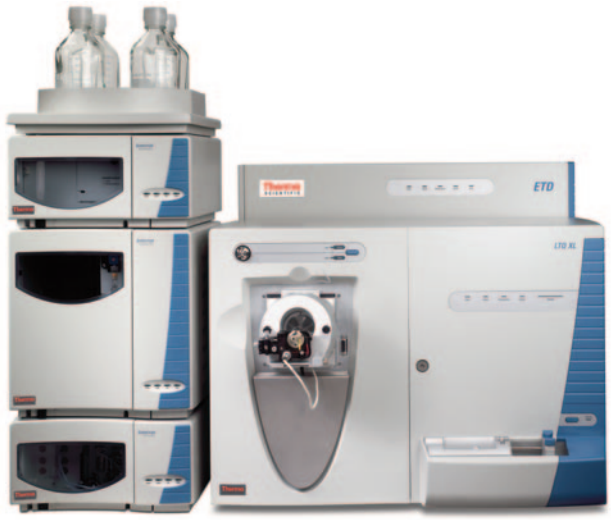
ETD generates enriched peptide fragmentation for increased protein coverage and post-translational modification (PTM) site identification.

Electron Transfer Dissociation (ETD)

Improving Protein Characterization with Ion/Ion Chemistry

Thermo Scientific ETD technology is a "landmark advance in the field of proteomics" according to renowned protein researcher, Prof. Donald F. Hunt of the University of Virginia.



- Identifies both the type and site of PTMs
- Alternating ETD and CID data scans provide greater protein sequence coverage
- Automated identification of ETD spectra with Thermo Scientific Proteome Discoverer software using the Z-Core algorithm optimized for ETD data
- Compatible with proton transfer reaction (PTR) chemistry
- Available for LTQ™ series linear ion traps

Electron transfer dissociation (ETD) is a powerful new tool for peptide structure analysis and protein identification. It dramatically improves identification of important post-translational modifications for better protein characterization.

The high ion storage capacity and fast cycle times of Thermo Scientific LTQ series linear ion traps provide an ideal environment for ETD, offering an unprecedented new view of entire proteomes.

Traditional fragmentation techniques, such as collision-induced dissociation (CID), generate mainly y- and b-type peptide fragment ions. In contrast, ETD produces complementary c- and z-type ions while also preserving structural information related to labile PTMs.

The fast cycle times of Thermo Scientific linear ion traps allow for rapid, alternating CID and ETD scanning during LC/MS^n analysis, delivering more comprehensive information about the sample.

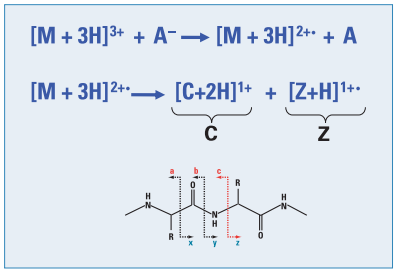
Electron transfer dissociation is just one type of useful ion-ion reaction; the ETD source option hardware supports multiple ion-ion reaction types, including proton transfer reaction (PTR).

Product Specifications

System Specifications

ETD Installation Specification

A 3 µL/min infusion of a 1 pmol/µL solution of Angiotensin I will produce an electron transfer dissociation fragmentation efficiency of at least 15%.



Electron transfer dissociation mechanism

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: 89 × 82 × 125 cm (h × w × d)
- MS: ~137 kg
- Two roughing pumps: 38.6 kg each

Product Specifications

Mass Range

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

Resolution

- Down to 0.05 FWHM (full width half maximum) with Ultra ZoomScan™

Polarity Switching

- 100 msec between positive and negative

MS Scan Power

- MS^n, for n = 1 through 10

Contact Closure

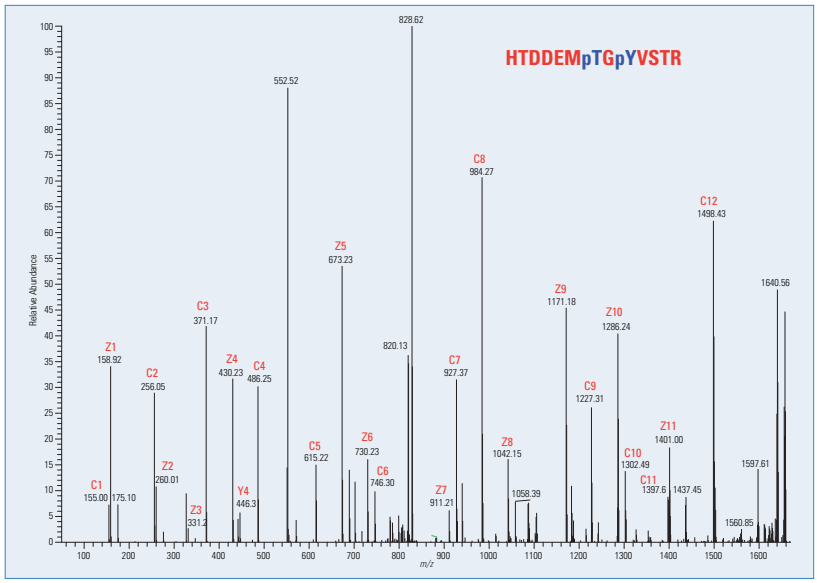
- Start In/Out
- Start Out is programmable

Analog Inputs

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

Access

- 100 cm access required at the rear of the instrument



ETD Spectrum of doubly phosphorylated peptide from SAPK2a

Reference

Syka JEP, Coon JJ, Schroeder MJ, Shabanowitz J and Hunt DF.
Peptide and protein sequence analysis by electron transfer dissociation mass spectrometry.
Proc. Natl. Acad. Sci. U.S.A. **2004**, 101, 9528–9533.

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