Break free from the time, cost, and complexity of manual proteomics sample preparation

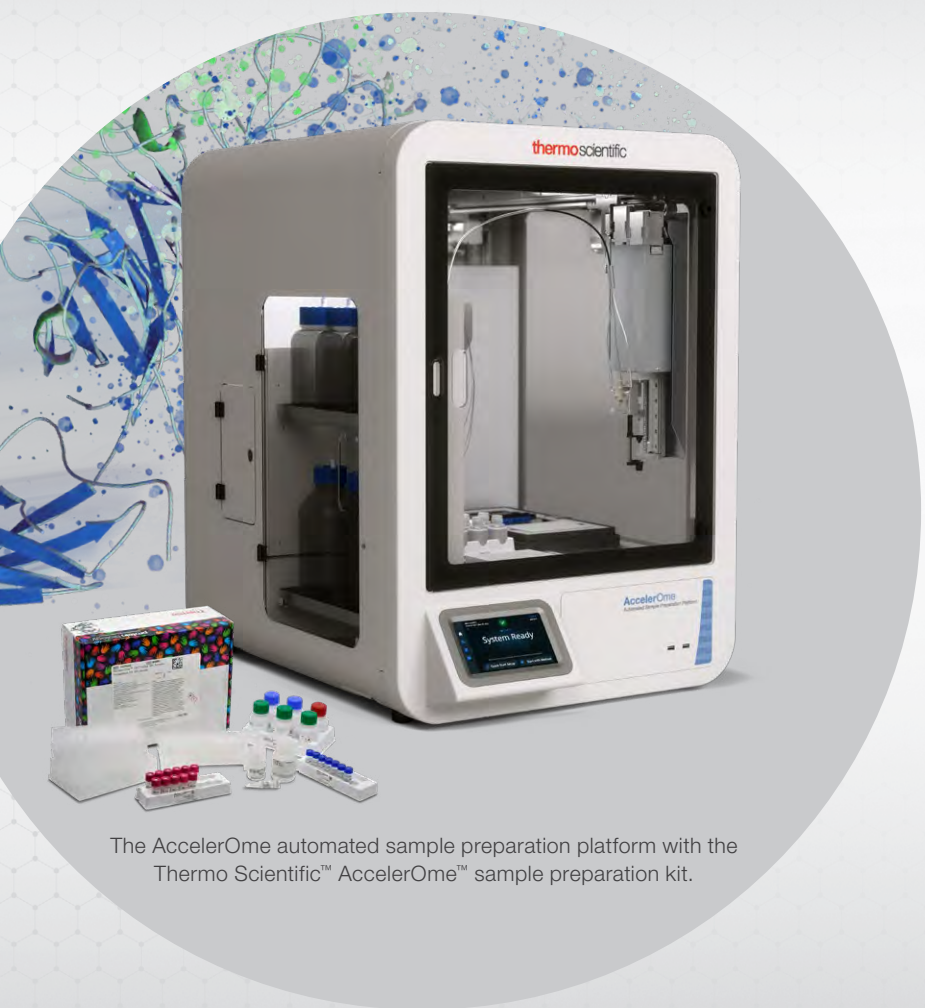The AccelerOme automated sample preparation platform with the Thermo Scientific™ AccelerOme™ sample preparation kit.

Transforming sample preparation with speed, accuracy, and high reproducibility

Completing comprehensive proteomics studies with confidence requires high levels of performance and precision at every step of the workflow. Nowhere is that more important than with sample preparation, where manual preparation protocols are complex, time-consuming, and highly prone to errors that can compromise even the best LC-MS performance.

Thermo Fisher Scientific has extended its proteomics innovation and developed the Thermo Scientific™ AccelerOme™ automated sample preparation platform that enables scientists to overcome the challenges of sample preparation and deliver confident results, regardless of the laboratory. With factory-supplied reagents and kits and step-by-step onscreen instructions that include both label-free and Tandem Mass Tag (TMT) multiplexing strategies, the AccelerOme platform makes short work of complex tasks. Designed with a unique experimental design experience, the AccelerOme platform is optimized to fit into the Thermo Scientific™ Orbitrap™ mass spectrometry ecosystem delivering confident results with speed, accuracy, and high reproducibility, allowing researchers to spend more time on more valuable tasks.

Hardware

Software

Chemistry

The first platform designed for comprehensive workflow integration to achieve the best results

Easy to use

Simplify method set-up using a software wizard that walks through pre-validated sample preparation workflow steps. With fit-for-purpose reagents that are pre-made and pre-packaged, the AccelerOme platform provides a walk-away solution for any user.

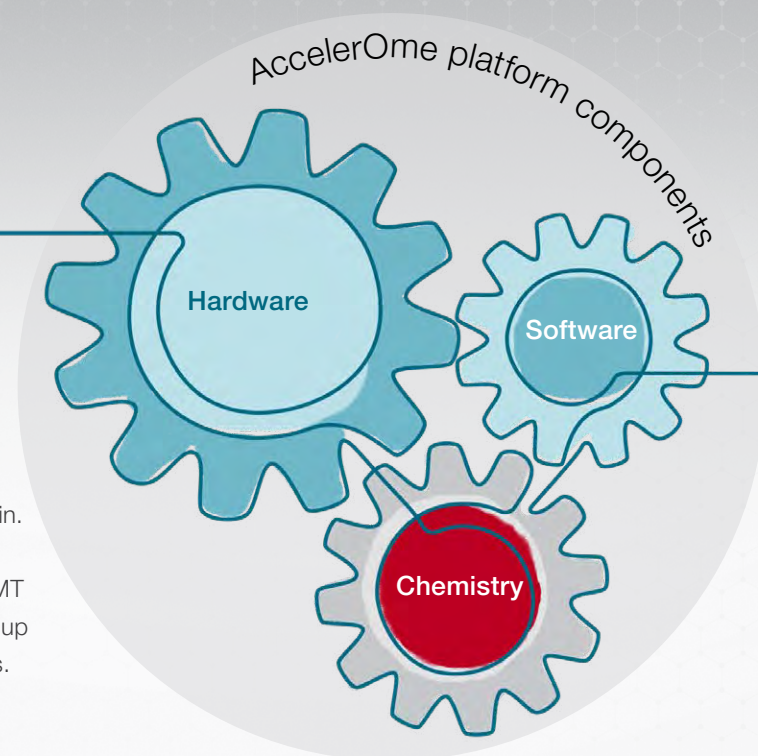### Meet your demands with experimental flexibility

The set of workflows supported by the AccelerOme platform extends confident performance for a wide range of applications, from label free to TMT multiplexing on small- and large-scale studies. Reagents and buffers have been optimized to prepare cells, tissue, biofluids, and purified proteins for high-quality data acquisition.
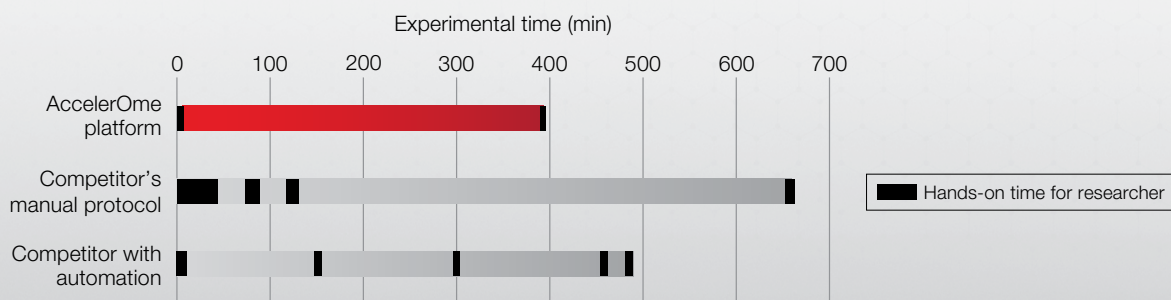
Ensure high-quality samples

Factory-made, pre-packaged kits ensure reproducible digestion and labeling performance time and time again. Validated sample preparation methods and reliable robotics drive automated routines for label-free and TMT multiplexing experiments. On-line µSPE sample clean-up and UV concentration analysis confirm reaction results.

Maximize productivity

Built on a proven liquid handling format with key instrument features and optimized chemistries and reagents, the AccelerOme platform confidently delivers more processed samples reproducibly with minimal human touchpoints, enabling you to focus on other tasks.

Increased productivity by minimizing frequent touchpoints

Experimental time (min)

	0	100	200	300	400	500	600	700

AccelerOme platform

Competitor's manual protocol

Competitor with automation

■ Hands-on time for researcher

Unlike manual or other automated methods that require frequent hands-on intervention during sample processing, the AccelerOme platform requires only two touchpoints, at the start and end, to prepare 36 label-free samples.

Automated end-to-end solution to streamline performance

Key features built on a trusted platform to deliver automated sample preparation success
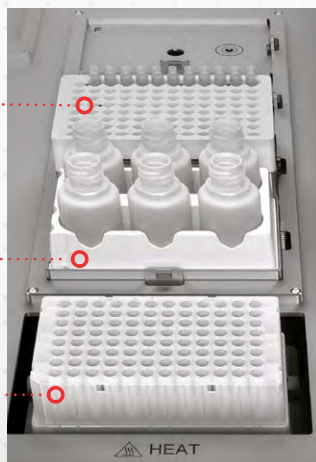
Dilutor module and solvents

With 1 mL syringe and capacity for 2 × 1 L or 3 × 500 mL bottles for wash solvents or buffer dilutors

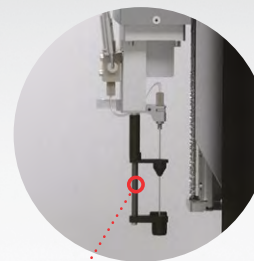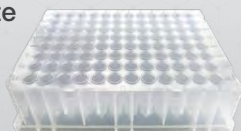**µSPE cartridges**

Sample conditioning/clean-up

Peptide clean-up buffer module

Thermal Mixer

For sample input position— 96-well plate format

Sample input/output plate

Diluter tool and integrated UV flow cell

Integrated in-line UV spectrophotometer and liquid delivery to measure final peptide concentration and dilute samples to desired levels

Reagent tray with optional tray cooling plate for temperature range of 5–40 °C

3 × 54 2 mL vials or 3 × MTP 96 15 × 10 mL reagent vials

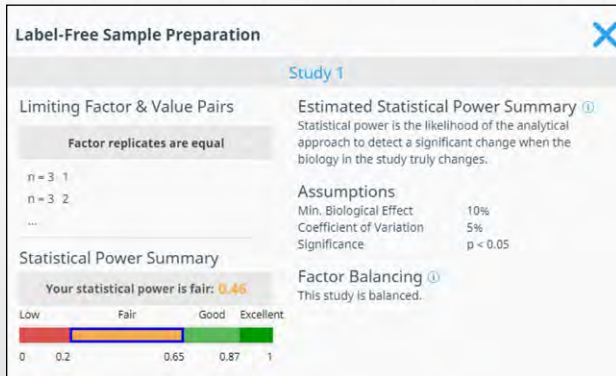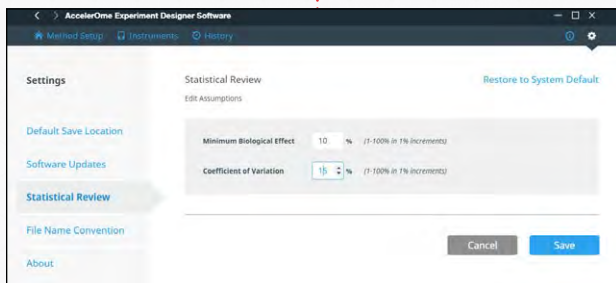**Cartridge waste positions**

Wash positions

Touchscreen display

AccelerOme platform user interface wizard for simple operation

Simplifying the operational process with intuitive software

Obtain rigorous results with unique experiment design software

| Design the experiment | Test the experiment | Capture metadata | Manage sample preparation | Sample output | Data acquisition and processing |

The unique Experiment Designer software starts with entering the study parameters, experiment type, and statistical assumptions used to assess the outcomes (top) that are evaluated for analytical rigor based on the assumptions provided (bottom).

Metadata from the experimental method creation is captured to manage the entire workflow from randomization of the sample processing order, sample name, vial position, and study factors. The metadata can be exported to the Thermo Scientific™ Orbitrap™ mass spectrometer to populate the acquisition queue as well as Thermo Scientific™ Proteome Discoverer™ software to streamline data processing.

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Maximizing digestion efficiency, increasing productivity

Ideal for small- and large-scale proteomics studies

Performing studies with more than 100 samples requires researchers to balance sample preparation with data acquisition and processing to maximize productivity. The AccelerOme platform takes approximately 6.5 hours to prepare 36 samples for LC-MS analysis requiring minimal hands-on time. Preparation of the remaining samples can be performed in parallel with data acquisition, requiring approximately 80 hours to fully analyze 144 samples while spending almost no time in the wet lab. Comparatively, manual preparation often incubates sample digestion overnight to fully prepare sample batches with multiple touchpoints required throughout the digestion workflow, delaying the onset of data acquisition and diminishing productivity. Using "home-brew" kits can also lead to lower sample reproducibility and increased random artifacts such as missed cleavage, incomplete cysteine alkylation, and increased oxidation/deamidation that can disrupt data acquisition and interpretation.

- 0 missed cleavage sites
- 1 missed cleavage site
- 2 missed cleavage sites
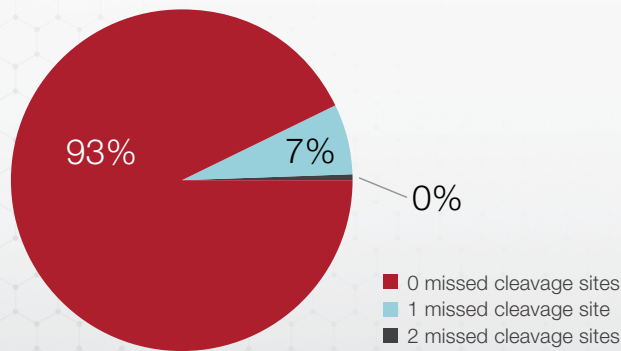
Comparative analysis of red blood cell proteomes for large-cat studies. The study consisted of 144 samples from 18 cats prepared and analyzed using the Thermo Scientific workflow. Following the data acquisition and processing using Proteome Discoverer software, key metrics were evaluated within big-cat class as well as across the study. The pie chart shows the digestion efficiency with 93% of all measured peptides being fully tryptic and the other 7% having 1 missed cleavage site.
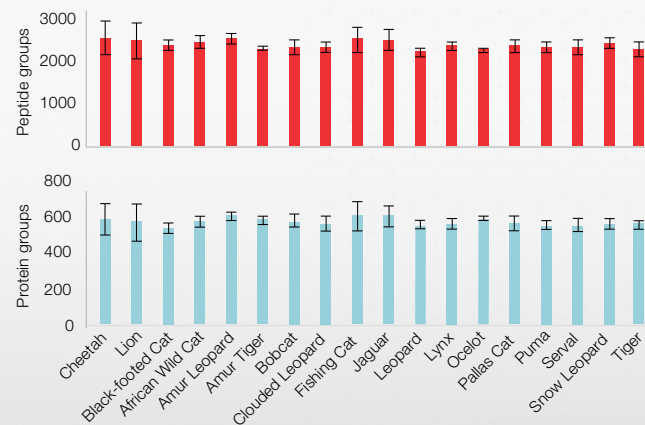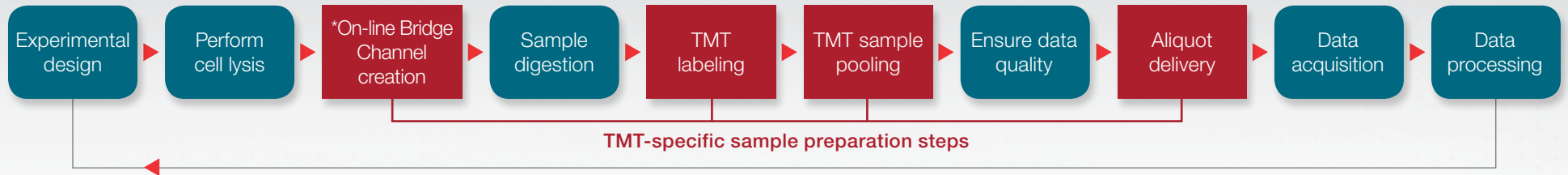
Evaluation of the peptide and protein groups identified across the study. Each large cat had 8 samples collected and randomized prior to digestion and analysis. Most groups showed similar numbers of protein and peptide groups with almost all sample groups showing less than 10% variance.

Generating accurate and precise results

Cost-effective solutions for functional proteomics

Experimental design → Perform cell lysis → *On-line Bridge Channel creation → Sample digestion → TMT labeling → TMT sample pooling → Ensure data quality → Aliquot delivery → Data acquisition → Data processing

**TMT-specific sample preparation steps**

Tandem mass tags provide unrivaled quantitation for multiplexed proteome analysis. The Thermo Scientific TMT reagents and Orbitrap mass spectrometers combine to deliver a complete workflow for the identification and quantitation of thousands of proteins in a single experiment. However, sample preparation presents additional challenges to maintain experimental confidence with additional sample handling steps, precise pooling, and for accurate interpretation of resulting data analysis.
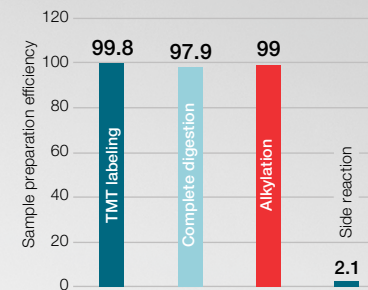
The AccelerOme platform overcomes these challenges from designing experiments to managing the entire sample preparation process delivering high-quality samples ready for LC-MS analysis. With on-line pooling, clean-up, UV measurement, and integrated solvent dilution capabilities, the AccelerOme platform ensures high-quality samples to maximize laboratory productivity.

*On-line bridge channels are used to introduce normalization for studies larger than the multiplexing capabilites.

Human cell lysates

8 × 30 µg

8 × 60 µg

×2

Input plate
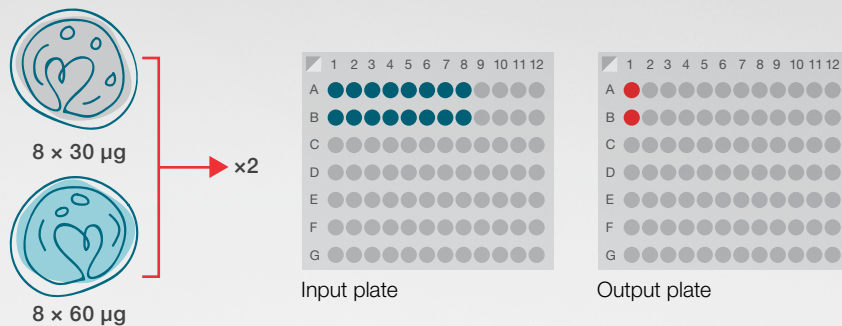
Output plate

Human cells were prepared into 30 and 60 µg samples groups. Eight replicates per group were added to the input plate to create two pooled samples. The Experiment Designer software automates randomization of the TMT tags to remove bias prior to automated sample digestion, TMT labeling, pooling, concentration measurement, and balancing the aliquot pooled sample extraction eliminating the need for determining the post-analysis TMT correction factors.

Sample preparation efficiency: TMT labeling 99.8, Complete digestion 97.9, Alkylation 99, Side reaction 2.1

Maximizing reaction efficiencies reduce unpredicted artifacts that can disrupt downstream data acquisition and interpretation.

CV — %CV 30 µg 10.7%, %CV 60 µg 9.8%

Ratios (60 µg/30 µg) — Median 2.:1, Ratio
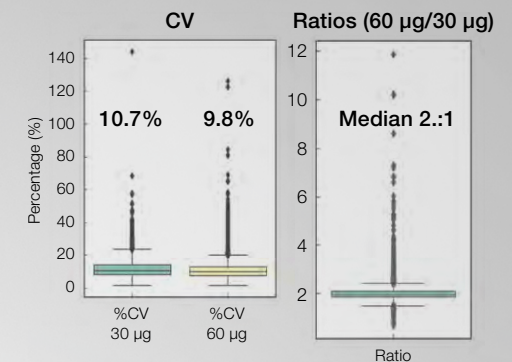
Demonstrating the effectiveness of the entire Thermo Scientific TMT multiplexing workflow with key metrics confirming the 2x fold change at 115 ng/µL.

Thermo Scientific™ AccelerOme™
sample preparation kits

Maximizing your laboratory's potential with leading proteomics workflow solutions

Thermo Fisher Scientific offers integrated proteomics workflow solutions that maximize your analytical performance from start to finish. As an industry leader and innovator of proteomics technologies and applications, we continue to deliver the products and expertise needed to acquire the most comprehensive data and powerful data-processing software, enabling you to achieve greater results across the broadest set of applications. With the introduction of the AccelerOme platform, high-quality sample preparation is fast, easy, and reproducible to deliver the highest-quality data that provides rigorous biological insights for every laboratory.
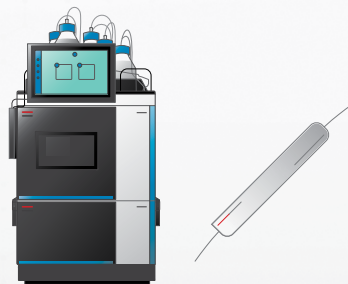
Automated sample preparation	▶	Chromatographic separations	▶	Mass spectrometry data acquisition	▶	Data processing
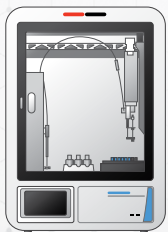
Thermo Scientific™
AccelerOme™ automated sample
preparation platform

Thermo Scientific™ Vanquish™ Neo UHPLC
system with the
Thermo Scientific™ µPAC™ HPLC column

Thermo Scientific™ Orbitrap Exploris™ 480 and
Orbitrap Eclipse™ Tribrid™ mass spectrometers with
the Thermo Scientific™ FAIMS Pro Duo interface

Thermo Scientific™ Proteome
Discoverer™ software with
MSAID GmbH's CHIMERYS
search engine

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