

Proteome Discoverer software
Harness the potential of proteomics



Transform proteomics mass spectrometry data into insights

Thermo Scientific™ Proteome Discoverer™ software enables comprehensive proteomics data processing workflows empowered by artificial intelligence.

Flexible analysis framework—supports diverse acquisition methods, third-party-developed nodes, and multi-search engine workflows, including INFERYS™ Rescoring and the CHIMERYS™ intelligent search algorithm, for artificial intelligence (AI)-driven insights.

Integrated study management—design studies to statistical significance and generate publishable results—all within the software.

Biological annotation—match identified proteins with gene ontology (GO), symbols, and pathway terms. Enhance your interpretation with built-in enrichment analysis tools.

Dynamic results visualization—interactively explore proteins, peptides, and quant data through volcano plots, PCA, heat maps, and more. Easily visualize biological insights and patterns in complex data.

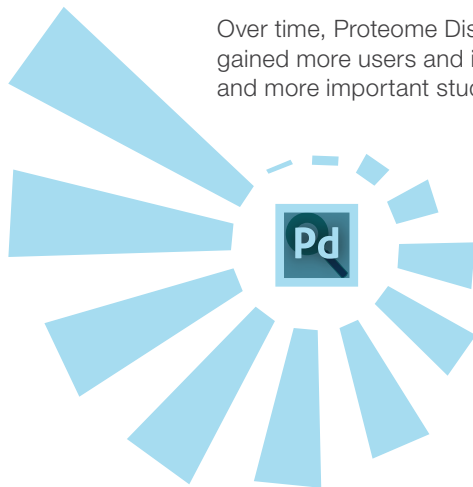
Thermo Scientific™ Ardia™ Platform connectivity—bring together all proteomics workflows, data, and results into a centralized location, enabling users to retrieve and share results in a collaborative and connected platform.

More than a search engine. A platform built for proteomics.

Since its release in 2009, Proteome Discoverer software has been trusted in thousands of peer-reviewed publications—not just for database searching, but for powering complete proteomics workflows. From study design and spectral processing to quantification, annotation, and interpretation, it's a modular, scalable platform that evolves with your science.

Turning data into insights

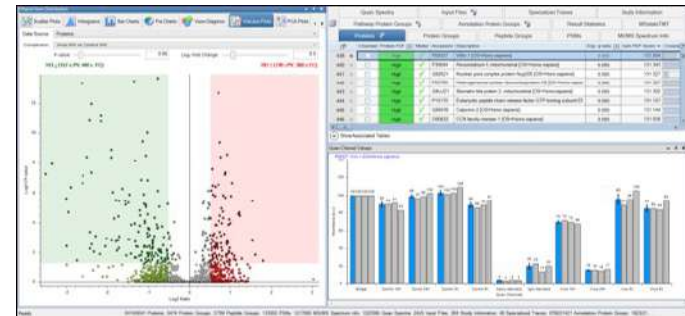
Over time, Proteome Discoverer software has gained more users and is being used in more and more important studies.



From design to discovery: End-to-end flexibility

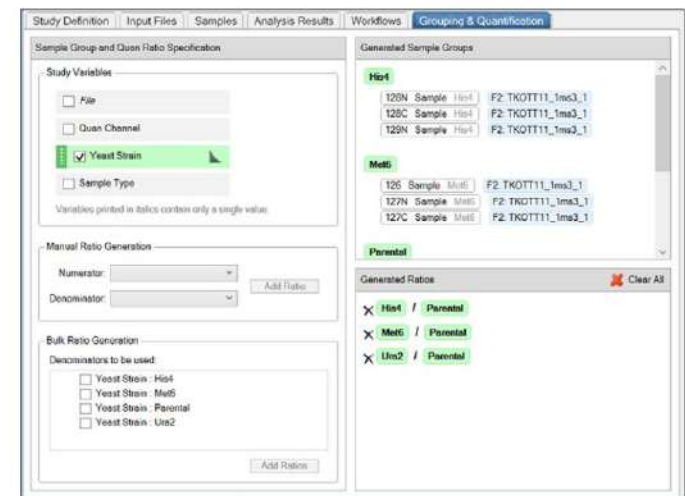
Integrated study management

Proteome Discoverer software includes tools for study management that make it easy to assign study factors to quantification measurements. With a small up-front investment, you can set up replicates, define ratios, and link conditions directly to results tables and charts. Instead of viewing results only by file or quantification channel, you can quickly compare outcomes by experimental condition—streamlining analysis and supporting confident scientific conclusions.



The figure shows a table of sample types, quantification channels, and yeast strains. The table has columns for 'Sample Type', 'Quant Channel', and 'Yeast Strain'. The rows show various sample types (e.g., 126N, 127N, 127C, 128N, 128C, 129N, 129C, 130N, 130C, 131N, 131C) and their corresponding quantification channels (e.g., 126N, 127N, 127C, 128N, 128C, 129N, 129C, 130N, 130C, 131N, 131C) and yeast strains (e.g., Met6, His4, Parental, Ura2).

Proteome Discoverer software enables the creation and mapping of sample types, study factors, and quantification channels to data files for simplified and integrated study management.



Generate ratios from study variables or sample types for comparative and statistical analyses.

Pre-defined and customizable processing workflows

With a customizable, node-based workflow system, you can create workflows to match your unique experimental needs or use ready-to-go templates for common proteomics studies.

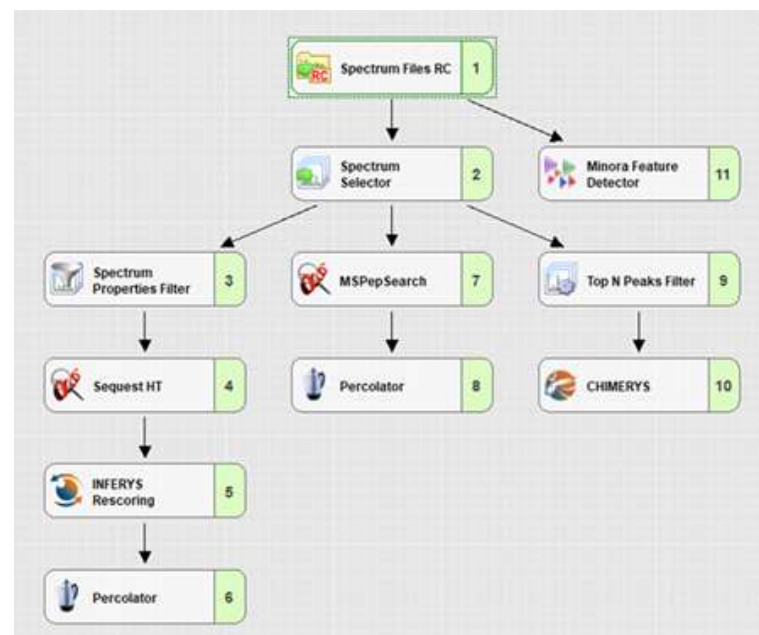
Support for proteomics workflows, including:

- Bottom-up identification
- Isobaric tags (TMT and other labelled approaches)
- Stable isotope labeling by/with amino acids in cell culture (SILAC) precursor quantification
- Hybrid DIA with PRM or Thermo Scientific™ SureQuant™ analysis
- Targeted quantitation with high-resolution mass spectrometry (HRAM)
- Label-free quantification (LFQ)-DDA and DIA
- Single-cell proteomics
- Immunopeptidomics
- Metaproteomics
- Top-down proteoform analysis with multiple fragmentation methods and Thermo Scientific™ ProSightPD™ software
- Crosslinked peptide ID with the XlinkX algorithm
- Post-translational modification analysis

Flexibility across acquisition and analysis

Supporting a wide range of acquisition strategies and compatibility with multiple search algorithms, Proteome Discoverer software offers an open, extensible framework that adapts to diverse experimental needs, giving you the freedom to design workflows that match the complexity of your studies.

Workflows can be customized to include multiple search engines or complex strategies to maximize data interpretation. Filters can direct spectra based on mass analyzer, fragmentation method, or mass spectrometry (MS) level for different search approaches. This extensible system allows third-party partnerships for new search methods. Co-developed search algorithms are available, and other nodes can be downloaded from third-party websites.



The workflow system in the software allows for customizable workflows to analyze complex data.

Data visualization and statistics

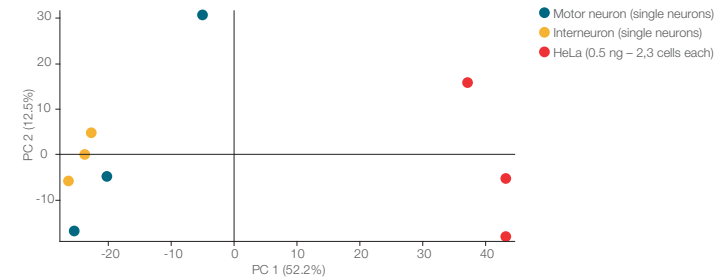
Intuitive interface for results interpretation

Proteome Discoverer software features powerful, interactive tools for visualizing and interpreting results. Each plot is linked back to the underlying source data, allowing users to highlight, select, and analyze related proteins or peptides directly within the results tables. Visualizations can reveal changes across experimental conditions, quantify differences between groups, and classify complex datasets, such as single-cell proteomics.

Key visualization tools include:

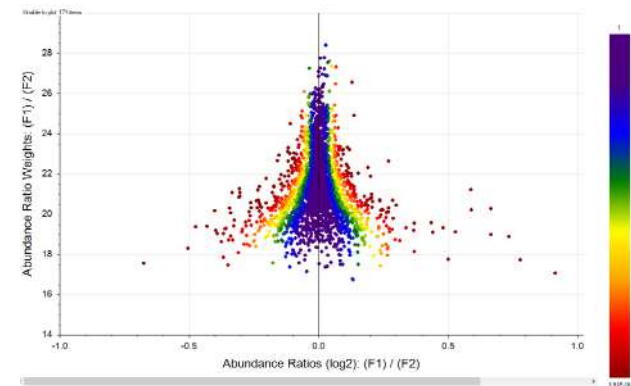
- Hierarchical tables with dynamic filters
- Abundance charts
- Annotated spectra and chromatograms
- Scatter plots
- Volcano plots
- Histograms
- Heat maps
- Venn diagrams
- PCA plots

PCA analysis



Principal component analysis (PCA) simplifies trends in complex datasets. Identify patterns and highlight variations in protein expression across samples.

Confidence interval chart with abundance ratios

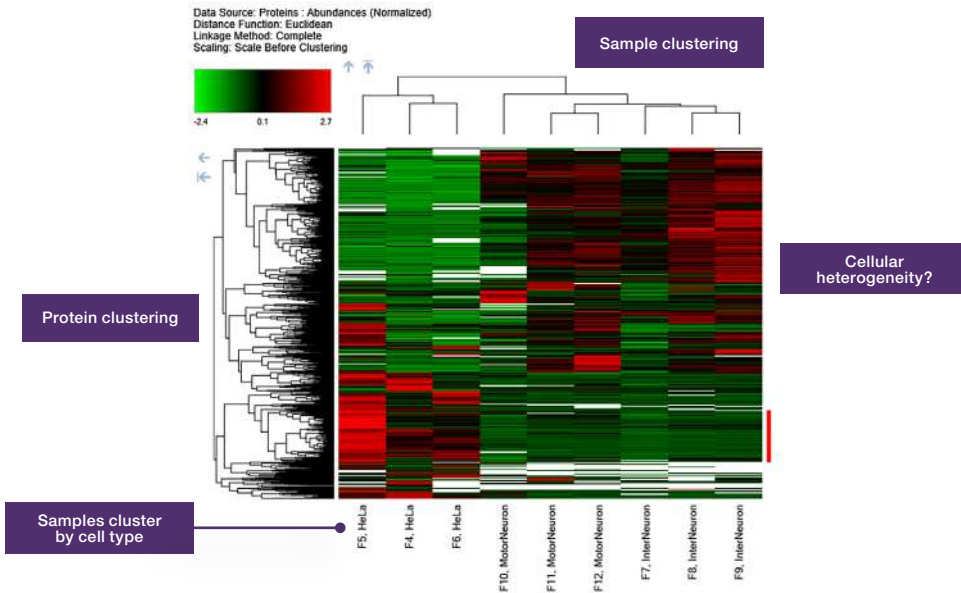


Interactive abundance ratios comparing groups can be visualized with shading according to the confidence interval, allowing for a more confident interpretation of proteome changes across a large dynamic ratio range using a background-based p-value calculation.



Volcano plots allow for the visualization and selection of proteins or peptides in comparisons with customizable p-value and log2 fold change values.

Heat map analysis



Heat map analysis showing the differentiation of HeLa, motor neurons, and interneurons from single-cell experiments.

Advanced statistical insights

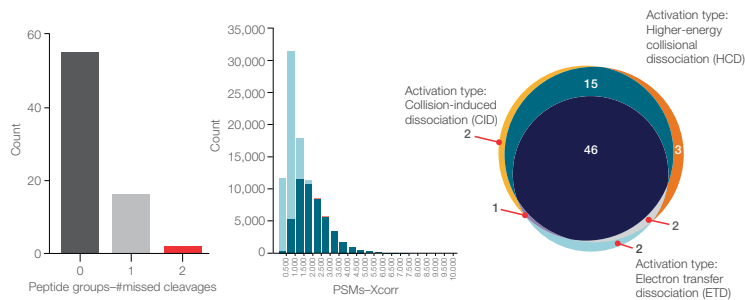
The post-processing Statistics Insights node enables a customizable way to present statistics using filtered data. It can be added to any consensus workflow and produces minimal statistics by default (high-confidence counts).

For deeper insights, tailored statistics can be defined using the Stats Configuration parameters. You can use any custom filter applied to the data to calculate sample or file-specific statistics, such as:

- Median CV for high-confidence proteins per group
- Median ratios
- Number of proteins with CV <10%
- High-confidence proteins by sample

The combination of rich visualization and advanced statistics ensures that every dataset yields clear, interpretable, and actionable insights.

Distribution charts



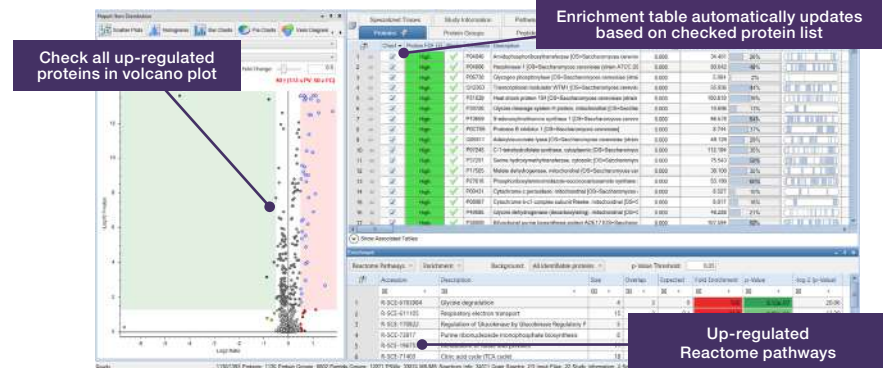
Distribution charts can be utilized to visualize, interpret, and optimize experimental procedures, data acquisition settings, and results. For example, a bar graph can display the number of missed cleavages, a histogram can show the Xcorr values for peptide-spectrum matches (PSMs) passing the pre-set false discovery rate (FDR) filter (dark red) and excluded hits (salmon), and Venn diagrams can display peptide sequences identified by different fragmentation techniques.

Biological annotation and pathway mapping

Annotation and pathway mapping

In addition to the identification and quantification of peptides and proteins, Proteome Discoverer software offers biological interpretation of results. The addition of the Protein Annotation node to the consensus workflow creates the Pathway Protein Groups and Annotation Protein Groups results tables. Also, proteins can be selected from volcano plots, PCA plots, and heat maps to generate an enrichment table to display overrepresented or underrepresented pathways, GO, and protein families (Pfam) database terms to quickly convert results into biological insights. The annotation service is regularly updated to provide the most up-to-date terms. The service also supports full proteome FASTA file downloads and allows for easy updates over time as entries are modified in the database.

Interactive enrichment table from graphical results to find overrepresented pathways



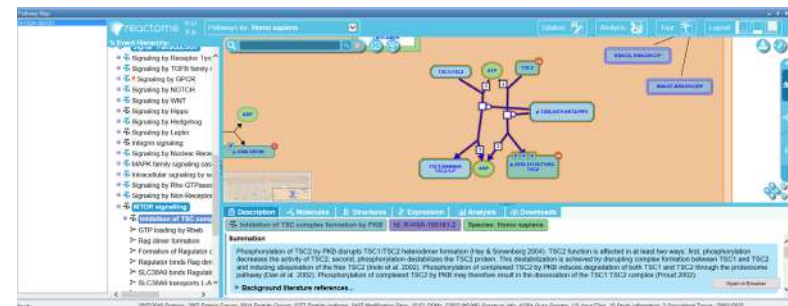
Interactive enrichment tables allow for the selection of up- or down-regulated proteins or peptides in any view, including volcano plots, PCA plots, and heat maps, and the visualization of corresponding Reactome pathways from the checked proteins to help derive biological interpretation of results. In addition to Reactome pathways, Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways and WikiPathways, as well as GO and Pfam terms, can be visualized in the enrichment table.

GO annotation: Identify biological processes, cellular components, and molecular functions. Map results onto pathways to understand biological context.

Proteins	Protein Groups	Peptide Groups	Peptide Isoforms	Modification Sites	PSMs	MS/MS Spectrum Info	Input Files	Specialized Tracers	Path
Accession	Description	Biological Process	Cellular Component	Molecular Function					
1	P21333	Filamin-A OS=Homo sapiens CXN-9							
2	Q15149	Plectin OS=Homo sapiens CXN-960							
3	P55072	Transitional endoplasmic reticulum							

Accession	Description	Biological Process	Cellular Component	Molecular Function
1	P21333	Filamin-A OS=Homo sapiens CXN-9		
2	Q15149	Plectin OS=Homo sapiens CXN-960		
3	P55072	Transitional endoplasmic reticulum		

An annotation service with frequent updates allows for the display of overrepresented pathways and GO and Pfam terms associated with selected proteins.



Pathways can also be directly visualized, providing biological context and background literature references using pathway maps.

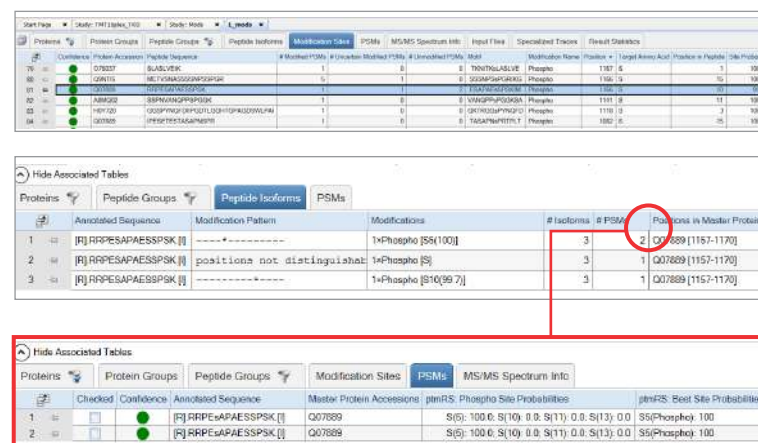
Bioinformatic analysis

The software also provides tools for bioinformatic analysis through a cloud-hosted annotation service. When the Protein Annotation node is included in a workflow, the resulting protein table is automatically annotated with several ontologies, including GO, pathways, Pfam, chromosomes, and more—all with links to pathway diagrams.

Proteome Discoverer software also provides enrichment analysis, which returns GO or pathway terms that are significantly overrepresented or underrepresented in a selected set of proteins in a dataset, helping to reveal deeper biological context.

A complete path from data to biological meaning

Proteome Discoverer software enables a foundation that supports our advanced acquisition methods from Thermo Scientific™ mass spectrometers and powerful tools for visualization, annotation, and enrichment to help you translate raw MS data into biological discovery.

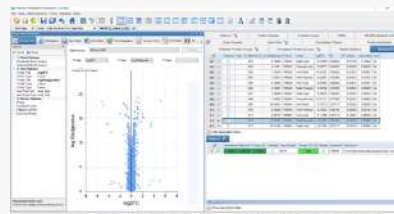


PTMs can be easily identified and visualized through the modification sites table, which allows for the selection of peptide sequences and the display of peptide isoforms. Within each peptide isoform, the modification pattern can be identified and annotated through the use of post-translational modification localization scoring (ptmRS) site probabilities as well as the CHIMERY5 algorithm.



The protein sequence coverage view shows the location of identified peptides as well as identified and localized post-translational modifications (PTMs). If the Protein Annotation node is used in the Consensus workflow, the PTMs annotated in UniProt for the selected protein will be displayed.





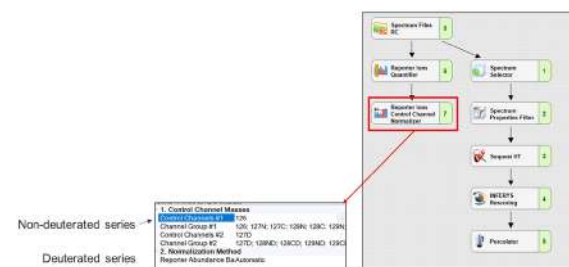
Improved identification and confidence for TMT workflows

Adding artificial intelligence capabilities to tandem mass tag (TMT) workflows allows for additional identifications (IDs) and more confident quantification. Using the CHIMERYS intelligent search algorithm in MS²-based TMT workflows and INFERYS Rescoring for MS³-based TMT workflows will provide improved confidence. Both CHIMERYS and INFERYS Rescoring models can also help improve the number of identified and quantified peptides and proteins by digging deeper into the data.

Integrate intelligent data acquisition strategies with sophisticated data analysis to maximize insights

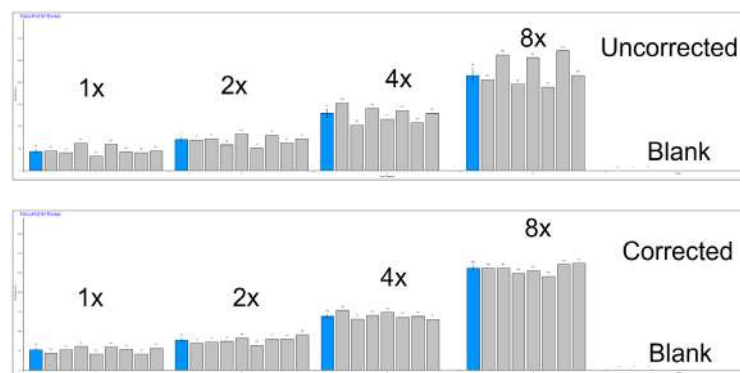
TMT and Thermo Scientific™ TMTpro™ reagents allow for the multiplexing of proteomics samples up to 32-plex with robust and efficient derivatization for better quantitative accuracy and precision. Proteome Discoverer software offers default TMT methods to match the various reagents to enable accurate and precise results and offers predefined workflows to support Thermo Scientific™ Orbitrap™ mass spectrometers with the capability to do both MS²- and MS³-based quantification, along with the ability to customize workflows to increase the number of identified and quantified peptides and proteins.

TMT protein quantification is performed using signal-to-noise summed protein abundances from the peptide to protein level values for improved confidence in quantification accuracy and precision. Larger datasets with multiple runs are supported using scaling with pools or control channels. Results are easily visualized and filtered, and can be customized using the Scripting Node, for example, with the integration of the MSstatsTMT R libraries.



Expanding capacity with new TMTpro reagents

TMTpro reagents now support up to 35 quantitative measurements in a single spectrum. These include deuterated variants, which nearly double the number of quantification channels compared to previous methods. Because deuterated and non-deuterated tags elute at slightly different retention times during liquid chromatography-tandem mass spectrometry (LC-MS/MS), there are differences in the relative abundances of the deuterated and non-deuterated series for nearly every tandem mass spectrometry (MS/MS) spectrum. A new Proteome Discoverer node called Reporter Ions Control Channel Normalizer attaches to the Reporter Ions Quantifier. This node allows the user to designate one or more control channels in both the deuterated and non-deuterated series that will be used to rescale the abundances of the two series to ensure accurate, reliable quantification across all channels.



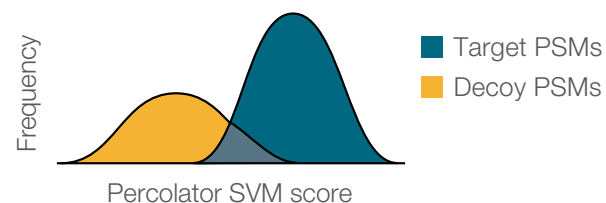
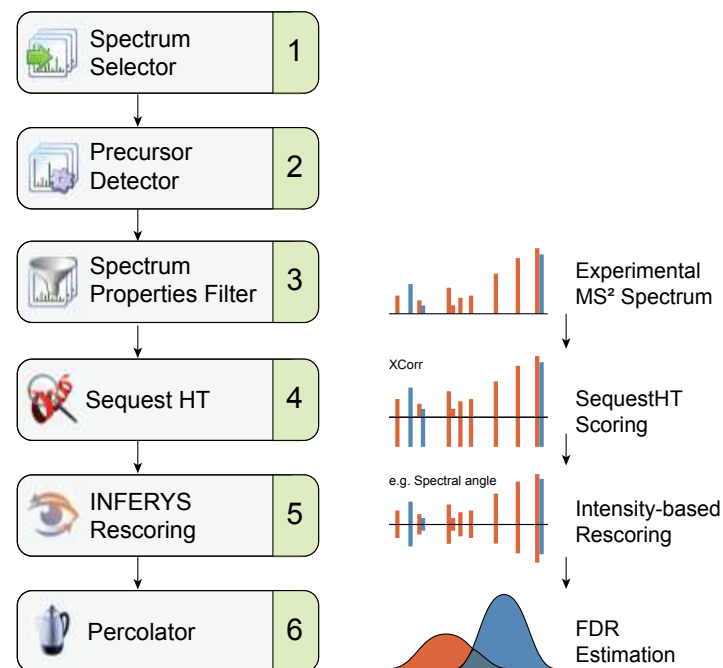
Thermo Scientific™ Pierce™ 6 Protein Digest is spiked at different levels in a human proteome background in this comparison of uncorrected and corrected abundances for cytochrome c peptide TCQAPGFSYTDANK. The uncorrected abundances show an alternating abundance pattern between the deuterated and non-deuterated series.

Improved confidence with INFERYS Rescoring

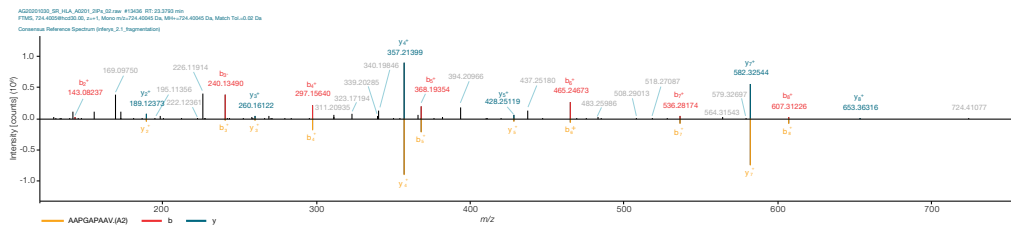
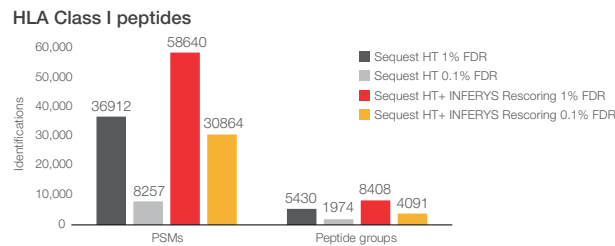
Boost confidence with deep-learning validation

INFERYS Rescoring uses deep-learning predictions to significantly improve the reliability of peptide and protein IDs. More than just a node in Proteome Discoverer software, it serves as a powerful validation tool by predicting spectral libraries directly from protein or peptide lists and storing them natively within the software.

These predictions can also be exported in standard formats, such as .msp, for use in external tools such as Skyline software, ensuring results are both robust and widely compatible. By incorporating predicted fragment intensities into FDR calculations, INFERYS Rescoring increases the number of peptides and proteins identified across all proteomics applications, with a particular impact in challenging studies, such as single-cell proteomics, metaproteomics, and immunopeptidomics.

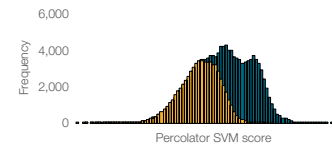


The INFERYS Rescoring workflow. Experimental MS² spectra are scored by Sequest™ HT by matching all theoretical b and y ions, each weighted equally by the search engine. The INFERYS Rescoring node subsequently reads the peptide sequences identified by Sequest HT, predicts their fragment intensities, and correlates the predicted spectrum to the original. Values corresponding to this correlation are included as features in Percolator, helping increase confidence for PSMs whose fragment abundances closely match those from the prediction.

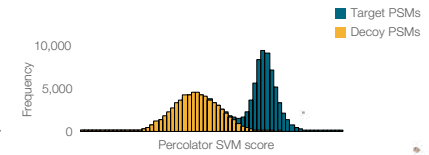


(A) INFERYS Rescoring model predicts peptides on the fly during a workflow for only those peptides identified by the Sequest HT algorithm in the target and decoy database searches. These predictions offer additional figures of merit to increase the confidence for any given PSM. INFERYS Rescoring model substantially improves the analysis of human leukocyte antigen (HLA) peptides because of the very large search space required. At the same 1% FDR threshold, with the inclusion of INFERYS Rescoring, the number of PSMs increases by 58%, and the unique peptides by 55%.

Sequest HT



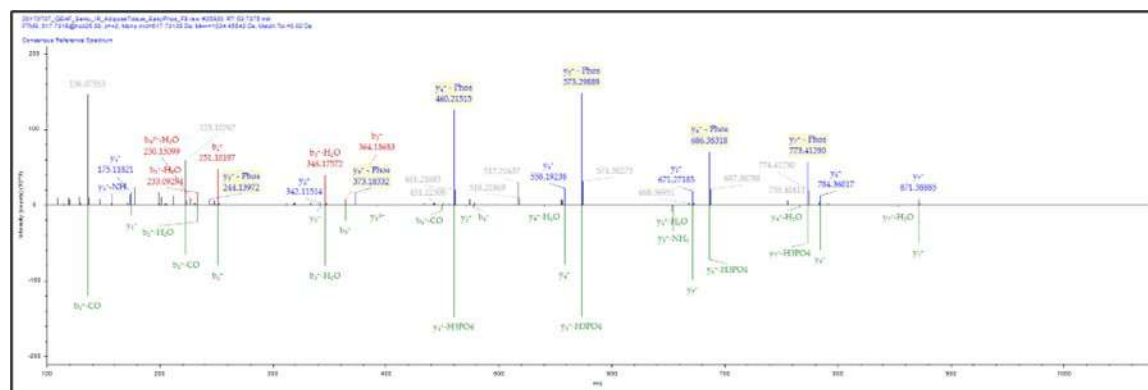
Sequest HT with INFERYS Rescoring



(B) INFERYS Rescoring predictions are done accurately based on fragmentation method, including HCD, CID, and collision energy. The prediction has also been improved to include TMT and TMTpro reagents. This result is an increased Percolator support vector machine (SVM) score for well-matched target PSMs.

(C) The mirror plot shows how close the predicted spectrum below matches to the experimental MS/MS spectrum above for the selected PSM.

YSILSES (Phospho) R



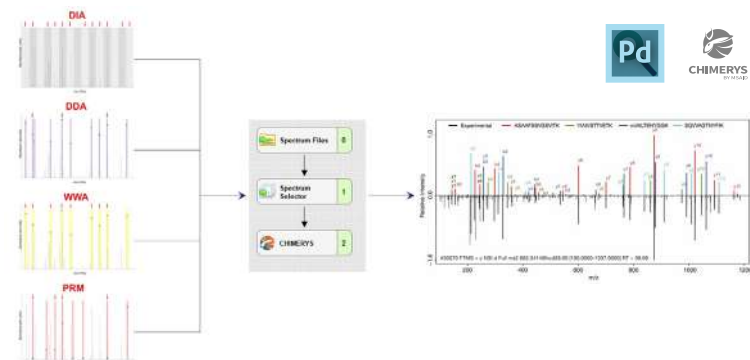
This spectrum illustrates a new feature in INFERYS Rescoring—support for phosphopeptide ID. The predicted spectra now include neutral losses in the predicted spectra and do not include just phosphate loss, such as water, ammonia, and carboxyl losses. The prediction algorithm shows accurate abundances for the phosphate loss off of the y-ions here and also accurately predicts water and ammonia losses. This new prediction algorithm also accounts for the a2 ion as a b2-CO. This helps give more confidence in the ID by confirming the amino acid composition of the first two amino acids in the identified peptide.

LFQ workflows

AI-powered quantification, simplified

The CHIMERYS algorithm is a unifying intelligent search algorithm designed to work with various acquisition methods such as data-independent acquisition (DIA), data-dependent acquisition (DDA), wide window acquisition (WWA), and parallel reaction monitoring (PRM). It is built on the INFERYYS spectral prediction algorithm and goes multiple steps further to deconvolute complex MS/MS spectra to produce peptide IDs and, in the cases of DIA and PRM, accurate quantification values.

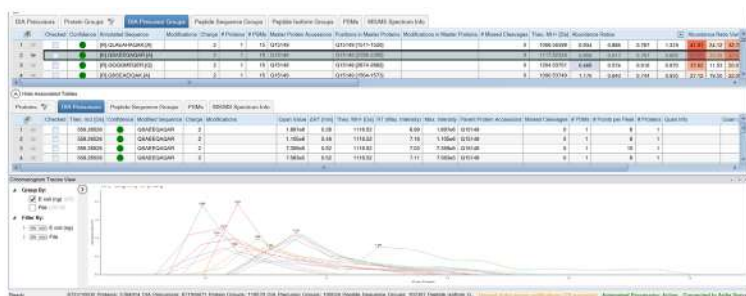
Because it leverages advanced AI tools, the CHIMERYS algorithm requires a specialized computing environment and is deployed either in the cloud or on the Ardia Platform. It supports identification across all major acquisition methods while offering MS²-level quantification and PTM localization for INFERYYS-supported modifications.



Advanced quantitation tools

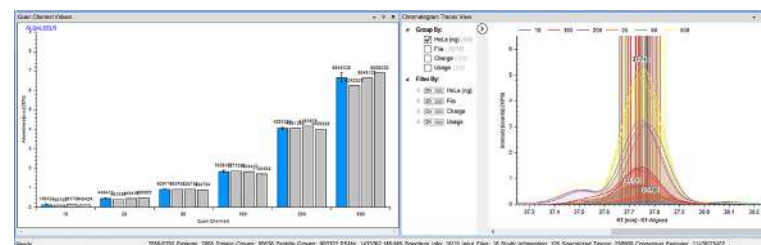
To support advanced DIA analysis, Proteome Discoverer software offers results tables that enable greater clarity and control over quantification data.

- **DIA precursor**—displays peptide, modification, and charge state information for each individual file, including points per peak
- **DIA precursor group**—matches peptide, modification, and charge state across all files, with all tables fully FDR-controlled



The CHIMERY algorithm generates relative quantitative values for every peptide detected within an MS/MS spectrum during deconvolution. For DIA or PRM workflows, it calculates quantitative values for all PSMs across consecutive DIA cycles, spanning the entire elution profile. Users can choose whether to report apex abundance or full peak area, depending on their quantification strategy.

Unlike targeted approaches, peptides are identified independently in each spectrum across the elution profile. Proteome Discoverer software then processes these values just as it does for TMT or LFQ data—rolling up DIA precursor measurements into peptide and protein-level quantification for integrated downstream analysis.



LFQ results can be visualized with chromatograms, principal component analysis plots, heat maps, quantitation channel charts, and more within the Proteome Discoverer software framework, allowing for quick and easy interpretation of results.

Integrated, targeted quantification workflows

Raise confidence with united DIA and PRM workflows

Hybrid DIA with PRM workflows and SureQuant workflows are supported through the Minora feature detector node in the processing workflow, along with the CHIMERYYS algorithm for DIA data processing. The spectrum selector is used to send only DIA scans to the CHIMERYYS algorithm for searching, while the Minora feature detector node handles targeted MS² scans.

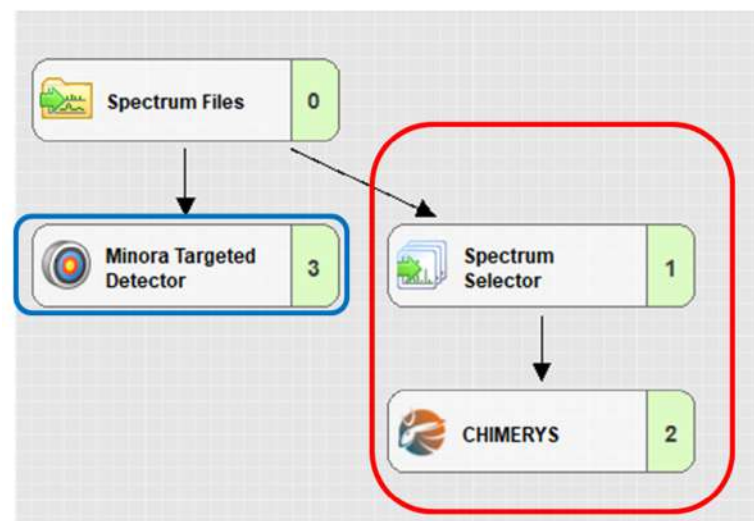
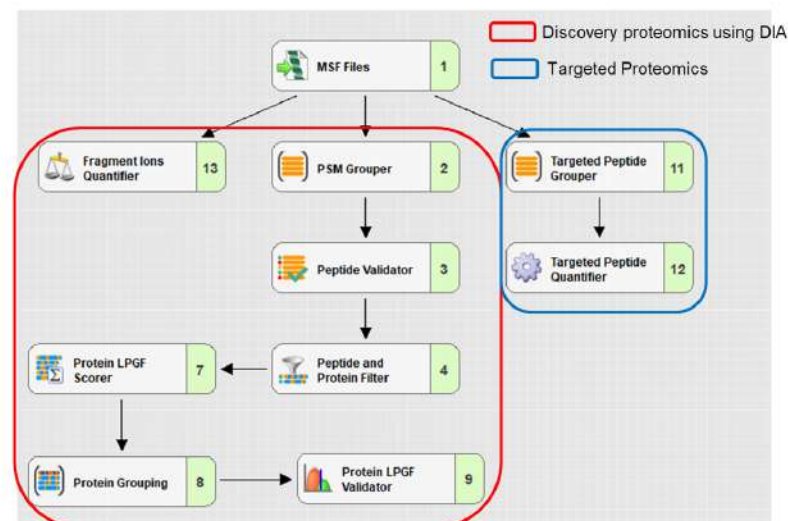
The consensus workflow combines two complementary elements:

Discovery—DIA quantification is performed by the Fragment Ions Quantifier node

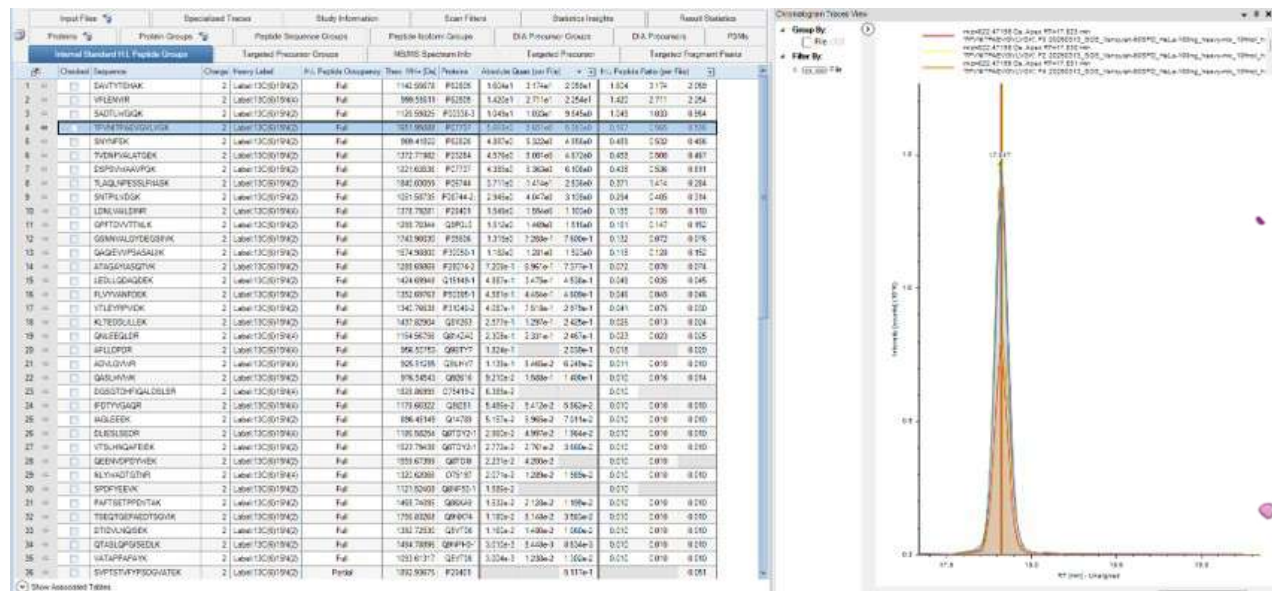
Targeted—targeted peptide detection and quantification are managed by the Targeted Peptide Grouper and Targeted Peptide Quantifier nodes

These elements enable precise fragment selection—using both experimental fragments of interest and library-predicted fragments—to enable high-confidence, targeted quantification. With study management, samples can be grouped and statistical analyses automatically calculated, including abundance ratios, p-values, heavy:light peptide ratios, and absolute concentrations.

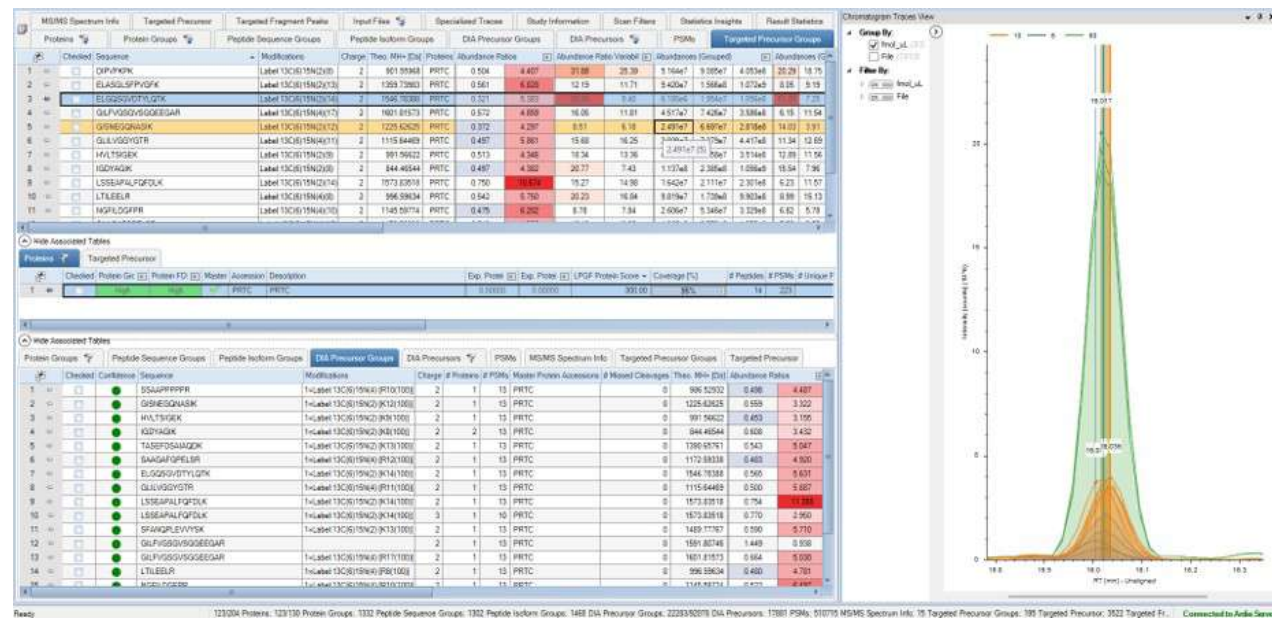
Results tables link targeted PRM/SureQuant data directly to DIA-derived protein and peptide quantification, consolidating results into a single, unified dataset for streamlined interpretation and reporting.



The transition list loader tool supports ease of use, allowing the user to load their target list directly from a raw file or list of peptide sequences. From this list, a library of predicted fragments can be generated easily for fragment selection/ filtering and quantification.



New target peptide tables for heavy/light peptide pairs provides heavy:light peptide ratios across all files in an experiment, along with chromatograms for heavy:light peptides.

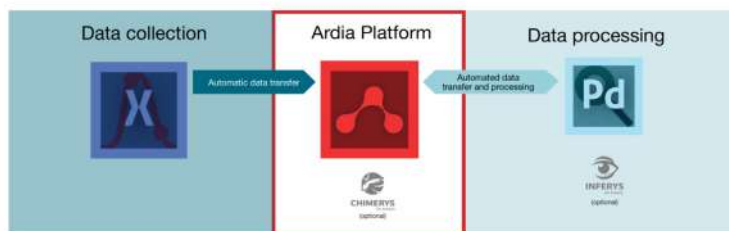


Hybrid DIA results output provides tables with abundance ratios, CVs, and p-values for target peptides. These tables link to the protein results containing DIA data for comparison of targeted and DIA results.

Open, flexible, and connected proteomics

Integrated, automated, and scalable

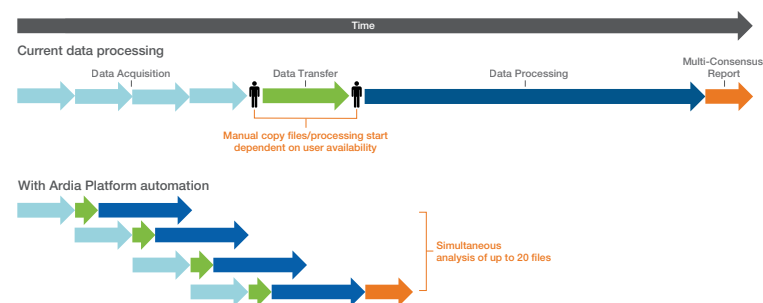
Proteome Discoverer software integrates with the Ardia Platform and a range of third-party applications, enabling flexible, automated, and scalable proteomics workflows.



With streamlined proteomics analysis, data is acquired and automatically uploaded to the Ardia Platform. The data is subsequently processed in Proteome Discoverer software and results are automatically sent back to the platform for secure storage.

The proteomics software solution combines powerful data analysis with secure, scalable data management to accelerate discovery. When Thermo Scientific™ Xcalibur™ software and Proteome Discoverer software are connected to the Ardia Platform, researchers benefit from automated data handling, streamlined collaboration, and access to advanced AI-driven tools such as the CHIMERYS search algorithm deployed on-premises.

With open integration to third-party applications, the solution adapts to diverse research needs, empowering scientists to turn complex proteomics data into meaningful biological insights.

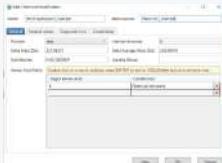
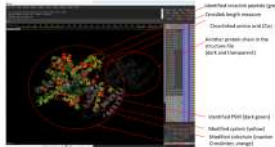


Visual representation of the Ardia platform design, demonstrating how multi-stream multitasking of processes enhanced with automation functions reduces wait time and increases data analysis throughput.

Proteome Discoverer software brings together the tools researchers need to address a broad spectrum of proteomics challenges. With support for diverse acquisition strategies and integrated connectivity to specialized workflows, the software adapts to the unique demands of each study. This flexibility enables scientists to scale from routine experiments to advanced applications, gaining deeper insights while maintaining confidence in their results.

Protein crosslinking with XlinkX

Combine crosslinked peptide identification with TMT and LFQ analysis for quantitative structural biology insights.

Key features for XlinkX for Proteome Discoverer software	Crosslink modifications	User interface for crosslink modification definition	Predefined workflows	LFQ and TMT quantification	Annotated XlinkX spectra	Exporting to third-party tools
	- Predefined crosslinks - Cleavable and non-cleavable - Heterobifunctional crosslinkers 	Users can add their own crosslinker 	- Cleavable and non-cleavable - Support for different acquisition modes 	Uses same nodes as for standard proteomics workflows 	- Chromatograms, aligned and unaligned - Abundance plots - Extracted ion chromatograms 	- xiView visualization - PyMOL 3D molecular visualization 

Protein crosslinking enables structural proteomics studies to be performed using MS to pinpoint residues in close proximity to the interaction interfaces between protein complexes and interfaces. The XlinkX nodes in Proteome Discoverer software allow for easy analysis of crosslinked peptide data, supporting both cleavable and non-cleavable crosslinkers. These nodes can also be combined with the TMT and the LFQ nodes in Proteome Discoverer software for quantification.

Top-down proteomics with ProSightPD software

Comprehensive, top-down data analysis and visualization to support multiple fragmentation modes, Thermo Scientific™ FAIMS Pro Duo interface, and detailed proteoform analysis.

Key features of ProSightPD software	Prebuilt and flexible top-down workflows	Advanced acquisition methods and quantification support	Powerful database management	Versatile proteoform identification	Unique, top-down results visualization	Extensive reporting capabilities
	- Discovery LC-MS - Native top-down - Complex-down MS⁴ and more 	- PTCR - LFQ - ETD, ETHcD, and UVPD - FAIMS Pro Duo interface 	- ProSight Annotator - Precise control of all proteoforms - Intuitive user interface 	- Fast ProSight database search algorithms - Searches include truncated forms and unknown modifications via Δm mode - Supports unresolved precursors 	- Visualizations from Proteome Discoverer software - TD Validator application - Fragment map view 	- TD Viewer application - ProForma Annotated Sequences 

ProSightPD software enables the identification, characterization, and quantification of top-down proteomics datasets within the Proteome Discoverer software framework. ProSightPD software includes a database manager to import proteins of interest and add or remove isoforms or PTMs in tandem with workflows equipped to address the challenges of finding and annotating known and unknown proteoforms, including processing capabilities for all fragmentation modes, such as HCD, CID, ETD, electron-transfer/higher-energy collision dissociation (ETHcD), ultraviolet photodissociation (UVPD), and proton transfer charge reduction (PTCR), along with FAIMS Pro Duo interface data. Mix and match search types and deconvolution strategies to match acquisition and processing strategies to identify intact proteoforms and sub-sequences of proteoforms. Visualize and filter results with the capabilities of Proteome Discoverer software, including automated discovery and characterization of proteoforms and instantly validated results with TD Validator.



Offering a complete biotherapeutic solution—explore the applications

Identify and quantify peptides and proteins in complex biological samples using Proteome Discoverer software. Simplify a wide range of proteomics workflows with software that supports multiple dissociation techniques, quantitation technologies, and database search algorithms for comprehensive protein identification, characterization, and quantitation.

thermofisher.com/proteomediscoverer



Connecting your laboratory—discover new functionality

Connecting instruments and software on the Ardia Platform powers enhanced functionality for Thermo Scientific™ chromatography and MS software. Discover the functional enhancements provided by the Ardia Platform.

thermofisher.com/ardiaplatform



Offering in-depth support—visit the help portal

Connect with support and explore operation manuals, release notes, quick start guides, and more—all from one location.

docs.thermofisher.com

Learn more at thermofisher.com/proteomediscoverer

General Laboratory Equipment – Not For Diagnostic Procedures. © 2022, 2026 Thermo Fisher Scientific Inc. All rights reserved. All trademarks are the property of Thermo Fisher Scientific and its subsidiaries unless otherwise specified. CHIMERYS and INFERYS are trademarks of MSAID GmbH. SEQUEST is a trademark of the University of Washington. UniProt is a trademark of the European Molecular Biology Laboratory. XlinkX was developed by Fan Liu and Richard Scheltema in Albert Heck's group at Utrecht University and is licensed to Thermo Fisher Scientific. Specifications, terms and pricing are subject to change. Not all products are available in all countries. Please consult your local sales representatives for details. **BR62847-EN 0126**

thermo scientific