C146-E440

SHIMADZU
Excellence in Science

Kit for Direct Probe Ionization Mass Spectrometer

DPiMS QT

DPiMS™ QT

Quick, Simple Measurements with Simple Pretreatment

- Analysis can start immediately with just simple pretreatment.
- Capable of connections to quadrupole TOF mass spectrometers, enabling high-resolution mass spectrometry.
- The slight amount of the sample adhering to the probe is ionized, so the analysis is highly resistant to contamination of the MS unit.

3 Step Workflow

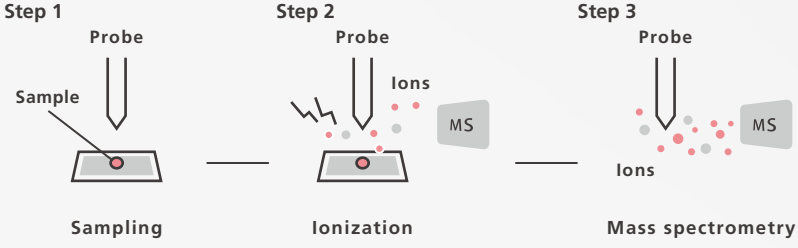
Analysis

Step 1
Collect the sample.

Step 2
Add it to the plate.

Step 3
Start the analysis.

Ionization




SHIMADZU
LCMS-9030

DPiMS™ Can be Used in All Sorts of Fields

Measure Liquid and Solid Samples with Simple Pretreatment

- Reduces the time required to analyze blood, urine, and other biological samples with conventional methods by approximately 50 %.
- Foods, tissue sections, and other solid samples can be analyzed as it.

  Pretreatment times are significantly reduced.

  Note: Analytical precision can be improved even for solid samples by performing simple pretreatment such as dilution and centrifugation.

Biological sample **Solid sample**

The Functional Components of Foods Can be Detected Quickly with Simple Pretreatment

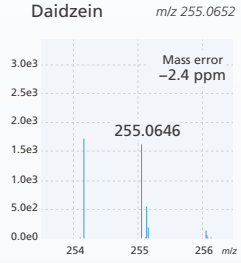
Quick and Easy Detection of Isoflavones in Processed Soy Bean Foods

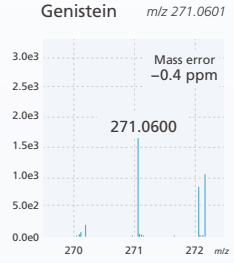
10 mg of each food product was permeated with 1 mL of 50 % ethanol. This mixture was agitated and centrifuged, after which the supernatant was measured, and each component was detected on-plate.

MS Measurement Conditions

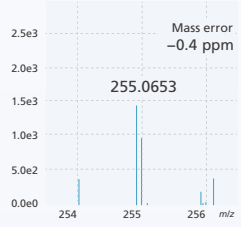
Mass range: *m/z* 100–800 / IF Voltage: 3.5 kV
Desolvation line temp: 250°C
Heat blocktemp: 50°C
Polarity:Positive / Event Time: 0.02sec

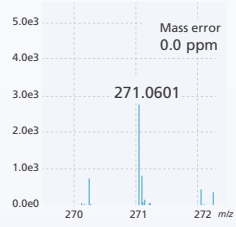
Boiled soy beans





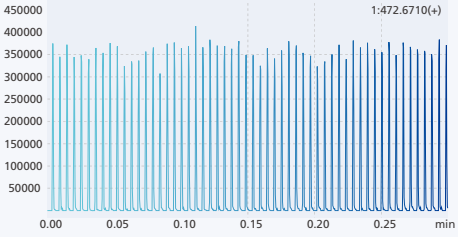
Chocolate made with processed soy beans





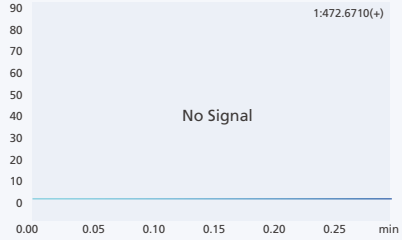
Analysis System with No Carryover

Only a few dozen pL of the sample adheres to the probe after each sampling. There is no worry of contamination inside the mass spectrometer. Carryover can even be prevented by changing probes. Concentrated samples and samples of unknown concentration can be measured.



NaI (400 mg/L) Base Peak (*m/z* 472.6710) MS Chromatogram

Blank solvent measurement after 30 analyses of high concentration samples

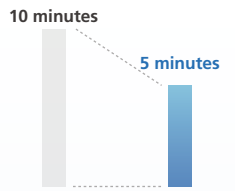


Blank Solvent

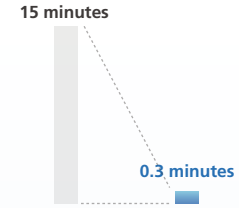
Speedy Qualitative Analysis

The qualitative analysis sequences for DPiMS QT and Q-TOF LC/MS were compared. Using DPiMS QT, it was possible to significantly reduce the measurement time in comparison to conventional methods using Q-TOF LC/MS.

Comparison of Sample Pretreatment Times

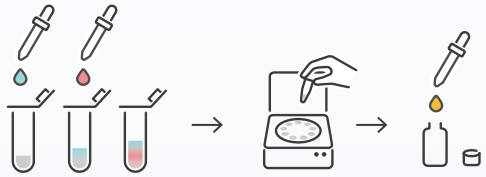


Comparison of Qualitative Analysis Times



Comparison of Pretreatment Times

Q-TOF LC/MS Measurement: 10 minutes



Add 300 µL of acetonitrile, 200 µL of water, and 100 µL of whole blood to the Micro Volume QuEChERS kit.

Centrifugation

Instill the supernatant into an LC vial.

DPiMS QT Measurement: 5 minutes

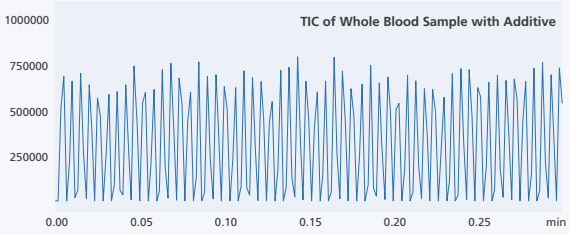
Mix 20 µL of whole blood and 200 µL of ethanol with 180 µL of water.

Centrifugation

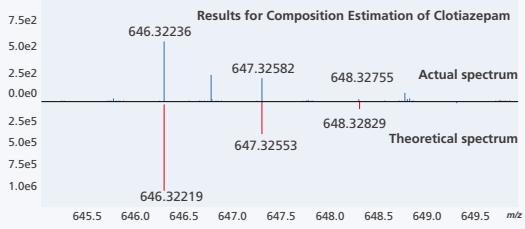
Instill the supernatant onto the sample plate.

Speedy Qualitative Analysis

Only a few dozen seconds are spent on DPiMS QT qualitative analysis. When performing qualitative screening analyses, the time before results are checked can be reduced, improving procedural efficiency.



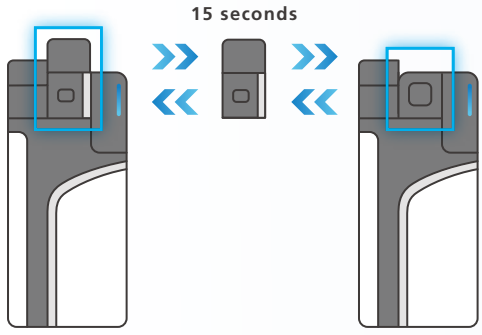
Single DPiMS QT Measurement: 0.3 minutes



Implementing Accurate Mass and Composition Estimation from the MS Spectrum

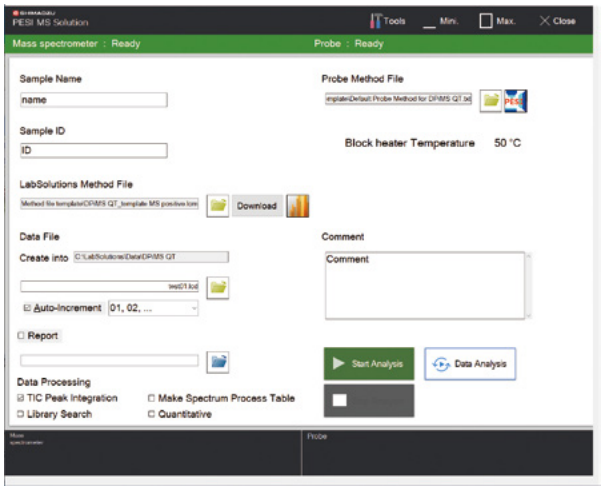
Switching between DPiMS QT and Q-TOF LC/MS is Simple

Only about 15 seconds are required to remove the DPiMS QT unit, reconfiguring the system for Q-TOF LC/MS. The resources (solvents and columns) required for Q-TOF LC/MS analysis can be reduced by implementing qualitative analysis and primary screening via DPiMS QT, thereby reducing the number of samples requiring quantitative analysis.



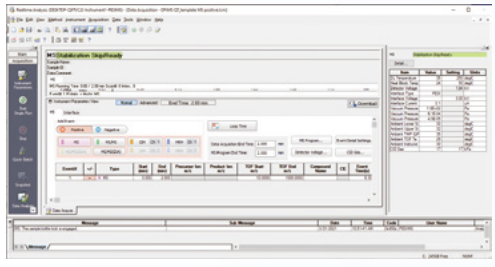
PESI MS Solution Software

PESI MS Solution software is used to control the probe, edit MS method files, and start measurements. Detailed MS analytical conditions are configured from the LabSolutions™ LCMS method editing window. Analysis can be started easily by selecting the probe control mode and MS method in PESI MS Solution. During analysis, the status can be confirmed in the LabSolutions LCMS window.



PESI MS Solution

Probe control method file

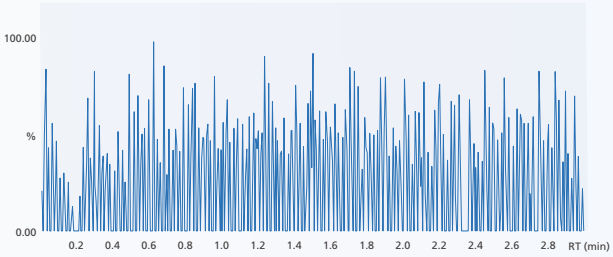


LabSolutions method file

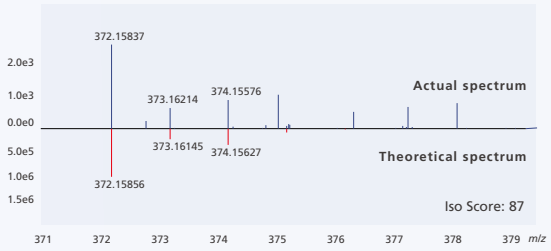
Sequence for Qualitative Analysis via MS and MS/MS

A qualitative analysis was performed on a whole blood sample mixed with trazodone (500 ng/mL). A cycle of MS and MS/MS measurements was performed simultaneously. LabSolutions Insight Explore was used for the data analysis. LabSolutions Insight Explore enables composition estimation, library searches, and structural analysis.

MS Measurement



Trazodone C19H22ClN5O **Chromatogram extracted at *m/z* 372.1586**



MS spectrum in the vicinity of *m/z* 372.1586

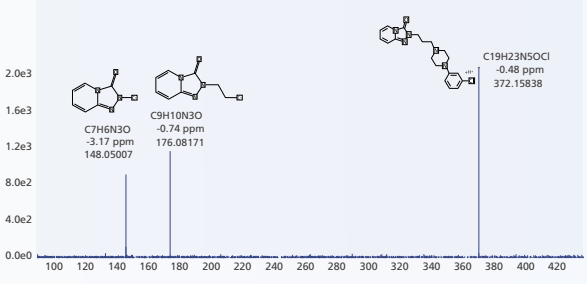
Checking for Peaks

The chromatogram extracted for the target is depicted by entering the composition formula or the applicable ion *m/z* into the compound table.

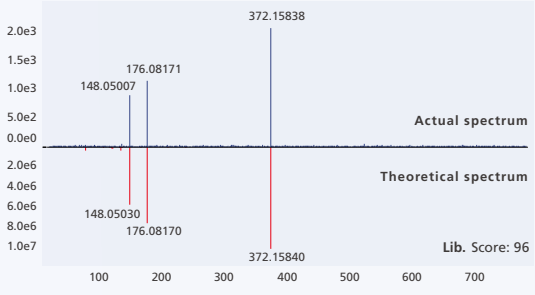
Composition Estimation

From the measured spectrum, select a spectrum of any *m/z* and use the composition estimation function to list estimated composition formulas in order by score.

MS/MS Measurement



Results for the Structural Estimation of Trazodone



Product Ion Spectrum Measured with DPiMS QT

Assigning Fragments

Using the structural analysis assign function in LabSolutions Insight Explore, fragments are assigned with respect to the product ion spectrum.

Scoring via the Spectral Library

Scoring is performed with respect to the spectrum measured with DPiMS QT by creating a spectral library using Q-TOF LC/MS.

Specifications

Hardware	DPiMS QT controller	Control of the DPiMS QT unit (Installed in the mass spectrometer)
	DPiMS QT unit	Probe Voltage: ±5 kV max. (set voltage)
		Probe Stroke: 46.30 mm max.
		Number of Extraction Cycles: 300 max.
		Probe Speed: 300 mm/sec max.
		Probe Acceleration: 1 G max.
		Probe Stop Time: 60,000 msec max.
Software	PESI MS Solution LabSolutions	Used to select analytical conditions and start analysis
		Used to specify MS analysis method settings and analyze data
	(Probe Control Software)	Used to specify probe control method settings
Consumables	Probe	Set of 10 or 50 pcs.
	Plate	Plates available for both liquid and biological samples (set of 100 pcs. each)
Installation requirements*	Room temperature	18 to 28 °C
	Humidity	20 to 70 % (No-condensing and no-discharge due to static electricity)
	Others	Should be installed in an environment without dust, oscillation, electromagnetic noise, corrosive gas and electromagnetic interference.

*Equivalent to the installation requirement of mass spectrometer.

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