

Liquid Chromatograph Mass Spectrometer

LCMS-2020

UFMS
ULTRA FAST MASS SPECTROMETRY



LCMS-2020

—*Seeing is Believing.*

Ultra Fast
UFswitching[™]

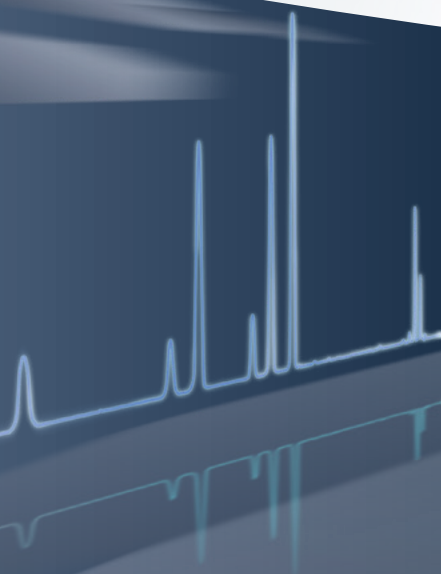
Rapid 15 msec Polarity Switching

Ultra Fast
UFsensitivity[™]

Superior Sensitivity with UHPLC

Ultra Fast
UFscanning[™]

15,000 u/sec Fast Scanning Speed





Speed Beyond Comparison

UAMS

ULTRA FAST MASS SPECTROMETRY

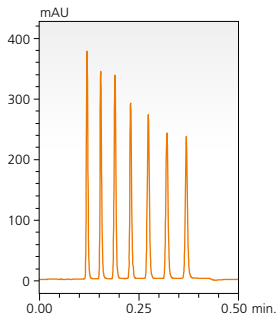
Speed is Power.

Greater speed.
Greater sensitivity.



From HPLC to UHPLC

UHPLC achieves excellent speed and resolution, while offering the high precision not available with conventional HPLC and expandability options.



Ultra Fast

Not only high-speed analysis, but increased overall speed through rapid sample injection and fully automatic analysis functions.

Unquestionable Fidelity

UHPLC offers exceptional injection reproducibility as well as ultra high-speed operation. In terms of minimizing sample carryover, essential in LC/MS analysis, the LCMS-2020 stays ahead of the competition.

Ultra Flexible

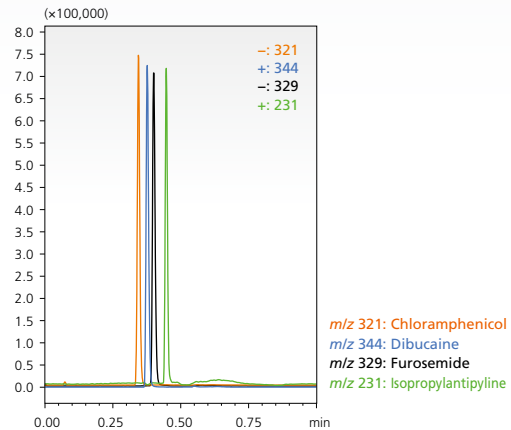
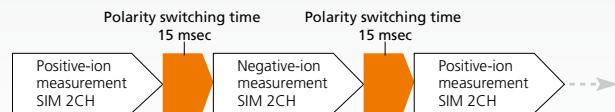
Covers an extensive range from ultra-fast analysis to conventional HPLC and semi-preparative analysis.

Ultra-fast

UFswitching

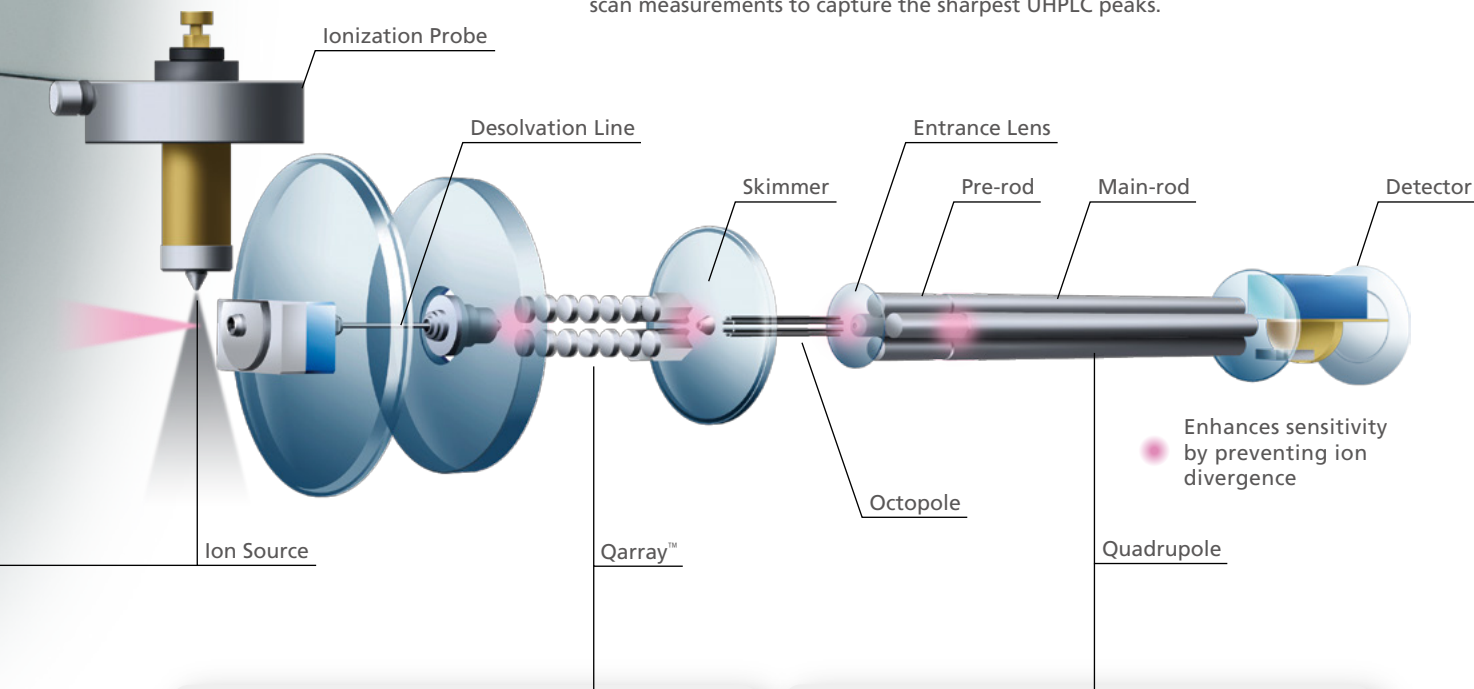
Rapid 15-millisecond positive/negative ionization switching

To detect both positive and negative ions, analysis is performed while switching between the positive and negative ionization modes. The LCMS-2020 adopts patented high-voltage power supply technology (Patent: US7855355) to achieve an ultra-fast polarity switching time of just 15 ms.



Accurate mass analysis of sharp chromatographic peaks obtained by UHPLC requires ultra-fast MS detection capabilities.

The LCMS-2020 offers UFSwitching for rapid polarity switching between the positive and negative ionization modes and UFScanning for ultra-fast scan measurements to capture the sharpest UHPLC peaks.

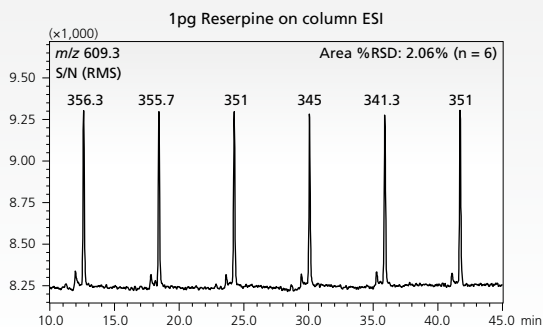


Ultra-fast

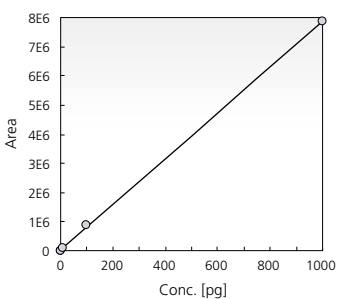
UFSensitivity

Superior sensitivity from UHPLC

Newly developed Qarray™ Optics achieve superior sensitivity, reproducibility, and linearity.



Calibration curve: 0.1, 1, 10, 100, 1000 pg

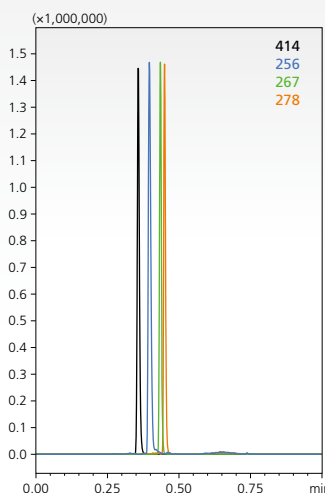


Ultra-fast

UFScanning

15,000 u/sec scan speed

Shimadzu's proprietary scanning technology (Patent: US8188426) maintains resolution and achieves high ion transmission even at high scanning speeds.

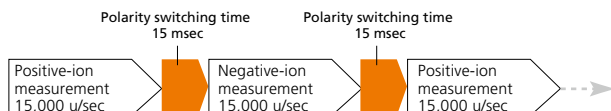


m/z 414: L- α -Narcotine
 m/z 256: Diphenhydramine
 m/z 267: Desipramine
 m/z 278: Amitriptyline

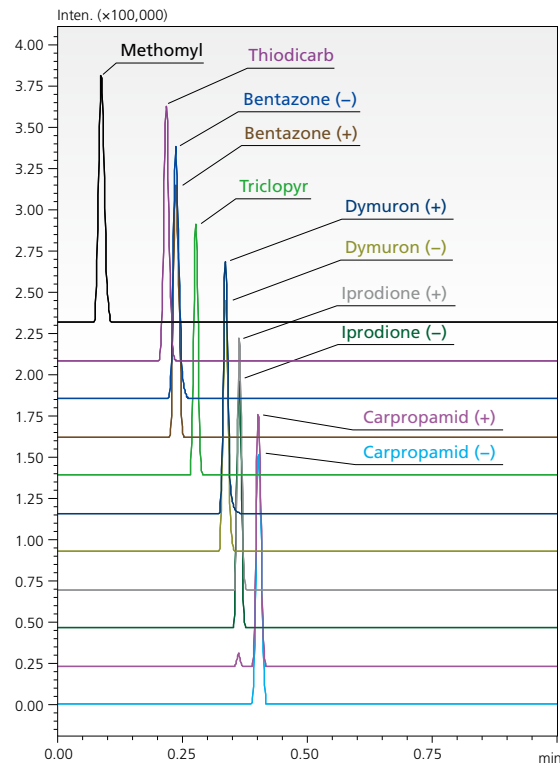
UFscanning & UFswitching

UFswitching and UFscanning for Ultra-fast Analysis

Rapid elution and sharp chromatographic peaks require Ultra Fast MS acquisition. The three-second wide peaks in this chromatogram were acquired on multiple SIM channels with polarity switching to demonstrate the outstanding quantitative performance of the LCMS-2020.

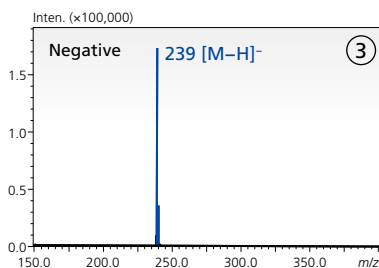


| Sample: Polarity | |
|------------------|----------------------------|
| ① | Methomyl: m/z 163 (+) |
| ② | Thiodicarb: m/z 355 (+) |
| ③ | Bentazone: m/z 239 (-) |
| ④ | Bentazone: m/z 241 (+) |
| ⑤ | Triclopyr: m/z 256 (-) |
| ⑥ | Dymuron: m/z 269 (+) |
| ⑦ | Dymuron: m/z 313 (-) |
| ⑧ | Iprodione: m/z 330 (+) |
| ⑨ | Iprodione: m/z 243 (-) |
| ⑩ | Carpropamid: m/z 334 (+) |
| ⑪ | Carpropamid: m/z 378 (-) |

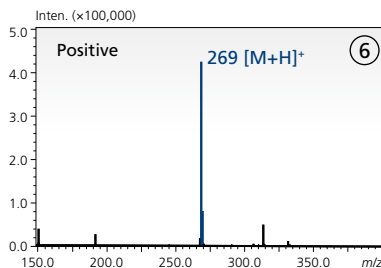


Examples of ionization in positive and negative modes

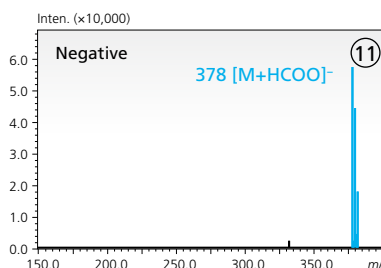
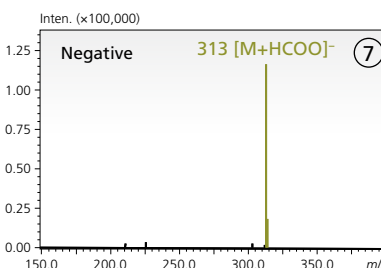
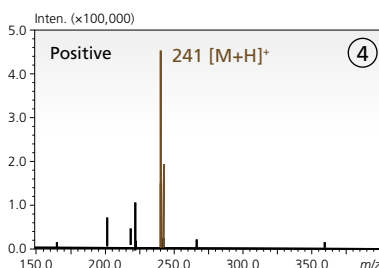
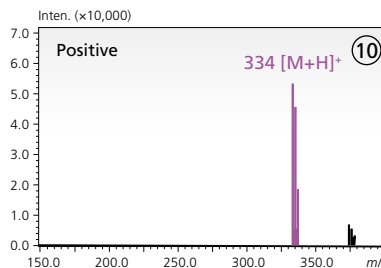
● MS Spectra of Bentazone



● MS Spectra of Dymuron



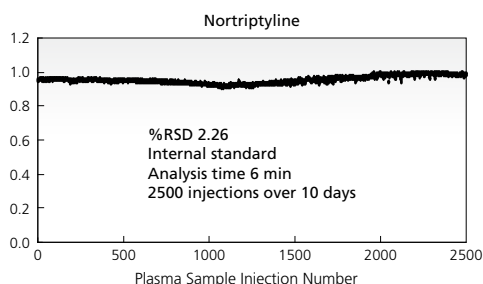
● MS Spectra of Carpropamid



Rugged Yet Sophisticated Hardware

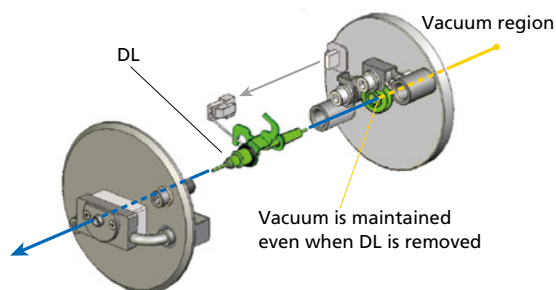
Stands Up to Difficult Matrices

Complex biological matrices can easily foul a mass spectrometer, but the LCMS-2020 possesses proven durability. The graph below shows the results of 2,500 consecutive injections (1 μ L each) of protein precipitated plasma over the course of 10 days. Excellent stability and precision were demonstrated; Nortriptyline peak area %RSD = 2.26%.



Easy Maintenance

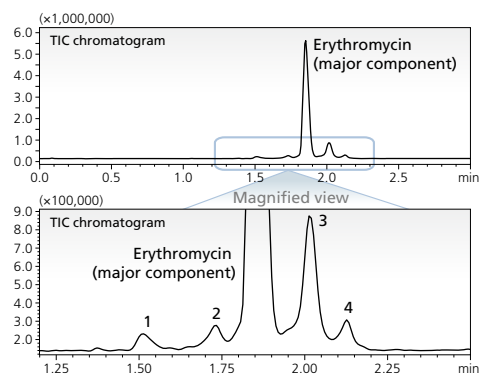
The desolvation line (DL) that introduces the sample from the ion source into the vacuum chamber can be installed and uninstalled without breaking the vacuum, which dramatically improves ease-of-maintenance.



Fragment Ion Information by In-source CID

In-source CID (collision-induced dissociation) is effective for confirming the molecular weight of synthetic compounds and for the quantitation of impurities.

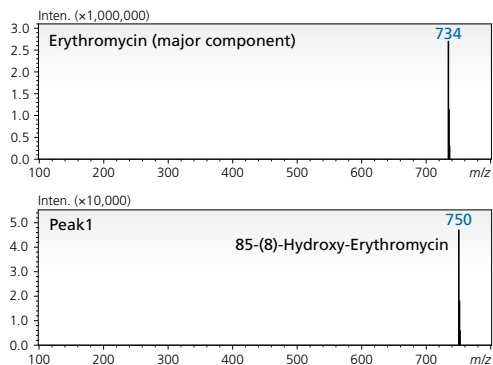
● MS Chromatogram for Erythromycin Measurements DL = 0 V, Qarray DC = 0 V



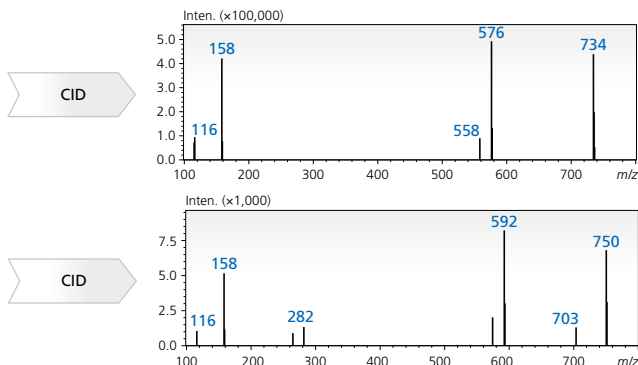
Using in-source CID allows the generation of fragment ions. This example shows the structure of impurities in erythromycin estimated from fragment ions generated by in-source CID.

The multi-sequence mode permits several other methods within a single analysis, such as CID, positive/negative ion switching modes, and SCAN/SIM modes. Utilize single quadrupole mass spectrometry to its fullest potential by conducting multiple experiments in a single run.

● MS Spectra (Normal mode) DL = 0 V, Qarray DC = 0 V



● MS Spectra (In-source CID mode) DL = 0 V, Qarray DC = 60 V



Diverse Ionization Methods Expand the Range of Applications

Selecting the ionization method appropriate for the target compound achieves superior analysis results.

LCMS-2020 offers APCI and DUIS in addition to ESI. Diverse ionization methods support a wide range of applications.

Selecting the most appropriate Ionization Method

| | | ESI | APCI | DUIS |
|------------|------------------------|-----|------|------|
| Compounds | DNA | B | — | B |
| | Proteins | A | — | B |
| | Peptides | A | — | B |
| | Amino acids | B | — | B |
| | Macromolecules | B | C | B |
| | Carbohydrates | B | A | A |
| | Triglycerides | B | A | A |
| | Aromatic hydrocarbons | C | C | C |
| | Aliphatic hydrocarbons | — | C | C |
| Properties | Polar | A | B | A |
| | Non-polar | — | B | B |
| | Volatile | A | A | A |
| | Non-volatile | A | — | A |
| | Thermostable | A | A | A |
| | Thermolabile | A | — | C |

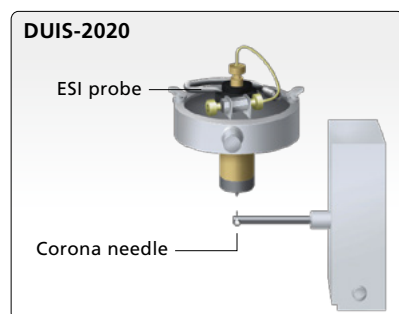
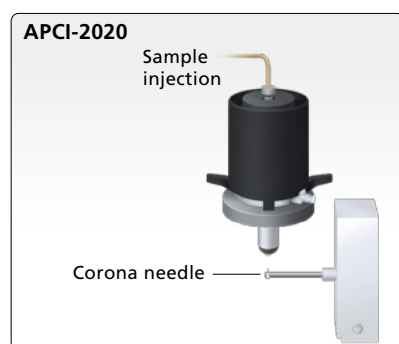
| | | ESI | APCI | DUIS |
|-------------------|----------|-----|------|------|
| Functional groups | Acid | A | B | A |
| | Alcohol | C | B | B |
| | Aldehyde | C | B | B |
| | Alkyne | — | C | C |
| | Amino | A | A | A |
| | Carbonyl | C | B | B |
| | Ester | B | A | A |
| | Ether | C | B | B |
| | Phenol | B | A | A |

A Extremely suitable
B Suitable
C Analysis possible with appropriate parameters
— Inherently unsuitable

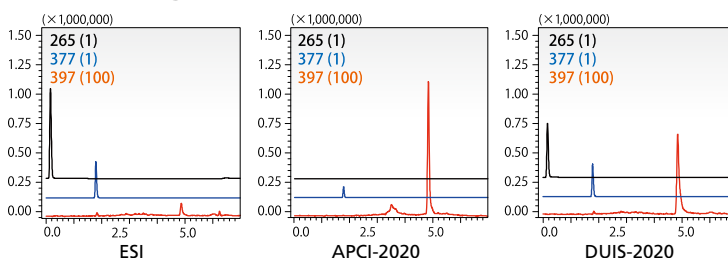
Ion Source Options

While the water-soluble vitamins thiamine and riboflavin can be detected by ESI, they are virtually undetectable by APCI. Conversely, the fat-soluble vitamin calciferol can be detected by APCI but ESI does not offer adequate detection sensitivity.

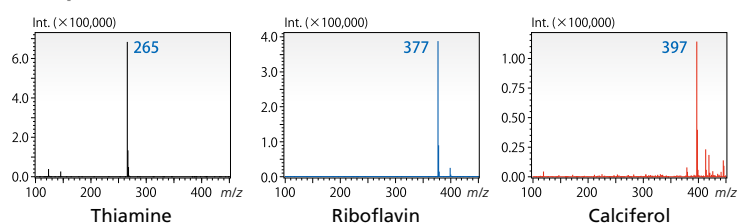
DUIS-2020 allows detection of a mixture of compounds suited to ESI or APCI, without missing any compounds.



MS Chromatograms



MS Spectra from DUIS Measurements

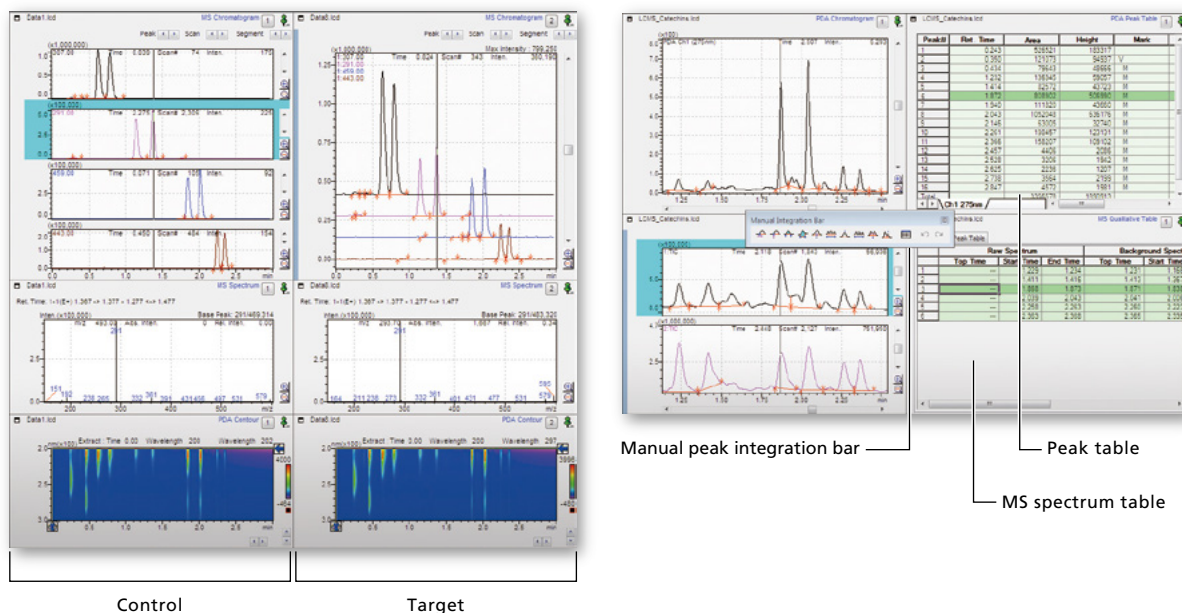


Mixed Sample of Three Water-soluble/Fat-soluble Vitamins
 1. Thiamine: m/z 265, $[M]^+$, water-soluble vitamin
 2. Riboflavin: m/z 377, $[M+H]^+$, water-soluble vitamin
 3. Calciferol: m/z 397, $[M+H]^+$, fat-soluble vitamin

LabSolutions™ LCMS

Unified software for LCMS data acquisition and processing. Single point of control for UHPLC/LCMS-2020 LCMS systems.

Easily create LC and MS acquisition parameters in a single method, and quickly review results in the Data Browser window.



Data Comparison

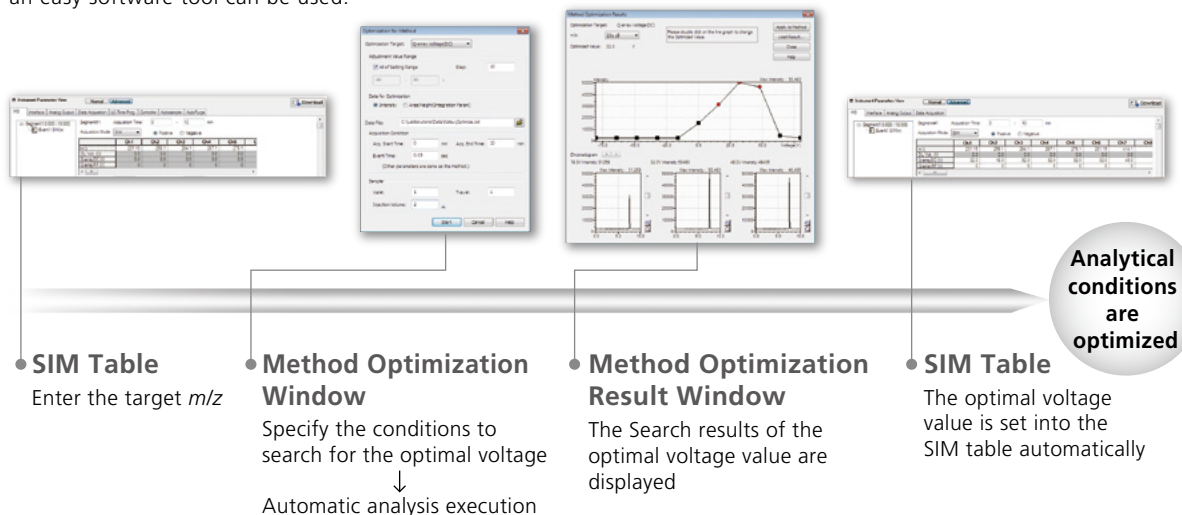
Mass spectrometer (MS) and photodiode array (UV) data can be overlaid or arranged for simultaneous viewing to discover differences in sample characteristics. A wide variety of user preferences is available to interrogate spectra and chromatograms.

Quantitative Analysis

Use total ion chromatograms, extracted ion chromatograms, or individual UV wavelength chromatograms for quantitative analysis. The browser window simultaneously loads calibration curve and sample data for rapid analysis and review of an entire batch.

Automated MS Voltage Optimization

Shimadzu's sophisticated auto-tune file comprehensively establishes MS voltages. For individual compound optimization, an easy software tool can be used.

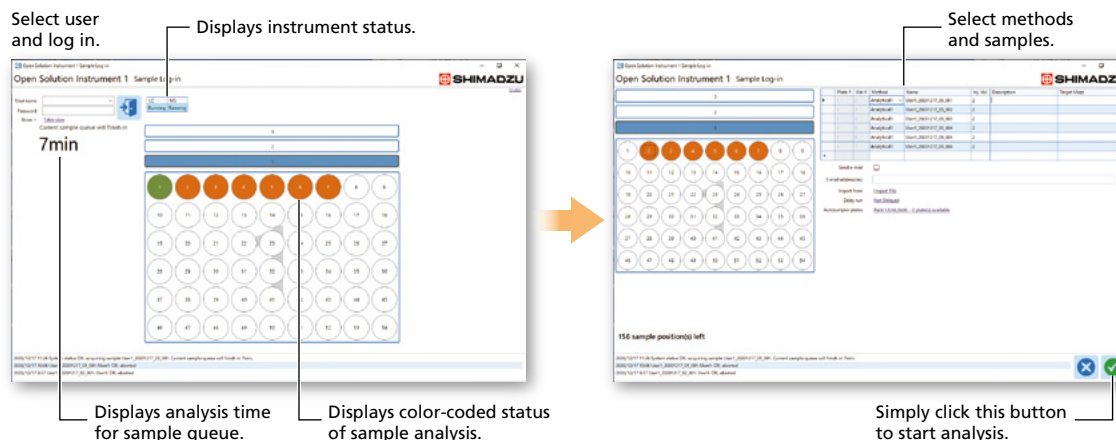


Optional Open Access Software for Analytical and Purification

Open Solution

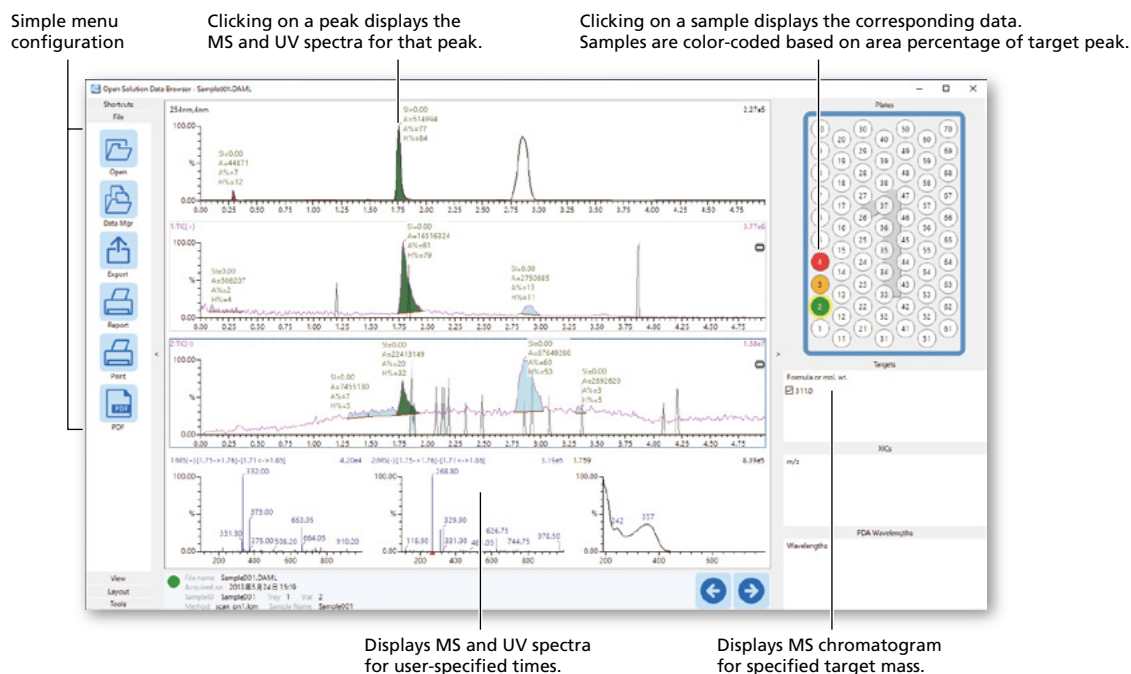
Simple and Intuitive Sample Logging and Data Review

- After logging in to the [Sample Log-in] window, simply select methods and samples to start analysis.
- Open-access functionality for sharing instruments among multiple users.
- Performs automated method switching for multiple users, including column and mobile phase switching, and automatic rinsing of flow lines.
- LC, PDA and MS instrument status.



Data Browser—Display and Analyze Data

- Quickly display data by simply clicking on samples in the rack diagram.
- The data browser can be launched on any networked computer by simply installing software on that computer.
- Peak integration (adding or deleting peaks) for LC chromatograms can be performed easily.
- Displays MS and UV spectra for user-specified times.
- Calculates and displays peak purity based on similarity score of MS spectrum.

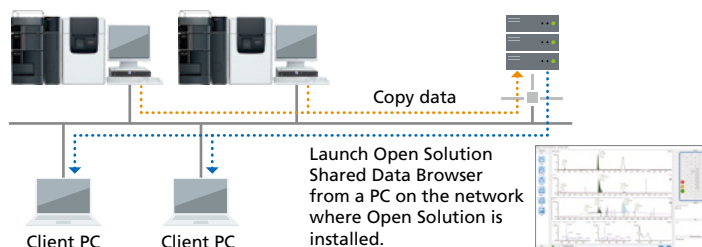


Anywhere data can be viewed in Shared Browser

Data can be viewed from Open Solution Shared Data Browser from the client PC on the network. No software installation is required on the client PC*. Simply launch Open Solution Shared Data Browser from a PC on the network where Open Solution is installed.

* Microsoft® .NET Framework 4.6.1 or later and Visual Studio 2017 redistribution module are required.

- Automatically copy data to a PC on the network.
- From the client PC, launch Open Solution Shared Data Browser and view the data of the PC on the network.
- The manual peak integration can be simply performed for LC and PDA chromatogram.



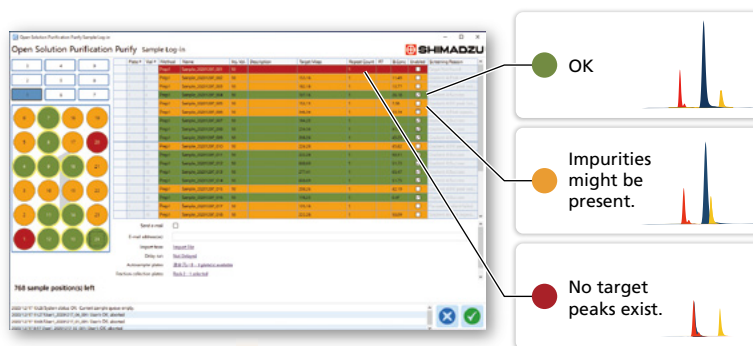
Preparative option—Purification

Supports Reverse Phase Preparative Scale-Up

- The same sample is automatically analyzed by multiple methods (multiple mobile phases, columns) using a scale-up algorithm from analysis results to preparative analysis. From the analysis result, the optimum conditions (initial B. Conc.) are automatically generated.
- Easy display of fractionation results.

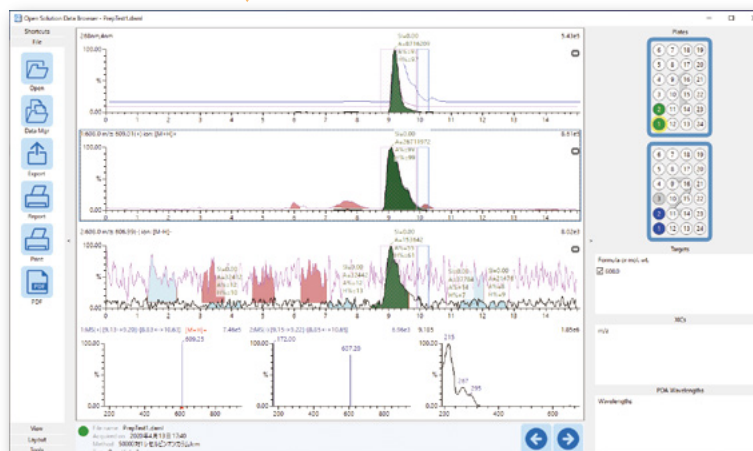
Fractionation

- Automatically creates a batch queue for purification works with three color coding when analysis results files (Excel® or Text) are loaded.
- Green signal means “Go ahead for purification” but orange signal tells you there is a risk of impurity when you conduct the purification with the given method.



Purification Results

- Display fractionation results using Open Solution data browser from any networked PC.
- Click on any collection vessel in the display window to examine MS or UV spectra for that fraction. Purity results are color-coded in the display window.



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