METABOLITE PROFILING OF SOY BY-PRODUCTS: A COMPREHENSIVE APPROACH

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1 ABSTRACT

Soy is the major oilseed crop as soybeans are widely used to produce biofuel, food, and feed. Other parts of the plant have been left on the ground after the harvest. The accumulation of such by-products on the soil can cause environmental problems. This work presents for the first time a comprehensive metabolite profiling of soy by-products collected directly from the ground just after mechanical harvesting. A two-liquid-phase extraction using *n*-heptane and EtOH-H₂O 7:3 (v/v) provided extracts with a complete characterization by gas chromatography and ultra-high-performance liquid chromatography both coupled to time-of-flight mass spectrometry. A total of 146 metabolites, including flavones, flavonols, isoflavonoids, fatty acids, steroids, mono-, sesqui-, di-, and triterpenoids, were tentatively identified in soy by-products and soybeans. These proved to be sources of a wide range of bioactive metabolites, thus suggesting that they could be valorized while reducing potential environmental damage in line with a circular economy model.

20	Keywords: Me	tabolomics; W	aste valorization;	Bioeconomy	: Biorefinery	; Green chemistr	v
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23 INTRODUCTION

Plants are an important source of compounds with a wide range of therapeutic uses.¹ Agricultural 24 by-products, a highly abundant source of natural products, can still be considered underexplored for 25 this purpose.²⁻⁴ Most of them are currently used for low value-added applications, such as animal feed, 26 energy production, or simply left in the field with the aim of maintaining soil fertility.²⁻⁴ However, an 27 excessive accumulation of such by-products from consecutive harvests can also contribute to pest and 28 weed infestation, greenhouse gas emission, soil microbiome deregulation, and water and soil 29 contamination.^{4–7} These problems are expected to increase due to the high demand for food caused by 30 population growth.⁸ Efforts to mitigate such problems through sustainable chemistry and engineering 31 approaches are advocated by the United Nations (UN), the European Environment Agency, among 32 other institutions. These institutions warn of the urgent need to convert agricultural by-products into 33 raw-materials for high value-added products employing green technologies.^{9,10} 34

The soy crop (Glycine max (L.) Merr.) deserves special attention, since it is the major oilseed crop 35 worldwide.¹¹ The production of soybeans and associated by-products, which are left on the fields (i.e., 36 branches, leaves, pods, and roots), were expected to be around 362 and 597 million tonnes in 2020/21, 37 respectively.^{12,13} Chemical studies of soy plants at different growth stages reported a wide dynamic 38 39 range of metabolites in their different organs, such as flavonoids, isoflavonoids, prenol lipids, fatty acids, and other organic acids, with potential applications in cosmetic, food, chemical, and 40 pharmaceutical industries.^{14–16} However, to the best of our knowledge, the literature does not report 41 42 the untargeted metabolite profiling of soy by-products left on the ground after harvest. Previous works focused only in isoflavonoids and in an alkaloid (trigonelline) in such materials.^{17,18} 43

Thus, a comprehensive extraction and identification procedure to tentatively identifying a widely range of metabolites in soy by-products would be desirable to estimate alternative applications for them. Previous works with sugarcane and coffee by-products evidenced that the best conditions for one type of by-product would not necessarily be the best for another one.^{19,20} In other words, an optimization should be pursued for each type of complex matrix. A Design of Experiment (DoE) should be preferred to a trial-and-error approach to achieve a global optimization of the extraction procedure in a minimum number of experiments.²¹ Unlike DoE, a trial-and-error approach is very often a time and resource (i.e., solvents and energy) consuming strategy, involving a large number of experiments without leading to reliable optimization, in a clear contradiction with Green Chemistry principles.²²

Therefore, this work aimed to conduct metabolite profiling for the first time of soy by-products 54 collected directly from the ground just after mechanical harvesting (branches, leaves, pods, and roots). 55 To achieve this goal, DoE was initially employed to optimize a (i) an ultra-high performance liquid 56 57 chromatography-PDA/UV-mass spectrometry (UHPLC-PDA/UV-MS) method, (ii) a gas chromatography-mass spectrometry (GC-MS) method, and (iii) a two-liquid phase extraction to extract 58 simultaneously polar, medium polarity, and nonpolar compounds. Subsequently, (iv) the optimized 59 60 procedures were applied for tentative identification of metabolites in each soy by-product (and in the commodity soybeans, which were used as reference material) by employing a dereplication strategy 61 that crosses chromatographic, spectral, and chemotaxonomic information. Global Natural Product 62 Social Molecular Networking (GNPS) was employed for tentative identification of high to medium 63 polarity compounds in hydroethanolic extracts, while GC-MS data were matched against NIST 64 (National Institute of Standards and Technology) and Fiehn libraries. 65

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67 MATERIALS AND METHODS

68 *Reagents and materials*

HPLC grade ethanol and MS grade acetonitrile and methanol were purchased from Merck
(Germany). P.A. (practical grade) formic acid and *n*-heptane were from Sigma Aldrich (Germany).

71 *Plant material*

Soy by-products from NA5909 cultivars were collected directly from the ground after mechanical 72 harvesting of soybean at the School of Agricultural Sciences of São Paulo State University in Botucatu 73 74 city, São Paulo State, Brazil (-22.8296354, -48.42553) and Santa Fé Farm in Pardinho city, São Paulo State, Brazil (-23.0268717, -48.3859183). The collected materials were then separated into branches, 75 leaves, pods, and roots. Similar mass portions of the same type of material (e.g., pods) from the two 76 collection sites were mixed and grounded in a basic analytical mill (IKA® A11, Germany). For 77 extraction optimization purposes, the resulting material was separated by ranges of granulometry on 78 79 an electromagnetic sieve shaker (Bertel, Brazil).

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81 *Optimization of methods by Design of Experiments (DoE)*

Optimizations were pursued using Protimiza Experimental Design® software (Protimiza
Experimental Design, Brazil) and GraphPad Prism 9 software (GraphPad Software, USA).

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Method optimization of ultra-high-performance liquid chromatography coupled to photodiode array and mass spectrometry (UHPLC-PDA/UV-MS)

87 The liquid chromatography analyses were performed using a UHPLC Nexera UC system (Shimadzu, Japan), consisting of two LC-30AD pumps, SIL-30AC auto-injector, CTO-20AC column 88 oven, SPD-M20A photodiode network detector, unit degasser DGU-20A5R, coupled to a LCMS-2020 89 single quadrupole mass spectrometer equipped with an ESI ionization source and a CBM-20A 90 communications module. The separations were achieved in a Zorbax Eclipse Plus C18 column, 150 91 mm \times 2.1 mm; 1.8 μ m (Agilent Technologies, USA), a widely used column that has already been 92 employed for soy metabolomics.^{23–25} A 1 µL UltiMate[™] 3000 Pre-Heater (Thermo Fisher Scientific, 93 USA) was installed inside the column compartment. A two-factor central composite rotatable design 94

(CCRD, $\alpha = (2^k)^{1/4}$) was employed. Initial % of B (MeOH) (x_1) and % of formic acid (HCOOH) in the 95 mobile phases (x_2) were the selected factors. The flow rate and analysis temperature were kept at 0.3 96 97 mL/min and 30 °C, respectively. An aliquot of 2 µL of a non-concentrated EtOH:H₂O 7:3 (v/v) (prepared as the central point described in the section "method optimization of two-liquid-phase 98 dynamic maceration (2-Mac)") was filtered with a syringe-filter of 0.22-µ nylon prior to injection. 99 100 The CCDR (Central Composite Rotatable Design) itself as well as the outcomes are shown in Table 101 1. The monitored responses were the total number of peaks detected by PDA/UV at 254 nm (y_l) (the 102 samples analyzed here were expected to be rich in subclasses of flavonoids which absorbs at this wavelength)²⁶ and the sum of the peaks in positive (ESI+) and negative (ESI-) ionization mode for MS 103 104 analysis (y_2 and y_3 , respectively). Only peaks with signal/noise (S/N) greater than 3 were considered. Mass spectrometer parameters were set as: nebulization gas flow at 1.5 L/min; drying gas flow at 15 105 106 L/min; heat block temperature at 400 °C; dissolution line temperature at 250 °C, and a voltage detector of 0.1 kV. The optimized condition was H₂O (A) and MeOH (B), both acidified with 0.1% formic acid 107 108 (v/v) in the following gradient elution: 15–100% B from 0 to 60 min, at 0.3 mL/min and 30 °C. The data were processed using Shimadzu's LabSolutions software. 109

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111 *Method optimization of gas chromatography coupled to mass spectrometry (GC-MS)*

112 Gas chromatography analyses were performed using a GC-MS Clarus 680 chromatograph (Perkin Elmer, USA) coupled to a Clarus SQ 8 T mass Detector. Chromatographic separations were performed 113 using a PerkinElmer Elite-5MS column (30 m \times 0.25 mm, 0.25 μ m). A two-factor CCRD design was 114 used to optimize the chromatographic separation, where x_1 = temperature rate and x_2 = carrier gas flow 115 (Table 2). The total number of peaks was the monitored response. The final optimized separation was: 116 the oven temperature was held isothermal at 150 °C for 2 min and then increased to 350 °C at the rate 117 of 7 °C/min. The GC injector and MS transfer line temperatures were set at 330 °C and 310 °C, 118 respectively. The injection volume of the non-concentrated *n*-heptane extract (central point described 119 6

120 on 2.3.3) was 2 μ L with a split flow of 5 ml/min. Helium gas was used as the carrier gas at a constant 121 flow rate of 1.6 ml/min, and 6 min solvent delay. The ionization of the sample was performed in EI 122 mode (70 eV), and the acquisition mass range was set at 50–600 amu.

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124 *Method optimization of two-liquid-phase dynamic maceration (2-Mac)*

Two-liquid-phase dynamic maceration (2-Mac) with magnetic stirring with a temperature sensor 125 (Heidolph MR Hei-Tec, Germany) was selected as the extraction technique to be optimized.²⁷ A mix 126 of the different parts of the soy by-products collected directly from the ground on the day of mechanical 127 harvesting, plus soybeans (60 mg of beans, branches, leaves, pods, and roots, in a total of 300 mg) was 128 added to a 22.5 mm inner diameter beaker. Then, 3 mL of EtOH-H₂O 7:3 (v/v) and 3 mL of *n*-heptane 129 130 were added into the beaker. The other parameters varied according to a four-factor Doehlert design as shown in Table 3. All produced extracts were centrifuged at 4000 rpm for 5 min (Eppendorf 5810 R, 131 Germany) to speed phase separation. The simultaneously produced EtOH-H₂O 7:3 (v/v) and n-heptane 132 extracts were then syringe filtered (0.22 µm nylon filter) and analyzed by UHPLC-PDA/UV-MS and 133 GC-MS, respectively (see final conditions of 2.3.1 and 2.3.2). The sum of peaks observed in both types 134 135 of chromatograms was selected as the response (y) to be monitored in each experiment presented in Table 3. The final optimized condition of extraction was Time: 35 min; Temperature: 45 °C; Magnetic 136 stirring: 1400 rpm; Granulometry of the plant material: 48-115 Mesh. For peak annotation purposes, 137 this condition was applied to the individual parts of soy by-products or soybeans which were then 138 analyzed by UHPLC-QToF-MS/MS and GC-QToF MS. 139

140 Ultra-high-performance liquid chromatography coupled to time-of-flight mass spectrometry

141 (UHPLC-QToF-MS/MS)

Metabolite profiling of concentrated EtOH-H₂O 7:3 (v/v) extracts (10 mg/mL) was carried out in an Agilent 1290 UHPLC system (Agilent Technologies, USA) coupled to an Agilent 6540 quadrupole-

time-of-flight mass spectrometer (QToF-MS), equipped with an orthogonal ESI source (Agilent Jet 144 Stream, USA). The UHPLC condition was the optimized condition described in previously. 145 146 Additionally, a shorter UHPLC-QToF-MS/MS analysis in negative mode was performed using a Zorbax Eclipse Plus C18 column, 100×2.1 mm; 1.8 µm (Agilent Technologies, USA), and H₂O and 147 148 ACN, both acidified with 0.01% formic acid (v/v) (A and B, respectively) in the following gradient 149 elution: 0-30% B in 0-7 min, 30-80% B in 7-9 min, 80-100% B in 9-11 min, 100% B in 11-13 min, 150 and 0% B in 13-14 min. The flow rate and analysis temperature were kept at 0.5 mL/min and 30 °C, and the sample injection volume was 5 µL. MS parameters were capillary voltage, 4000 V; nebulizer 151 152 pressure, 40 psi; drying gas flow rate, 10 L/min; gas temperature, 350 °C; skimmer voltage, 45 V; fragmentor voltage, 110 V. Both MS and Auto MS/MS modes were acquired in m/z values of 50 and 153 1100 and 50-800, respectively, and at a scan rate of 5 spectra per second. Agilent Mass Hunter 154 Qualitative analysis software (B.07.00) was applied for postacquisition data processing.²⁸ Metabolites 155 present in the EtOH-H₂O 7:3 (v/v) extracts were annotated using Global Natural Product Social 156 157 Molecular Networking (GNPS) (http://gnps.ucsd.edu) and MZmine 2.53 software (https://mzmine.github.io/).²⁹⁻³¹ First, MS/MS data were converted to mzML format with 158 ProteoWizard 3.0.6002 package MSConvert software (ProteoWizard, USA). 159

160 The converted files were uploaded to GNPS platform, and a molecular network was created using the online workflow (https://ccms-ucsd.github.io/GNPSDocumentation/). The data were filtered by 161 removing all MS/MS fragment ions within +/- 17 Da of the precursor m/z. MS/MS spectra were 162 window filtered by choosing only the top six fragment ions in the +/- 50Da window throughout the 163 spectrum. The precursor ion mass and MS/MS fragment ion tolerances were set to 0.02 Da. A cosine 164 165 score above 0.65 and more than four matched peaks were used to create the edges of the network. The spectra in the network were searched against spectral libraries of GNPS. The library spectra were 166 filtered in the same manner as the input data. The matches between network spectra and library spectra 167 were required to have a score above 0.65 and at least four matched peaks. MolNetEnhancer, a tool of 168

GNPS, and Cytoscape version 3.7.2 (Cytoscape Consortium, USA) were used for the network visualization. The product ion spectra presented in GNPS were manually verified with previous literature annotation. The mass error tolerance adopted was ≤ 10 ppm (Table 4). The final classification of the compounds was performed using JChem for Excel 21.1.0.787 - ChemAxon (https://www.chemaxon.com) and NPClassifier, with the final classification using ClassyFire.^{32,33}

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175 *Gas chromatography coupled to time-of-flight mass spectrometry (GC-QToF-MS)*

Metabolite profiling of concentrated *n*-heptane extracts (10 mg/mL) was done using a 7890B 176 Agilent system (Agilent Technologies, USA) coupled to a quadrupole time-of-flight (OToF) 7200 177 (Agilent Technologies, USA) equipped with an electronic ionization (EI) interface. An Agilent Zorbax 178 179 DB5- MS + 10 m Duragard Capillary Column ($30 \text{ m} \times 250 \mu \text{m} \times 0.25 \mu \text{m}$), similar to the column used in the GC-MS method optimization, was employed for chromatographic separation. The sample 180 injection volume was 1 µL using a split flow of 8.4 mL/min, and the other parameters were the same 181 as in the optimized GC-MS method. Metabolites present in the *n*-heptane extracts were annotated using 182 the match of mass spectra in the Agilent Mass Hunter Unknown Analysis tool and mass spectral 183 databases (i.e., NIST MS Search v.2.0 and Fiehn Lib). 184

185 **RESULTS AND DISCUSSION**

186 *Optimization of Analytical methods*

As the main goal of this work was to identify the greatest possible number of metabolites in the different soybean crop by-products, the methods were optimized to obtain the greatest number of chromatographic peaks with signal/noise $\geq 3.^{19,34}$ For the optimization of separations by employing a two-factor central composite rotatable design (CCRD), UHPLC-PDA/UV-MS and GC-MS systems were used due to their higher availability when compared with the systems later employed in the application step, when high-resolution mass spectrometers were used for tentative identification of

compounds. At this optimization step, the injected samples in the UHPLC-PDA/UV-MS and GC-MS 193 systems were a EtOH-H₂O 7:3 (v/v) and a n-heptane extract, respectively, prepared with a mix of sov 194 195 by-products and soybeans (reference material) by Two-Liquid-Phase Dynamic Maceration (2-Mac). The extraction condition was that of the central point of the experimental design that should be used 196 197 later for the optimization of the extraction condition (Table 3). Once the UHPLC-PDA/UV-MS and GC-MS optimizations were achieved, they were used to monitor the extraction efficiency during the 198 optimization of 2-Mac extraction itself.²¹ In both cases, the simultaneously produced EtOH-H₂O 7:3 199 (v/v) and n-heptane extracts by 2-Mac were injected into the chromatographic systems just after 200 201 filtration. This means without any concentration and resuspension step to enhance sample throughput while saving solvents and energy, in line with principles 1, 2, 6, 7, 9, 10, 11, and 12 of the 12 Principles 202 of Green Analytical Chemistry (GAC).35 203

204 Optimization of the UHPLC-PDA/UV-MS method

The variables and levels selected for the CCRD (Table 1) were based on preliminary tests and on a 205 literature review.^{23–25,36} Initial % of B (MeOH) was set as a factor in the CCRD (Table 1), because 206 preliminary tests with mobile phase ranging from 5 to 100% of MeOH led to peaks mainly spread out 207 208 in the second half of the chromatogram (late elutions - data not shown). Therefore, finding the gradient of B that best distributed the peaks across the chromatogram would lead to the highest number of 209 peaks. On the other hand, % HCOOH in the mobile phase was selected as the other factor in the CCDR, 210 211 because this acid has been used in soy metabolomics works and could improve chromatography separation and ionization efficiency in mass spectrometry.^{23-25,37-40} Thus, selecting the best % of 212 HCOOH would be also important. Methanol was chosen as the organic modifier since it is available 213 214 as a MS grade solvent, being classified as a "recommended" solvent in the CHEM21 solvent selection guide.⁴¹ Although acetonitrile is also available as a MS grade solvent, it is classified as a "problematic" 215 one according to Prat et al. (2016).⁴¹ 216

217	Considering the UHPLC-PAD/UV outcomes at 254 nm (Table 1), factors x_1^2 , x_2 , and x_2^2 showed a
218	significant influence in the number of chromatographic peaks (y_l) at 95% confidence level, with p-
219	value of 5.7 \times 10 ⁻⁵ , 8.1 \times 10 ⁻⁵ , and 8.5 \times 10 ⁻³ , respectively. When considering the UHPLC-MS
220	chromatograms at 95% confidence level, x_1^2 and x_2 were significant factors, with <i>p</i> -value of 2.7×10^{-10}
221	² and 5.2 × 10 ⁻³ to ESI+ (y_2), and 3.9 × 10 ⁻² and 1.7 × 10 ⁻³ to ESI- (y_3), respectively. The resulting
222	mathematical models from UHPLC-PAD/UV at 254 nm, UHPLC-MS in positive and negative mode
223	outcomes (Table 1) are presented in Equations 1, 2, and 3, respectively.

- 224 $y_1 = 40.60 4.74 x_1^2 4.22 x_2 2.24 x_2^2$ (Equation 1)
- 225 $y_2 = 74.48 1.90 x_1^2 2.47 x_2$ (Equation 2)
- 226 $y_3 = 37.52 2.60 x_1^2 2.94 x_2$ (Equation 3)

The determination coefficients (R^2) of the models described by Equations 1, 2, and 3 were 0.92, 227 0.66, and 0.77, respectively. The statistical significance of the models was verified by the ANOVA F 228 test. The regressions were significant (p < 0.05) without lack of fit; therefore, the experimental data 229 230 were successfully described by the models. Figure S1 illustrates the response surface of the model for the response v_l , which predicts the highest number of peaks (43) when using 15% of MeOH and 0.16– 231 0.30% of HCOOH. Thus, the lowest concentration of HCOOH in the optimum range (0.16%) was 232 preferred to reduce the amount of HCOOH used, in line with principle 7 of GAC.³⁵. Furthermore, the 233 predicted optimal conditions for the negative and positive modes of MS (y_2 and y_3 , respectively) were 234 15% of MeOH and 0.10% of HCOOH, which would lead to 42 and 78 peaks, respectively. Both 235 optimal predicted conditions were tested experimentally in triplicate, resulting in 40±3, 42±0, and 236 79±1 for UHPLC-PAD/UV at 254 nm, and UHPLC-MS in negative and positive modes, respectively. 237 238 All these values matched the predicted ones, evidencing that the optimizations for both detectors were achieved. Representative chromatograms of the optimized conditions are shown in Figure 1, with clear 239 240 distributions of peaks across the whole chromatogram.

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Another two-factor CCRD was applied to optimize the GC-MS separation for the analysis of *n*heptane extracts obtained by 2-Mac. The experiments of the CCRD and their outcomes are presented in Table 2.

At 95% confidence level, factors x_1 , x_1^2 , x_2^2 , and their interaction (x_1x_2) showed significant influence in the number of peaks, with *p*-value of 3.5×10^{-3} , 7.9×10^{-3} , 7.9×10^{-3} , and 2.4×10^{-2} , respectively.

Equation 4 is the resulting mathematical model.

249 $y_4 = 63.60 + 5.74 x_1 - 5.30 x_1^2 - 5.30 x_2^2 + 5.50 x_1 x_2$ (Equation 4)

The R^2 of the model described by Equation 2 was 0.85. The statistical significance of the model 250 251 was verified by the ANOVA F test and evaluation of p-values. The regression was significant (p=0.002) without lack of fit, indicating that the models describe well the experimental data. Figure 252 S2 illustrates the response surface of the model for v_4 , which predicted the highest number of peaks 253 (66) when using 7 °C/min and 1.6 mL/min. Thus, the optimum predicted condition was tested in 254 triplicate, resulting in 66±3 peaks, matching the predicted value and evidencing again that 255 optimization was achieved. A representative chromatogram with the optimum condition is provided 256 in Figure 2. 257

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259 *Optimization of a two-liquid-phase dynamic maceration (2-Mac)*

A Doehlert design was applied to optimize a 2-Mac. The experimental conditions and the corresponding responses are listed in Table 3. The monitored response (y_5) was the sum of the peaks of the EtOH-H₂O 7:3 (v/v) and *n*-heptane extracts as determined with the previously optimized UHPLC-PDA/UV-MS and GC-MS methods, respectively.¹⁹

At 95% confidence level, experimental factors x_1 , x_2 , and x_4 exhibit a significant influence in the total number of peaks, with *p*-value of 2.5×10^{-3} , 3.1×10^{-3} , and 1.1×10^{-6} , respectively, leading to the mathematical model shown in Equation 5:

267 $y_5 = 241.88 + 19.80 x_1 + 22.20 x_2 + 35.55 x_4$ (Equation 5)

The R² was 0.77, and the statistical significance of the model was confirmed by the ANOVA F test 268 269 and evaluation of p-values. The regression was significant ($p=8.2 \times 10^{-7}$) without lack of fit, indicating 270 that the model satisfactorily describes the experimental data. Figure S3 illustrates the response surface of the model for y₅. The coefficients of the variables were all positive; therefore, the highest response 271 272 would be achieved by setting the levels of the variables x_1 , x_2 , and x_4 to their highest, which corresponds to 35 min of extraction time, 45 °C, and particle sizes of 48–115 Mesh. The rotation of the magnetic 273 bar (x_3) was fixed at 1400 rpm. The predicted optimum condition would lead to 270 peaks. Then, this 274 optimal condition and the best experimental condition of the original CCRD itself (exp. 5 of Table 3) 275 were performed in triplicate on the same day, leading to 275±6 and 270±13, respectively. This result 276 277 is compatible with the optimum predicted response, indicating that another optimization was achieved successfully. Chromatograms of UHPLC-PDA/UV-MS and GC-MS obtained for the EtOH-H2O 7:3 278 (v/v) and *n*-heptane extracts produced from the optimum extraction condition are presented in Figures 279 280 1 and 2, respectively.

281 Applying the optimized conditions for metabolite profiling of the soy by-products

Once the separation and extraction methods were optimized, the next step was to apply the optimal separation conditions for the first untargeted metabolite profiling of soy by-products from collected directly from the ground after mechanical harvesting. Due to the fact that high-resolution mass spectrometers were used in this step, adjustments in some parameters were necessary to get to the best identification conditions, as mentioned in UHPLC-QToF-MS/MS and GC-QToF-MS methods. Two NA5909 cultivars were sampled since this cultivar has been widely cropped in Brazil, which is the major producer of soybean. The outcomes confirmed that a comprehensive and optimized 13

procedure was achieved. Considering the annotation of compounds in the simultaneously produced 289 EtOH-H₂O 7:3 (v/v) and n-heptane extracts, a total of 76, 76, 66, and 79 compounds were tentatively 290 291 identified for branches, leaves, pods, and roots, respectively. These were 50 in the commodity soybeans (Tables 4 and 5). The tentatively annotated compounds were grouped according to 292 Classyfire³³ and summarized in Figure 3. Considering all matrices together, fatty acyls was the most 293 294 representative group, with 30 metabolites. Fatty acyls are formed by the chain-elongation of an acetyl-295 CoA primer with malonyl-CoA or methylmalonyl-CoA and contain a vast functionality as biological lipids.⁴² Flavonoids and isoflavonoids were the second and third most represented groups, with 16 and 296 297 15 metabolites, respectively (Figure 3, Table 4). Both have been widely known activities in plant defense, in addition to human health benefits.^{43,44} Then, prenol lipids (14), steroids and steroid 298 derivatives (10), and carboxylic acids and derivatives (8) appeared (Figure 3, Tables 4 and 5). These 299 300 correspond to fundamental substances in plants, being the precursor of several specialized metabolites and constituting vitamins, mono-, sesqui-, and triterpenes, and other high value-added compounds.⁴² 301 302 The abundance of such metabolites in soy by-products increase their potential as a source of bioactive compounds, especially for the food and pharmaceutical industry. A more detailed analysis by 303 304 extract/matrix follows.

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Annotation of compounds in the $EtOH-H_2O$ 7:3 (v/v) extracts by UHPLC- ESI-QToF-MS/MS

The EtOH-H₂O 7:3 (v/v) extracts of the individual by-products as well of soybeans were analyzed by UHPLC-ESI-QToF-MS. The annotation of the ions was performed comparing the MS/MS data against the GNPS spectral reference library.²⁹ Additionally, the candidates obtained by GNPS had their compatibility challenged with the acquired high-resolution masses as well as with previous reports of their occurrence in soy by-products as organized in a database published elsewhere.¹⁴

A total of 67 metabolites were tentatively identified in EtOH-H₂O 7:3 (v/v) extracts of soy parts as summarized in Table 4. Sixteen of them were isoflavonoids, a class of compounds that have been 14

widely known for their bioactive properties. These were 11, 10, 10, 9, and 4 in pods, branches, 314 soybeans, roots, and leaves, respectively (Table 4). Formononetin 7-O-glucoside (ononin) and 315 316 genistein, which are isoflavonoids, were identified in all soy by-products (Table 4). Ononin has been reported as a potential anti-angiogenesis and neuroprotective effects, while genistein administration 317 has been related to the reduction of some cardiovascular risk factors.^{45–47} Additionally, a systematic 318 319 review about phytoestrogens and menopausal symptoms pointed to the potential of extracts with high levels of genistein (> 30 mg/d) in the treatment for hot flushes.⁴⁸ Flavonoids corresponded to 16 320 compounds, with 11, 9, 8, 6, and 2 identified in pods, branches, soybeans, leaves, and roots, 321 322 respectively, with four of them only identified in soybeans (Table 4). Flavonoid glycosides, such as kaempferol 3-O-glucoside (astragalin), kaempferol 3-O-sophoroside (sophoraflavonoloside), and 323 luteolin 7-O-glucoside (cynaroside), were identified in at least one soy by-product. Among them, 324 sophoraflavonoloside was only present in soybeans (Table 4). These compounds have shown 325 antitumor and anti-inflammatory properties.⁴⁹⁻⁵¹ 326

327 It is important to highlight that compounds identified in EtOH-H₂O 7:3 (v/v) extracts of soy byproducts, such as daidzein, daidzin, genistein, genistin, and glycitin are classified as phytotoxins.⁶ 328 Zoccolo (2010)⁷³ and later Hama et al. (2021)⁶ reported the presence of such compounds in agricultural 329 330 soils and streams close to soy crops, which in turn were close to human settlements. Thus, recovering such isoflavonoids from at least part of soy by-products would be an advantage from an environmental 331 point of view to decrease the potential undesirable effects associated with large build-up of 332 isoflavonoids in the environment.¹⁷ This would be in line with a "responsible production" of soybeans, 333 as recommended by the number 12 of the 17 Sustainable Development Goals of the UN. Additionally, 334 335 this practice might potentially lead to economic gains in soy production chain by developing valueadded commercial extracts standardized in bioactive isoflavones from by-products in a biorefinery 336 337 approach.

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Annotation of compounds in the n-heptane extracts by GC-QToF-MS

The *n*-heptane extracts of the individual by-products as well of soybeans were analyzed by GC-340 QToF-MS (Figure S4). MS data were matched against NIST and Fiehn libraries. High match factors 341 342 (>70) were achieved between the MS spectrum of the candidates and of these libraries, as demonstrated in Table 5. A total of 79 metabolites were tentatively identified in *n*-heptane extracts of soy by-products 343 or soybeans, as summarized in Table 5. Most of them (50) were identified for the first time in soy plant 344 345 tissues, which could be because few works in the literature have used nonpolar solvents for the extraction and subsequent analyses of soy parts or by-products. Nonpolar solvents, such as hexane, 346 have been used mainly to degrease plant matrices by solid-liquid extractions or liquid-liquid 347 partitioning in a so called "clean-up" sample pre-treatment.^{74,75} The produced nonpolar extract or 348 fraction are often discarded without analysis of their composition, potentially losing valuable 349 phytochemical information ^{19,20} as confirmed in this work. Twenty-six metabolites tentatively 350 identified in *n*-heptane extracts were fatty acyls, which is the group with the highest number of 351 annotated compounds (Table 5). Most of these compounds was identified in soy roots (18), followed 352 353 by leaves (13), branches (11), pods (8), and soybeans (6). Fatty acyls, such as hexadecenoic, octadecanoic, and eicosanoic acids, have been used in dermatologic, nutraceutical, and other industries 354 since they present anti-inflammatory properties and antibacterial activities.^{76,77} The second most 355 representative group of compounds present in *n*-heptane extracts was steroids and their derivatives, 356 with 14 annotated compounds. Particularly, *a*-tocopherol, campesterol, and stigmasterol were 357 identified in all soy by-products. α-Tocopherol has been used in nutraceutical and dermatological 358 applications, as it presents antioxidant, anti-inflammatory, and other human health benefits.^{78,79} On the 359 other hand, campesterol and stigmasterol have been explored for potential treatment of human ovarian 360 cancer and neuroprotective properties, respectively.^{80,81} Moreover, prenol lipids, phytosteroids, 361 unsaturated, and saturated hydrocarbons were identified in soy by-products, representing a diverse 362 363 range of compounds in such materials.

364

365 ABBREVIATIONS USED

- 366 United Nations (UN), Design of Experiment (DoE), Ultra-High Performance Liquid Chromatography-
- 367 PDA/UV-Mass Spectrometry (UHPLC-PDA/UV-MS), Global Natural Product Social Molecular
- 368 Networking (GNPS), Gas Chromatography- Mass Spectrometry, NIST (National Institute of
- 369 Standards and Technology), HPLC (High Performance Liquid Chromatography), P.A. (practical
- 370 grade), Two-Liquid-Phase Dynamic Maceration (2-Mac), Ethanol (EtOH), Methanol (MeOH), Formic
- 371 Acid (HCOOH), Electrospray Ionization (ESI), Central Composite Rotatable Design (CCDR), Ultra-
- 372 High-Performance Liquid Chromatography coupled to Time-Of-Flight Mass Spectrometry (UHPLC-
- 373 QToF-MS/MS), Gas Chromatography coupled to Time-of-Flight Mass Spectrometry (GC-QToF-MS).

374 SUPPORTING INFORMATION DESCRIPTION

- 375 Response surfaces and contour plots of all optimized methods (Figures S1-S3) and GC-QToF-MS
- 376 chromatogram of the individual soy by-products (Figure S4).
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FIGURE CAPTIONS



Figure 1. Representative UHPLC-PDA/UV-MS chromatograms of a mix of soy by-products (branches, leaves, pods, and roots) with beans. Column: Agilent Zorbax Eclipse Plus C18 column (150 mm \times 2.1 mm \times 1.8 µm). Mobile-phase: 0.1 % HCOOH in H₂O and MeOH from 15 to 100 % of MeOH in 60 min. Flow rate: 0.3 mL/min. Analysis temperature: 30 °C. Injection volume: 2 µL of non-concentrated EtOH-H₂O 7:3 (v/v) extract.



Figure 1. Representative optimized GC-MS chromatogram of the mix of soy by-products (branches, leaves, pods, and roots) with beans. Column: PerkinElmer Elite-5MS column (30 m × 0.25 mm, 0.25 μ m). Injector and MS transfer line temperature: 330 and 310 °C, respectively. Helium flow rate: 1.6 mL/min. Oven temperature: 150 °C (2 min); followed by 350 °C at the rate of 7 °C/min. Injection volume: 2 μ L of the non-concentrated n-heptane extract with a split flow of 5 mL/min.



Figure 3. Number of compounds identified in the different extracts of by-products and soybeans. They were grouped according to Classyfire³³. For annotation of the compound, please refer to Tables 4 and 5.

TABLES

Table 1. Experimental conditions determined by the two-factor central composite rotatable design foroptimization of an UHPLC-PDA/UV-MS condition for EtOH-H2O 7:3 (v/v) extracts

	Initial 0/ of D	% of UCOOU in	Total numbers of peaks							
Experiment	$\frac{1}{(x_1)^a}$	the M.P. $(x_2)^a$	254 nm (y1)	ESI(+) (y ₂)	ESI(-) (<i>y</i> 3)					
1	-1 (7.90)	-1 (0.16)	41	72	37					
2	1 (22.10)	-1 (0.16)	36	75	39					
3	-1 (7.90)	1 (0.44)	29	70	30					
4	1 (22.10)	1 (0.44)	27	70	31					
5	-1.41 (5)	0 (0.30)	32	73	33					
6	1.41 (25)	0 (0.30)	31	70	33					
7	0 (15)	-1.41 (0.10)	41	81	42					
8	0 (15)	1.41 (0.50)	32	72	36					
9 (CP) ^b	0 (15)	0 (0.30)	40	73	35					
10 (CP) ^b	0 (15)	0 (0.30)	41	73	36					
11 (CP) ^b	0 (15)	0 (0.30)	40	74	36					
12 (CP) ^b	0 (15)	0 (0.30)	40	73	40					
13 (CP) ^b	0 (15)	0 (0.30)	42	77	39					

^{*a*}Codified values are given without brackets, whereas the corresponding real values are indicated in Brackets; ^{*b*}Central point.

Table 2	. Two-factor	central comp	osite rotatable	design the op	timization of a	GC-MS cor	ndition for <i>n</i> -
heptane	extracts						

Evn ovim or 4	Ramp rate $(x_1)^a$	Carrier gas flow (<i>x</i> ₂) ^{<i>a</i>}	Total numbers of peaks
Experiment	(°C/min)	(mL/min)	(GC-MS)
1	-1 (4.60)	-1 (1.20)	56
2	1 (22.10)	-1 (1.20)	51
3	-1 (4.60)	1 (1.80)	44
4	1 (22.10)	1 (1.80)	61
5	-1.41 (4)	0 (1.50)	41
6	1.41 (8)	0 (1.50)	65
7	0 (6)	-1.41 (1.00)	50
8	0 (6)	1.41 (2.00)	56
9 (CP) ^b	0 (6)	0 (1.50)	67
10 (CP) ^b	0 (6)	0 (1.50)	65
11 (CP) ^b	0 (6)	0 (1.50)	66
12 (CP) ^b	0 (6)	0 (1.50)	59
13 (CP) ^b	0 (6)	0 (1.50)	61

^{*a*}Codified values are given without brackets, whereas the corresponding real values are indicated in Brackets; ^{*b*}Central point.

Evenoviment	Time	Temperature	Stirring	Granulometry	\sum number of peaks
Experiment	(min) $(x_1)^a$	(°C) $(x_2)^a$	(rpm) (<i>x</i> ₃) ^{<i>a</i>}	(mesh) $(x_4)^a$	(y) ^b
1	0 (20)	0 (35)	-0,75 (700)	1 (48)	268
2	0 (20)	1 (45)	0 (1000)	0 (31)	277
3	1 (35)	0,5 (40)	0 (1000)	0 (31)	274
4	0,33 (25)	0,5 (40)	1 (1400)	0 (31)	254
5	0,33 (25)	0,5 (40)	0,25 (1100)	1 (48)	293
6	0 (20)	-1 (25)	0 (1000)	0 (31)	212
7	-1 (5)	-0,5 (30)	0 (1000)	0 (31)	199
8	-0,33 (15)	-0,5 (30)	-1 (600)	0 (31)	255
9	-0,33 (15)	-0,5 (30)	-0,25 (900)	-1 (14)	183
10	-1 (5)	0,5 (40)	0 (1000)	0 (31)	244
11	-0,33 (15)	0,5 (40)	-1 (600)	0 (31)	239
12	-0,33 (15)	0,5 (40)	-0,25 (900)	-1 (14)	189
13	1 (35)	-0,5 (30)	0 (1000)	0 (31)	249
14	0,67 (30)	0 (35)	-1 (600)	0 (31)	235
15	0,67 (30)	0 (35)	-0,25 (900)	-1 (14)	222
16	0,33 (25)	-0,5 (30)	1 (1400)	0 (31)	236
17	-0,67 (10)	0 (35)	1 (1400)	0 (31)	233
18	0 (20)	0 (35)	0,75 (1300)	-1 (14)	206
19	0,33 (25)	-0,5 (30)	0,25 (1100)	1 (48)	279
20	-0,67 (10)	0 (35)	0,25 (1100)	1 (48)	244
21 (CP) ^c	0 (20)	0 (35)	0 (1000)	0 (31)	228
22 (CP) ^c	0 (20)	0 (35)	0 (1000)	0 (31)	268
23 (CP) ^c	0 (20)	0 (35)	0 (1000)	0 (31)	264
24 (CP) ^c	0 (20)	0 (35)	0 (1000)	0 (31)	238
25 (CP) ^c	0 (20)	0 (35)	0 (1000)	0 (31)	258

Table 3. Doehlert design with four variables (x) normalized to one, used for the optimization of a twoliquid phase extraction by dynamic maceration, and the result for each experiment (y).

^{*a*}Codified values are given without brackets, whereas the corresponding real values are indicated in Brackets; ^{*b*}The sum of number of peaks obtained by UHPLC-UV/MS (UV at 254 nm, and MS at positive and negative modes) and GC-MS for EtOH-H2O 7:3 (v/v) and n-heptane extract, respectively; ^{*c*}Central point.

Table 4. List of tentatively identified compounds in the EtOH- H_2O 7:3 (v/v) extracts of the soy by-products, branches (B), leaves (L), pods (P),and roots (R), and seeds (S) by UHPLC-ESI-QToF-MS.

Peak Number	Rt (min)	Tentative identification	Classification	Molecular formula	Molecular Ion	Measured mass (∆ ppm)	MS/MS fragments (relative abundance)	в	L	Р	R	s	Ref.
1	1.54	Acetyl-L-Carnitine	Fatty Acyls	C9H17NO4	$[M+H]^+$	204.123(-6.5)	85.0289 (100), 43.0190 (41.9), 87.0419 (29.8)		x		x		*
2	1.57	Adenine	Imidazopyrimidines	C5H5N5	$[M+H]^+$	136.0618(0.9)	119.0360 (100), 94.0520 (34.8), 82.0490 (17.1)	X	X	x	x		52
3	1.79	5'-Deoxy-5'-(methylsulfinyl)adenosine	5'-deoxyribonucleosides	C11H15N5O4S	$[M+H]^+$	314.0918(2.7)	136.0639 (100), 97.03099 (61.2), 164.0570 (10.7)	X			x		52–54
4	1.86	Meglutol	Fatty Acyls	C ₆ H ₁₀ O ₅	[M-H] ⁻	161.0455(8.4)	57.0359 (100), 59.0149 (33.1), 41.0040 (32.1)	X	x	x	x	X	55
5	1.88	Adenosine	Purine nucleosides	$C_{10}H_{13}N_5O_4$	[M+H] ⁺	268.104(-3.5)	136.0619 (100), 137.0610 (11), 119.0350 (8.8)	x	x	x	x	x	52–54

6	1.93	Tyrosine	Carboxylic acids and derivatives	C ₉ H ₁₁ NO ₃	$[M+H]^+$	182.0812(0.2)	91.0530 (100), 56.9430 (59.8), 136.0740 (49.6)				x	52,53
7	2.32	Pantothenic acid	Carboxylic acids and derivatives	C9H17NO5	[M-H] ⁻	218.1034(7.8)	71.0459 (100), 44.0149 (72.1), 88.0459 (64.6)	x	X	X	x x	52 ⁵²
8	2.37	N-Fructosyl isoleucine	Carboxylic acids and derivatives	C12H23NO7	$[M+H]^+$	294.1547(-4.2)	230.1269 (100), 258.1340 (99.9), 86.0940 (88.1)	x	X	X	x	*
9	2.58	3-[(2S,3R,4S,5S,6R)-6-[[(2R,3R,4R)-3,4- dihydroxy-4-(hydroxymethyl)oxolan-2- yl]oxymethyl]-3,4,5-trihydroxyoxan-2-yl]oxy-2-	Organooxygen compounds	C17H24O12	$[M+H]^+$	421.1341(2.5)	127.0390 (100), 69.0329 (11.3), 128.0410 (7.4) 317.0830 (100), 149.0189 (29.5)	x	x	x	x	*
	2.95	methylpyran-4-one			[M+Na]	443.116(-4.9)	149.0189 (29.5), 214.0879 (21.2)					
10	2.61	Leucine	Carboxylic acids and derivatives	C ₆ H ₁₃ NO ₂	$[M+H]^+$	132.1019(6)	72.9369 (100), 43.0499 (98.7), 44.0489 (71)	x	X	x	x	52,56,57
11	2.77	Pelargonin	Flavonoids	$C_{27}H_{31}O_{15}$	[M]	595.1657(5.6)	271.0639 (199), 433.1099 (77.9), 272.0669 (55.2			x	x	*
12	2.81	Dianthoside	Organooxygen compounds	C12H16O8	[M+H] ⁺	289.0918(1.1)	127.0390 (100), 256.0559 (11.1), 128.0449 (10.6)	x	x	x	x	*

13	2.92	Benzoic acid + 2O, O-Hex	Organooxygen compounds	$C_{13}H_{16}O_9$	[M-H] ⁻	315.0722(4.9)	109.0299 (100), 153.0209 (41.3)	x	x	x	x	X	*
14	3.43	Glutamyltyrosine	Carboxylic acids and derivatives	C14H18N2O6	$[M+H]^+$	311.1238(0.1)	136.0740 (100), 84.0439 (98), 165.0540 (77.3)			x		X	58
15	3.47	D-Pantothenic acid	Organooxygen compounds	C9H17NO5	$[M+H]^+$	220.1179(-3.4)	90.0540 (100), 58.0639 (27.8), 98.0220 (22.8)			x	X	X	52
16	3.64	Coatline B	Linear 1,3- diarylpropanoids	C ₂₁ H ₂₄ O ₁₁	[M-H] ⁻	451.1246(5.4)	149.0489 (100), 176.0359 (79.8), 207.0429 (77.8)				X		*
17	4.15	2,6-Dihydroxy-2-[(4-hydroxyphenyl)methyl]-4- [(2S,3R,4S,5S,6R)-3,4,5-trihydroxy-6- [[(2R,3R,4R,5R,6S)-3,4,5-trihydroxy-6- methyloxan-2-yl]oxymethyl]oxan-2-yl]oxy-1- benzofuran-3-one	Flavonoids	C27H32O15	[M-H] ⁻	595.1668(1.3)	269.0469 (100), 259.0639 (82.9), 125.0250 (47.1)					X	*
18	4.22	1-[2,4-Dihydroxy-3-[(2S,3R,4R,5S,6R)-3,4,5- trihydroxy-6-(hydroxymethyl)oxan-2-yl]phenyl]- 2-hydroxy-3-(4-hydroxyphenyl)propan-1-one	Linear 1,3- diarylpropanoids	C ₂₁ H ₂₄ O ₁₀	[M-H] ⁻	435.1297(4.9)	315.089 (100), 163.0410 (81.2), 190.0290 (76.5)	x		x	X	X	*
19	4.25	3,5-Dihydroxy-2-(4-hydroxyphenyl)-7-[3,4,5- trihydroxy-6-(hydroxymethyl)oxan-2-yl]oxy-2,3- dihydrochromen-4-one	Flavonoids	$C_{21}H_{22}O_{11}$	[M-H] ⁻	449.1089(5.5)	125.0260 (100), 259.0639 (46.8), 269.0480 (46)	x		x	x	x	*

20	4.36	12-Hydroxyjasmonate sulfate	Fatty Acyls	$C_{12}H_{18}O_7S$	[M-H] ⁻	305.07(9.4)	96.9629 (100), 59.0139 (43.7), 79.9580 (20.1)	X	X	X	X	X	*
21	4.39	Salicylamide	Phenols	C7H7NO2	[M-H] ⁻	136.0404(7.3)	41.9990 (100), 93.0350 (99.2), 91.0199 (33.2)	X		x	x	;	*
22	4.64	3-[(1-Carboxyvinyl)oxy]benzoic acid	Benzene and substituted derivatives	C ₁₀ H ₈ O ₅	[M-H] ⁻	207.0299(9.2)	93.0329 (100), 79.9560 (40.4), 135.0379 (25.3)				X	:	*
23	4.69	4-Hydroxycinnamic acid	Cinnamic acids and derivatives	C9H8O3	[M-H] ⁻	163.0401(8.8)	119.0490 (100), 93.0339 (53.6), 117.0189 (19.2)	x	х		X	x	56,57
24	4.79	Isoflavone base + 20, O-Hex	Isoflavonoids	C21H20O9	[M+HCOO] ⁻	461.1089(1.9)	253.0529 (100), 44.9980 (48.6), 252.0449 (48.3)	X		x	x	X	*
25	5.00	3-(4-hydroxyphenyl)-7-methoxy-5- [(3R,4S,5S,6R)-3,4,5-trihydroxy-6- (hydroxymethyl)oxan-2-yl]oxychromen-4-one	Isoflavonoids	C22H22O10	[M+FA-H] ⁻	491.1195(4.3)	283.0620 (100), 282.0580 (41.1), 445.1170 (36.5)				2	X	*
26	5.08	N-Acetyltryptophan	Carboxylic acids and derivatives	C ₁₃ H ₁₄ N ₂ O ₃	[M-H] ⁻	245.0932(9.1)	74.0250 (100), 58.0330 (63.3), 116.0500 (40.4)	X		x	x	X	59

27	5.15	Kaempferol 3-O-sophoroside	Flavonoids	$C_{27}H_{30}O_{16}$	[M-H] ⁻	609.1461(3.3)	284.0350 (100), 285.0419 (60.5), 255.0319 (28)	x	X	X		X	54
28	5.16	Prunin	Flavonoids	C ₂₁ H ₂₂ O ₁₀	[M-H] ⁻	433.114(6.6)	151.0040 (100), 119.0490 (58.1), 271.0640 (53.4)					X	60
29	5.32	Daidzin	Isoflavonoids	C ₂₁ H ₂₀ O ₉	[M-H] ⁻	415.1035(6.1)	252.0460 (100), 253.0520 (58.5), 223.0429 (35.6)	x		X	x	x	17,54,57,6 1–68
30	5.52	D-Tryptophan	Indoles and derivatives	$C_{11}H_{12}N_2O_2$	$[M+H]^+$	205.0972(-0.8)	146.0579 (100), 118.0660 (36.9), 144.0800 (25.6)	х	x	x	x	x	54,57,62
31	5.52	L-Tryptophan	Indoles and derivatives	$C_{11}H_{12}N_2O_2$	$[M+H]^+$	205.0972(-0.8)	118.0650 (100), 91.0530 (97.5), 115.0540 (65.7)	x	X	X	x	X	54,57,62
32	5.54	Indole-3-carboxyaldehyde	Indoles and derivatives	C9H7NO	[M-H] ⁻	144.0455(6.3)	115.0429 (100), 99.9260 (59.9), 65.9990 (44.1)	x		x	x		*
33	5.62	Luteolin 7-O-glucoside	Flavonoids	$C_{21}H_{20}O_{11}$	[M-H] ⁻	447.0933(6.3)	285.0429 (100), 286.0469 (34.9), 284.0360 (30.4)			X			57

34	5.65	5,7-Dihydroxy-2-(4-hydroxy-3-methoxyphenyl)- 3-[3,4,5-trihydroxy-6-[[(2R,3R,4R,5R,6S)-3,4,5- trihydroxy-6-methyloxan-2-yl]oxymethyl]oxan-2- yl]oxychromen-4-one	Flavonoids	C ₂₈ H ₃₂ O ₁₆	[M-H] ⁻	623.1618(3.6)	299.0230 (100), 314.0469 (56.4), 300.0419 (35.5)	X				*
35	5.78	Methylthioadenosine	5'-deoxyribonucleosides	C ₁₁ H ₁₅ N ₅ O ₃ S	$[M+H]^+$	298.0968(0.9)	136.0619 (100), 84.9589 (22.4), 61.0099 (11.2)				x	53,54
24	17.91				$[M+H]^+$	433.1129(1.1)	271.0580 (100), 272.0660 (20.7), 273.0650 (2.1)		v	37		69
36	6.19	Apigenin 7-O-glucoside*	Flavonoids	C ₂₁ H ₂₀ O ₁₀	[M-H] ⁻	431.0984(5.6)	268.0400 (100), 269.0459 (25.4), 211.0420 (8)	х	х	Х	2	<u>í</u>
37	6.05	Kaempferol 3-O-glucoside	Flavonoids	$C_{21}H_{20}O_{11}$	[M-H] ⁻	447.0933(3.6)	284.0350 (100), 255.0319 (88.3), 227.0379 (79.2)	x	x	x		70
38	6.26	Isoleucyl-glutamic acid	Carboxylic acids and derivatives	$C_{11}H_{20}N_2O_5$	$[M+H]^+$	261.1445(3.5)	84.0439 (100), 86.0960 (87.5), 44.0499 (15)	X	x		x	ζ *
39	6.37	Isoflavone base + 40, O-MalonylHex	Flavonoids	C24H22O14	[M-H] ⁻	533.0937(4.5)	285.0429 (100), 489.1090 (75), 284.0350 (58.6)	X		X		*
40	6.38	Benzenesulfonimidic acid	Benzene and substituted derivatives	C ₆ H ₇ NO ₂ S	[M-H] ⁻	156.0125(7.2)	63.9630 (100), 79.9639 (97.6), 92.0500 (73)			x	x	*

41	6.89	Formononetin 7-O-glucoside	Isoflavonoids	CarHarOa	[M+HCOO] ⁻	475.1246(3.4)	44.9980 (100), 267.0690 (91.4), 252.0460 (54.8)	x	x	x	x		54,61
	22.10	romononem 7-0-gracoside	isonavonolus	022112209	$[M+H]^+$	431.1337(-2.2)	269.0790 (100), 270.0820 (20.6), 213.0899 (10.9)	Λ	Λ	Λ	Λ		
42	6.97	Genistein	Isoflavonoids	$C_{15}H_{10}O_5$	[M-H] ⁻	269.0455(8)	117.0350 (100), 63.0239 (64.8), 65.029 (57.1)	x	x	X	x	X	17,61– 64,68
43	6.98	Kynurenic acid	Quinolines and derivatives	C10H7NO3	[M+H] ⁺	190.0499(4.9)	116.0479 (100), 89.0390 (83.8), 144.0420 (29.9)		x	x			60
44	7.01	Isoliquiritigenin	Linear 1,3- diarylpropanoids	C15H12O4	[M-H] ⁻	255.0663(9.1)	91.0189 (100), 119.0490 (81.7), 44.9990 (63.5)	x	x	x	x		71
45	7.36	Biochanin A	Isoflavonoids	C16H12O5	[M-H] ⁻	283.0612(5.3)	91.0189 (100), 211.0429 (91.1), 135.0099 (83.4)	х	x		x		54
46	7.57	4-O-Beta-D-glucosyl-trans-4-coumaric acid	Organooxygen compounds	$C_{15}H_{18}O_8$	[M+NH4] ⁺	344.134(-1.7)	147.0440 (100), 165.0540 (84.8), 85.0299 (60.3)			x			*
47	8.15	Naringenin	Flavonoids	C15H12O5	[M-H] ⁻	271.0612(9.2)	119.0500 (100), 65.0029 (54.2), 107.0139 (47.2)			x		x	59

48	8.62	Retusin 7-methyl ether	Isoflavonoids	$C_{17}H_{14}O_5$	[M-H] ⁻	297.0768(8.9)	239.0380 (199), 195.0470 (85.5), 117.0320 (80.5)	X	X	x	x		*
49	8.95	Neobavaisoflavone	Isoflavonoids	$C_{20}H_{18}O_4$	[M-H] ⁻	321.1132(9.6)	265.0530 (100), 277.0540 (58.3), 91.0190 (38.3)	X			x		57,61
50	9.07	(2S,3S,4S,5R,6R)-6-[[(3S,6aR,6bS,8aS,14bR)-8a- carboxy-4,4,6a,6b,11,11,14b-heptamethyl- 1,2,3,4a,5,6,7,8,9,10,12,12a,14,14a- tetradecahydropicen-3-yl]oxy]-3,4,5- trihydroxyoxane-2-carboxylic acid	Prenol lipids	C36H56O9	[M-H] ⁻	631.3852(4)	75.0090 (100, 85.0289 (86.9), 113.0210 (78.3)		X				*
51	9.09	2-Methyl-4-oxo-4H-pyran-3-yl 6-O-(4-carboxy-3- hydroxy-3-methylbutanoyl)-beta-D- glucopyranoside	Saccharolipids	C ₁₈ H ₂₄ O ₁₂	$[M+H]^+$	433.1341(-5.4)	127.0390 (100), 128.0410 (6.8), 85.0279 (6.6)	x	X	x	x	x	*
52	9.60	9-Hydroxy-10,12-octadecadienoic acid	Fatty Acyls	C ₁₈ H ₃₂ O ₃	[M-H] ⁻	295.2279(9.6)	277.2210 (100), 195.1410 (68.4), 59.0149 (56.9)		X	X	x	X	72
	10.69	1 (07 Ostadasaraul) ar alusara 2			[M+HCOO] ⁻	564.3307(3.2)	279.2359 (100), 78.9589 (32.3), 44.9980 (24.1)						
53	52.56	phosphoethanolamine	Glycerophospholipids	C ₂₆ H ₅₀ NO ₇ P	$[M+H]^+$	520.3398(-2.4)	184.0690 (100), 104.1029 (30.4), 89.9280 (19.4)	Х	х		Х	Х	*
54	11.23	2,4,6-Trihydroxy-2-[(4-hydroxyphenyl)methyl]-1- benzofuran-3-one	Aurone flavonoids	C15H12O6	$[M+H]^+$	289.0707(-3)	243.0630 (100), 215.0690 (68.8), 149.0240 (63.7)					x	*

55	12.28	Loliolide	Benzofurans	$C_{11}H_{16}O_3$	$[M+H]^+$	197.1172(-6.2)	133.1000 (100), 107.0859 (81.2), 179.1049 (44)		x				*
56	14.08	Biochanin A 7-O-glucoside	Isoflavonoids	C ₂₂ H ₂₂ O ₁₀	$[M+H]^+$	447.1286(-4.6)	285.0729 (100), 286.0780 (19.6), 270.0509 (9.3)			х		x	54
57	16.56	Undecaethylene glycol	Organooxygen compounds	C ₂₂ H ₄₆ O ₁₂	$[M+H]^+$	503.3062(-6)	45.0330 (100), 89.0589 (96.6), 133.0839 (34.9)	x					*
58	17.03	3-[(2S,4S,6R)-6-[[(2R,3R,4R,5S,6S)-3,5- dihydroxy-6-methyl-4-[(2S,3R,4S,5S,6R)-3,4,5- trihydroxy-6-(hydroxymethyl)oxan-2-yl]oxyoxan- 2-yl]oxymethyl]-3,4,5-trihydroxyoxan-2-yl]oxy- 5,7-dihydroxy-2-(4-hydroxyphenyl)chromen-4- one	Flavonoids	C ₃₃ H ₄₀ O ₂₀	[M+Na] ⁺	779.2005(-3.7)	493.1530 (100), 494.1539 (29.7), 347.0929 (8.7)	x	x	X			*
59	17.25	Genistin [¥]	Isoflavonoids	$C_{21}H_{20}O_{10}$	$[M+H]^+$	433.1129(-2.8)	271.0589 (100), 272.0629 (22.8), 153.0180 (7.5)	x		х	X	X	17,57,61– 65,67
60	17.28	Salipurposid	Flavonoids	C ₂₁ H ₂₂ O ₁₀	[M+Na] ⁺	457.1105(-8.1)	185.0429 (100), 295.0549 (91.8), 337.0520 (74.8)					x	*
61	17.78	Kaemnherol 3-0-(2 6-di-0-rhamnosyl)galactoside	Flavonoids	C22H40Q10	$[M+H]^+$	741.2237(-2.6)	287.0549 (100), 129.0540 (25.4), 288.0570 (19)	x	x	x			62
61	18.54			0,51140017	$[M+Na]^+$	763.2056(-3.4)	477.1579 (100), 478.1549 (23.6), 331.1000 (22)						

62	18.02	Kaempferol 3-O-beta-sophoroside	Flavonoids	C ₂₇ H ₃₀ O ₁₆	[M+Na] ⁺	633.1426(1.9)	347.0939 (100), 348.0989 (14.8), 308.0270 (7.2)	х	x	x	х	54
63	20.57	6"-O-Malonylglycitin	Isoflavonoids	C25H24O13	$[M+H]^+$	533.129(-4.8)	118.0640 (100), 91.0530 (64.8), 146.0580 (55.4)			x		54,62–64
64	20.76	6"-O-Malonyldaidzin	Isoflavonoids	C24H22O12	$[M+H]^+$	503.1184(-5.4)	255.0650 (100), 256.0660 (21.7), 199.0750 (2.36)	x		x	х	17,54,57,6 1–67
65	20.99	6"-O-Malonylgenistin	Isoflavonoids	C24H22O13	$[M+H]^+$	519.1133(-4.1)	271.0590 (100), 272.0650 (24.8), 153.0170 (3.0)				х	54,57,61– 65,67
66	25.33	Daidzein	Isoflavonoids	$C_{15}H_{10}O_4$	$[M+H]^+$	255.0652(-2.3)	137.0220 (100), 91.0530 (89.9), 199.0749 (73.9)	X		X	x x	17,54,56,5 7,61–68
67	27.22	Formononetin 7-O-glucoside-6"-O-malonate	Isoflavonoids	C25H24O12	$[M+H]^+$	517.1341(-4.4)	269.0799 (100), 270.0840 (17.5), 271.0880 (1.3)			x	х	57

*Means that no corresponding compound was reported in "soybean" or "Glycine max" on SciFinder.

¥Apigenin 7-O-glucoside and genistin present the same molecular formula and similar fragment ions in MS

 Table 5. List of tentatively identified compounds in the *n*-heptane extracts of the soy by-products, branches (B), leaves (L), pods (P), and roots

 (R), and seeds by GC-QToF-MS.

Peak Number	Rt (min)	Tentative identification	Classification	Match Factor	Molecular formula	B	L	Р	R	S	Ref.
1	7.29	4-Nonene, 3-methyl-, (Z)-	Unsaturated hydrocarbons	89.5	$C_{10}H_{20}$		X				*
2	7.30	1-Pentene, 3,3-dimethyl-	Unsaturated hydrocarbons	74.3	C ₇ H ₁₄			x			*
3	7.42	(S)-3-Ethyl-4-methylpentanol	Organooxygen compounds	73.7	C ₈ H ₁₈ O		X				*
4	7.61	1,3-Dioxolane, 4-methyl-2-propyl-	Dioxolanes	72.3	$C_7H_{14}O_2$			X			*
5	7.62	Decanoic acid, 3-methyl-	Fatty Acyls	79	$C_{11}H_{22}O_2$		Х				82
6	7.68	Methyl 2-hydroxydecanoate	Fatty Acyls	76.9	$C_{11}H_{22}O_3$		X				*
7	7.78	Cyclohexane, (1,2-dimethylbutyl)-	Saturated hydrocarbons	72.8	$C_{12}H_{24}$			x			*
8	7.95	Ethanone, 1-cyclopropyl-	Organooxygen compounds	81	C ₅ H ₈ O	x					*
9	8.09	4-Octene, 2,3,6,7-tetramethyl-	Unsaturated hydrocarbons	85.2	$C_{12}H_{24}$	x	x	x			*
10	8.87	2,4-Dimethylcyclopentanone	Organooxygen compounds	83.5	C ₇ H ₁₂ O		x				*
11	9.05	5-Undecene, 7-ethenyl-	Unsaturated hydrocarbons	72.7	C ₁₃ H ₂₄		x				*
12	10.02	3-Hepten-1-ol	Fatty Acyls	71	C7H14O			X			83
13	10.08	cis-7,10-hexadecadienal	Fatty Acyls	90.6	C ₁₆ H ₂₈ O				X	Х	*
14	10.17	1,6-Octadiene, 5,7-dimethyl-, (R)-	Unsaturated hydrocarbons	84.8	C10H18				x		*

15	10.41	Hexadecanoic acid	Fatty Acyls	89.5	$C_{16}H_{32}O_2$	X	X	X	X	X	84
16	10.50	17-Octadecynoic acid	Fatty Acyls	79.5	$C_{18}H_{32}O_2$				X		*
17	11.22	1,4,9-Decatriene, (E)-	Unsaturated hydrocarbons	82.1	C ₁₀ H ₁₆				x		*
18	11.99	E-2-Octadecadecen-1-ol	Organooxygen compounds	72.7	$C_{18}H_{36}O$		X				*
19	12.03	Cyclopentane	Unsaturated hydrocarbons	76.1	C_5H_8	x					*
20	12.30	Phytol	Prenol lipids	90.5	$C_{20}H_{40}O$		х				85,86
21	12.62	trans-13-Octadecenoic acid	Fatty Acyls	75.9	$C_{18}H_{34}O_2$	X	Х	X		X	87
22	12.64	9,12,15-Octadecatrienoic acid, (Z,Z,Z)-	Fatty Acyls	90.2	$C_{18}H_{30}O_2$	X	х	X	X	X	54,56,57
23	12.68	Oxalic acid, cyclohexyl hexyl ester	Carboxylic acids and derivatives	72.3	$C_{14}H_{24}O_4$		x				*
24	12.75	cis-Vaccenic acid	Fatty Acyls	89.7	$C_{18}H_{34}O_2$				X		88
25	12.94	9,12-Octadecadienoic acid, methyl ester, (E,E)-	Fatty Acyls	80.7	$C_{19}H_{34}O_2$				X		89
26	13.00	Octadecanoic acid	Fatty Acyls	87	$C_{18}H_{36}O_2$	Х	X	Х	Х	Х	90
27	13.13	Nonanamide	Fatty Acyls	70.4	C ₉ H ₁₉ NO		Х				*
28	13.17	Hexadecanamide	Fatty Acyls	81.3	C ₁₆ H ₃₃ NO	X			X		70
29	14.56	2-(2,3-dimethylcyclopentyl)propan-1-ol	Prenol lipids	82.4	$C_{10}H_{20}O$		X				*
30	14.57	Cyclopentane, 1-methyl-3-(1-methylethyl)-	Saturated hydrocarbons	77.8	C9H18				x		*
31	14.59	4-Undecene, 6-methyl-	Unsaturated hydrocarbons	82.1	$C_{12}H_{24}$	x					*
32	15.00	E,Z-2,13-Octadecadien-1-ol	Fatty Acyls	71.2	C ₁₈ H ₃₄ O				X		*
33	15.00	Cyclohexanemethanol	Organooxygen compounds	81.5	C ₇ H ₁₄ O		X				*

34	15.35	9-Octadecenamide, (Z)-	Fatty Acyls	88.7	C ₁₈ H ₃₅ NO				X		91
35	15.39	Eicosanoic acid	Fatty Acyls	84.3	$C_{20}H_{40}O_2$	X	Х	X	X		92
36	15.52	Bicyclo[5.2.0]nonane, 4-methylene-2,8,8-trimethyl-2-vinyl-	Unsaturated hydrocarbons	79	C ₁₅ H ₂₄		X				*
37	15.65	Tetradecanamide	Fatty Acyls	78.5	C14H29NO	Х			X		93
38	16.60	Methyl (8Z,11Z,14Z,17Z)-icosa-8,11,14,17-tetraenoate	Fatty Acyls	70.3	$C_{21}H_{34}O_2$					X	*
39	16.61	1,Z-5,E-7-Dodecatriene	Unsaturated hydrocarbons	74.3	C ₁₂ H ₂₀	x					*
40	16.96	5-Undecene, 4-methyl-	Unsaturated hydrocarbons	77.6	C ₁₂ H ₂₄	x					*
41	17.89	Heptanoic acid	Fatty Acyls	91.6	$C_{7}H_{14}O_{2}$				X		94
42	19.16	5-Octen-4-one, 7-methyl-	Organooxygen compounds	71.3	C ₉ H ₁₆ O				x		*
43	19.92	13-Docosenamide, (Z)-	Fatty Acyls	82.5	C ₂₂ H ₄₃ NO	Х	х		X		*
44	20.30	Squalene	Prenol lipids	88.2	C ₃₀ H ₅₀		х				95
45	20.30	(3E,7E)-4,8,12-Trimethyltrideca-1,3,7,11-tetraene	Prenol lipids	76.6	C ₁₆ H ₂₆	Х					*
46	20.87	Docosanoic acid	Fatty Acyls	70.3	$C_{22}H_{44}O_2$				X		92
47	21.18	Octane, 3-ethyl-2,7-dimethyl-	Saturated hydrocarbons	76.6	$C_{12}H_{26}$				x		*
48	21.19	Nonacosane	Saturated hydrocarbons	70.8	C29H60			х			*
49	21.35	1,3-Bis-(2-cyclopropyl,2-methylcyclopropyl)-but-2-en-1-one	Prenol lipids	85.4	$C_{18}H_{26}O$		Х		X		*
50	21.55	delta-Tocopherol	Prenol lipids	90.6	C ₂₇ H ₄₆ O ₂		X	X	X	X	96
51	22.10	Ergost-5-en-3-ol, acetate, (3.beta.,24R)-	Steroids and steroid derivatives	77.9	$C_{30}H_{50}O_2$	x	x	x			*

52	22.35	Cholesta-6,22,24-triene, 4,4-dimethyl-	Steroids and steroid derivatives	78.5	C ₂₉ H ₄₆	x	x		X		*
53	22.40	.betaTocopherol	Prenol lipids	84.1	$C_{28}H_{48}O_2$		Х				97
54	22.54	.gammaTocopherol	Prenol lipids	90.3	$C_{28}H_{48}O_2$	X	X		Х	X	96–98
55	22.59	4,7,10,13,16,19-Docosahexaenoic acid, methyl ester, (all-Z)-	Fatty Acyls	73.8	$C_{23}H_{34}O_2$				Х		*
56	22.72	Cholesta-4,6-dien-3-ol, (3.beta.)-	Steroids and steroid derivatives	70.5	C ₂₇ H ₄₄ O		x				*
57	23.08	(S)-4-methyloctadecanal	Fatty Acyls	96.1	C ₁₉ H ₃₈ O	X	Х	X	Х		*
58	23.09	Heptacosane	Saturated hydrocarbons	79.8	C ₂₇ H ₅₆	X					99,100
59	23.09	(R)-4-methyloctadecanal	Fatty Acyls	94.1	C ₁₉ H ₃₈ O		X	X	Х		*
60	23.29	alpha-Tocopherol	Prenol lipids	92.7	$C_{29}H_{50}O_2$	x	х	x	Х	x	97,98,10 1
61	23.98	Ergosterol	Steroids and steroid derivatives	85.2	C ₂₈ H ₄₄ O	x	x		X		102,103
62	24.17	Campesterol	Steroids and steroid derivatives	83.7	C ₂₈ H ₄₈ O	x	x	X	X	x	95,101
63	24.40	Stigmasterol	Steroids and steroid derivatives	91.2	C ₂₉ H ₄₈ O	x	x	X	X	x	103
64	24.76	Obtusifoliol	Steroids and steroid derivatives	79.1	C ₃₀ H ₅₀ O		x				91,104,1 05
65	24.84	Cholesta-22,24-dien-5-ol, 4,4-dimethyl-	Steroids and steroid derivatives	84.3	C ₂₉ H ₄₈ O				X		*
66	24.86	Vitamin A	Prenol lipids	72	C ₂₀ H ₃₀ O			X			*

67	24.86	Pentacosane	Saturated hydrocarbons	88	C ₂₅ H ₅₂	х				96,100
68	24.96	.betaSitosterol	Steroids and steroid derivatives	93.1	C ₂₉ H ₅₀ O	x	x		x x	103
69	25.06	Stigmastanol	Steroids and steroid derivatives	77.9	C ₂₉ H ₅₂ O				x	106,107
70	25.29	Cholesta-8,24-dien-3-ol, 4-methyl-, (3.beta.,4.alpha.)-	Steroids and steroid derivatives	72.4	C ₂₈ H ₄₆ O	x				*
71	25.38	Stigmastane, 3-oxo-	Steroids and steroid derivatives	79.8	C ₂₉ H ₅₀ O				x	*
72	25.46	2H-Cyclopropa[g]benzofuran, 4,5,5a,6,6a,6b-hexahydro-4,4,6b-trimethyl-2-(1-methylethenyl)-	Dihydrofurans	85.6	C ₁₅ H ₂₂ O		x			*
73	25.46	Ergosta-4,6,8(14),22-tetraen-3-one	Steroids and steroid derivatives	79.9	C ₂₈ H ₄₀ O				x	*
74	25.52	4,22-Stigmastadiene-3-one	Steroids and steroid derivatives	86.9	C ₂₉ H ₄₆ O	x			x	*
75	25.72	Lupeol	Prenol lipids	85.3	C ₃₀ H ₅₀ O	X		Х	X	105
76	26.93	7,11,15-trimethyl-3-methylidenehexadec-1-ene	Prenol lipids	82.9	$C_{20}H_{38}$		Х			*
77	28.36	Isopropyl linoleate	Fatty Acyls	81.7	C ₂₁ H ₃₈ O ₂	X	X			*
78	30.11	Eicosanoic acid, octadecyl ester	Fatty Acyls	73.2	C ₃₈ H ₇₆ O ₂	X	X			*
79	32.11	1,6,10,14-Hexadecatetraen-3-ol, 3,7,11,15-tetramethyl-, (E,E)-	Prenol lipids	77.5	C ₂₀ H ₃₄ O		X			*

*Means that no corresponding compound was reported in "soybean" or "Glycine max" on SciFinder.

GRAPHIC FOR TABLE OF CONTENTS



"For Table of Contents Only"

METABOLITE PROFILING OF SOY BY-PRODUCTS: A COMPREHENSIVE APPROACH

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SUPPORTING INFORMATION



Figure S1. Response surface and contour plot for the total number of peaks in UHPLC-PDA/UV at 254 nm (A), and UHPLC-MS in positive (B) and negative mode (C), respectively, as a function of the variables x_1 (initial % of B) and x_2 (% of HCOOH in the M.P.)



Figure S2. Response surface and contour plot for the total number of peaks GC-MS as a function of the variables x_1 (Ramp rate - °C/min) and x_2 (carrier gas flow – mL/min)



Figure S3. Response surface and contour plot for the 2-Mac using the sum of total number of peaks in UHPLC-PDA/UV-MS and GC-MS as a function of the variables x_1 (time - min), x_2 (temperature – °C), and x_4 (granulometry – mesh size)



Figure S4. Representative optimized GC-QToF-MS chromatogram of the individual soy by-products, i.e., branches (A), leaves (B), pods (C), and roots(D), and soybeans (E). Column: Agilent Zorbax DB5- MS+10 m – Duragard Capillary Column $(30 \text{ m} \times 250 \text{ }\mu\text{m} \times 0.25 \text{ }\mu\text{m})$. Injector and MS transfer line temperature: 330 and 310 °C, respectively. Helium flow rate: 1.6 mL/min. Oven temperature: 150 °C (2 min); followed by 350 °C at the rate of 7 °C/min. Injection volume: 1 μ L of *n*-heptane extract (10 mg/mL) with a split flow of 8.4 mL/min.