Unlock the future of proteomics

Ardia Platform

thermo scientific

Over the years, the throughput, sensitivity, and sophistication of mass spectrometers have improved dramatically, producing results with increasingly rich biological information for proteomics datasets.

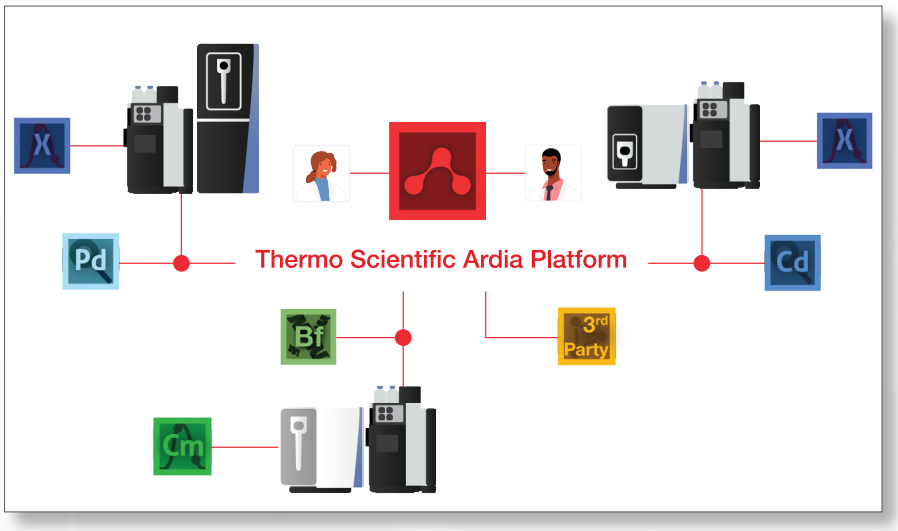
We are collecting more and more meaningful data, but with this comes new challenges around data management, security, throughput, and collaboration.

The Thermo Scientific™ Ardia™ Platform brings together scientific data and results into a centralized location, enabling users to interface intuitively with data, set up automated processing, and easily share results with colleagues and collaborators.

Power your data analysis with the platform that brings your data, instruments, and applications together to deliver the future of proteomics workflows.

Learn more >

Solving the proteomics data challenges



The Ardia Platform revolutionizes mass spectrometry (MS) applications by connecting data, instruments, and a growing list of software tools and applications to accelerate project timelines and drive innovation.

Unlock the power of centralized data management

Recent generations of analytical instruments, such as the Thermo Scientific™ Orbitrap™ Astral™ Mass Spectrometer, produce substantially more data than their predecessors, posing new data-management challenges for laboratories.

To meet the demands of ever-increasing scientific information, the Ardia Platform provides your laboratory with single-point data storage and automated file transfer, enhancing data accessibility and preventing unnecessary data duplication. Built-in backup and archive functionality provides resilience against data loss with easy recovery or retrieval in case of disaster or additional investigations.

Efficiency redefined

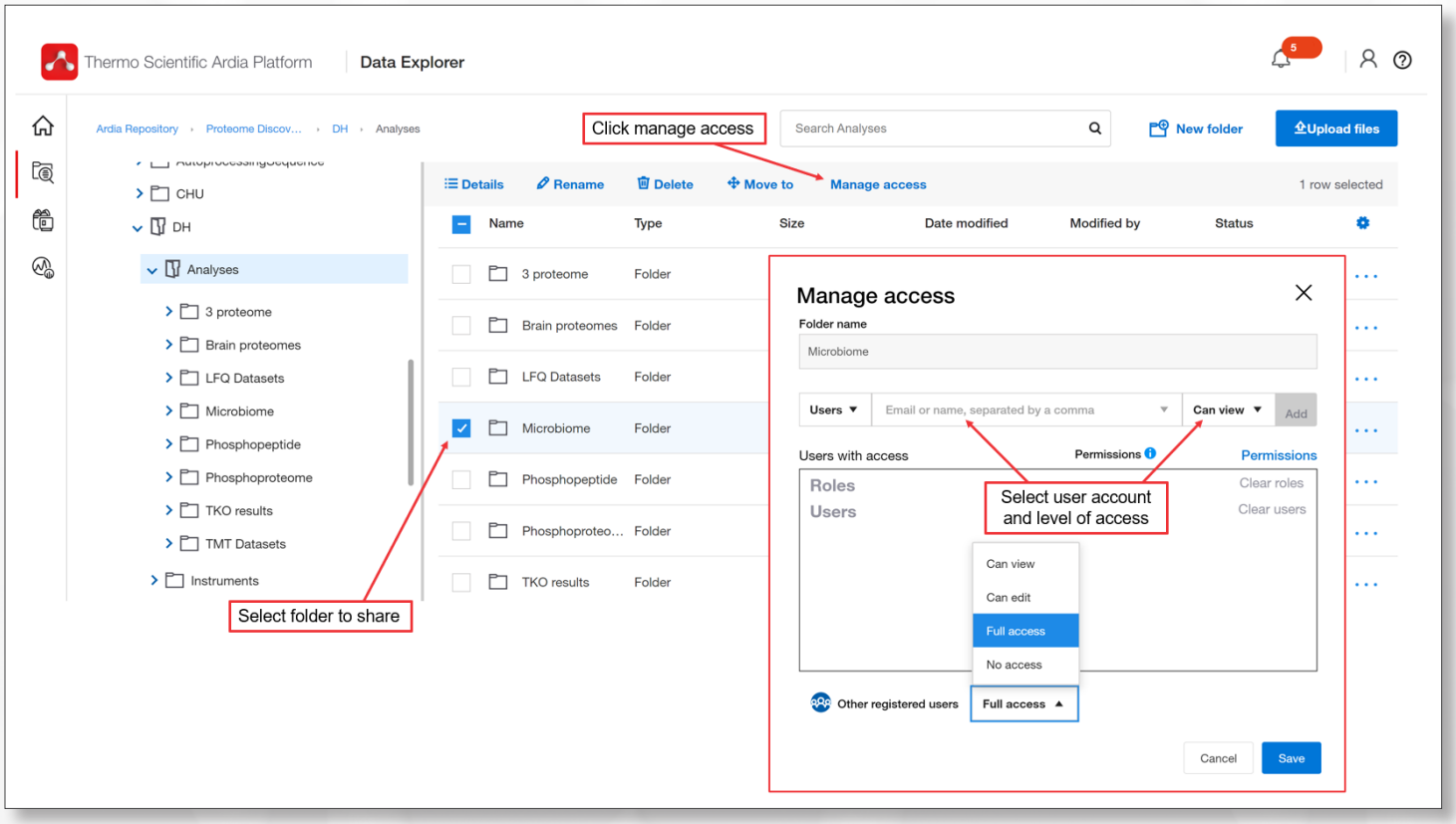
Remove the complexities of managing data scattered across various systems and locations. The Ardia Platform integrates with a growing list of software tools and applications for direct data access. For third-party applications that are not yet connected, you can eliminate time-consuming manual processes with automated data transfers to and from your repository via the Ardia Platform's Data Sync tool.

Accelerate discovery with collaboration on a shared platform

Collaborate with peers and easily view, process, and share data and other related information on cooperative study initiatives from anywhere. Real-time data updates, shared dashboards, and collaborative tools facilitate efficient teamwork and help accelerate project timelines.

User management made simple

Amid growing concerns over data security and privacy, you get access-controlled, secure, and audit-ready user and role management capabilities. Customizable to your organization's unique requirements, you can provide access to essential services and files on an individual or role basis. Designate specific folders to share with collaborators via the Ardia Platform's Data Explorer and Data Sync tools.



The Ardia Platform enables controlled access to data. Define privileges for which user actions can be performed within the platform and control access to data using a role-based approach.

Data throughput

With proteomics studies becoming increasingly large and throughput ever increasing, the flexibility and throughput of the corresponding data analysis software must be advanced accordingly. This challenge is further amplified in larger laboratories or collaborative settings where multiple instruments are generating data simultaneously for a given study.

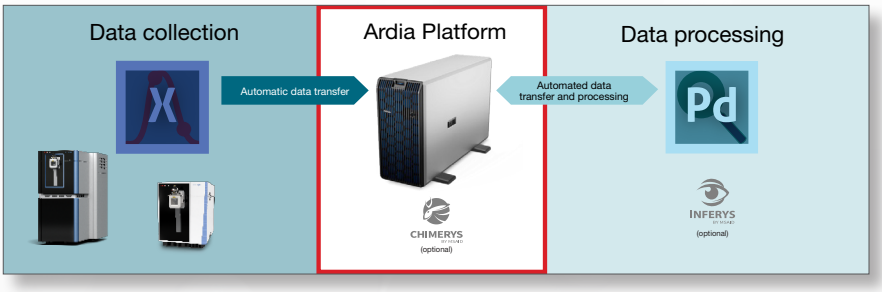
Designed to tackle the complexities of proteomics sample throughput by harnessing the power of parallelization and optimizing the algorithm efficiency, the Ardia Platform, combined with Thermo Scientific™ Proteome Discoverer™ software, significantly boosts data analysis throughput, allowing researchers to extract insights from their data with unprecedented speed and precision.

Learn more >

Automate data processing to deliver results faster

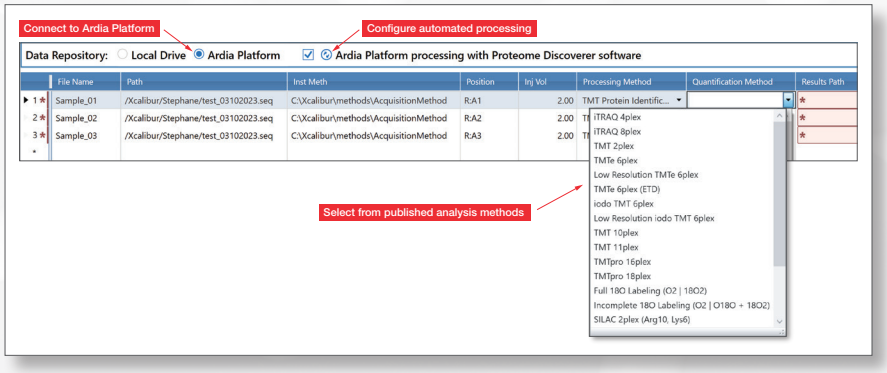
Proteome Discoverer software powered by the Ardia Platform

Reap the benefits of an integrated workflow to improve productivity and faster time-to-results with automated transfer, processing, and storage of data. When Thermo Scientific™ Xcalibur™ and Proteome Discoverer software are connected to the Ardia Platform, you can automatically process data files as soon as they are acquired.



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.

This automation capability is not restricted to any workflow or acquisition method. Diverse proteomics workflows can be automated, including data-independent (DIA), data-dependent (DDA), wide window DDA, label-free quantification (LFQ), Thermo Scientific™ Tandem Mass Tag™ (TMT™) studies, SILAC, MS1-based label-free quantitation, and cross-linked peptide ID.



To set up the automation process, users have the simple task of indicating before submitting an acquisition request to publish the data to the Ardia Platform and choose the methods to use for data processing within Proteome Discoverer software.

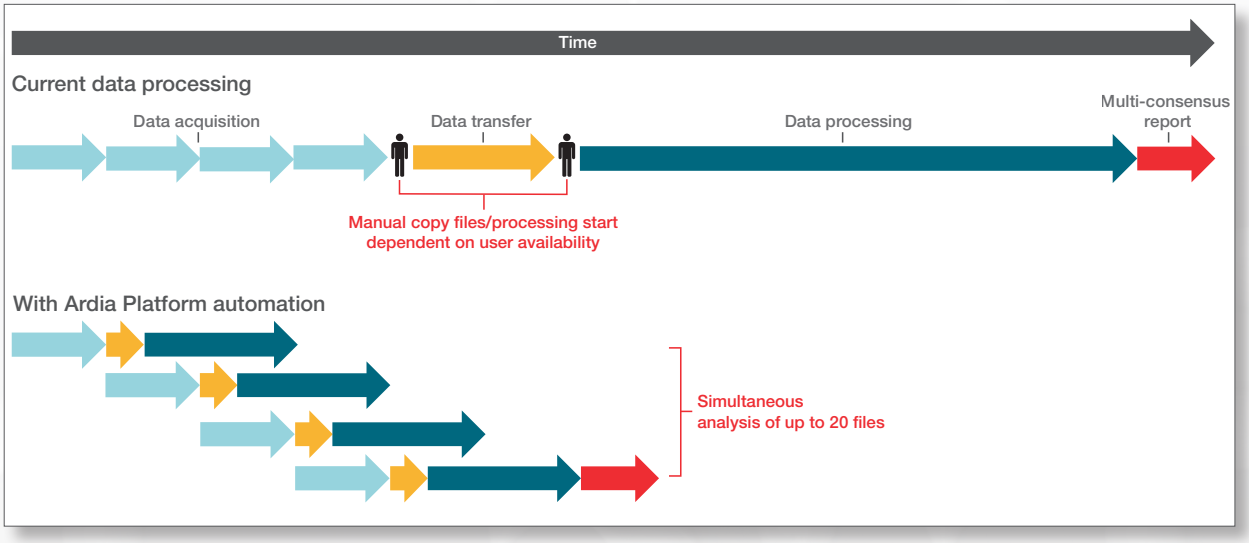
CHIMERYS algorithm on the Ardia Platform server

In proteomic applications, there is a common need for extensive bioinformatics algorithms to convert MS data to biological context. In partnership with MSAID, we have developed two algorithms, the INFERYS™ algorithm, a deep machine-learning algorithm that accurately predicts peptide fragmentation, and the CHIMERYS™ Intelligent Search Algorithm, which deconvolutes and quantifies chimeric MS/MS spectra for DDA, wide window DDA, and DIA analysis.

Previously only available as a cloud service, the CHIMERYS algorithm can now be locally installed on the Thermo Scientific™ Ardia™ Advanced Tower Server. This setup enables multiple users to access the local version, eliminating the need for multiple licenses and data transmission to the cloud. Moreover, the annual recurring cost associated with the cloud-based CHIMERYS algorithm is eliminated.

Unlock unparalleled processing power

With the CHIMERYS algorithm on the Ardia Platform server, 20 concurrent analyses from multiple client PCs can be processed, delivering 10 times more capacity than the highest-capacity cloud service.



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.

The automated processing for larger datasets saves about half of the time compared to traditional linear methods.

Flexible workflows

Proteins are intricate molecules, which necessitate diverse techniques for their identification and characterization. Proteome Discoverer software excels in this realm, offering a comprehensive solution for analyzing complex protein MS data.

Its versatile workflow-based system seamlessly handles datasets with various MSn levels and multiple identification strategies, encompassing DIA, DDA, SILAC, and TMT-based quantification.

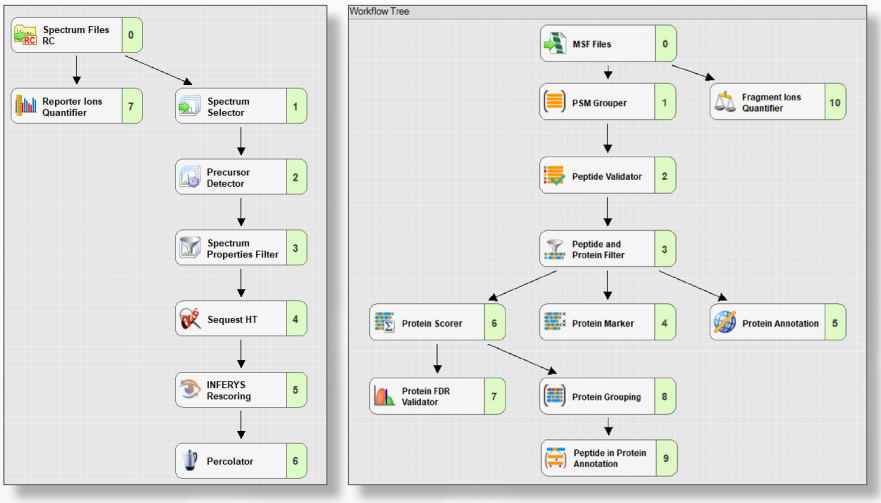
With a range of protein identification methods covering peptides, post-translational modification, and proteoforms, you can eliminate the need for multiple software platforms to fully characterize protein and proteomics samples.

Learn more >

Providing solutions for all your proteomics workflows

Powerful protein characterization using customizable workflows

The powerful workflow system of Proteome Discoverer software features a node-based architecture, enabling connections in linear or branched pathways to enhance the extraction of insights from proteomics datasets, while providing automated processing capabilities. New users can effortlessly deploy predefined workflows, while advanced users can customize workflows to analyze intricate proteomics datasets with ease.

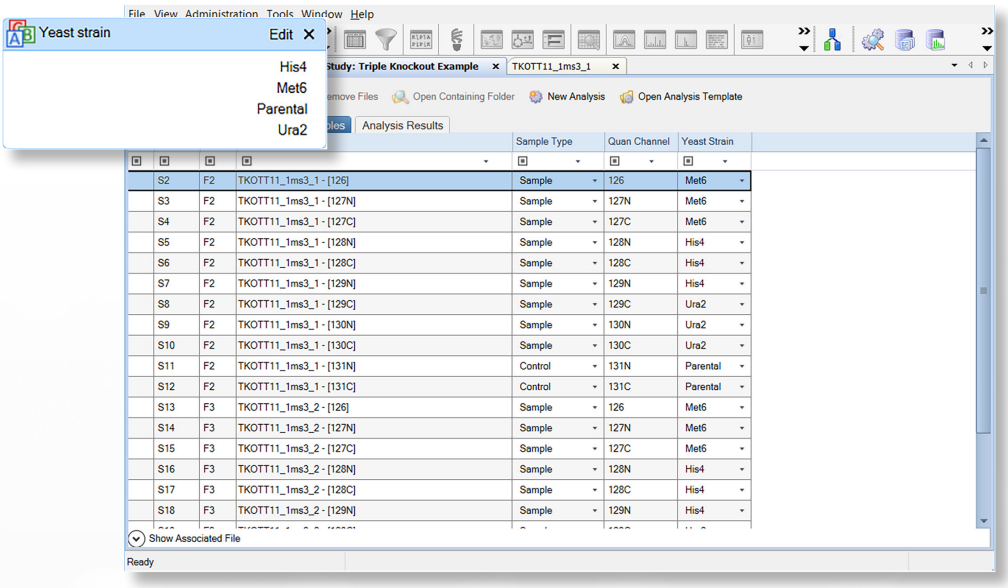


Spectra are streamed from the top of the workflow and pass through nodes that perform filtering, peptide ID, quantification, FDR calculation, grouping, and more.

The workflow system is easily extensible, allowing for rapid development of new nodes. We have several collaborations with third parties that develop nodes for the platform, including the XlinkX nodes for cross-linked peptide ID, Thermo Scientific™ ProSightPD™ nodes for top-down proteoform identification and characterization, and the IMP-ptmRS node for PTM site localization.

Study management for statistical analysis of large datasets

Performing complex proteomics experiments requires the ability to map data files to experimental study conditions for statistical comparison. Proteome Discoverer studies allow selection of data files, association of the data files with a quantification method, the creation of experimental variables as study factors, and the mapping of study factors to data files and quantification channels. Each data file or collection of fractionated data files can be mapped to one or more study factors and then used to perform comparative and statistical analyses.



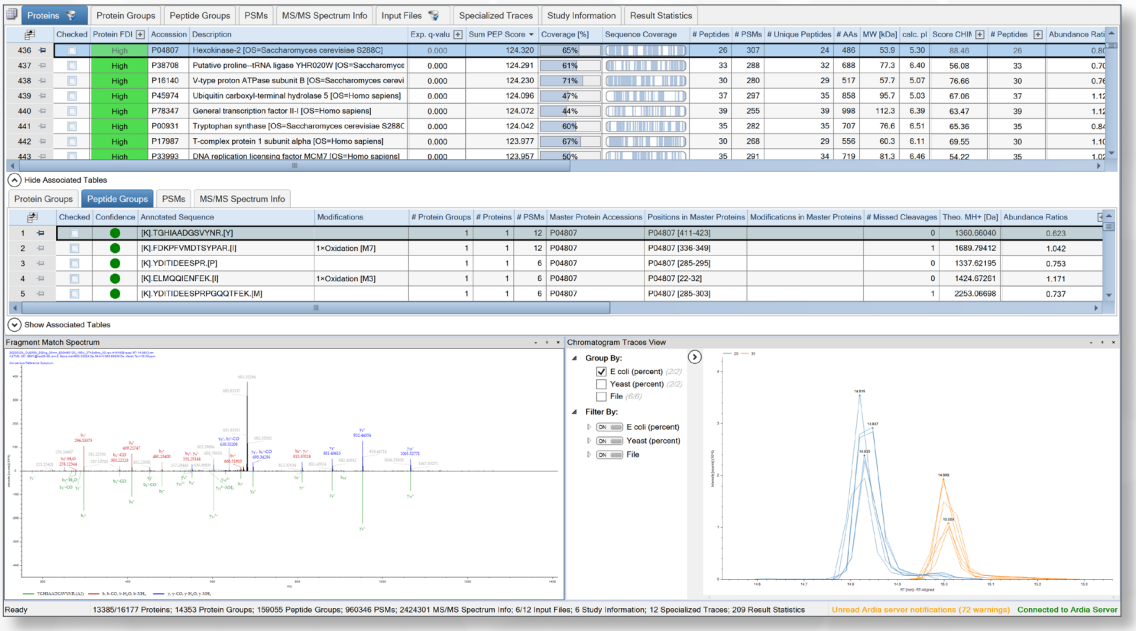
Proteome Discoverer software enables the creation and mapping of sample types, study factors, and quantification channels to data files for simplified and integrated study management.

Powerful visualization tools for analysis of results

Statistical analysis and visualization tools allow for rapid filtering, visualization, and interpretation of results. LFQ results include chromatograms, principal components analysis (PCA) plots, heat maps, quantification channel charts, user-defined plots, and more. Quantification channel charts can quickly display changes for a given peptide or protein group across different experimental variables in tandem with chromatogram traces to visualize the detected peaks across all conditions.

Complex datasets in applications with samples containing diverse protein expression, such as single-cell proteomics, can be quickly visualized using multivariate tools such as PCA plots and hierarchical clustering heat maps. These interactive plots simplify the selection and filtering of peptides or proteins that differentiate groups, aiding in tasks like classifying different cell types in single-cell proteomics data.

Discover how you can confidently and efficiently interpret your data with integrated statistical and visualization tools for a faster time to meaningful results.



Proteome Discoverer software provides interactive plots and customizable layouts for validation, statistics, and bioinformatics analysis.

Learn more at **thermofisher.com/ardia**