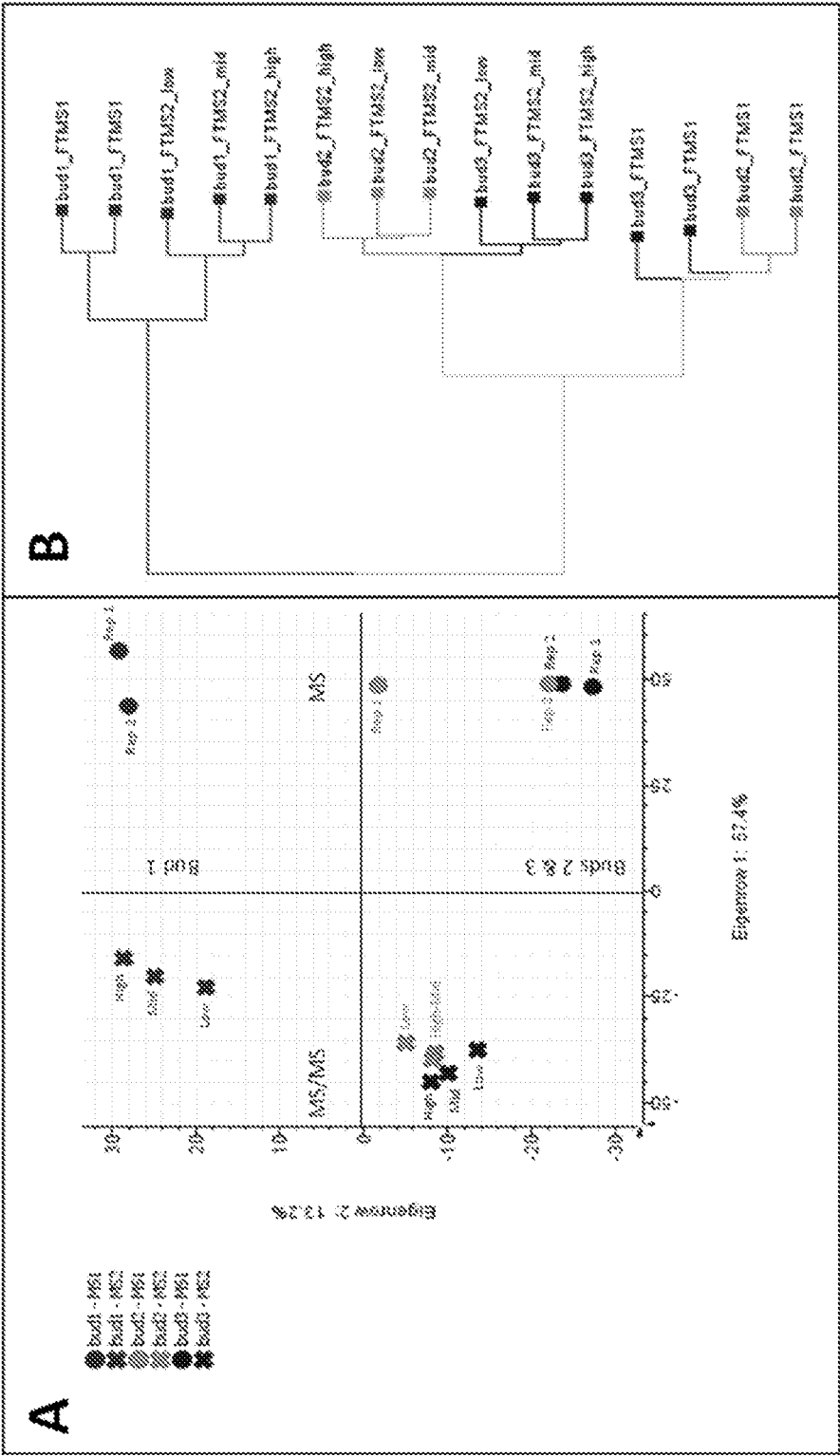
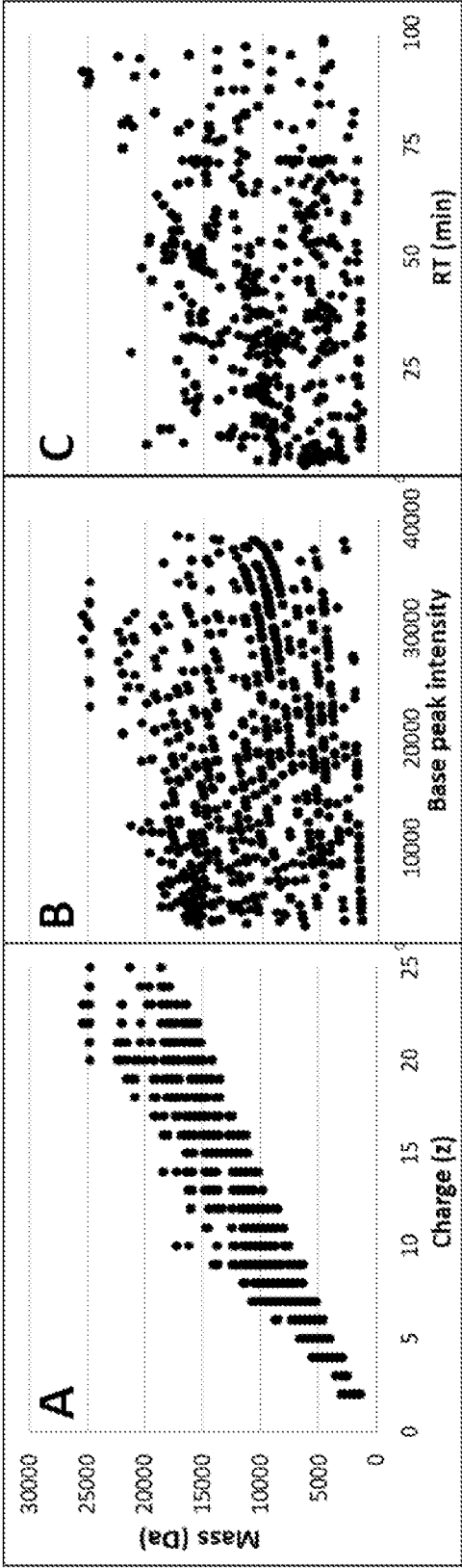
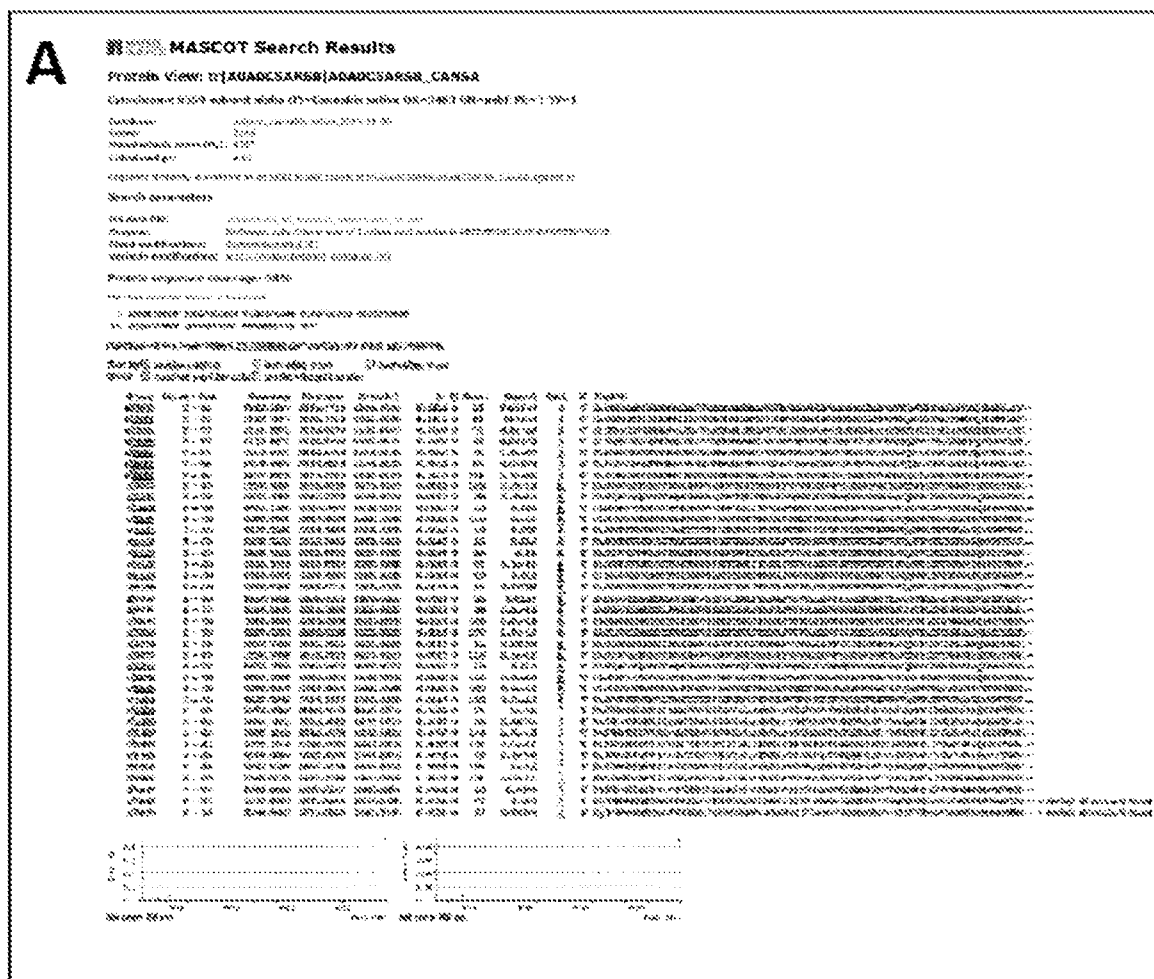
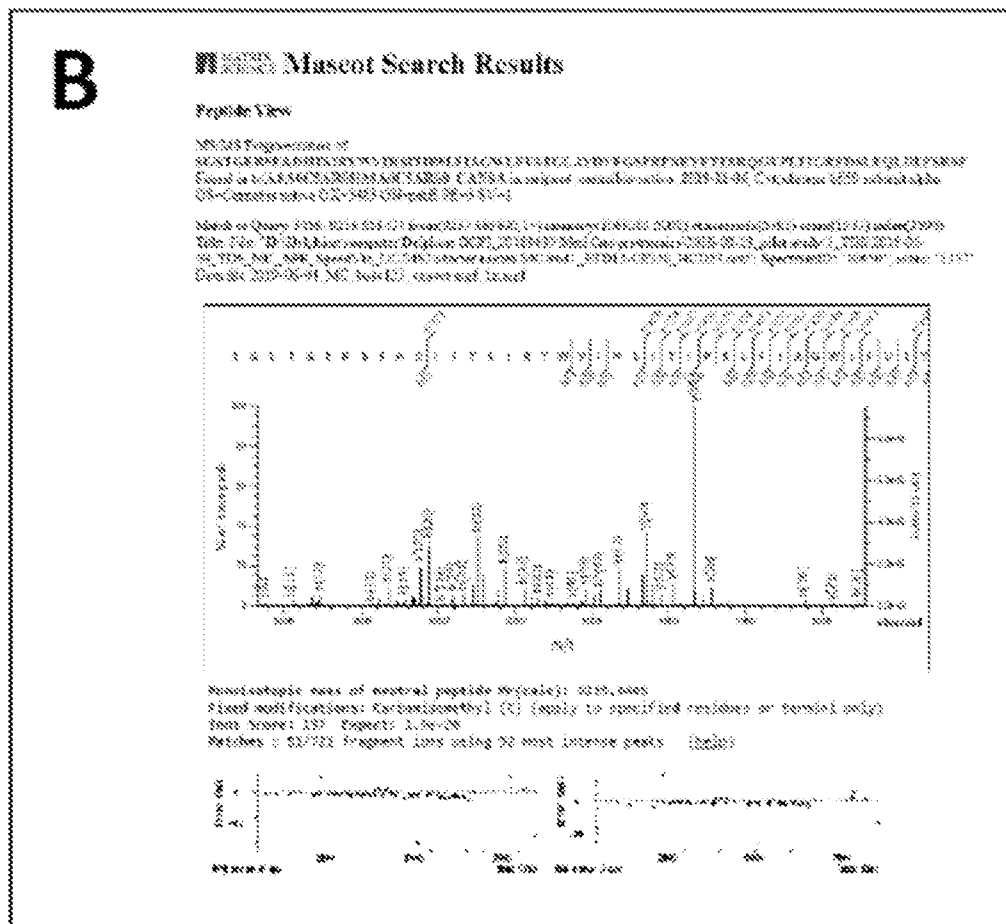


FIGURE 15

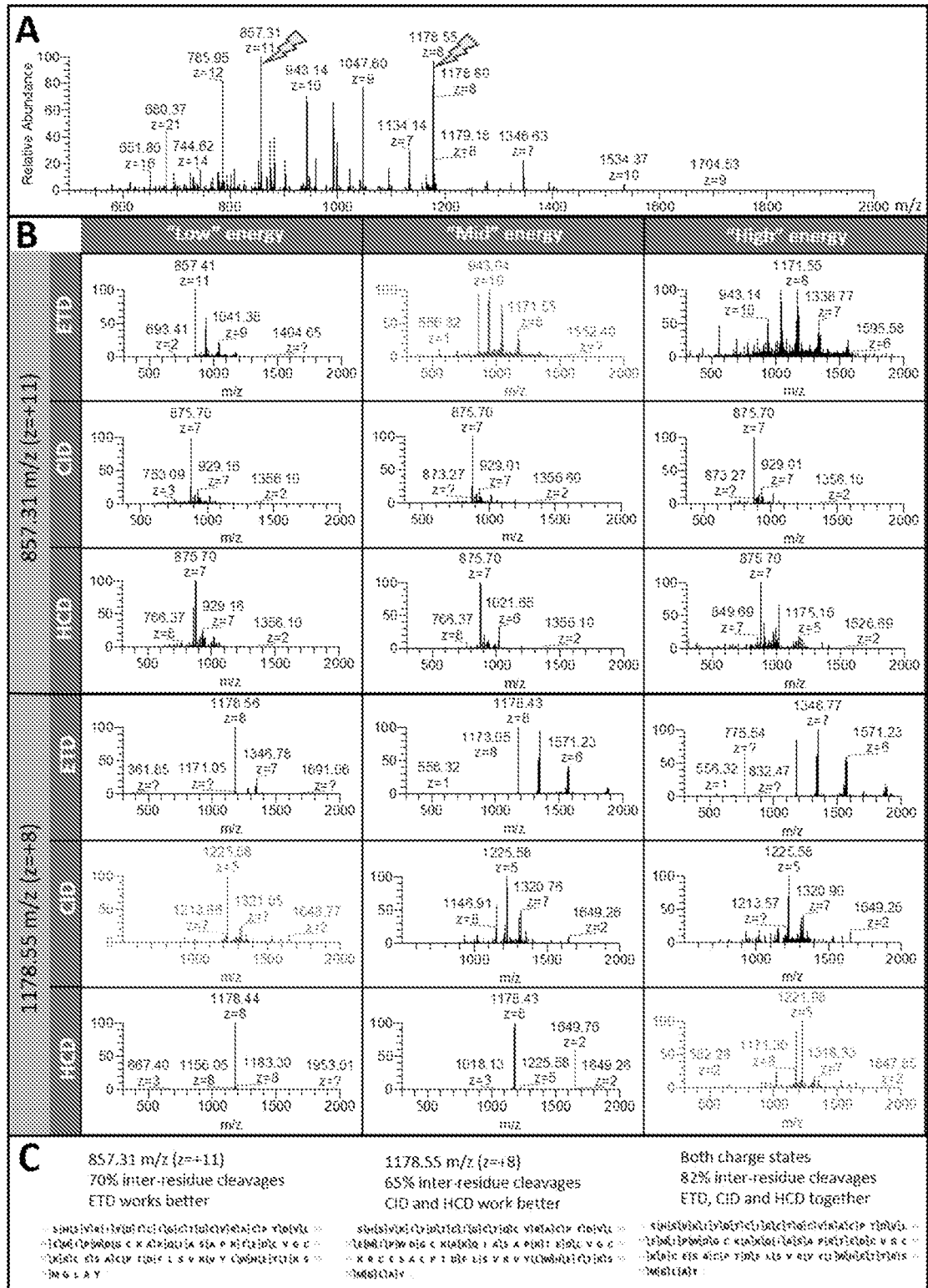






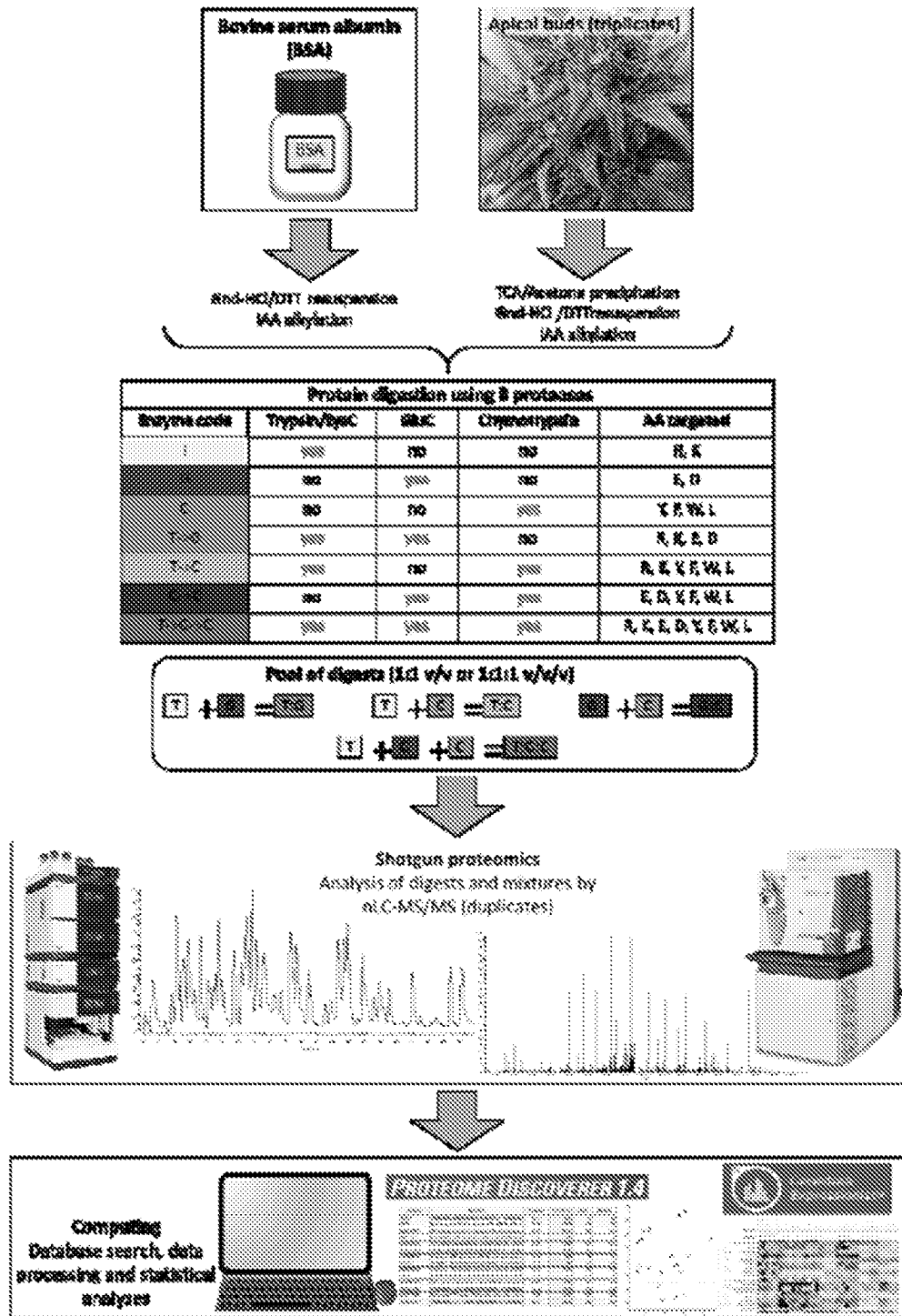
19/35

FIGURE 17



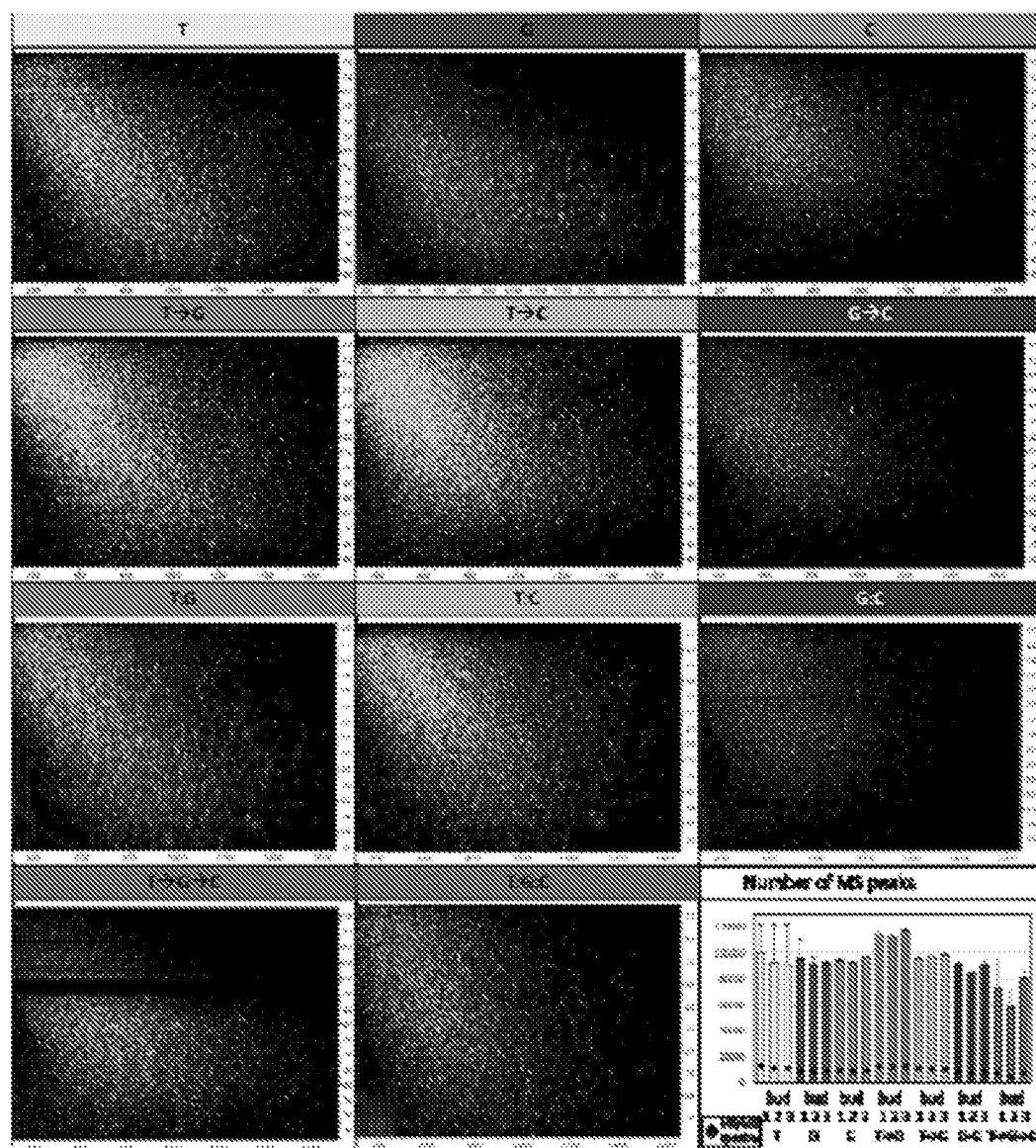
20/35

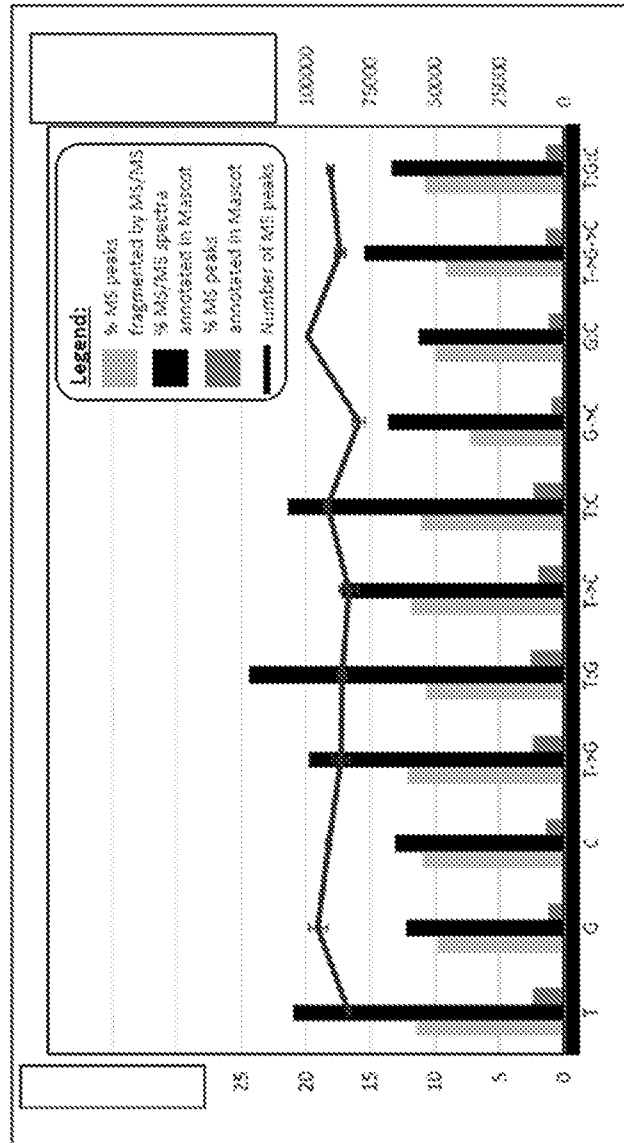
FIGURE 18



21/35

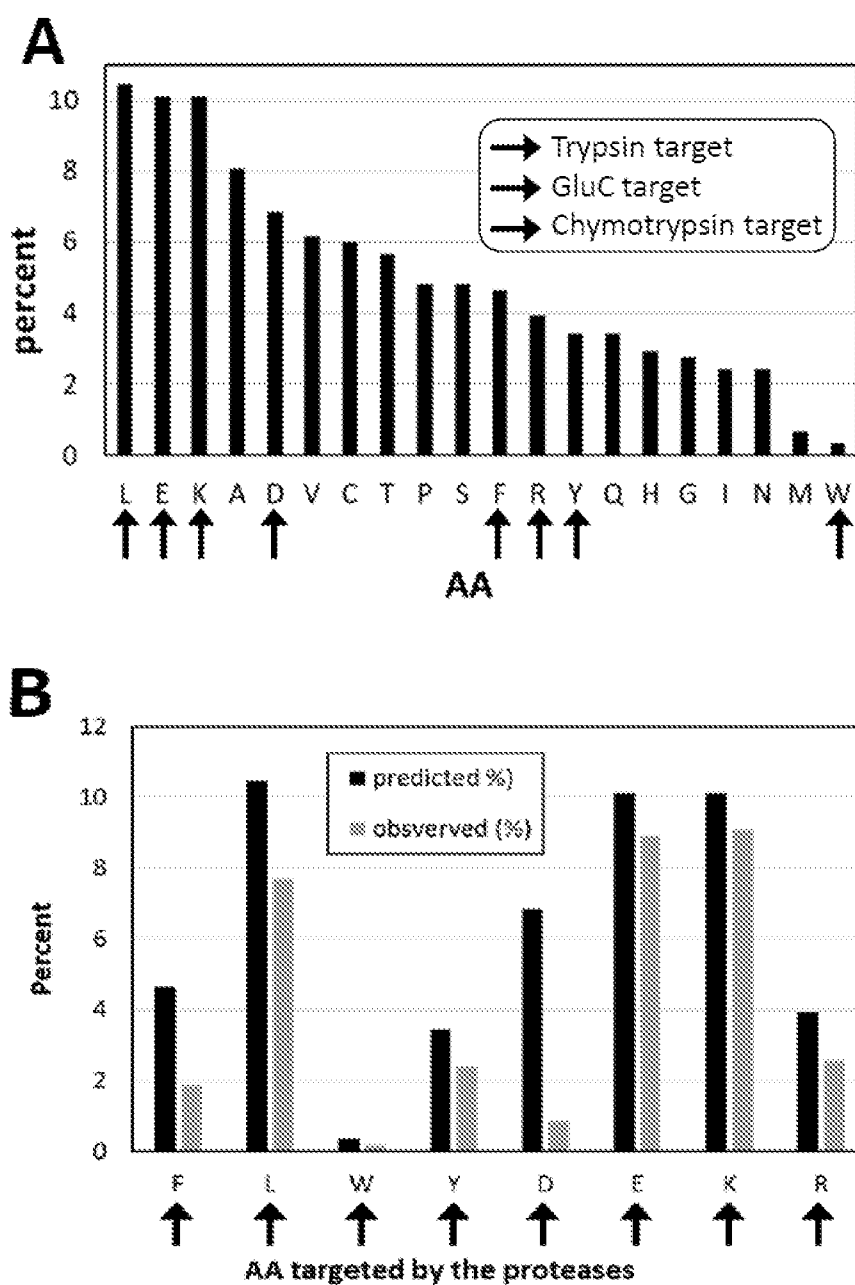
FIGURE 19





23/35

FIGURE 21



24/35

FIGURE 22

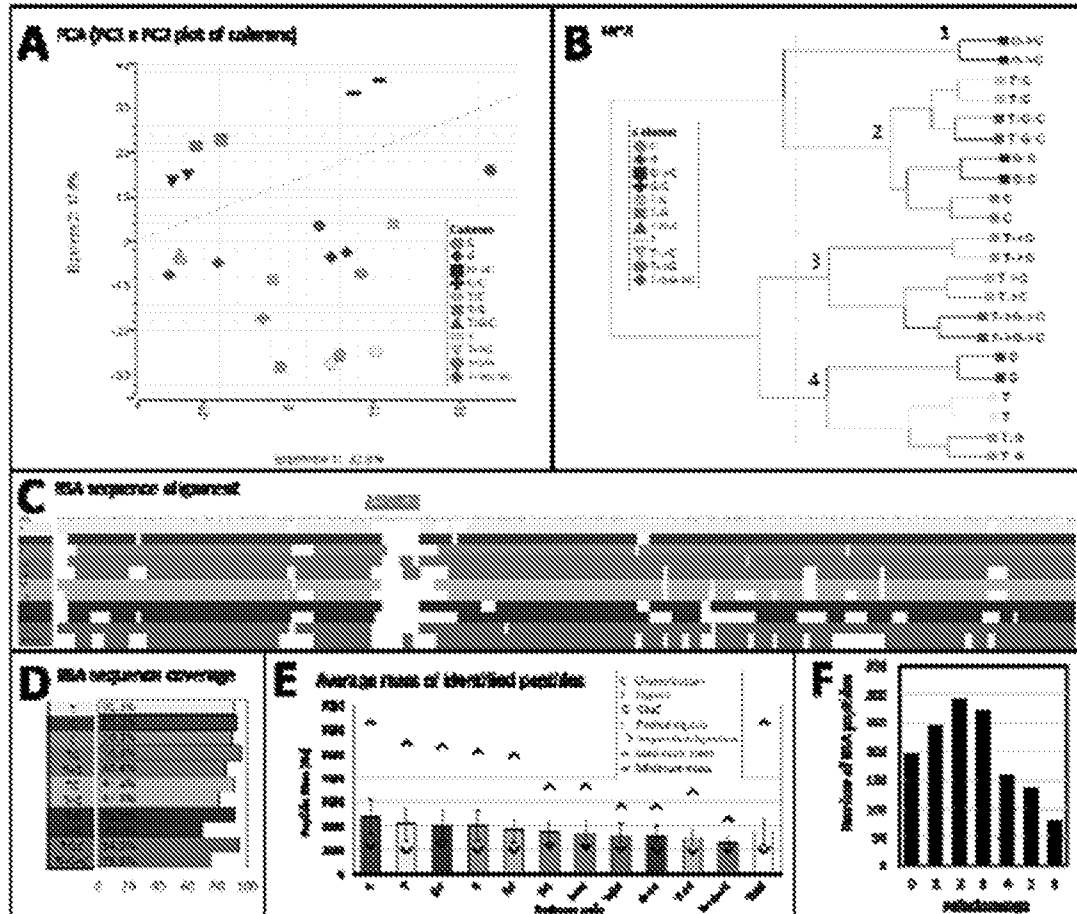
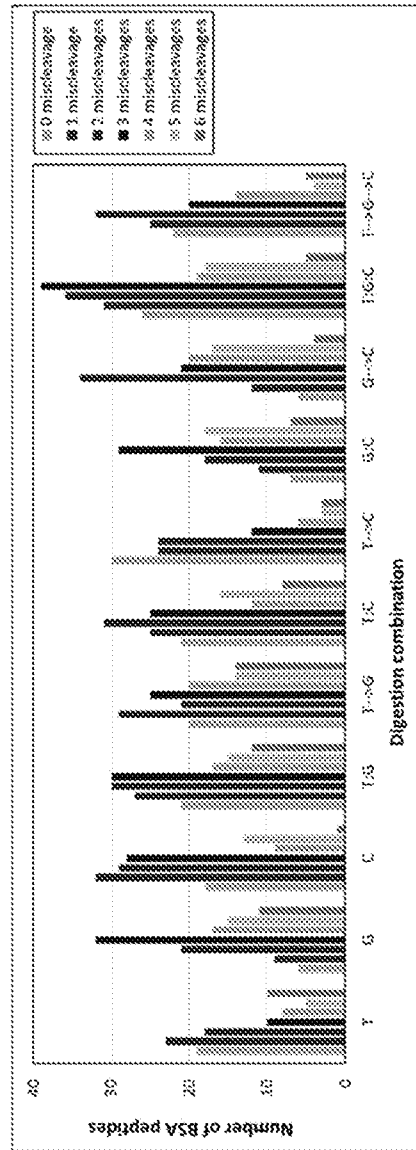
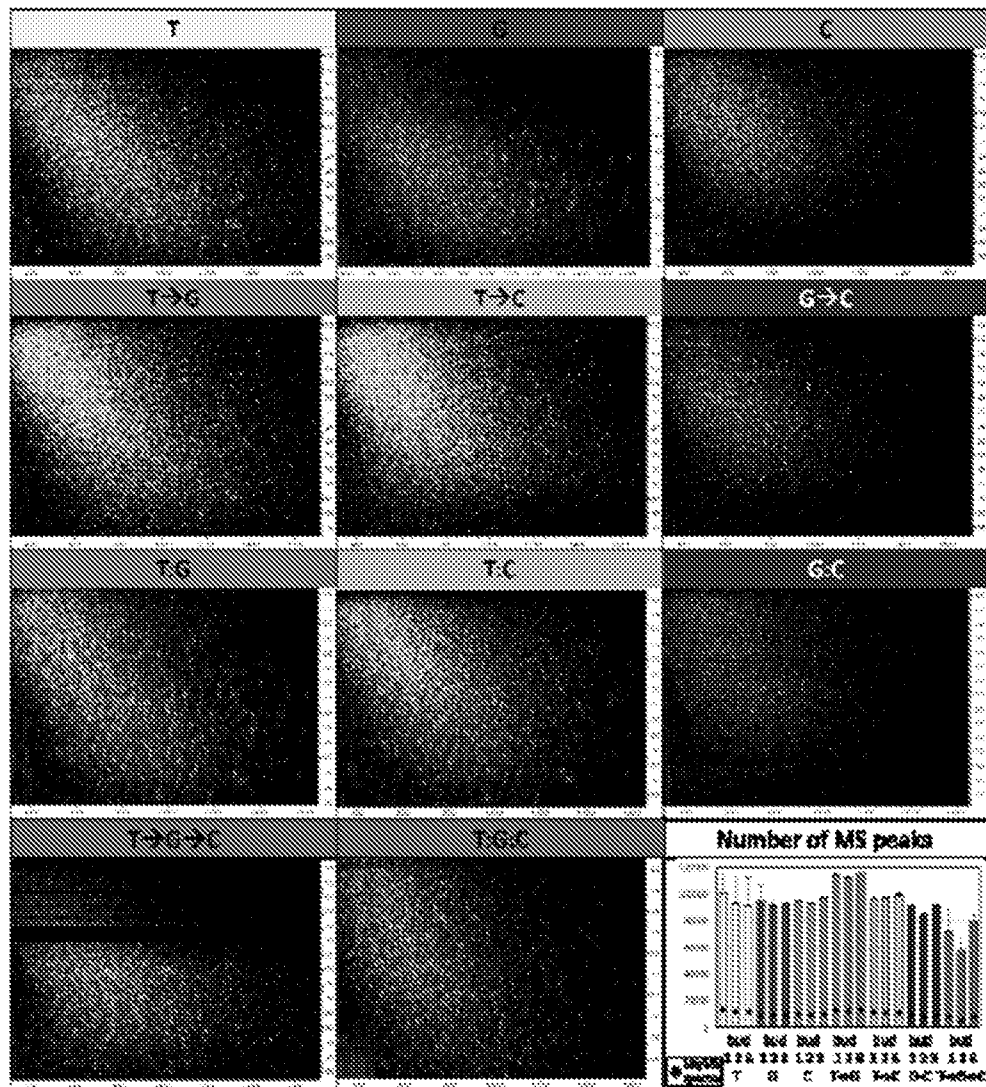


FIGURE 23

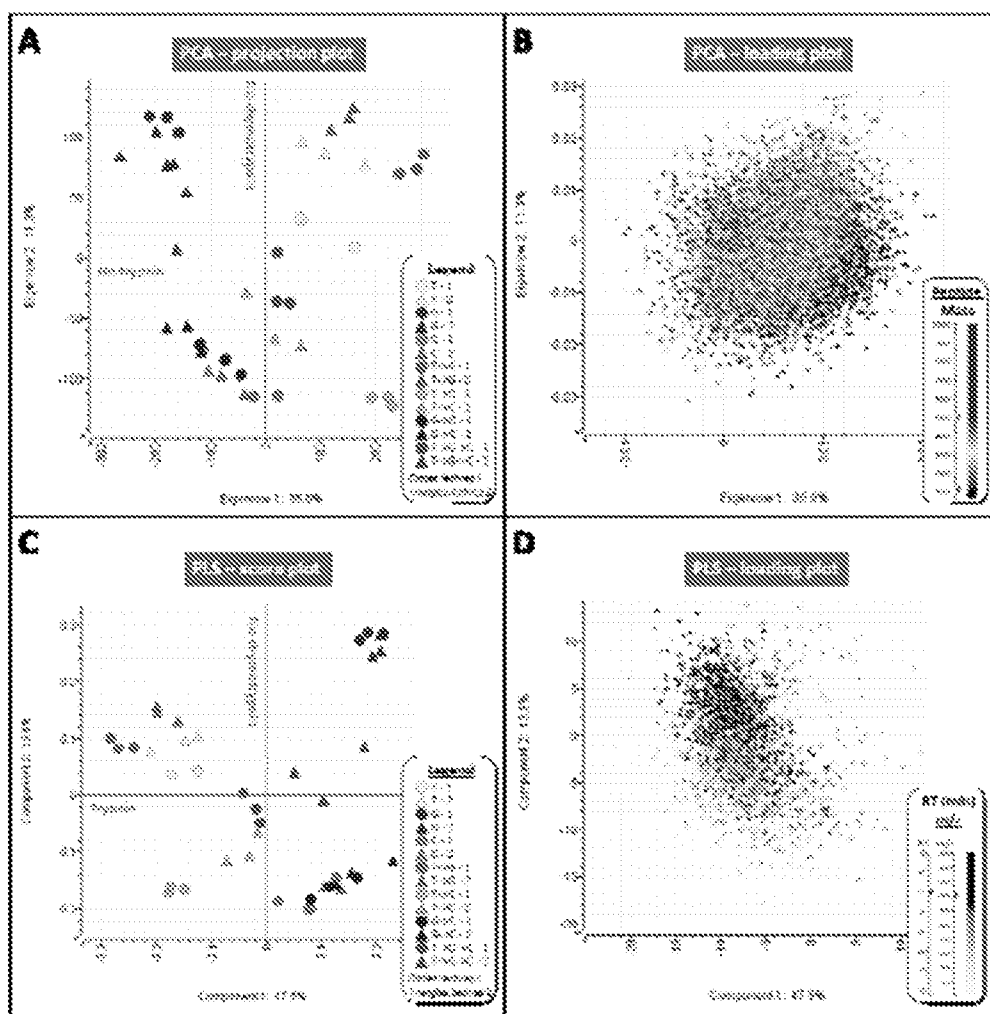
26/35

FIGURE 24



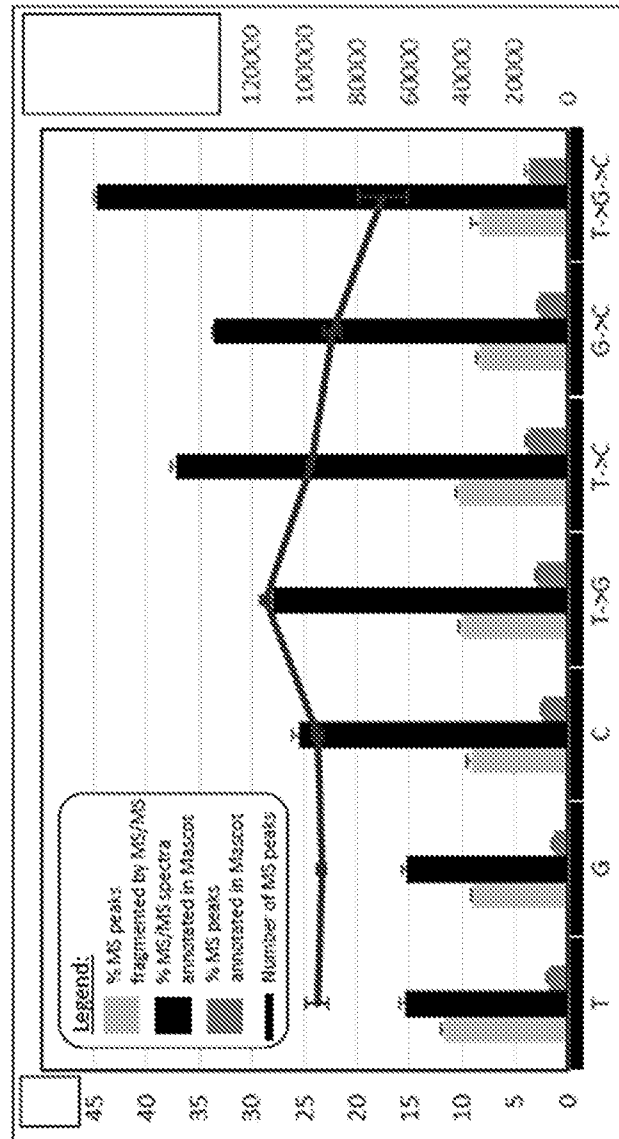
27/35

FIGURE 25



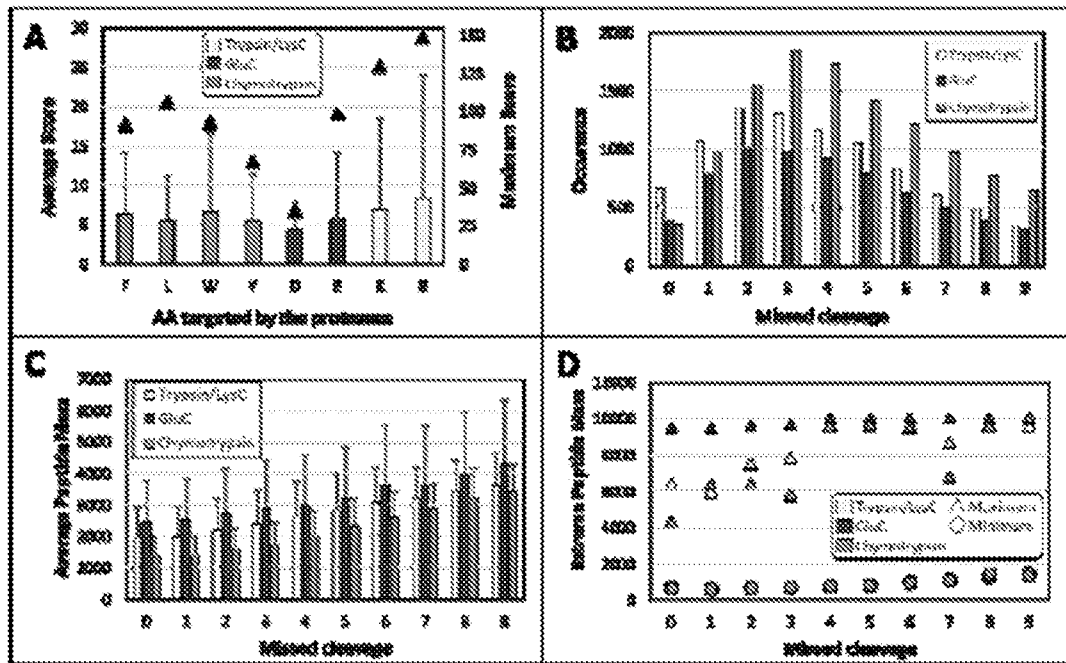
28/35

FIGURE 26



29/35

FIGURE 27



30/35

FIGURE 28

Peak	Spectrum	Peptide	Modifications	Protein	Start	End	Length	m/z	Calc. Mass	Charge	Mass	Ion	Identity	Missed	Ion	Ion
Peak_15871	Spectrum_5594	YDTRDTHAAGPVTQGVAPGAGAAQAE		Gluc	29	62	32	1565.23	311.67	3	-0.0075	51.79	16.80	4	19	169
Peak_176141	Spectrum_6785	RYTQKQWPFELSGGLVADELTHW		Chromogrysin	41	56	26	1281.64	252.25	2	0.0055	70.15	21.61	4	32	85
Peak_178513	Spectrum_08434	YTPQIQTPKELCAKAAASLQITWTVWTPGLTSKIQ		Tryptophan	42	79	38	1286.90	305.86	3	0.0239	42.77	18.89	0	21	136
Peak_184431	Spectrum_09773	GSYHSHFTSKVNTQK		Tryptophan	114	128	19	961.49	242.95	2	0.0074	102.43	18.92	0	14	13
Peak_188936	Spectrum_08435	GSYHSHFTSKVNTQK		Tryptophan	114	128	19	961.49	242.95	2	0.0052	48.24	20.61	0	14	91
Peak_190540	Spectrum_00316	LSCTHKK	Carbamidomethyl (C)	Tryptophan	170	177	8	305.18	91.53	3	-0.0026	21.51	18.18	1	8	20
Peak_198178	Spectrum_1005	LCCHKPTLGLDKNYSI	Carbamidomethyl (C), Phospho (T, Y)	Tryptophan	170	182	19	534.77	215.04	4	-0.0195	15.17	25.14	1	4	10

FIGURE 28 (continued)

Gluc

Y Q T K D T D I L A A F R V T P Q P G V P P E E A G A A V A A E

1973 b(130)

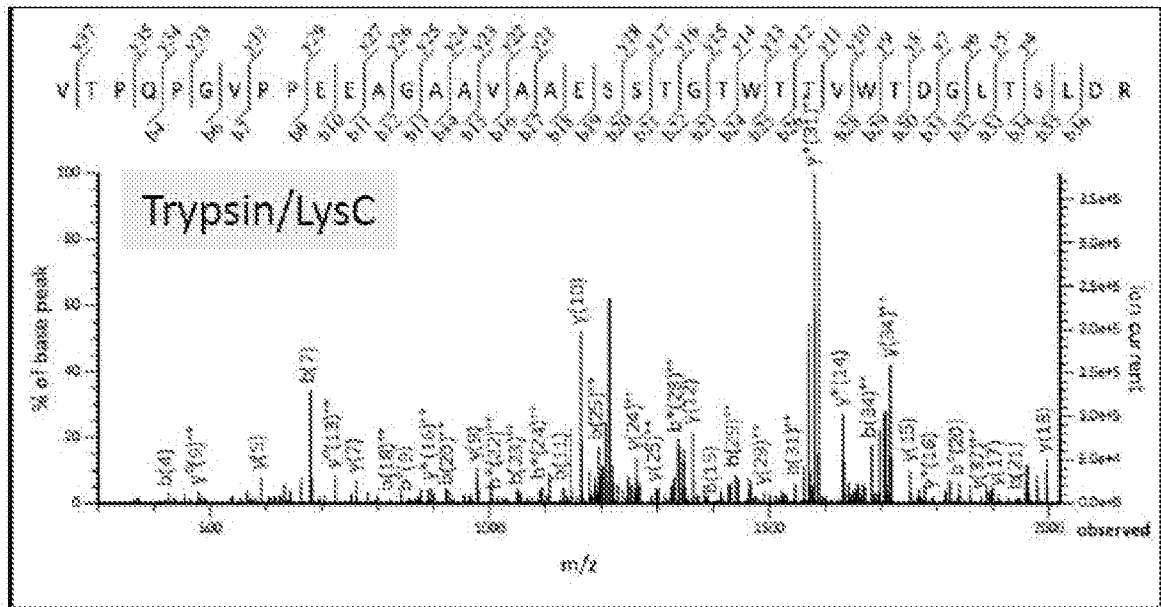
Chymotrypsin

R V T P Q P G V P P E A G A A V A A E S S T G T W

1183 b(130)

32/35

FIGURE 28 (continued)

B (continued)

Peptide alignment:

QT KDTDLAAFRVTPQPGVPPPEEAGAAVAAL

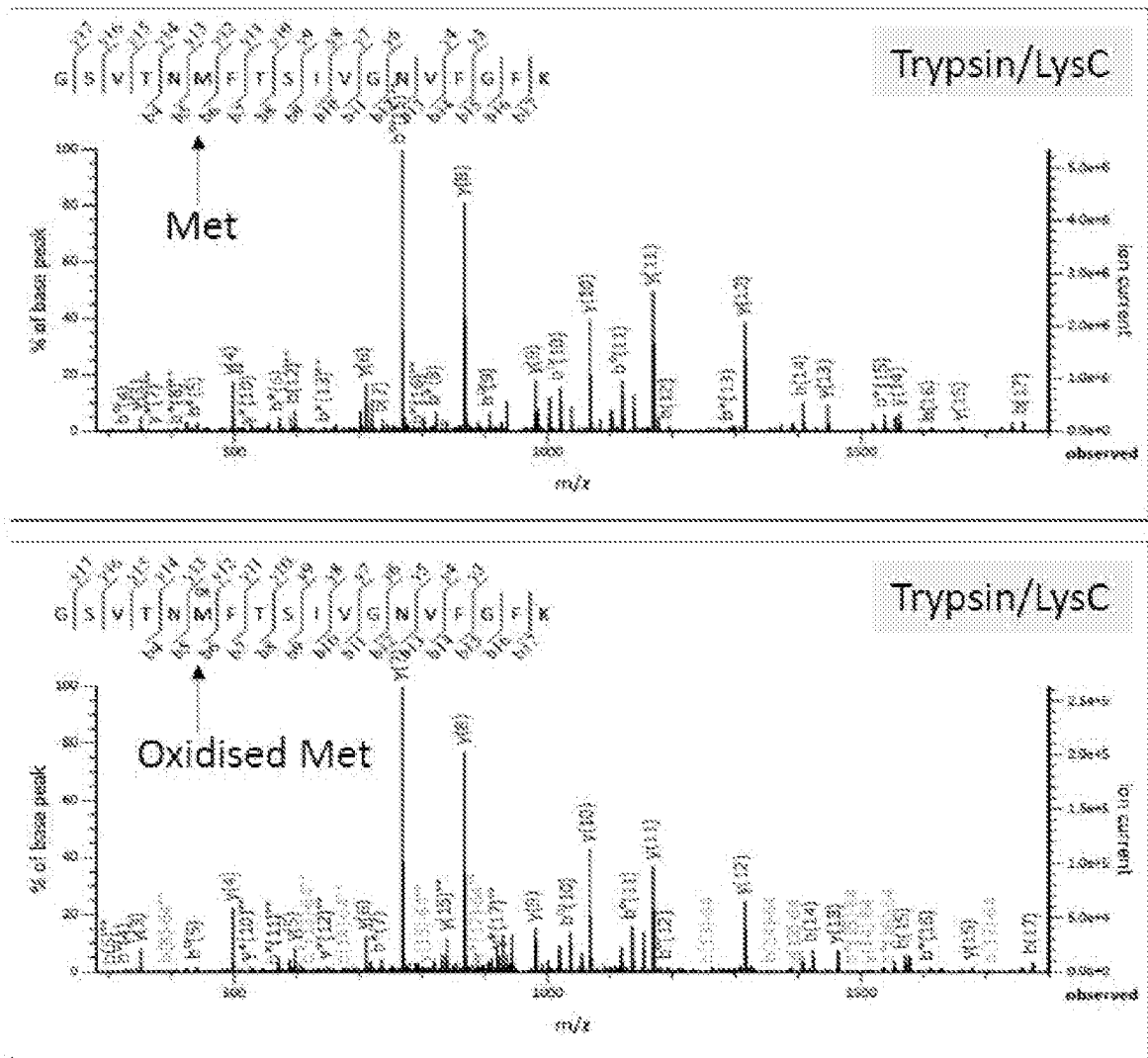
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VTPQPGVPPPEEAGAAVAESAESTGTWTTVWTDGLTSLDR

33/35

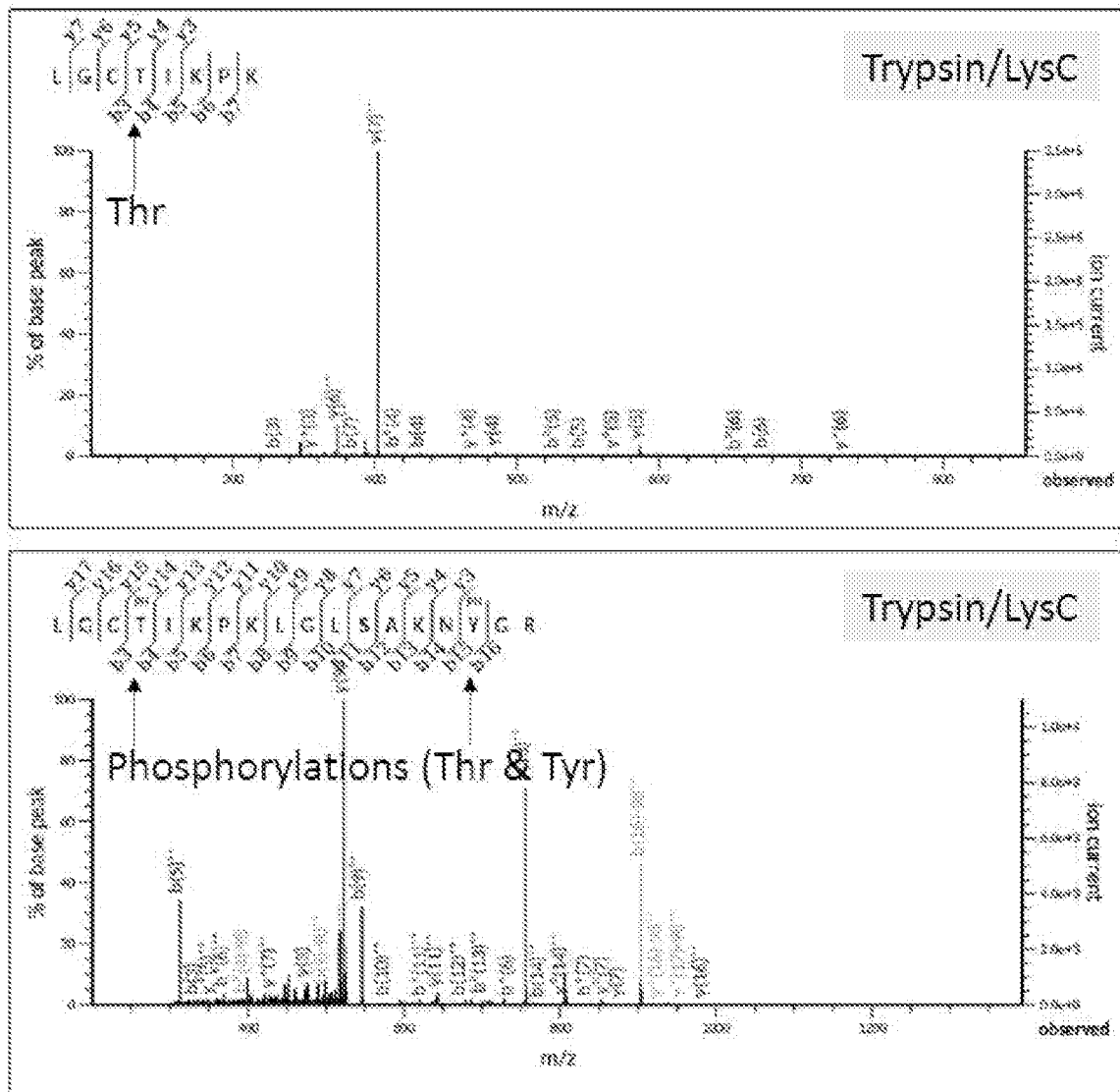
FIGURE 28 (continued)

C



34/35

FIGURE 28 (continued)

D

35/35

FIGURE 29