Genedata Expressionist® is a powerful software platform that revolutionizes the data processing, analysis, management, and reporting of biotherapeutics characterization studies based on mass spectrometry.

Genedata Expressionist accelerates state-of-the-art characterization processes from research to production, from high-throughput plate-based screening to deep characterization studies and quality control of production lots. Offering complete automation across instruments and labs, the software streamlines complex processes such as peptide mapping and intact protein mass, released glycan, and host cell protein analyses. With intuitive visualization, flexible reporting, and data and method management, Genedata Expressionist ensures reproducible high-quality results with significant time and cost savings.
Intact Protein Mass Analysis

Genedata Expressionist automates and streamlines the complete intact protein mass analysis process, from raw data to final report. It determines the molecular mass of intact, partially-, and fully-reduced therapeutic proteins and their respective subunits. It enables rapid decision making by reliable and efficient confirmation of amino acid sequences, glycosylations, PTMs, degradation products, non-covalent interactions, and protein aggregations across instruments, labs, and departments.

- Automated, assisted, or manual intact protein deconvolution
- Classic 1D deconvolution from (partially) summed retention time ranges
- Unique 2D time-resolved deconvolution for best identification and quantitation
- Orthogonal algorithms for optimal deconvolution, reducing the number of false positives
- Fully automated protein mapping or interactive verification and confutation of annotations
- Intuitive visualization for objective, unbiased, and untargeted analysis
- Identification of in-source and in-sample effects
- Fully automated batch analysis for high-throughput screening
- Characterization of antibody drug conjugates (ADCs) and multi-specific antibodies

2D time-resolved deconvolution for in-depth characterization
Peptide Mapping

Genedata Expressionist automates peptide mapping, dramatically reducing analysis time. Its scalable architecture and refined algorithms enable analysis of large data sets with fast and accurate sequence confirmation, identification of sequence variants, mapping of disulfide bonds, and quantitation and localization of PTMs and glycosylations.

- Reliable identification and accurate quantitation of expected and unexpected PTMs
- User-defined individual constraints in PTM search reduce false positive rates
- Mapping of known and unknown disulfide bonds
- Sequence variant analysis, also supported by fragment (MS/MS) information and scoring
- Comprehensive libraries of glycan structures for complex glycosylation studies
- Sophisticated data processing, visualization, and statistical tools enable batch comparison
- Integration of multiple charge states, adducts, and in-source fragments into one single signature
- Flexible reporting in a variety of formats

Interactive customizable workflows

Data analysis and management can be automated by combining different activities in a workflow tailored to specific needs.

Each step can be fine-tuned and managed to ensure end-to-end automation, maintaining full control throughout the process.

Analysis of stress-induced PTMs on multiple samples

- Noise reduction
- RT alignment
- Peak detection and clustering

Peptides

<table>
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<tr>
<th>Peptides</th>
<th>Control 1</th>
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</table>
Host Cell Protein Analysis

Genedata Expressionist builds on its proven proteomics capabilities to identify and quantify host cell proteins (HCPs) right down to the detection limit. It uniquely supports a wide range of HCP search strategies and enables reliable batch comparisons. Further, reproducible results combined with flexible reporting support the submission of regulatory dossiers.

- Automated HCP identification and quantitation
- Sophisticated raw data pre-processing enables detection of low abundant species
- Integration with one or multiple search engines (including Mascot, Sequest, and X! Tandem)
- Targeted and untargeted search strategies
- False discovery rate assessment through target-decoy or model-based approaches
- Reliable and robust RT alignment enables batch comparison and identification of spurious signals

Released Glycan Analysis

Genedata Expressionist supports the structural elucidation of released glycans, including glycan sequence and branching patterns, and provides robust quantitative information.

- Resolves co-eluting glycans
- Labeled and label-free quantitation
- Comprehensive glycan library
- Support for positive and negative ion mode
- Integration of fragmentation information

Genedata Expressionist® is part of the Genedata portfolio of advanced software solutions that serve the evolving needs of drug discovery, industrial biotechnology, and other life sciences.

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