

Matrix-Assisted Laser Desorption/Ionization Digital Ion Trap Mass Spectrometer

# MALDImini-1



# MALDImini™ -1

MALDI Digital Ion Trap Mass Spectrometer

## “Minimum”

Towards new possibilities with the compact MALDImini-1

Despite its light and compact shape, the MALDImini-1 allows high-sensitivity MS<sup>n</sup> measurements, making it suitable for a large number of applications.



## **“Minimum” footprint**

With its simple configuration and compact size, it is possible to install the MALDImini-1 in places where mass analysis devices could not previously be used. Through ingenious engineering and innovation its footprint has been reduced to the size of a piece of paper.

## **“Minimum” time**

Miniaturization allows rapid, "on-the-spot" analysis and simplifies data acquisition.

## **“Minimum” sample volume**

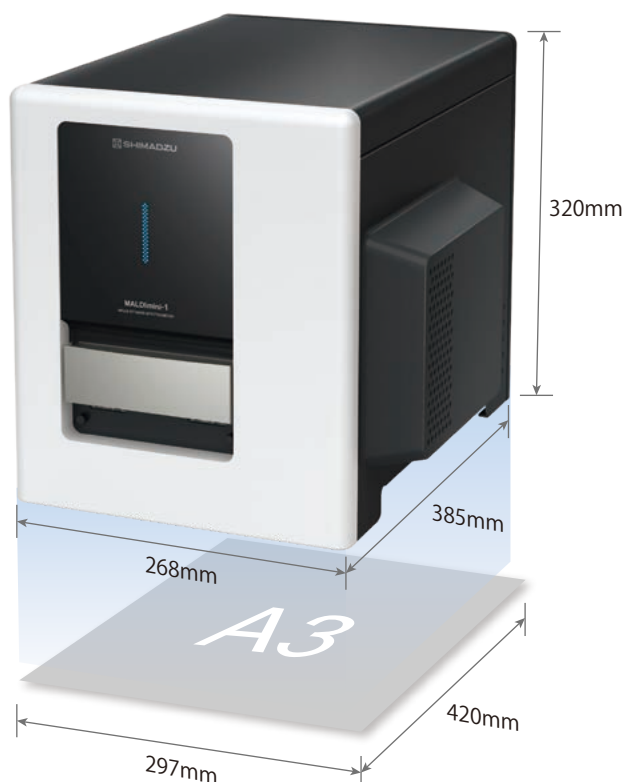
Complex structural analysis can be performed even with sub- $\mu\text{L}$  sample volumes.



# “Minimum” footprint

## The MALDI-MS that can be installed anywhere

Until now, devices for MS<sup>n</sup> have had strenuous installation requirements, but the MALDImini-1's compact size and power requirements make it easy to install almost anywhere. Easy access to the instrument allows users to quickly acquire data and check their results, creating a more convenient workflow right on the bench.



# “Minimum” time

## Begin taking measurements quickly without fuss

MALDI lends itself to quick analysis through simple sample preparation and acquisition. Once the sample is loaded, users can acquire a spectrum in a few minutes at the click of a button.

With such a smooth and quick setup, it is possible to carry out detailed structural analyses in a very short time span.



Place the sample onto the plate  
(FlexMass™-SR or FlexMass-DS can be used)

Insert the plate into the device  
and wait for the vacuum

Begin analysis

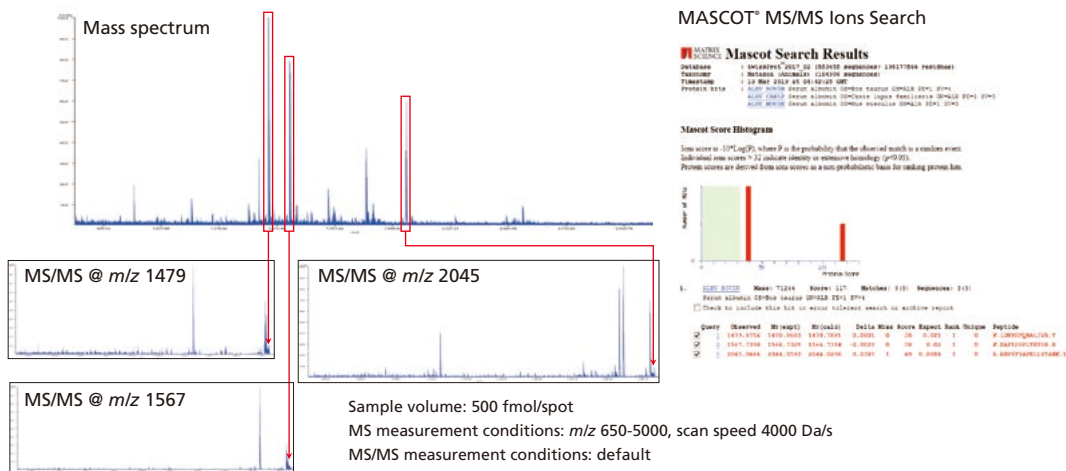
# “Minimum” sample volume

MS<sup>n</sup> analysis is possible over a wide mass range, even with microquantity samples

By combining a MALDI ion source with Digital Ion Trap (DIT) technology, it is possible to carry out high-sensitivity MS and MS<sup>n</sup> analysis even on micro-quantity samples. Not only can the mass of various molecules be checked, but it is also possible to carry out a wide range of analyses such as identifying proteins and investigating the structure of glycans and glycopeptides.

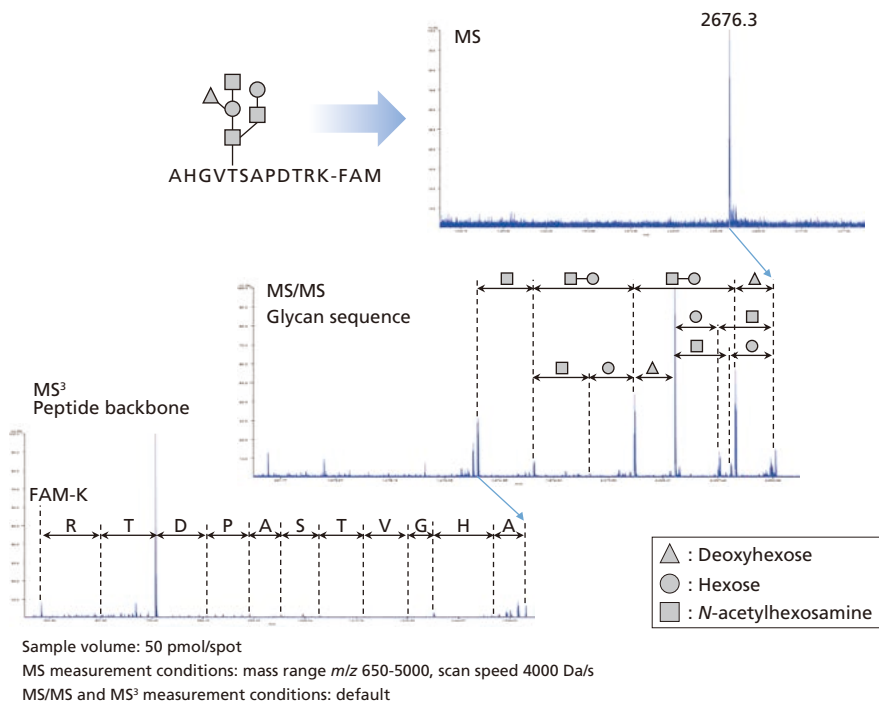
## Identifying protein digests

By carrying out MS and MS/MS measurements on protein digests, it is possible to determine the identity of a protein.



## Investigating glycopeptide structure

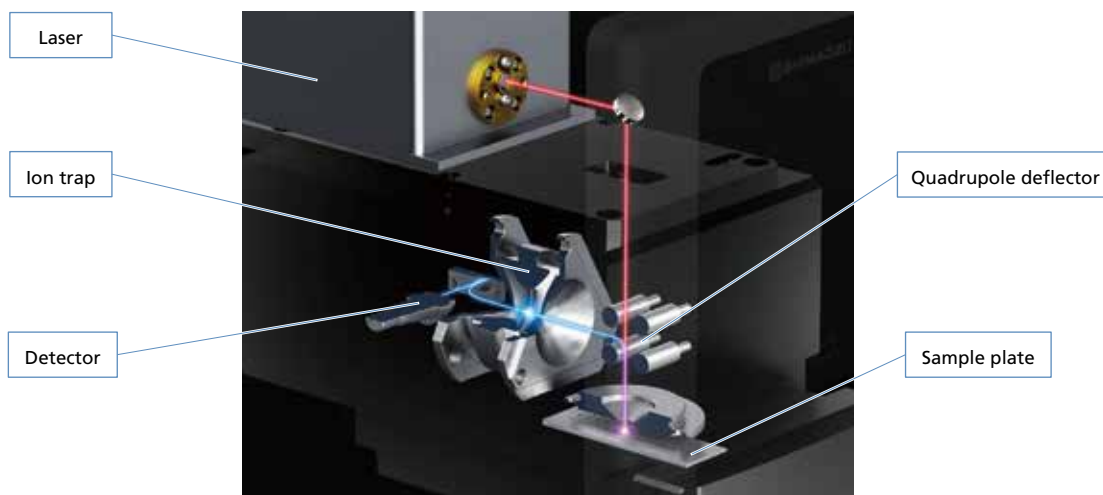
Through MS, MS/MS and MS<sup>3</sup> measurements of synthetic O-linked glycopeptides, the glycan sequence can be found from MS/MS data and the amino acid sequence of the peptide backbone can be found from MS<sup>3</sup> data.



# The Technology Behind MALDImini-1

## ■ Compact design with unique ion optics system and layout

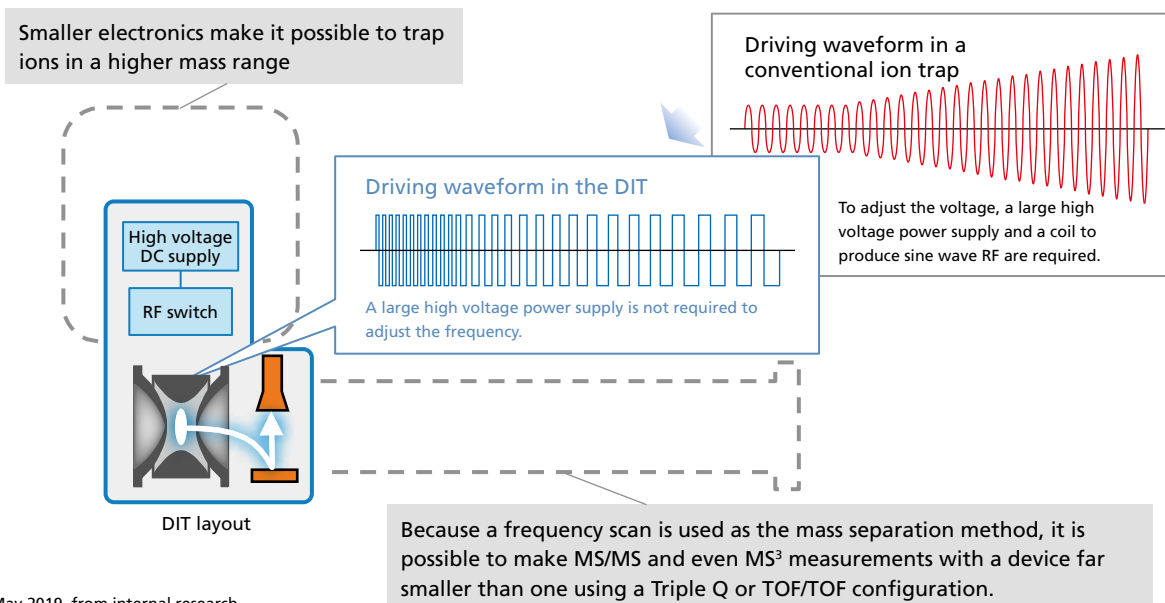
The laser optic system, sample stage, and vacuum exhaust system have all been finely optimized to reduce the size of the device.



Ion and laser optics steer the laser beam to hit the sample orthogonally to the plate, enabling high ion transmittance and a more compact layout. Following ionization, the beam is deflected 90° to ensure maximum transfer of ions to the ion trap.

## ■ Digital Ion Trap (DIT) technology provides high sensitivity over a wide mass range, despite the device's small footprint

The world-first\* Digital Ion Trap (DIT) technology, unique to Shimadzu, uses rectangular wave RF to trap ions rather than the sine wave RF which has been used in ion-trapping devices until now.



\* As of May 2019, from internal research

## ■ MALDImini Console

With the dedicated control software for MALDImini-1, you can take measurements just by setting simple analysis parameters. Switch quickly and easily between MS, MS/MS and MS<sup>3</sup> modes for seamless analysis. Data can be exported in mzML or mzXML formats.

- Adjust the laser strength
- Save measurement data
- Start or stop measurements

Control the laser position

Measurement parameters

**MS mode**

Mass range settings  
Scan speed settings

↕

**MS/MS mode**

Select precursor  
CID voltage settings

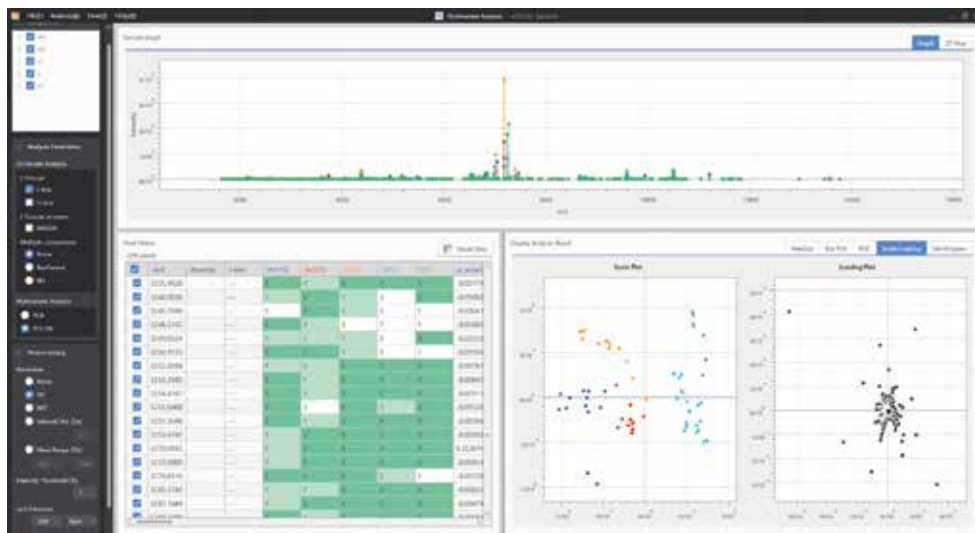
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**MS<sup>3</sup> mode**

Select precursor  
CID voltage settings

## ■ Compatibility with software solutions

Powerful processing tools can be used to analyze your exported mzML or mzXML data, such as MASCOT for identifying protein digests, SimGlycan™ for processing MS<sup>n</sup> data for glycans, and eMSTAT Solution™ for statistical analysis.



eMSTAT Solution

## Specifications

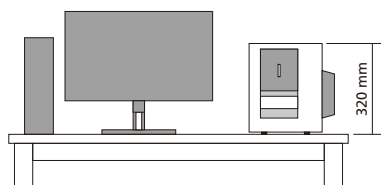
Mass range	<i>m/z</i> 650 to 70000
MS/MS mass range	<i>m/z</i> 350 to 5000
Separation ability	>4000 (FWHM, [Glu1]-Fibrinopeptide B <i>m/z</i> 1570.68, scanning speed 1000 Da/s)
Sensitivity (MS)	1 fmol ([Glu1]-Fibrinopeptide B <i>m/z</i> 1570.68)
	500 fmol (BSA <i>m/z</i> 66431)
Sensitivity (MS/MS)	10 fmol ([Glu1]-Fibrinopeptide B <i>m/z</i> 1570.68)
Mass accuracy	<200 ppm (external standard, <i>m/z</i> 1000 to 5000)
MS <sup>n</sup>	1 ≤ n ≤ 3
Laser	Medium: Nd:YLF, wavelength: 349 nm
Sample plate	FlexiMass-SR, FlexiMass-DS, size: 26 × 76 mm
Software	Data storage: Database format in SQLite
	Exported file format: mzML, mzXML
Dimensions	309 (W) × 320 (H) × 385 (D) mm
Weight	25 kg

## Installation requirements

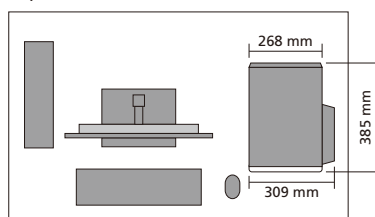
Utilities	Power	AC 100 to 240 V, 50/60 Hz, 960 VA
	Gas	Ar, He (99+%, 40 to 60 kPa)
Environment	Temp.	18 to 26 °C
	Humidity	40 to 70 % (without condensation)

## Installation example

Front view:



Top view:



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