Thermo Scientific Solutions for Intact-Protein Analysis

Better, Faster Decisions for Biotherapeutic Development
Therapeutic proteins and monoclonal antibodies (MAb) have transformed biotechnology and the pharmaceutical industry. Together they form the largest part of the rapidly growing biologics drug market. Protein-based drugs include blood factors, thrombolytic agents, hormones, hematopoietic growth factors, interferons, interleukins, tumor necrosis factor, and therapeutic enzymes.

Essential to the development of biotherapeutics is ability to quickly and accurately assess product quality and safety—including factors such as sequence integrity, glycan heterogeneity, and purity—at each step. Thermo Scientific workflows for intact-protein analysis enable these assessments early in the development process without the effort of complete characterization. Our workflows can provide insights that allow you to make better, faster decisions about how to proceed with your biotherapeutic development.
Traditional workflow for assessing MAb purity

High-quality, high-throughput analyses are key to development of monoclonal antibodies and other biotherapeutics. A typical intact-protein workflow involves MAb separation and fraction collection followed by fast cleanup, desalting, and separation by reverse-phase HPLC prior to mass spectrometric analysis. Intelligent Thermo Scientific HPLC platforms and innovative column chemistries give users the flexibility to adopt exactly the workflows needed for specific therapeutic development challenges.

With Thermo Scientific Dionex UltiMate 3000 HPLC, UHPLC+, and RSLCnano systems and Thermo Scientific EASY-nLC systems, the right combination of chromatographic performance and capabilities is always available. Thermo Scientific LCs offer:

- Superb accuracy and precision at flow ranges from mL down to nL
- Robust, reliable operation for greater productivity
- Biocompatible flow paths to maintain protein integrity and preserve labile PTMs
- Operating pressures up to 1000 bar for faster analyses
- Configurations for many 1D and 2D workflows
- Available fraction collection for automated re-injection in multidimensional or multistep analyses

All of these LC systems can be seamlessly integrated with Thermo Scientific MS systems for fast, sensitive and accurate analyses.

 Superior separations for
better results and higher throughput

Capture by Protein A

Aggregate analysis by SEC

Charge variant analysis by IEC

Optional on-line fraction collection

Hydrophobicity analysis by RP/HIC

MAb samples

Traditional workflow for assessing MAb purity
Fast, accurate mass spectrometry is essential to analysis of intact proteins like monoclonal antibodies. Thermo Scientific Orbitrap technology offers an unequalled combination of high resolution and accurate mass (HR/AM), sensitivity, and dynamic range. It enables fast confirmation of mass and primary sequence, heterogeneity, and purity, allowing quicker, more confident decisions about how to proceed with biotherapeutic development.

- 2X–4X better maximum mass resolution than TOF technology
- Isotopic resolution for proteins <50K Da
- No tradeoff of sensitivity or spectral quality to achieve high mass resolution
- Consistent performance for high- and low-abundance samples

For researchers who plan to dedicate an instrument primarily to intact protein screening, the Thermo Scientific Q Exactive hybrid quadrupole-Orbitrap instrument is an excellent option, providing:
- High-quality spectra
- 140K mass resolution, low-ppm mass accuracy, and outstanding sensitivity
- Robustness for high throughput
- Compact bench-top design

For researchers who plan to follow screening with complete top-down characterization or glycan and PTM structural analysis, the Thermo Scientific Orbitrap Elite hybrid ion trap-Orbitrap mass spectrometer offers the ultimate in performance and flexibility. It features:
- Stunning 240K mass resolution
- MS^n for complete top-down analysis
- Optional electron transfer dissociation (ETD) for fast, accurate location of PTM and glycosylation sites

Uncompromising high-resolution, accurate-mass MS/MS provides greater confidence

High-resolution, accurate-mass performance of Orbitrap technology clearly resolves IgG glycoforms.
Accurate deconvolution is essential for analysis of the multi-charge-state data from intact proteins. Thermo Scientific Protein Deconvolution software maintains the integrity of the high mass accuracy provided by Orbitrap™ technology. The software employs not one, but two deconvolution algorithms. The Xtract algorithm is specifically engineered to provide superb deconvolution results on data from smaller proteins (< ~50K Da) that can be isotopically resolved by Orbitrap technology. The ReSpect™ algorithm provides accurate deconvolution of unresolved data from larger proteins. It is dramatically faster than other common deconvolution algorithms. This deconvolution power is made accessible through an entirely new, simplified interface that guides users through the protein deconvolution workflow and produces clean, easy-to-interpret reports.

For researchers who need to follow up screening with complete top-down characterization or glycan and PTM structural analysis, we have the specialized software necessary to simplify those tasks, including:

- Thermo Scientific ProSightPC software for powerful top-down analysis with high-resolution, accurate-mass data
- SimGlycan® software from PREMIER Biosoft for glycan structural elucidation