

## Metabolomics Approach using LC-Orbitrap High Resolution Mass Spectrometry and Chemometrics for Authentication of Beef Meats from Different Origins in Indonesia

(Pendekatan Metabolomik menggunakan Spektrometri Jisim Resolusi Tinggi LC-Orbitrap dan Kemometrik untuk Pengesahan Daging Lembu daripada Asalan Berbeza di Indonesia)

ANJAR WINDARSIH<sup>1,2</sup>, ABDUL ROHMAN<sup>3,4,\*</sup>, NOR KARTINI ABU BAKAR<sup>1</sup> & YUNY ERWANTO<sup>4,5</sup>

<sup>1</sup>Department of Chemistry, Faculty of Science, University of Malaya, 50603 Kuala Lumpur, Malaysia

<sup>2</sup>Research Center for Food Technology and Processing (PRTPP), National Research and Innovation Agency (BRIN), Yogyakarta, 55861, Indonesia

<sup>3</sup>Department of Pharmaceutical Chemistry, Faculty of Pharmacy, Universitas Gadjah Mada, Yogyakarta, 55281, Indonesia

<sup>4</sup>Halal Centre, Universitas Gadjah Mada, Yogyakarta, 55281, Indonesia

<sup>5</sup>Faculty of Animal Science, Universitas Gadjah Mada, Yogyakarta 55281, Indonesia

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### ABSTRACT

Beef is one of the favourite meats consumed by people worldwide due to its high nutrition value needed by human development. It is highly susceptible for the adulteration practice by substituting beef with lower price meats by unethical meat traders due to the economic reasons. Therefore, the authenticity of beef meat (BM) is important because it is also related to halal status of meat which is required for certain religions. This research aimed to differentiate metabolites of BM from different origins using liquid chromatography-high resolution mass spectrometry (LC-HRMS) combined with chemometrics for the authentication purposes. Various metabolites mostly amino acids and lipids could be detected using methanol extraction. Principal component analysis (PCA), partial least square-discriminant analysis (PLS-DA) and sparse PLS-DA were successfully used to discriminate BMs from different origins. Fifty potential metabolite markers which are important for discrimination have been identified using variable importance projection (VIP) value extracted from PLS-DA analysis. Metabolites of (4S)-4-[(9Z)-3-Hydroxy-9-hexadecenoyl]oxy}-4-(trimethylammonio)butanoate, N,N-Diisopropylethylamine (DIPEA), D-sphingosine, (2E,4Z)-N-Isobutyl-2,4-octadecadienamide, 1-(14-methylhexadecanoyl)pyrrolidine, linoleic acid, 12-HAS, dodecylamine1, myristamide, and tributyl phosphate had high responsibility in discriminating BMs from different origins (VIP value > 2.0). It can be concluded that LC-HRMS based untargeted metabolomics combined with chemometrics could be used for authentication of BMs from different regions.

Keywords: Beef meat; *halal* authentication; LC- HRMS; PLS-DA; untargeted metabolomics

### ABSTRAK

Daging lembu ialah salah satu daging kegemaran yang dimakan di seluruh dunia kerana nilai pemakanannya yang tinggi yang diperlukan oleh tumbesaran manusia. Ia sangat terdedah kepada amalan pemalsuan dengan menggantikan daging lembu dengan harga daging yang lebih rendah oleh peniaga daging yang tidak beretika atas sebab ekonomi. Oleh itu, keaslian daging lembu (BM) adalah penting kerana ia juga berkaitan dengan status halal daging yang dituntut bagi agama tertentu. Penyelidikan ini bertujuan untuk membezakan metabolit BM daripada punca yang berbeza menggunakan spektrometri jisim resolusi tinggi kromatografi cecair (LC-HRMS) digabungkan dengan kemometrik untuk tujuan pengesahan. Pelbagai metabolit kebanyakannya asid amino dan lipid boleh dikesan menggunakan pengekstrakan metanol. Analisis komponen utama (PCA), analisis diskriminasi kuasa dua terkecil separa (PLS-DA) dan jarang PLS-DA berjaya digunakan untuk mendiskriminasi BM daripada punca yang berbeza. Lima puluh penanda

metabolit berpotensi yang penting untuk diskriminasi telah dikenal pasti menggunakan nilai unjuran kepentingan berubah (VIP) yang diekstrak daripada analisis PLS-DA. Metabolit (4S)-4-{{[(9Z)-3-Hidroksi-9-heksadesenoil]oksi}}-4-(trimetilammonio)butanoate, N,N-Diisopropylethylamine (DIPEA), D-sphingosine, (2E,4Z) -N-Isobutyl-2,4-octadecadienamida, 1-(14-metilheksadesenoil)pyrrolidina, asid linoleik, 12-HAS, dodecylamine1, myristamide dan tributil fosfat mempunyai tanggungjawab yang tinggi dalam mendiskriminasi BM daripada punca yang berbeza (nilai VIP > 2.0). Dapat disimpulkan bahawa metabolomik tidak disasarkan berasaskan LC-HRMS digabungkan dengan kemometrik boleh digunakan untuk pengesahan BM dari kawasan yang berbeza.

**Kata kunci:** Daging lembu; pengesahan halal; LC- HRMS; PLS-DA; metabolomik tidak disasarkan

## INTRODUCTION

Food authenticity is an important issue due to the increased reports of mislabelling, substitution, and adulteration in the food products. The main objective of these fraudulent practices is for economic reasons to gain more profits, for instance, high quality foods are often adulterated using lower price foods (Böhme et al. 2019). However, the adulteration is obviously associated with some negative impacts that could affect the quality and safety of food products (Schieber 2018). In addition, the adulteration using non-halal components such as in meat and meat-based food products is also a serious concern because several religions such as Muslim and Jewish have strict rule to avoid the consumption of non-halal meats (Martuscelli et al. 2020). The consumption of meat and meat products has increased every year which makes the increasing demand on meats. However, meat is susceptible for the adulteration practice because it is easy to blend high quality meat with other meats from other species without any significant change in visual appearance (Owolabi & Olayinka 2021). Beef meat (BM) is consumed worldwide due to its nutrition values which are benefits for the human health. Due to its high price of high-quality BM, BM is subjected to be adulterated using lower price and non-halal meats such as pork (Pranata et al. 2021). Therefore, the authentication of BM is required to ensure its authenticity, quality, and safety.

Numerous analytical methods could be used for the authentication of BM such as chromatographic-based methods including gas chromatography coupled with flame ionization and mass spectrometer detectors and liquid chromatography hyphenated with various detectors including UV-Vis, fluorescence, photodiode array, and mass spectrometer (Häfner, Kalkhof & Jira 2021; Perez-Palacios et al. 2022; Von Barga, Brockmeyer & Humpf 2014). Rapid methods based on vibrational spectroscopic techniques such as Fourier transform infrared (FTIR) (Rohman et al. 2016), near infrared

(NIR) (Leng et al. 2020), and Raman spectroscopy combined with chemometrics (Motoyama et al. 2018) have been used for the meat authentication using their fingerprint spectra. Currently, analytical methods for metabolomics approach such as nuclear magnetic resonance spectrometry (NMR) (Wang et al. 2020), gas chromatography mass spectrometry (GC-MS) (Trimigno et al. 2018), liquid chromatography mass spectrometry (LC-MS) (Jia et al. 2021) have been developed for food authentication including meat and meat products. Liquid chromatography high resolution mass spectrometry using time of flight (TOF) and Orbitrap mass analyser provides high resolving power associated to high sensitivity and high specificity for analysis of food products (Chan et al. 2021; Panseri et al. 2022). Powerful statistical analysis such as chemometrics or multivariate data analysis has been employed for treating big data analysis coming from instrumental responses obtained from metabolomics studies. Chemometrics is capable of processing and handling the vast number of data becoming more interpretable (Callao & Ruisánchez 2018).

The authentication of BM from different geographical origins (Australia, Korea, New Zealand, and United States) has been performed by metabolomics approach using NMR spectroscopy combined with principal component analysis (PCA) and orthogonal projections to latent structures-discriminant analysis (OPLS-DA) (Jung et al. 2010). Metabolomics analysis for authentication of BF from Japan, United States, and Australia has been successfully carried out by using LC-HRMS and GC-MS. The detailed chemical compositions could be obtained using these approaches which are important for BF differentiation (Man et al. 2021). In addition, lipidomics approaches using DART-QTOF (direct analysis in real time-quadrupole time of flight) and LC-ESI-QTOF (liquid chromatography-electrospray ionization-quadrupole time of flight) have been applied for differentiation of

BMs from six different countries, namely Argentina, Brazil, Canada, Australia, New Zealand and Uruguay. PCA and support vector machine (SVM) were applied for metabolite discrimination (Wang et al. 2021).

However, to the best of our knowledge, reports on the authentication study of BMs from different origins in Indonesia are still lacking. Therefore, this research was conducted to apply an LC-HRMS technique for metabolomics analysis in combination with PCA, PLS-DA, and sparse PLS-DA for authentication of BMs from different origins in Indonesia. Therefore, this study was important to ensure the authenticity of BMs which are related to the quality, safety, as well as halal status of beef meats to protect consumers from product's mislabelling and adulteration practices.

## MATERIALS AND METHODS

### CHEMICALS

The solvents of methanol and water (LC-MS grade) were purchased from Thermo Fisher (Thermo Scientific, USA). HPLC grade methanol and formic acid analytical grade were obtained from Merck (Darmstadt, Germany). The calibration solution for both ESI positive and ESI negative calibration was purchased from Thermo Fisher (Thermo Scientific, USA).

### BEEF MEAT COLLECTION AND PREPARATION

Beef meats (BMs) were purchased from ten different regions in Indonesia; namely Borobudur (B1), Muntilan (B2), Tempel (B3), Klaten (B4), Gunungkidul (B5), Yogyakarta (B6), Bantul 1 (B7), Gamping (B8), Godean (B9), and Bantul 2 (B10). The BMs were obtained from three bovines (*Bos taurus*) from the loin part for each region. Samples were stored in the freezer (-20 °C) prior being used for extraction.

### SAMPLES EXTRACTION

The BM samples from each different region were ground using a meat grinder (Tummy, China). Amount of  $100 \pm 5$  mg sample was weighed using an analytical balance and placed into a 2 mL centrifuge tube. Sample was added with 1 mL of LC-MS grade methanol for metabolite extraction. Subsequently, the sample was vortexed (Nemco, Velp Scientifica, Italy) at room temperature (25 °C) for 2 min. After that, ultrasonication (Elmasonic S 60 H, Elma, Germany) was performed for deeper extraction of the metabolites at room temperature for 30 min. Centrifugation (Megafuge 8R, Thermo Scientific,

USA) at 5000 rpm for 10 min was performed to separate pellet and supernatant. The supernatant was pipetted from each tube and a PTFE filter (0.22  $\mu$ m) was used to filter the supernatant into a clear HPLC glass vial.

### UNTARGETED METABOLOMICS USING LC-HRMS

A liquid chromatography (UHPLC Vanquish, Thermo Scientific, USA) connected with a mass spectrometer with high resolution (Q-Exactive, Orbitrap, Thermo Scientific, USA) was used for metabolomics analysis. The method used was according to previous method by Windarsih et al. (2022) with modification. Metabolite separation from methanol extract of meats was performed using an analytical column Accucore C18 (10 mm  $\times$  2.1 mm ID  $\times$  2.6  $\mu$ m). The mobile phase used was water (A) and methanol (B), both containing 0.1% formic acid. Samples were injected at 10  $\mu$ L and eluted with flow of 0.3 mL/min. The elution used was gradient mode as follows: 0-5 min (5% B), 5-16 min (5% B – 90% B), 16-20 min (90% B), 20-25 min (95% B – 5% B). The parameters for MS condition such as capillary temperature was set at 320 °C, sheath gas flow rate was 32 AU, and auxiliary gas flow rate was 8 AU. The spray voltage was 3.5 kV with collision energy of 10 NCE. Analysis was performed both in full MS and dd-MS2 with resolution of 70,000 and 17,500, respectively. Scanning was performed either using positive and negative ionization modes.

### DATA ANALYSIS

The total ion chromatogram (TIC) was exported using XCalibur (Thermo Scientific, USA). Compound Discoverer software (Thermo Scientific, USA) was used for data processing such as peak alignment, peak integration, baseline correction, and background correction. The identification of metabolites from TIC used untargeted metabolomics workflow. The metabolites were identified against databases of MzCloud (<https://www.mzcloud.org/>) and ChemSpider (<http://www.chemspider.com/>). Metabolites which have full match with MzCloud and ChemSpider were selected. The resulted compounds were filtered according to MS2 of DDA for preferred ion, mass tolerance of 5 ppm, and retention time tolerance of 0.2 min.

### CHEMOMETRICS ANALYSIS

Data pre-processing was carried out using MetaboAnalyst 5.0 prior to chemometrics analysis including normalization and data scaling. The metabolites and their peak area were used as variables during the chemometrics modelling.

Sum area was chosen for data normalization whereas auto-scaling was selected for data scaling. Chemometrics analysis was performed using MetaboAnalyst 5.0. Principal component analysis (PCA) was initially used to identify pattern of BM from different origins. Then, partial least square-discriminant analysis (PLS-DA) and sparse PLS-DA (sPLS-DA) was applied for the discrimination and classification of samples. The discriminating metabolites having important roles in meat differentiation among origins was observed from the PLS-DA model using variable importance for projections (VIP) value.

## RESULTS AND DISCUSSIONS

### LC-ORBITRAP HRMS BASED METABOLOMICS

The metabolites of BMs from different origins in Indonesia was successfully analysed using LC-Orbitrap HRMS. A total of 208 metabolites was annotated from both positive and negative ionization modes (Table S1). Various metabolites include amino acids, peptides, nucleotides, and lipids were found in BM extracted using methanol indicating high coverage of extraction using methanol. It has been reported that methanol become the most common extraction solvent used for the metabolomics analysis in plasma and tissue samples due to its high coverage to extract compounds (Zeki et al. 2020).

The amino acids contained in BMs obtained from this study were varied such as DL-lysine, L-histidine, N6,N6,N6-trimethyl-L-lysine, DL-alanine, D-(+)-Proline, L-glutamic acid, DL-glutamine, L-pyroglutamic acid, L-(-)-threonine, L-(-)-methionine, L-isoleucine, L-tyrosine, L-norleucine, alanyltyrosine, L-phenylalanine, DL-tryptophan, and leucylproline. Some lipids compound from different lipid classes were also found in BMs such as palmitoyl sphingomyelin, PC(o-18:0/18:2(9Z,12Z)), 1-stearoylglycerol, 1-oleoyl-2-hydroxy-sn-glycero-3-PE, lysoPC(18:3(9Z,12Z,15Z)), and fatty acids (oleic acid, linoleic acid,  $\gamma$ -linolenic acid, palmitoleic acid, 8Z,11Z,14Z-eicosatrienoic acid, 3-(Icosanoyloxy)-4-(trimethylammonio)butanoate, 3-[(12-hydroxyoctadecanoyl)oxy]-4-(trimethylammonio)butanoate, (4S)-4-[(9Z,12Z,15Z)-9,12,15-octadecatrienoyloxy]-4-(trimethylammonio)butanoate, and (4S)-4-[(9Z)-3-hydroxy-9-hexadecenoyl]oxy)-4-(trimethylammonio)butanoate). The amino acids and lipids varied among BMs from

different origins as shown by the variation in the peak area. Therefore, the information on the metabolite compositions is important for differentiation and discrimination of BM from the different origins. Moreover, the metabolites composition could be further used for developing the discrimination and classification models using chemometrics analysis.

Previous research on the metabolomics analysis for differentiation of BM obtained from Australia, Korea, New Zealand, and United States using <sup>1</sup>H-NMR technique demonstrated that the signals of carnosine and anserine were dominant in all samples. In addition, various amino acids such as glutamine, glutamate, tyrosine, phenylalanine, methionine, valine, leucine, isoleucine, and alanine were also found (Jung et al. 2010). Another study on the metabolomics analysis for differentiation of BM from Japan, Australia, and United States using a modified Bligh and Dyer extraction method showed different metabolites either polar such as amino acids and non-polar such as lipids in BM (Man et al. 2021). In the present study, the use of methanol as extraction solvent could extract various metabolites from polar to semi polar.

### ANALYSIS USING PRINCIPAL COMPONENT ANALYSIS (PCA)

PCA was applied to identify pattern of BM from different origins. Five principal components (PC) from PCA were successfully used to differentiate beef meat from different regions as depicted in the PCA score plot (Figure 1). BMs were clustered into four main clusters. The first cluster consist of beef B1, B4, B5, B6, and B7 which appeared in one tight cluster. Secondly, BMs of B8 and B9 are grouped into the similar area. Meanwhile BF of B2 appeared in one cluster close to the first cluster. The last, BM of B10 appeared in a different region far from the other clusters. Based on PCA's loading plots, the metabolites of hypaphorine, acetyl methyl choline, 3-Methylsulfolene, and inosine-5-monophosphate were responsible for differentiation of BM B10 (Bantul 2) among others. These compounds were significantly found in high peak area in B10, as shown in the Box-plot (Figure 2).

Samples which appeared close to each other in PCA score plot indicated their high similarity in their metabolite compositions, whereas samples which observed far from other samples indicated the high dissimilarity meaning the more differences in their

metabolite compositions. PCA is an unsupervised pattern recognition of qualitative chemometrics analysis to recognize pattern by reducing the vast number of variables into principal components (PC) (Worley & Powers 2016). It has been widely used as the first step in metabolomics analysis to identify pattern without time consuming. Previous study reported that PCA could be used to differentiate BM from six countries (Argentina, Australia, Brazil, Canada, New Zealand, and Uruguay) using the lipid compounds (Wang et al. 2021). In addition, PCA has also been successfully used in other meat research such as differentiation of concentrate-fed and pasture-fed of goat meat (Wang et al. 2021), and

differentiation of normally slaughtered and dead-on chicken meat (Sidwick et al. 2017).

The information in PCA analysis is essential to know the metabolite compositions of beef meat from different origins. The PCA analysis is very useful for differentiation of beef meats from different origins based on the similarity and dissimilarity of their metabolite compositions. It can be very helpful when choosing beef meat with certain metabolites target by using PCA. The PCA analysis is also important to authenticate beef meat from each origin that support the halal authentication to ensure the halal authenticity of beef meats obtained from different origins.

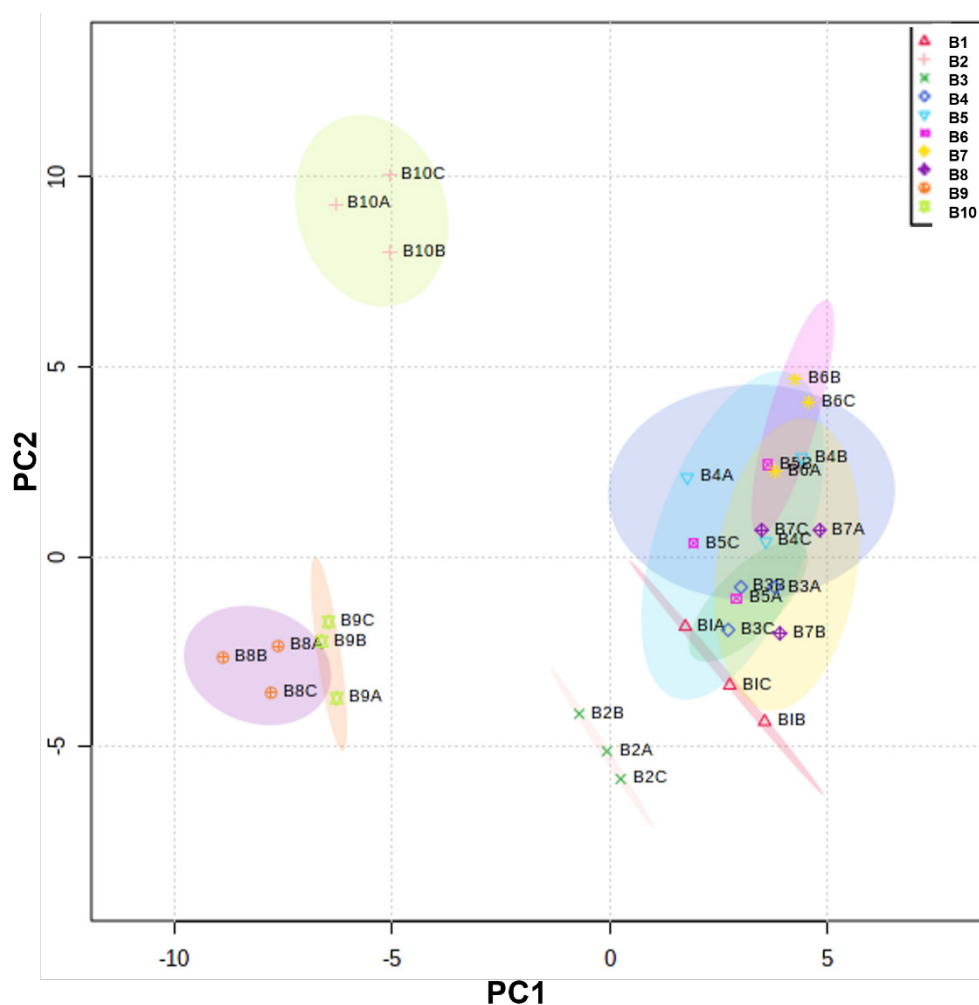


FIGURE 1. Principal component analysis (PCA) of beef meat obtained from different origins in Indonesia (B1=Borobudur, B2=Muntilan, B3=Tempel, B4=Klaten, B5=Gunungkidul, B6=Yogyakarta, B7=Bantul 1, B8=Gamping, B9=Godean, and B10=Bantul 2; each region was measured in three replicates)

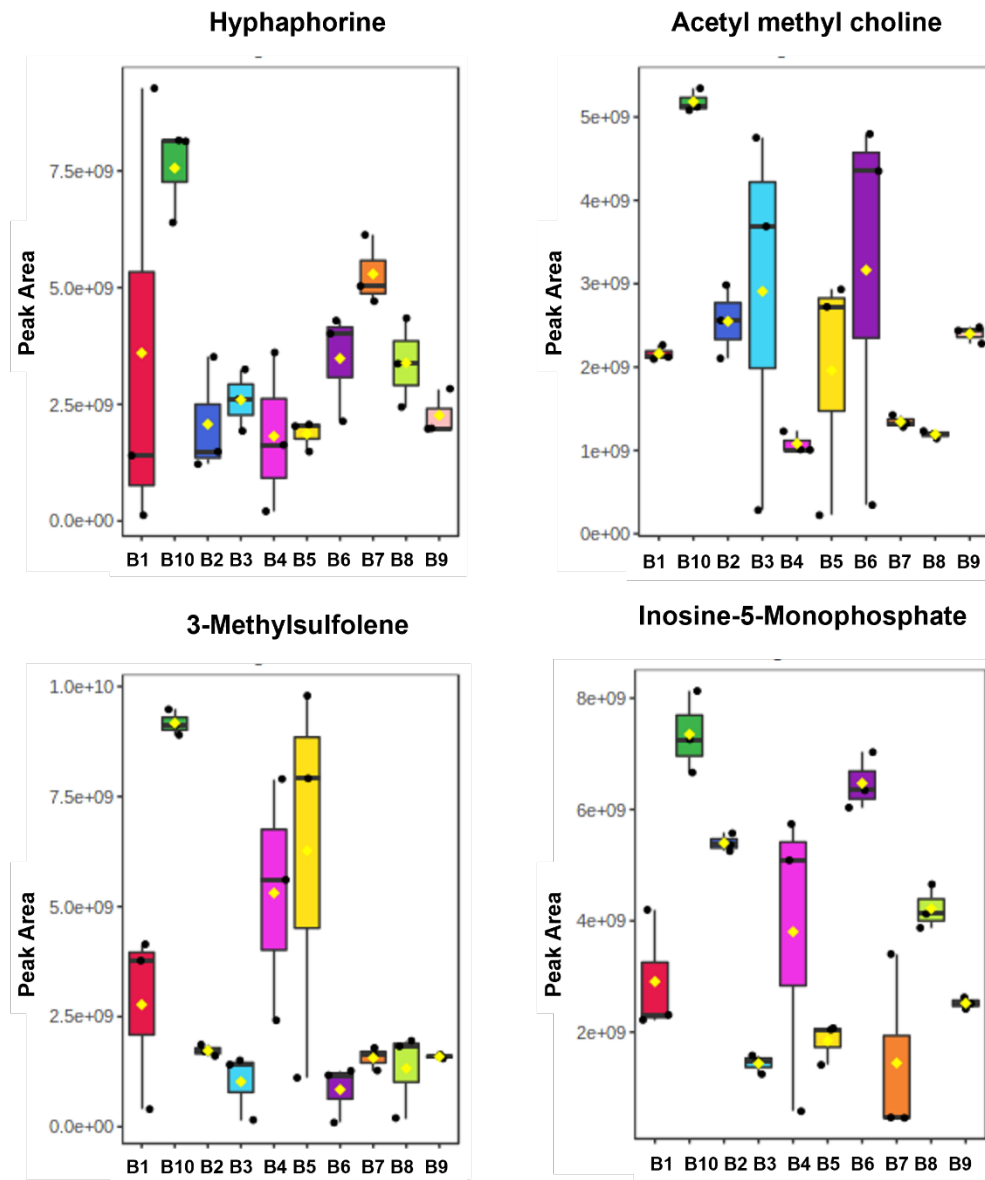


FIGURE 2. Box-plot of metabolites from PCA loading plot responsible for differentiation of beef meat B10 (B1=Borobudur, B2=Muntilan, B3=Tempel, B4=Klaten, B5=Gunungkidul, B6=Yogyakarta, B7=Bantul 1, B8=Gamping, B9=Godean, and B10=Bantul 2)

CLASSIFICATION USING SUPERVISED PATTERN  
RECOGNITIONS

Analysis using PLS-DA was successfully used for discrimination and classification of BMs from different origins. The result differs from the differentiation result obtained from PCA analysis. PLS-DA could maximize the variation in the dataset resulting better separation. Each class appeared in the separate cluster except in BF samples of B3 and B4 (Figure 3). PLS-DA search the latent variables among the datasets than only principal components. The latent variables are capable of searching the relationship between x-matrix and y-predicted to maximize the variation. The variables having high responsibility in discrimination of each class were observed using variable importance for projections (VIP) value. The value of VIP which is more than 1 is known for its big role in discrimination, thus potential to be identified as potential markers (Paul, De & Harrington 2021). Table 1 shows 50 metabolites obtained from VIP value more than 1, which were responsible in classification of BM samples from ten different origins. The metabolites are from fatty acids, lipids, and peptides class. Among those variables, 10 metabolites were found to have VIP value more than 2.0 such as (4S)-4-[[[(9Z)-3-Hydroxy-9-hexadecenyl]oxy]-4-(trimethylammonio)butanoate, N,N-Diisopropylethylamine (DIPEA), D-Sphingosine, (2E,4Z)-N-Isobutyl-2,4-octadecadienamide, 1-(14-methylhexadecanoyl)pyrrolidine, linoleic acid, 12-HAS, dodecylamine, myristamide, and tributyl phosphate. This indicated their crucial role of VIP in BM differentiation because the higher the VIP value of metabolites, the more the role of metabolites for discrimination. The distribution of these variables among BM from ten different origins were demonstrated in the Box-plot (Figure 4). The use of PLS-DA has been successfully proven to discriminate beef from Japan, Australia, and United States by previous researchers resulting better differentiation result than using PCA. Amino acids and their derivatives as well as lipids such as PC (phosphatidylcholine) and LysoPE (Lyso phosphatidylethanolamine) were found as potential biomarkers (Man et al. 2021). The differences in metabolites might be a result from the differences in bovine husbandry practices in each origin (Saleem et al. 2012).

Apart from PLS-DA, sparse PLS-DA was also applied for differentiation of BM from different origins. The result showed that the classification pattern had more similar overview (Figure 3) with the PCA result. However, B2 did not appear as a single class like in PCA. Only BM of B10 appeared in a single class far from other classes. Sparse PLS-DA is similar to PLS-DA; however, it has one step procedure in variable selection and classification. The contribution of irrelevant variables could be reduced; therefore, it could maximize the role of important variables to build the latent components which contributed to the most discrimination variables among BM samples (Jiménez-Carvelo et al. 2021). The metabolites important for discrimination in sPLS-DA observed using the loading plots were compiled in Table 2. The present study showed that PLS-DA resulted better discrimination of BM samples from different origins compared to sPLS-DA. It might be the simultaneous step of variable selection and classification does not always provide a better discrimination as in PLS-DA (Paul, De & Harrington 2021).

Supervised methods such as PLS-DA and sPLS-DA are susceptible for model overfitting. To avoid the negative effect of model overfitting, validation test is carried out to evaluate the developed PLS-DA and sPLS-DA models. The PLS-DA was validated using cross validation employing leave one out technique and permutation test. The cross-validation technique using 3 components (Q2) confirmed the PLS-DA model validity with R2Y value of 0.9960 and Q2 value of 0.5746. Meanwhile, permutation test also confirmed the validity through the significant p value ( $p$  value  $< 0.05$ ). The observed p-value from 1000 permutation was 0.031. The cross validation and permutation test results were supplemented in Figure S1 (supplementary files). Validation of sPLS-DA model using leave one out cross validation technique also confirmed the model validity. Therefore, both models had high accuracy and predictivity and were free from model overfitting. Validation techniques such as cross validation and permutation test have been widely used to validate supervised pattern recognition techniques such as PLS-DA, sPLS-DA, and OPLS-DA applied for discrimination of various types of samples. The results of validation test could warrant the performance of those models (Paul, De & Harrington 2021).

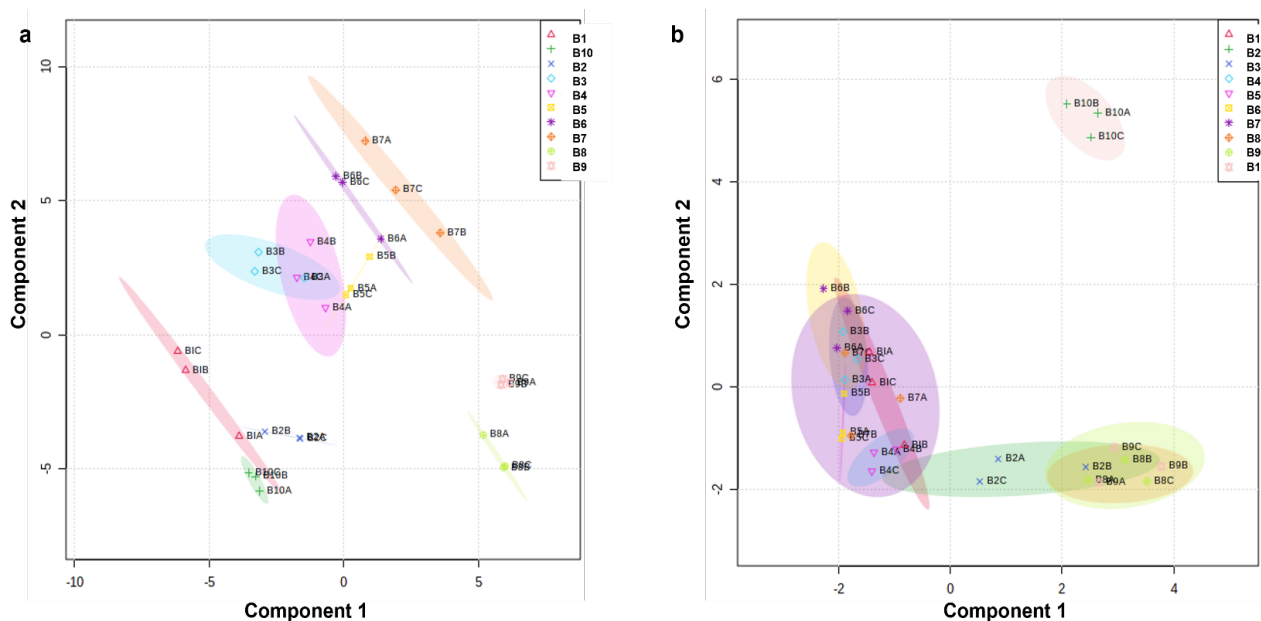


FIGURE 3. Partial least square-discriminant analysis (A) and sparse partial least square-discriminant analysis (B) for discrimination and classification of beef meats from different origins in Indonesia (B1=Borobudur, B2=Muntilan, B3=Tempel, B4=Klaten, B5=Gunungkidul, B6=Yogyakarta, B7=Bantul 1, B8=Gamping, B9=Godean, and B10=Bantul 2; each region was measured in three replicates)

TABLE 1. Potential metabolite markers to differentiate beef meats from different origins in Indonesia obtained from variable importance for projections (VIP) value analysis

No.	Compounds	VIP Value
1.	(4S)-4-[[[(9Z)-3-Hydroxy-9-hexadecenyl]oxy]-4-(trimethylammonio)butanoate	2.96
2.	N,N-Diisopropylethylamine (DIPEA)	2.71
3.	D-Sphingosine	2.37
4.	(2E,4Z)-N-Isobutyl-2,4-octadecadienamide	2.32
5.	1-(14-methylhexadecanoyl)pyrrolidine	2.30
6.	Linoleic acid	2.28
7.	12-HSA	2.25
8.	Dodecylamine.1	2.19
9.	Myristamide	2.12
10.	Tributyl phosphate	2.00
11.	cis-5-Tetradecenoylcarnitine	1.99
12.	3-Methylhistidine	1.98
13.	1-Heptanethiol	1.89
14.	4-Dodecylbenzenesulfonic acid	1.85
15.	1-Linoleoyl-2-Hydroxy-sn-glycero-3-PC	1.82



16.	(2E)-hexadecenoylcarnitine	1.80
17.	3-hydroxyhexadecanoylcarnitine	1.73
18.	Hexanoylcarnitine	1.73
19.	Ebelactone B	1.69
20.	Platelet-activating factor	1.63
21.	2-(2-amino-3-methylbutanamido)-3-phenylpropanoic acid	1.61
22.	1-(6-Nonyl-3-pyridinyl)-1-decanone	1.61
23.	4-Undecylbenzenesulfonic acid	1.59
24.	Octacosyl (2E)-3-(3-hydroxy-4-methoxyphenyl)acrylate	1.58
25.	Nicotinamide	1.57
26.	ACPC	1.52
27.	3-Methylsulfolene	1.51
28.	Biacetyl	1.50
29.	3-BHA	1.50
30.	D-ribose 5-phosphate	1.50
31.	O-heptanoylcarnitine	1.47
32.	N,N-Dimethyldecylamine N-oxide	1.47
33.	Propionylcarnitine	1.47
34.	Inosine	1.45
35.	Dodecyl sulfate	1.45
36.	Decanoylcarnitine	1.44
37.	Acetyl-methylcholine	1.37
38.	11(Z),14(Z)-Eicosadienoic acid	1.35
39.	N6,N6,N6-Trimethyl-L-lysine	1.35
40.	3-Hydroxy-3-[(3-methylbutanoyl)oxy]-4-(trimethylammonio)butanoate	1.32
41.	Leu-Leu	1.32
42.	8Z,11Z,14Z-Eicosatrienoic acid	1.30
43.	Urolithin B	1.30
44.	O-heptadecanoylcarnitine	1.30
45.	5-hydroxy-4-methoxy-5,6-dihydro-2H-pyran-2-one	1.28
47.	(+)-Nootkatone	1.28
47.	4-Acetamidobenzoic acid	1.26
48.	27-Norcholestane-3,7,12,24,25,26-hexol, (3Î±,5Î²,7Î±,12Î±)	1.25
49.	Benzoic acid	1.25
50.	2,2'-Methylenebis(4-methyl-6-tert-butylphenol)	1.22

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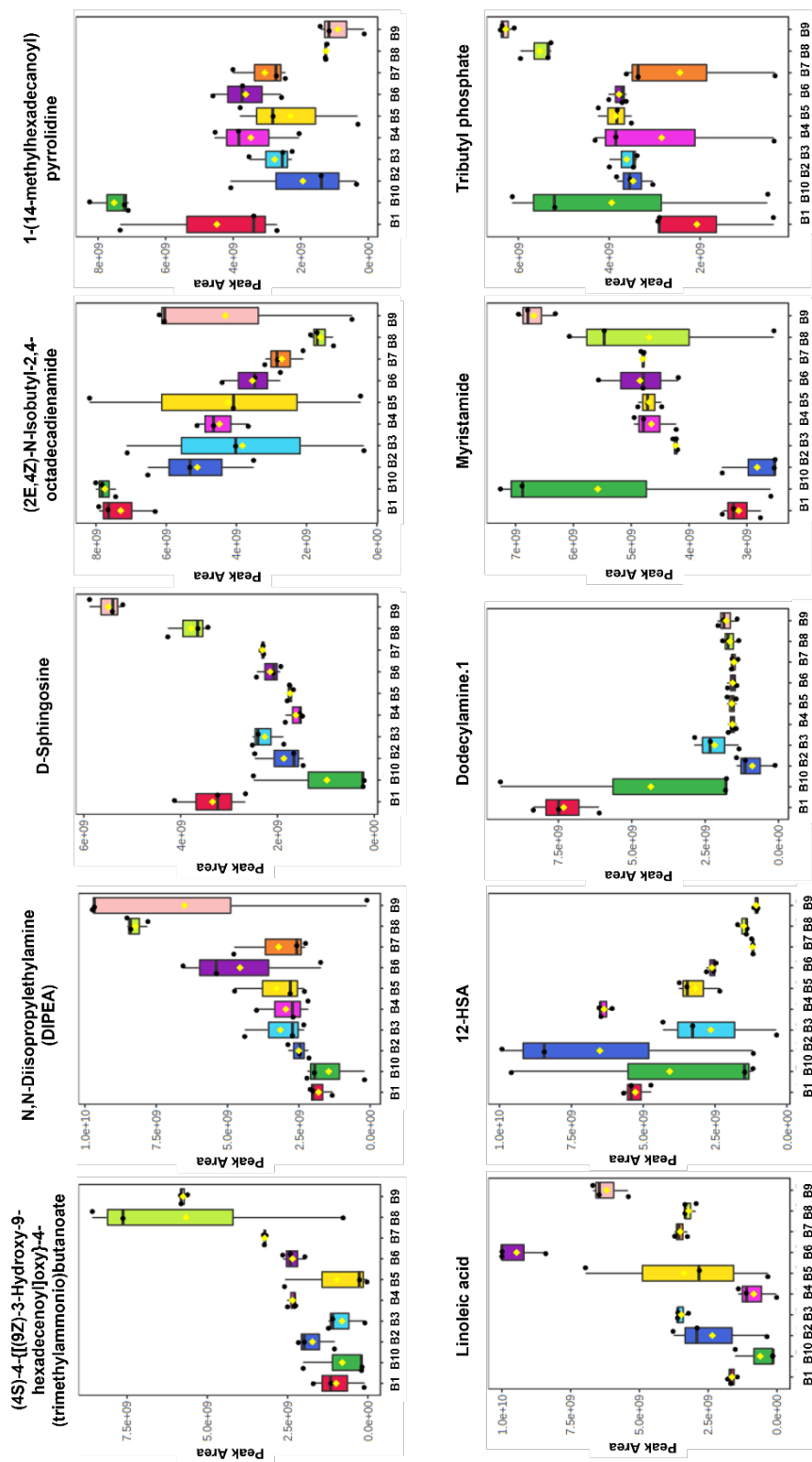


FIGURE 4. Box-plot of metabolites which have high responsibility for discrimination in PLS-DA model with VIP (variable importance for projections value) more than 2.0 (B1=Borobudur, B2=Muntilan, B3=Tempel, B4=Klaten, B5=Gunungkidul, B6=Yogyakarta, B7=Gamping, B8=Bantul 1, B9=Bantul 2)

TABLE 2. Responsible metabolites for classification using sparse partial least square-discriminant analysis through loading 1 and loading 2

No.	Compounds	
	Loading 1	Loading 2
1.	Bis(2-ethylhexyl) amine	Xanthine
2.	2,2'-Methylenebis(4-methyl-6-tert-butylphenol)	Octacosyl (2E)-3-(3-hydroxy-4-methoxyphenyl)acrylate
3.	D-ribose 5-phosphate	1-(14-methylhexadecanoyl)pyrrolidine
4.	Octadecanamine	2-(2-amino-3-methylbutanamido)-3-phenylpropanoic acid
5.	D-Panthenic acid	N,N-Dimethyldecylamine N-oxide
6.	DL-Carnitine	Acetyl-?-methylcholine
7.	Butyrylcholine	Tiglylcarnitine
8.	Stearic acid	hypaphorine
9.	Navenone A	Uric acid
10.	1-(2-Furyl)-N-((2R,4S,5R)-5-[1-methyl-3-(2-naphthyl)-1H-pyrazol-5-yl]-1-azabicyclo[2.2.2]oct-2-yl)methylmethanamine	Creatinine

### CONCLUSIONS

The authenticity of beef meat is important to warrant that the products are free from mislabelling, substitution, and adulteration. Metabolomics approach using LC-HRMS and chemometrics analyses demonstrated good capability for authentication of beef meats from different origins in Indonesia. Principal component analysis successfully identified separation of beef meats from different origins based on the metabolite compositions. The discrimination and classification of beef meats from ten different origins could be obtained using PLS-DA. Metabolites of (4S)-4-[[9Z)-3-Hydroxy-9-hexadecenoyl]oxy}-4-(trimethylammonio)butanoate, N,N-Diisopropylethylamine (DIPEA), D-Sphingosine, (2E,4Z)-N-Isobutyl-2,4-octadecadienamide, 1-(14-methylhexadecanoyl)pyrrolidine, linoleic acid, 12-HAS, dodecylamine, myristamide, and tributyl phosphate were identified as important metabolites for discrimination and classification of beef meats from ten different origins. Sparse partial least square-discriminant analysis allowed for classification of beef meats and the responsible metabolites for classification both in loading 1 and loading 2 could be observed. Among the chemometrics used, PLS-DA provided the

best discrimination result for differentiation of BM from different origins. It can be summarized that metabolomics approach using LC-HRMS and chemometrics is a reliable analytical technique that can be used for beef meats authentication from different origins.

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\*Corresponding author; email: [abdul\\_kimfar@ugm.ac.id](mailto:abdul_kimfar@ugm.ac.id)

#### SUPPLEMENTARY FILES

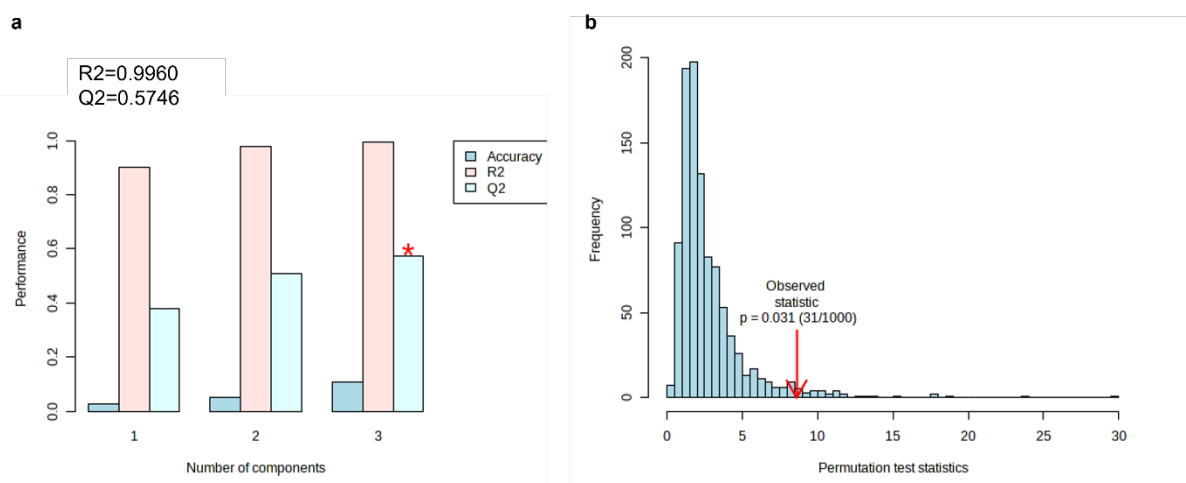


FIGURE S1. The graphic of cross validation (a) and permutation test (b) of the partial least square-discriminant analysis model to discriminate beef meats from different origins

SUPPLEMENTARY TABLE

Table with columns: Formula, Name, Aromatized MW, RT (min), BIA, BIB, BIC, B2A, B2B, B2C, B3A, B3B, B3C, B4A, B4B, B4C, B5A, B5B, B5C, B6A, B6B, B6C, B7A, B7B, B7C, B8A, B8B, B8C, B9A, B9B, B9C, B10A, B10B, B10C, B11A, B11B, B11C, B12A, B12B, B12C, B13A, B13B, B13C, B14A, B14B, B14C, B15A, B15B, B15C, B16A, B16B, B16C, B17A, B17B, B17C, B18A, B18B, B18C, B19A, B19B, B19C, B20A, B20B, B20C, B21A, B21B, B21C, B22A, B22B, B22C, B23A, B23B, B23C, B24A, B24B, B24C, B25A, B25B, B25C, B26A, B26B, B26C, B27A, B27B, B27C, B28A, B28B, B28C, B29A, B29B, B29C, B30A, B30B, B30C, B31A, B31B, B31C, B32A, B32B, B32C, B33A, B33B, B33C, B34A, B34B, B34C, B35A, B35B, B35C, B36A, B36B, B36C, B37A, B37B, B37C, B38A, B38B, B38C, B39A, B39B, B39C, B40A, B40B, B40C, B41A, B41B, B41C, B42A, B42B, B42C, B43A, B43B, B43C, B44A, B44B, B44C, B45A, B45B, B45C, B46A, B46B, B46C, B47A, B47B, B47C, B48A, B48B, B48C, B49A, B49B, B49C, B50A, B50B, B50C, B51A, B51B, B51C, B52A, B52B, B52C, B53A, B53B, B53C, B54A, B54B, B54C, B55A, B55B, B55C, B56A, B56B, B56C, B57A, B57B, B57C, B58A, B58B, B58C, B59A, B59B, B59C, B60A, B60B, B60C, B61A, B61B, B61C, B62A, B62B, B62C, B63A, B63B, B63C, B64A, B64B, B64C, B65A, B65B, B65C, B66A, B66B, B66C, B67A, B67B, B67C, B68A, B68B, B68C, B69A, B69B, B69C, B70A, B70B, B70C, B71A, B71B, B71C, B72A, B72B, B72C, B73A, B73B, B73C, B74A, B74B, B74C, B75A, B75B, B75C, B76A, B76B, B76C, B77A, B77B, B77C, B78A, B78B, B78C, B79A, B79B, B79C, B80A, B80B, B80C, B81A, B81B, B81C, B82A, B82B, B82C, B83A, B83B, B83C, B84A, B84B, B84C, B85A, B85B, B85C, B86A, B86B, B86C, B87A, B87B, B87C, B88A, B88B, B88C, B89A, B89B, B89C, B90A, B90B, B90C, B91A, B91B, B91C, B92A, B92B, B92C, B93A, B93B, B93C, B94A, B94B, B94C, B95A, B95B, B95C, B96A, B96B, B96C, B97A, B97B, B97C, B98A, B98B, B98C, B99A, B99B, B99C, B100A, B100B, B100C.







Entity Name	Value 1	Value 2	Value 3	Value 4	Value 5
C21H14O4	-0.5	22.8891	12.96	1740442.8	23203856.5
C18H33NO4	0.11	327.8699	12.77	894038.69	78232344.4
C17H33NO4	-0.2	315.2609	12.97	854318.79	7215799.32
C16H31NO4	0.15	157.1462	12.98	331346.56	22610994.4
C15H29NO2	-1.25	227.1825	13.14	1068233.37	63491.659
C15H29NO5	-0.56	392.6997	13.175	199483.29	7525804.19
C15H31NO5	-0.74	225.1152	13.49	488674.62	338892.13
C16H31NO2	0.52	163.0947	13.04	475232.31	472229.43
C16H31NO3	-1.2	253.2591	13.74	4545694.42	6525252.56
C18H39NO5	-1.78	317.2924	13.89	287037.66	140704.36
C14H31NO5	-0.94	213.2454	13.96	177444	1133302.42
C12H27NO5	-0.33	183.2429	14.06	317102.51	1590001.1
C12H29NO5	0.23	245.1401	14.43	780455.106	469101.68
C12H27NO6	-0.27	165.2445	14.24	610836.013	349379.24
C21H37NO4	-1.11	367.2785	14.36	612158.96	610332.4
C21H41NO5	-0.37	387.2883	14.84	815993.78	605582.12
C18H39NO2	-0.45	301.2993	15.26	392322.691	604677.67
C23H43NO5	-0.32	413.1399	15.43	1052865.69	14086.617
C25H43NO4	-0.08	421.1917	16.07	829646.65	152004.46
C23H45NO5	-0.69	413.2849	16.21	634938.22	878369.89
C18H37NO2	-0.57	292.8256	16.95	265783.23	132932.95
C23H43NO4	-0.89	397.3185	16.23	1009300.44	126323.1
C23H45NO4	-1.11	383.5185	16.27	425266.69	17510.78
C21H27O4P	-0.61	261.1453	16.19	203144.57	290256.49
C23H45NO4	-0.8	423.3452	16.56	1239706.4	132992.5
C23H45NO4	-0.51	473.3463	16.55	58169.35	70189.45
C16H31NO3	-0.17	241.23691	16.63	195253.013	25467.98
C23H45NO4	-1.54	393.2424	16.98	257833.33	322774.5
C15H29NO2	-0.04	218.1076	17.05	823262.33	92118.84
C23H45NO5	-0.59	443.4081	17.12	151657.33	1301420.74
C18H39O2	-1.14	278.2426	17.2	1610798.23	3231588.9
C24H47NO4	-1.31	413.4997	17.39	132142.06	880972.46
C27H59NO4	-2.51	432.8809	17.44	1266245.5	1446226.51
C18H39NO5	-0.33	293.8816	17.44	1106348.06	448123.89
C20H35NO4	3.89	432.9711	17.49	397344.49	7386184.6
C18H49O3	3.61	302.2573	17.57	3579417.25	473236.74



