Comprehensive, Fast, Flexible Mass Spectrometry Software
Achieve unprecedented simplicity and speed

**TraceFinder software is the solution**
Thermo Scientific™ TraceFinder™ software makes the challenging steps of targeted and untargeted analysis simple, fast and productive. It is the only software that can be used to develop methods, acquire and process data, and generate reports with the full portfolio of Thermo Scientific quantitative mass spectrometers. Tracefinder software integrates the full range of popular front end chromatography systems, providing laboratories with the suite of features required to address their analytical demands. Now, regardless of the MS expertise of the user, the analytical requirements of every laboratory can be addressed with one software solution.

**TraceFinder empowers you to tackle the everyday challenges in your laboratory**

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<th>Challenge</th>
<th>TraceFinder</th>
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<td>Maintain or increase laboratory productivity</td>
<td>One software for both HRAM and triple quadrupole MS platforms. Scientists now have the ability to leverage information from method development in early stage work to quickly enable data review in routine quantitative analysis.</td>
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<td>Customizable reporting templates</td>
<td>Customized templates and automatic generation of reports save time and organizational resources.</td>
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<td>Efficient method development regardless of expertise</td>
<td>Method development wizard, comprehensive database, and the ability to address critical parameters for all molecule types enable development of sensitive, robust, and reproducible quantitation methods.</td>
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Comprehensive data review allows for rapid data quality determination.
Ensure increased productivity

TraceFinder software simplifies every step of routine mass spectrometry (MS) quantitation and targeted workflows, saving time and increasing productivity. From data acquisition to data processing, review and reporting, TraceFinder empowers you to streamline your processes and get answers faster.

- 4 click workflow from analysis to reports
- Comprehensive method development for screening and quantitative workflows
- Automated and manual flagging are reflected in final reports
- Template driven design to simplify routine workflows
- Automatic method creation with Method Forge™
Comprehensive flagging facilitates the technician’s role in reviewing data.

TraceFinder software speeds up each step in the analysis of routine MS quantification and screening workflows. Once a method is defined, data acquisition is an easy four-click process that can be monitored in real-time. Data review is fast with comprehensive flagging, and enables association of a sample set with a previous calibration. When needed, the software makes it easy to edit results, and the edits are dynamically reflected in the final report. Customized nomenclature for environmental testing, food safety, clinical research and forensic toxicology applications is available.

**Comprehensive method development**

TraceFinder software enables the development of better, and more robust methods in a shorter amount of time. Powerful tools enable method developers to meet the demands of advanced users, and address regulatory requirements and existing laboratory protocols.

- Method templates for data processing
- Batch templates use previously defined methods for rapid data acquisition, processing and reporting
- Compound databases (CDB) for selected reaction monitoring (SRM) and high-resolution accurate mass (HRAM) workflows
- Customizable report templates
- User-defined flags for nearly every parameter
- Method association with any previously saved calibration
- Method Forge tool to upload a raw data file and detect peaks via a library search

**Four-click data acquisition**

Submitting sample batches and initiating analyses is performed in four simple steps:

1. Select the appropriate batch template.
2. Review the selected batch template.
3. If needed, choose a system start-up and shut-down method, or extend a historical calibration curve.
4. Submit the samples.

**Increased efficiency with compound databases**

The CDB retains all instrument parameters for targeted analysis allowing the method developer to select compounds and develop methods rapidly. New analytes and all corresponding instrument parameters can be readily added to the CDB.

Comprehensive flagging facilitates the technician’s role in reviewing data.
Potent method creation

Multiple confirmation criteria and reporting is streamlined with automatic predefined criteria for identification of targeted molecules to include ion ratios, library searches, isotopic distributions, and defined fragmentation patterns. Identification criteria are automatically reported in the customizable report templates. Depending on laboratory requirements, the software offers multiple resources for identification.

TraceFinder software provides user-defined flags for almost every parameter, and the flags chosen are reflected in data review and reports.

Simplified screening

Screening capabilities draw from proven Thermo Scientific screening software, making TraceFinder an easy-to-use tool that substantially simplifies MS/MS targeted screening workflows. The software supports SRM, HRAM, and MS/MS workflows, and uses the widely accepted NIST spectra library and mZCloud libraries software for compound identification.

The heat map reporting templates allow for the quick evaluation of the presence of components and their relative abundance across the sample set.
TraceFinder software offers simple, yet exceptionally feature-rich data review capabilities. The intuitive, workflow-driven arrangements of the software windows simplify your role in reviewing data, and views can be customized to streamline daily tasks. You can quickly and easily observe the data processing status, view compound-related flags to locate compounds which need attention, and take appropriate steps to correct any problems.

To address compound-related difficulties, it's easy to perform compound specific edits such as manual peak rejection and integration, and to change peak-detection parameters. Feedback is immediate, as data is reprocessed and presented in the same software screen and in the final report automatically.

**Save time and samples with intelligent sequencing**

The Intelligent Sequencing module helps you take complete advantage of the powerful flagging system. It contains parameters that can be configured by sample type to enable actions on flagged results in real-time. Intelligent sequencing allows for real-time rejection of samples, insertion of blanks, and halting of sample sequences in which data has fallen outside of predefined criteria, saving you time and valuable sample resources.

Submitting sample batches and initiating analyses is straightforward. The Real Time Viewer offers immediate access to system status and queues.
Data reporting

- Automated reporting and numerous report templates.
- A large number of predefined and customizable report templates to meet a variety of regulatory requirements.
- Changes to the data processing method can immediately be seen in the report view – without manual intervention.
- If desired, save time and paper by choosing only to print reports for compounds above the LOD, LOQ or LOR.

User rights ensure increased security for audit trail

To protect the integrity of analytical data, the software includes a rights-based secure user login system and dual method hierarchy that limits access to methods and data. In addition, an e-signature and audit trails are available, which support the guidelines indicated in 21 CFR Part 11.

Highly customizable reports allow for fast decision making.

Optimized flagging for targeted screening analysis.
Discover the power of TraceFinder software to help you create, review and report scientific data and increase the efficiency of your team. Use TraceFinder software to easily acquire data, perform routine data review, and automatically report results on the fly. TraceFinder allows your laboratory to standardize on a single platform across all your Thermo Fisher Scientific mass spectrometry and chromatography products.

**System requirements**
- 3.0GHz or faster processor
- Internet Explorer 11
- 8GB of RAM (16GB recommended)
- 5GB of available hard-disk space (solid state hard drive recommended)
- 1024x576 screen resolution (1920x1080 recommended)
- DVD drive
- Video hardware acceleration (optional)

**Software**
- Microsoft® Windows® 7 SP1 Professional (64-bit only) English only
- Microsoft®.NET Framework 4.5.1
- Adobe® Reader® 10.1

**Thermo Scientific software (minimum versions listed):**
- Xcalibur 4.0
- Foundation 3.1 SP1
- mzVault 1.0 SP1
- Thermo FreeStyle 1.1 SP1
- Thermo LC Devices 3.0 or later
- Thermo Exactive Series 2.7
- TSQ Endura and Quantiva 1.2 or later
- Fusion 1.2 SP1 or later
- Aria MX 2.2 or later
- SII for Xcalibur 1.1 or later
- GC Devices 3.2 or later
- ISQ 3.2 SP1 or later
- TSQ 8000 3.2 or later
- LTQ Series 2.7 SP4 or later
- TSQ 2.5 or later