

Thermo Scientific™ Velos Pro™ dual-cell linear ion trap mass spectrometer

Accelerating innovation with MSⁿ

Keywords

Velos Pro dual-cell linear ion trap mass spectrometer, MSⁿ (CRM) capabilities, proteomics, metabolite identification, forensic analysis, clinical research, teaching

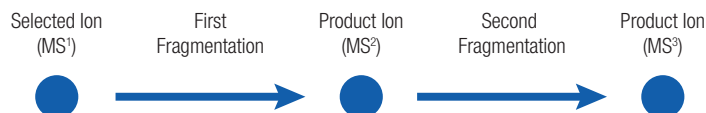
The Velos Pro mass spectrometer is an optimized dual-cell linear ion trap with high-pressure and low-pressure cells that blurs the lines between traditional ion trap and triple quadrupole performance.

The first high-pressure cell enables maximum ion trapping efficiency, higher ion isolation and fragmentation efficiency. The second low-pressure cell, enables better resolution and higher scan rates. All of which, results in higher sensitivity for full scan MS and MSⁿ analysis.

If you are in the market for an extremely powerful and flexible mass spectrometer, look no further than the Velos Pro dual-cell linear ion trap.

Applications include proteomics, metabolite identification, forensic analysis, clinical research and teaching. Now includes updated software with Windows 10 compatibility enabling full support today and into the future

A single quadrupole offers no more than Selected Ion Monitoring (SIM). A triple quadrupole adds Selected Reaction Monitoring (SRM) where a selected ion can be fragmented into a product ion. A linear ion trap goes further by enabling Consecutive Reaction Monitoring (CRM) where a selected ion is fragmented into a product ion and the resulting product ion further fragmented in additional consecutive steps (MSⁿ). Each additional fragmentation step makes compound identification more certain and facilitates structural characterization.



Powerful tools for structural characterization

Collision Induced Dissociation (CID)	
<ul style="list-style-type: none">• Resonance excitation of precursor at low q; low energy collisions with He• Universal, no tuning required, high efficiency	Included
Pulsed “q” Dissociation (PQD)	
<ul style="list-style-type: none">• Short resonant excitation of precursor at high q, rapid shift to very low q, high energy collisions with He• Selective, no low mass cutoff, low noise• Tuning required, low efficiency	Included
Higher Energy Collision Induced Dissociation (HCD)	
<ul style="list-style-type: none">• Acceleration of ion packet through N2 cell, high energy collisions with N2• High efficiency, no low mass cutoff• Tuning required	Software option

Hardware features

Thermo Scientific™ Ion Max™ API source

- With ESI, HESI, APCI and APPI options
- Sweep gas reduces chemical noise
- 60° interchangeable ion probe orientation
- Removable metal ion transfer tube provides vent-free maintenance

Transfer ion optics

- S-lens technology
- Generation II Ion optics with novel neutral blocking technology for improved robustness
- High stability and ion transmission efficiency

Dual-pressure 2D linear quadrupole ion trap mass spectrometer

- Dual-pressure for optimized performance
- Isolation waveforms during injection
- Balanced rf field
- Automatic system calibration
- High-efficiency radial ion ejection

Vacuum system

- Differentially-pumped vacuum system to 10⁻⁵ Torr
- Split-flow turbomolecular pump controlling vacuum in three regions
- Dual rotary vacuum pump configuration
- High-vacuum aluminum analyzer chamber

Detection system

- Proprietary dual conversion dynode detector
- Two off-axis discrete dynode electron multipliers with extended dynamic range
- 24-bit electrometer for high level linearity
- Digital electronic noise discrimination

Integrated liquid delivery

- Fully-automated data system with valve control enables user to divert the solvent front, gradient end point, and any other portion of the HPLC run to waste
- Syringe Pump allows automated infusion under data system control

Data system features

Hardware

- High performance PC
- 27 inch LED Monitor with 1920 x 1080 resolution

Operating system

- Microsoft Windows® 10 x 64 enterprise IoT LTSB 2016

Thermo Scientific™ software

- LTQ Instrument Control Software
- Thermo Scientific™ Xcalibur™ software for method setup, data acquisition, data processing, and reporting
- Thermo Scientific™ FreeStyle™ software to view and analyze data

Scan functions

- Predictive Automatic Gain Control (AGC) delivers up to 10 Hz data dependent MS/MS acquisition
- Full-scan mass spectra for sensitive analyses and rapid screening of unknown compounds
- Full-scan product ion spectra at sensitivities higher than any ion trap mass spectrometer
- Selected Reaction Monitoring (SRM) for traditional LC/MS/MS quantitative analytical experiments
- MSⁿ for multi-stage MS experiments to probe the structure of ions
- ZoomScan, a high-resolution, full-range scan to resolve isotopic envelopes often used for charge state determination
- Ultra ZoomScan for ultimate resolution
- Rapid Scan, the fastest scan mode for UPLC analytical data collection
- TurboScan an ultra-fast scan to improve signal-to-noise and sampling rate
- Unique Automatic Gain Control (AGC) ensures that the ion trap is always filled with the optimum number of ions for any scan type
- Dynamic Exclusion allows acquisition of MS/MS and MSⁿ spectra from lower intensity ion species

- WideBand Activation generates more structurally informative spectras
- Normalized Collision Energy provide reproducible data from instrument to instrument

System specifications

MS/MS sensitivity

Heated electrospray ionisation (HESI) – 2 µL of a 50 fg/µL solution of reserpine (100 femtograms total) injected at a flow of 400 µL/min will produce a minimum signal-to-noise ratio of 100:1, for the transition of the isolated protonated molecular ion at m/z 609 to the largest two product ions, m/z 397 and m/z 448, when the mass spectrometer is operated at unit resolution in the full-scan MS/MS mode, scanning the product ion spectrum from m/z 165–650.

Atmospheric pressure chemical ionization (APCI) – 2 µL of a 50 fg/µL solution of reserpine (100 femtograms total) injected at a flow of 400 µL/min will produce a minimum signal-to-noise ratio of 100:1, for the transition of the isolated protonated molecular ion at m/z 609 to the largest two product ions, 397 and 448, when the mass spectrometer is operated at unit resolution in the full-scan MS/MS mode, scanning the product ion spectrum from m/z 165–650.

MSⁿ sensitivity

Heated electrospray ionization (HESI) – A loop injection of 2 µL of a 50 fg/µL solution of reserpine (100 femtograms total sample) at a flow of 400 µL/min will produce a minimum signal-to-noise ratio of 100:1, for the transition of the unit isolated protonated molecular ion at m/z 609 to the product ion at m/z 397 which is further fragmented to the product ion at m/z 365, when the mass spectrometer is operated at unit resolution in the full-scan MS/MS mode, scanning the product ion spectrum from m/z 165–650.

Installation requirements

Power

- One 230 Vac ±10.0%, 15 Amps, 50/60 Hz, single phase, with earth ground dedicated to the instrument
- 120 or 230 Vac single phase, with earth ground for the data system

Gas

- One high-purity (99% pure, flow rate 15 L/min) nitrogen gas supply for the API source
- One ultra-high-purity helium gas supply (99.998% pure) with less than 1 ppm each of water, oxygen, and total hydrocarbons for the mass analyzer

Environment

- System averages 2300 W (8000 BTU/h) output when considering air conditioning needs
- Operating environment must be 15–27 °C (59–80 °F) and relative humidity must be 40–80% with no condensation
- Optimum operating temperature is 18–21 °C (65–70 °F)

Dimensions/weight

- MS: 56 cm × 79 cm × 59 cm (h × w × d)
- MS: ~120 kg
- Two roughing pumps: 38.6 kg each

Performance specifications

Mass range

- m/z 15–200
- m/z 50–2000
- m/z 200–4000

Linear dynamic range

- Under typical experimental conditions, at least six (6) orders of magnitude

Polarity switching

- 100 msec between positive and negative

Scan power

- MS^n for $n = 1$ through 10

Contact closure

- Start In/Out
- Start Out is programmable

Analog inputs

- One (1) analog Input (0–1 V)
- One (1) analog Input (0–10 V)

Scan Type	Mass Accuracy (Da)	Peak Width (FWHM)	Scan Rate (Da/Sec)
Turbo	1.5	3	125,000
Rapid	0.15	0.6	66,667
Normal	0.1	0.5	33,333
Enhanced	0.1	0.35	10,000
Zoom	0.1	0.25	2,222
Ultrazoom	0.1	0.075	28

Find out more at thermofisher.com/iontraps

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