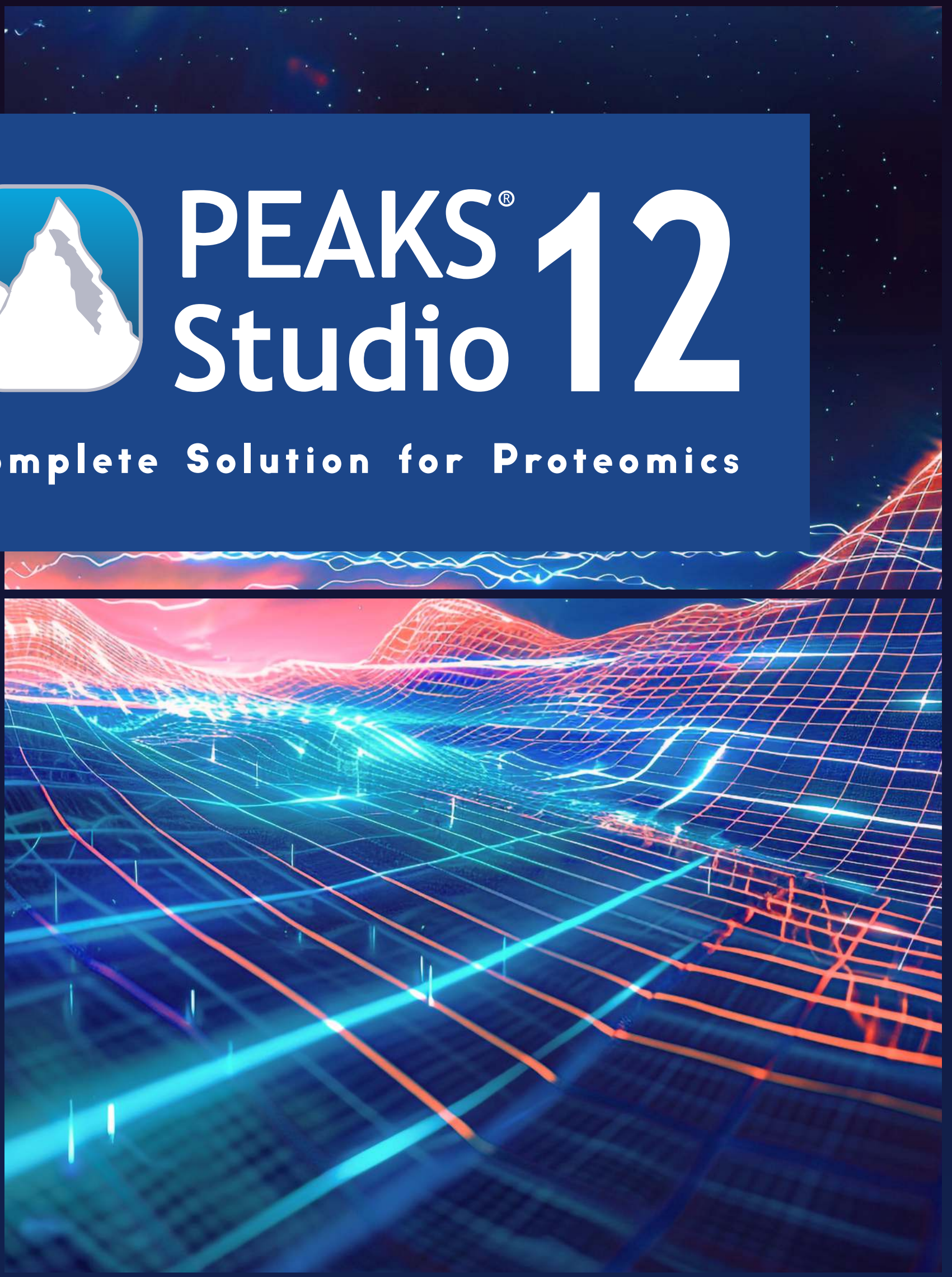
BIOINFORMATICS SOLUTIONS INC.

PEAKS® Studio 12

Complete Solution for Proteomics



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PEAKS® Studio 12

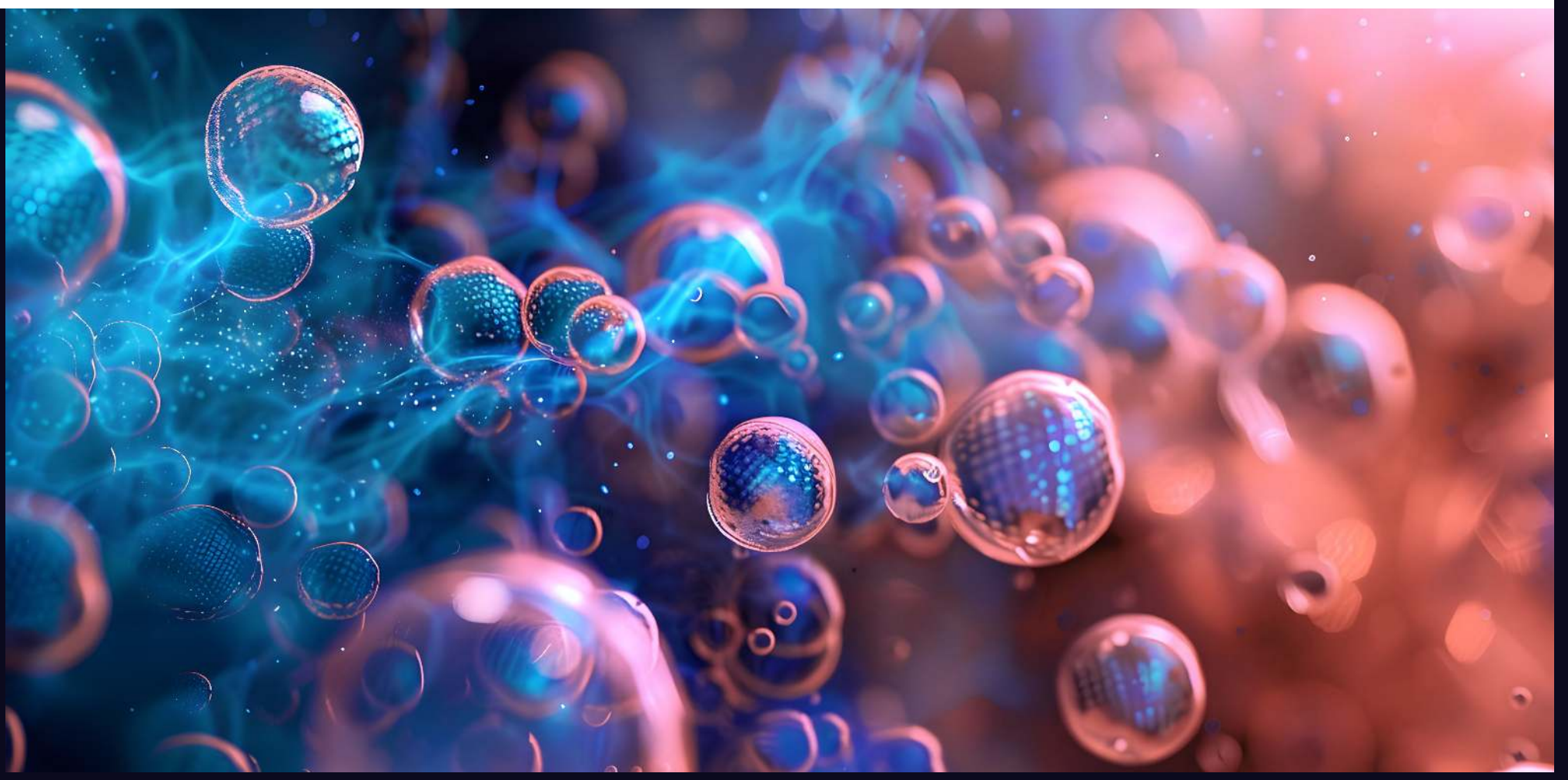
ASCEND TO NEW HEIGHTS
DEEP PROTEOMICS SOLUTIONS

Mass spectrometers and other related analytical techniques have continued to improve at a rapid pace over the past few decades. It is important for researchers to have software that is up to date and can handle the continuously improving data outputs. asdgipsum

Developing innovative software and applying AI-driven technology to proteomics data analysis is vital to advancing research by providing faster, more accurate and sensitive identification and quantification. Together the latest mass spectromery technology and PEAKS® Studio will advance the frontier of biological research and facilitate drug discovery.

NEXT GENERATION OF PEAKS®

PEAKS® Studio 12 is the next generation of the studio platform and features a completely redesigned architecture to provide increased speed and stability. With the updated Graphical User Interface, users still get the intuitive data visualization that PEAKS® is known for, but with a new look and optimized workflows to streamline your data analysis. From DDA to DIA data support, PEAKS® Studio 12 provides a complete solution to bring your research to new heights!



PEAKS® Studio is a powerful and comprehensive software suite designed for the analysis of mass spectrometry (MS) proteomics data. PEAKS® Studio is a versatile and powerful tool that supports a wide range of proteomics applications, from basic protein identification to advanced functional and clinical proteomics studies.

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Extending the
DISCOVERY PROTEOMICS
DEEP LEARNING REVOLUTION

PEAKS® Studio 12 harnesses deep learning technology to improve identification, accuracy, and sensitivity by using algorithms to predict retention time, fragment ion intensity, mass-to-charge ratios, and ion mobility.

Deep learning is utilized in DDA workflows for PEAKS® DeepNovo peptidome for immunopeptidomics and deep learning-boost in PEAKS® DB search results. While in DIA workflows, PEAKS® database search examines the dataset with an *in silico* spectral library generated from the protein sequence database. *In silico* peptide details including the fragment ion pattern, indexed retention time, and ion mobility are predicted using deep learning.

FACILITATE DRUG DISCOVERY AND ADVANCE THE FRONTIER OF BIOLOGICAL RESEARCH THROUGH AI-DRIVEN SOFTWARE SOLUTIONS

In PEAKS® Studio 12, we have integrated AI to advance the following workflows:
Peptide *de novo* sequencing: In this release, users will experience the most accurate and fastest peptide *de novo* sequencing available in any PEAKS® product. PEAKS® has been known as the gold standard for automated peptide *de novo* sequencing for many years but with the new GPU-enabled "DeepNovo", de novo sequencing in PEAKS® is the best it has ever been. In PEAKS® 12, users can now take advantage of the first *de novo* sequencing with FDR estimation.

DIA Workflow: Deep learning has been integrated into our DIA workflow for spectral library search, database search, and *de novo* sequencing. In this version, users can expect PEAKS® DIA workflow to be faster, increased sensitivity and accuracy, and better support for short gradients. New to PEAKS® 12, the software is integrated with parallel-reaction monitoring (PRM) for discover and validation.

***DeepNovo* Peptidome:** This workflow supports both DDA and DIA data analysis and is a specialized workflow for immunopeptidomics. In this version, we have integrated the latest *DeepNovo* algorithm to improve processing speed and identify peptides with a variety of modifications, sequence variants, and/or splice sites. New to PEAKS® 12, users can link the peptides to genes and bridge the gap between proteomics and genomics to help identify and validate peptides potentially originating from rare sequence variants and non-coding regions.

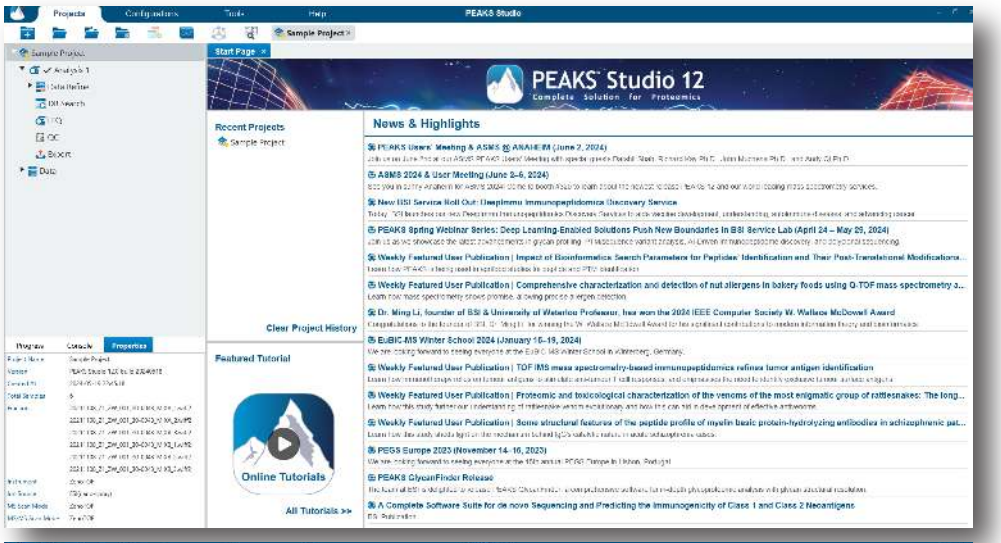
PEAKS® DB: PEAKS® provides a unique *de novo*-assisted database search called PEAKS DB to improve both sensitivity and accuracy. The users have the option to include the deep learning boost for MS2 rescoring and improving the number of identifications by ~10%.

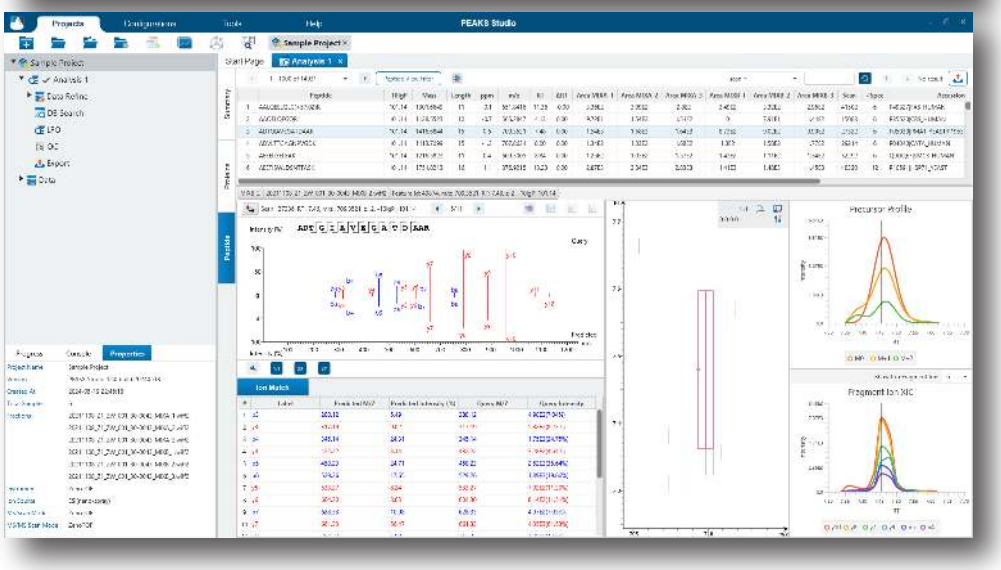
Updated Software Architecture and Graphical User Interface (GUI)

The updated software architecture provides increased speed and stability for identification and quantification. Support all your discovery proteomics research with higher throughput and robust data analysis for both, DDA and DIA support.

Users still get the intuitive data visualisation that PEAKS® is known for but with a new look and optimised workflows to streamline your data analysis.

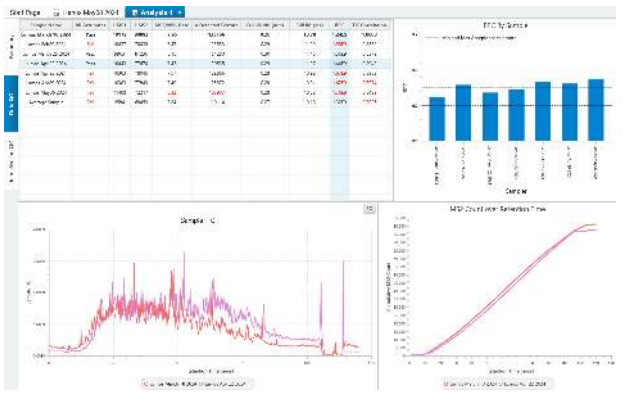
As a vendor neutral software, all DDA and DIA experiments can be performed in PEAKS® . Save your workflows and create customized post-translational modifications (PTMs), enzymes, labelled quantification methods, etc.





Automated Quality Control (QC) Tool

PEAKS® Studio presents a specialized QC tool designed to improve the accuracy of protein and peptide identification and quantification. This module delivers detailed QC analysis, presenting complex information in an organized and user-friendly manner, which aids in troubleshooting instrumentation and data processing issues. By seamlessly integrating database searching, quantification, and QC analysis into a single workflow, consolidating statistical analysis into a comprehensive report. Users can freely export data and figures as needed. The entire process is automated, systematic, and customizable.



Sample Name	All Attributes	# MS2	# Identified Feature	# PSM	# Peptide	# Sequence	# Protein Group	# Top Protein	# All Protein	Missed Cleavage Ratio	Enzyme Specificity Ratio	# PSM / # Peptide Rate	MS1 Error Mean(SD)	MS2
Lumos March 18 2024	Pass	80993	13162	21447	11773	11444	1917	1947	2198	0.29	0.97	1.82	2.0856(0.9542)	0.
Lumos Feb29 2024	Fail	78039	17783	29490	15977	15472	2385	2424	2699	0.32	0.96	1.85	0.8883(1.3507)	0
Lumos March 25 2024	Pass	81236	14687	24590	12772	12468	1962	1988	2238	0.31	0.97	1.93	0.8268(1.1208)	0
Lumos Apr 22 2024	Pass	77670	12389	23976	11000	10670	1734	1759	1958	0.32	0.97	2.18	0.8743(1.2699)	0
Lumos Apr 23 2024	Fail	78045	16048	29341	13783	13382	2099	2127	2376	0.33	0.97	2.13	0.8328(1.3165)	0
Lumos Apr29 2024	Fail	77849	11473	21417	10052	9837	1663	1692	1911	0.31	0.97	2.13	0.7509(1.0558)	0
Lumos May06 2024	Fail	72217	10792	20634	9593	9365	1658	1683	1885	0.31	0.97	2.15	0.9429(1.1476)	0
Average Sample	Fail	68459	13626	21689	12243	11916	1926	1958	2223	0.28	0.97	1.79	1.0042(1.1739)	0

DID YOU KNOW:

Both new DIA workflow and PEAKS® DeepNovo Peptidome enable GPU acceleration

Streamline your LC-MS/MS data analysis with

NEW WORKFLOWS

Both DDA and DIA technologies are rapidly advancing, and researchers need an analysis method that harmonizes the benefits of both acquisition methods. In recent years, DIA has become increasingly popular due to its parallel nature of acquiring all fragment ions for all precursors within a selected m/z range. This overcomes the limitations of sequential MS/MS acquisition in DDA.

***DE NOVO* SEQUENCING:**
Given a spectrum, find a peptide that has the best match with the spectrum.

DATABASE SEARCH:
Given a spectrum and a protein sequence database, find a peptide in the database that has the best match with the spectrum.

SPECTRAL LIBRARY SEARCH:
Given a spectrum and spectral library, find a peptide in the spectral library that has the best match with the spectrum.

DIRECT DATABASE SEARCH:
Given a spectrum and protein sequence database, construct an *in-silico* spectral library using spectrum and iRT prediction models to find a peptide in the spectral library that has the best match with the spectrum.

As a vendor neutral proteomics software developer, we strive to provide a comprehensive solution to facilitate proteomics research and support efficiency in mass spectrometry labs. Avoid the need to use different software for various analytical and acquisition methods.

1. When the peptides are believed to be in a protein sequence database, then a database search approach is preferred.
2. When studying a particular proteome, a peptide spectral library for the targeted biological system being studied can be used to focus your analysis.
3. However, when such a sequence database or spectral library is unavailable, de novo sequencing is needed to derive the peptide sequence directly from the spectrum.

PEAKS® provides a complete solution for all LC-MS/MS search methods to enhance laboratory efficiency, and reproducibility, and reporting. Seamlessly progress from raw file to report for all your bottm-up mass spectrometry based proteomics.

DDA WORKFLOWS

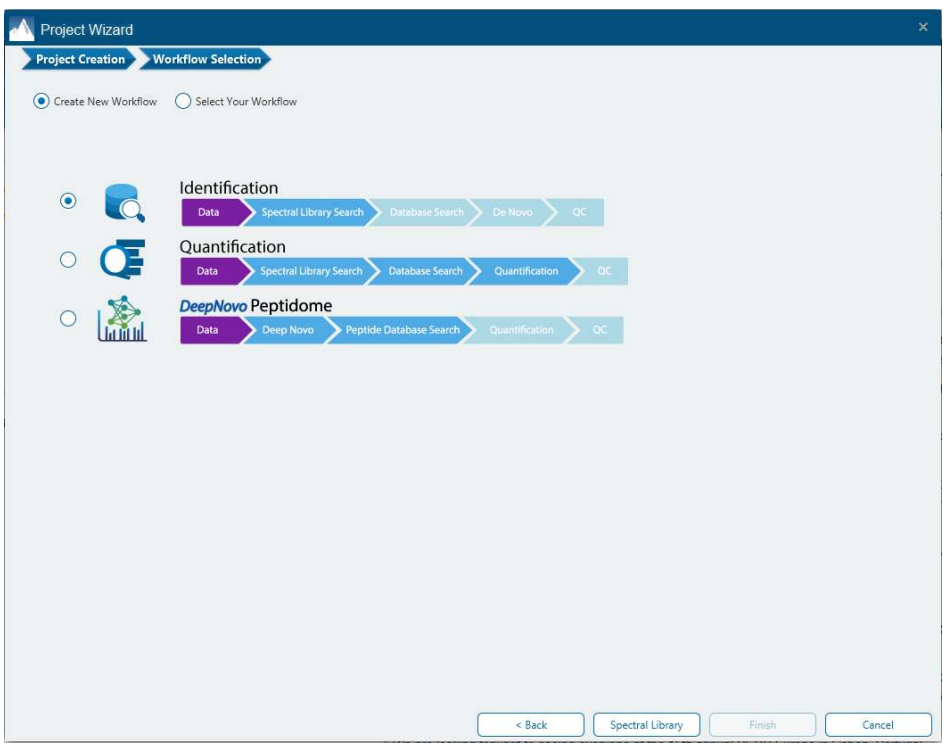
From *de novo* sequencing and database search to quantification, take advantage of the proven PEAKS® search algorithms efficiently as established workflows.

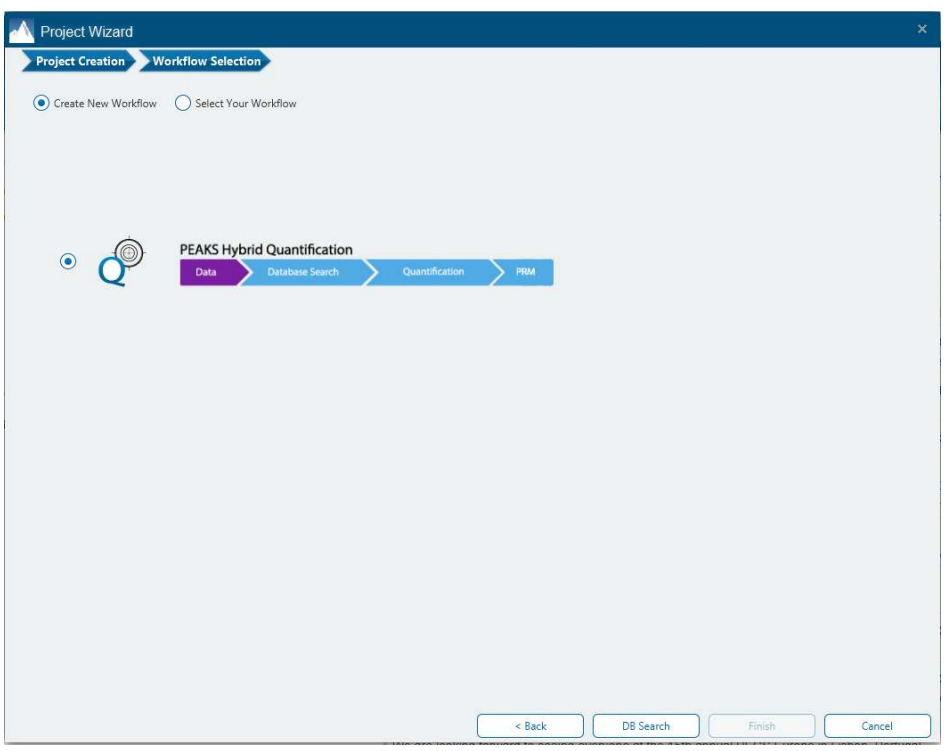
New to PEAKS® Studio 12:
The PEAKS® 12 DeepNovo workflow now uses the new GraphNovo algorithm. For the first time, FDR estimation is available for de novo sequencing results.

DIA WORKFLOWS

PEAKS® Studio 12 features an advanced DIA workflow that incorporates three methods of peptide identification: spectral library search, direct database search, and *de novo* sequencing. For quantification, the label-free method is available as an add-on module.

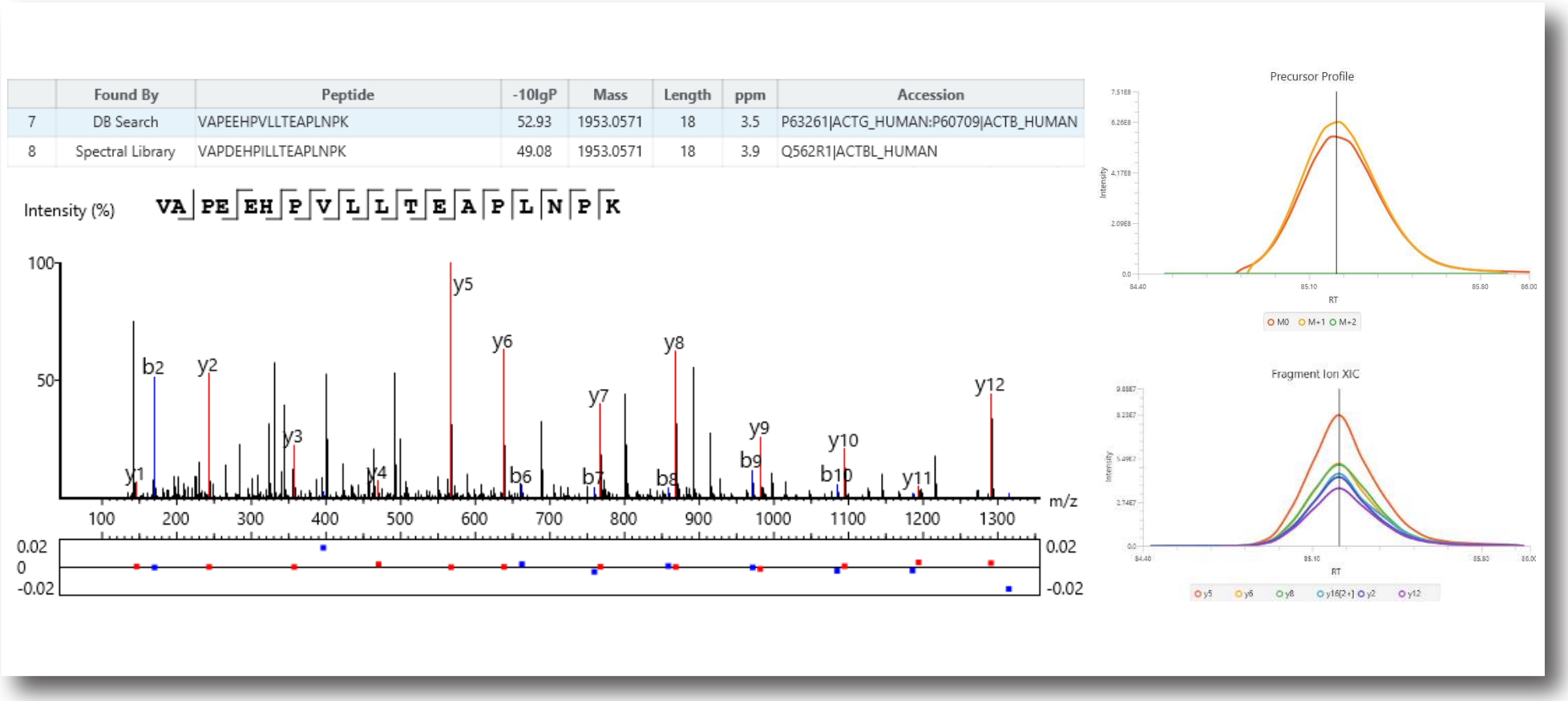
New to PEAKS® Studio 12:
Match Between Runs is now available in the identification workflow.





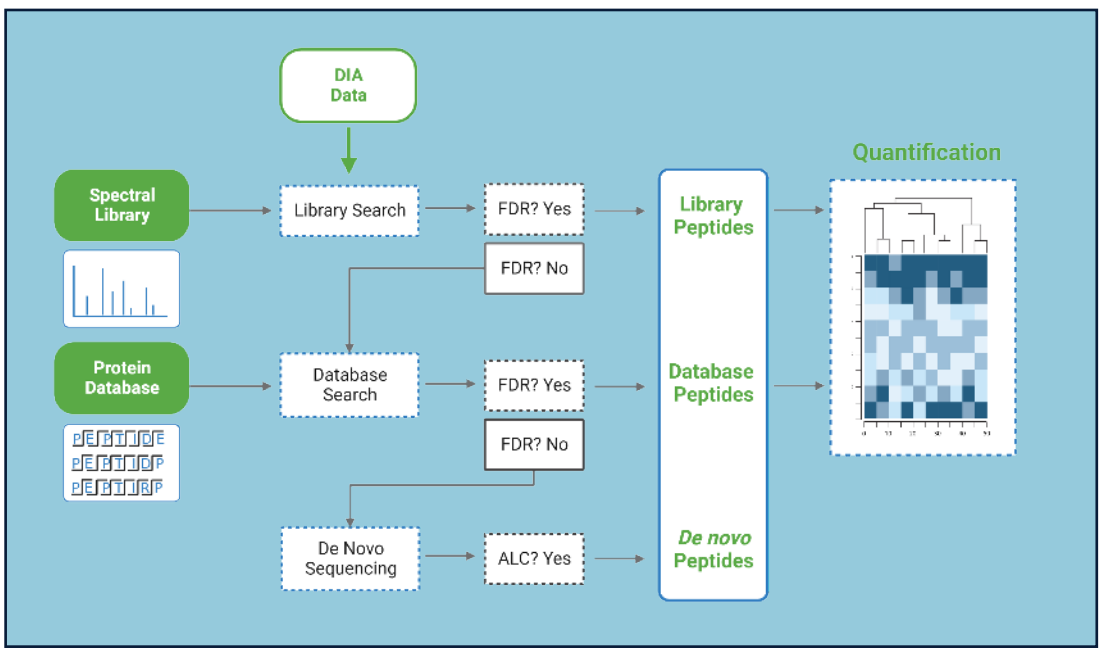
PRM & HYBRID-DIA WORKFLOWS

New to PEAKS® Studio 12 users can perform discovery and targeted proteomics in one software package with the new PRM and hybrid-DIA workflows.



Advantages of a DIA Workflow

- Decrease bias by including all peptides in analysis
- Reproducibility of peptide detection and quantification across MS runs
- Quantify proteins in complex mixtures over a dynamic range
- Eliminate under sampling
- Increased sensitivity and depth of proteome coverage
- Increased precision and reproducibility when compared to DDA
- Eliminate the cost and time with label free quantification



PEAKS® new DIA Workflow

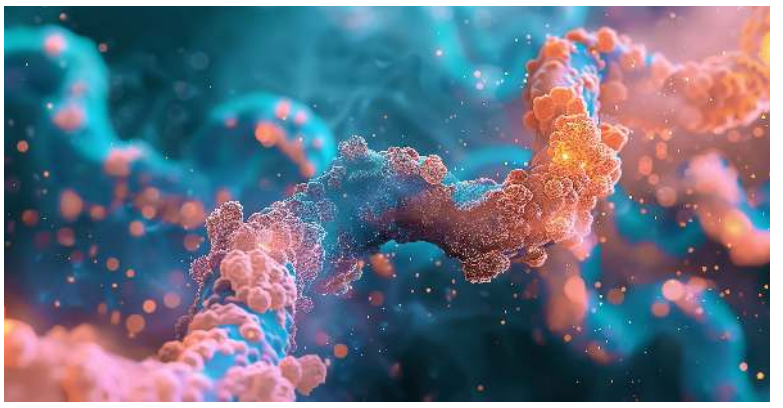
PEAKS® offers a robust solution for DIA data analysis. It incorporates three methods of peptide identification: spectral library search, direct database search, and de novo sequencing. The search is performed using an expanding search space. First, a library search is performed against a library of previously identified spectra. By estimating the false discovery rate, peptides that pass the filter are saved. MS/MS spectra that don't match a peptide within the false discovery rate threshold are brought forward to a direct database search. Confident database matches are added to the result. Then, using the same FDR approach, unmatched spectra from the database search are analysed using *de novo* sequencing. In this workflow, users can also use the Automated Quality Control (QC) tool to provide sophisticated and systematic QC analysis of raw data and both, identification and quantification results.

DID YOU KNOW:

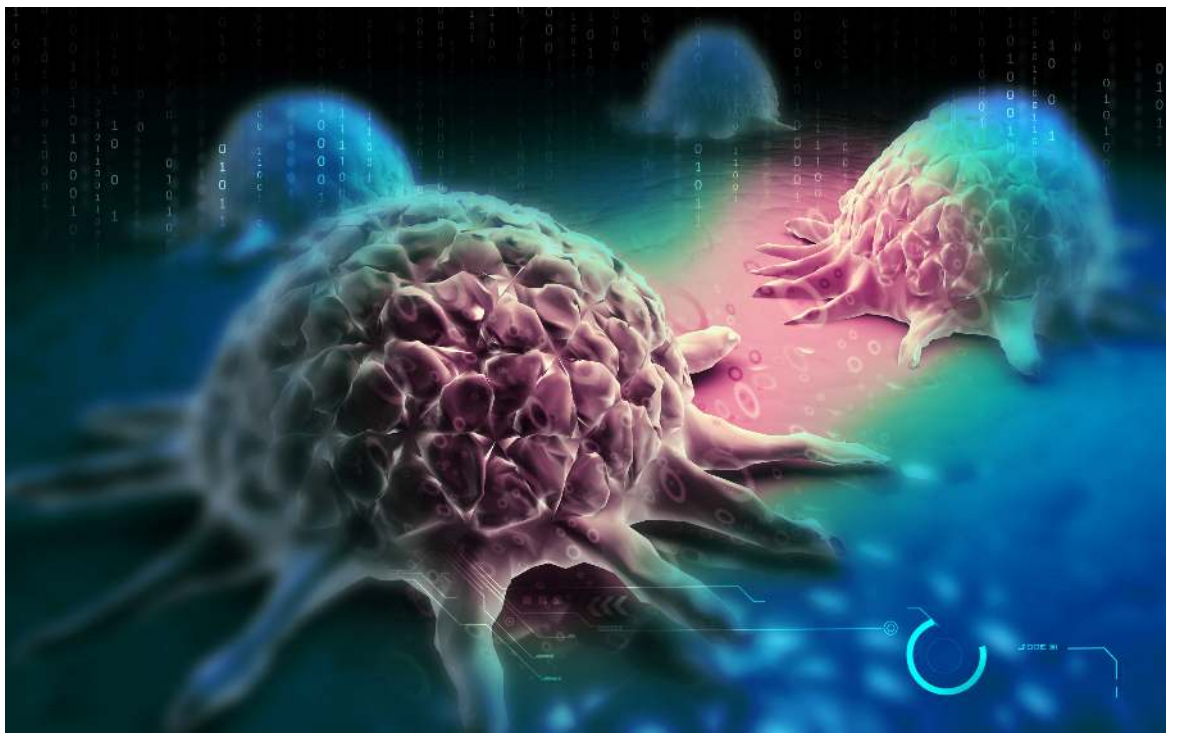
PEAKS® 12 offers hybrid-PRM/DIA that combines targeted and discovery proteomics

The gold standard for peptide *de novo* sequencing, got even better

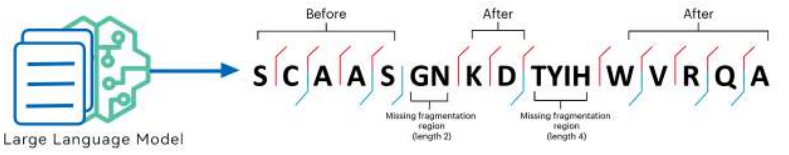
Next generation PEAKS® *DeepNovo*



In mass spectrometry, *de novo* sequencing derives an amino acid sequence from a mass spectrum without the need of a sequence database. In contrast to the popular 'database search' peptide identification approach, *de novo* sequencing is the only choice when the sequence database is not available. This makes PEAKS® the preferred method for identifying novel peptides and proteins from unsequenced organisms.

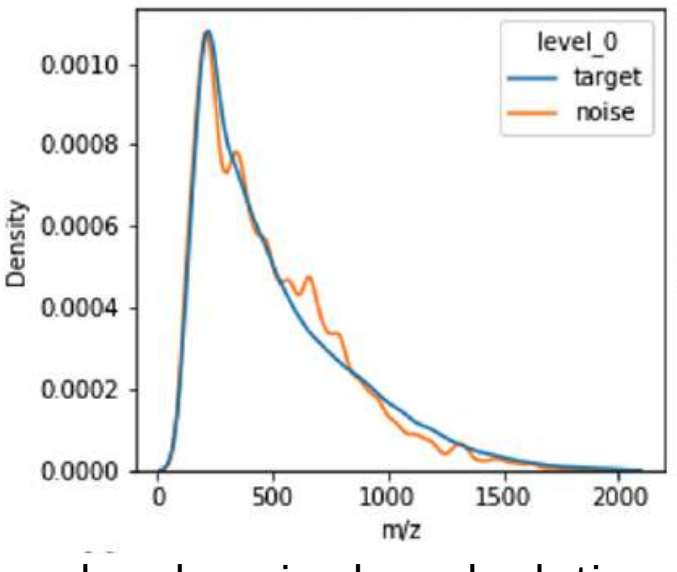


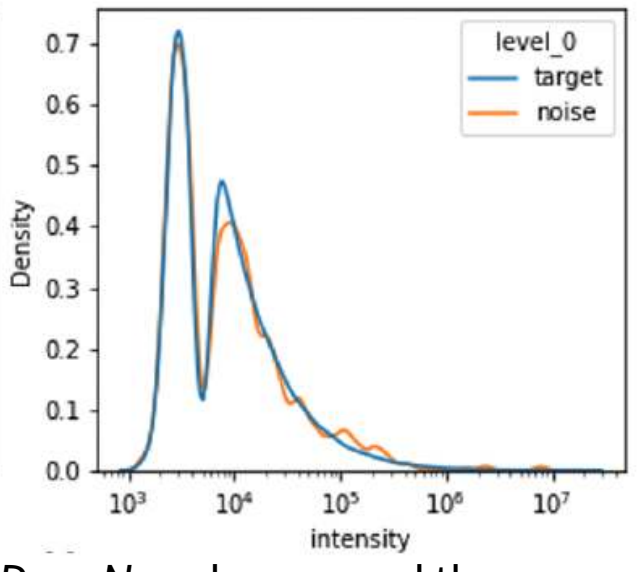
Empowered by the latest *GraphNovo* algorithm, the new *DeepNovo* resolved the issue of accumulated prediction errors due to missing fragment ions by finding the optimal path in the first stage to guide sequence prediction in the second stage.

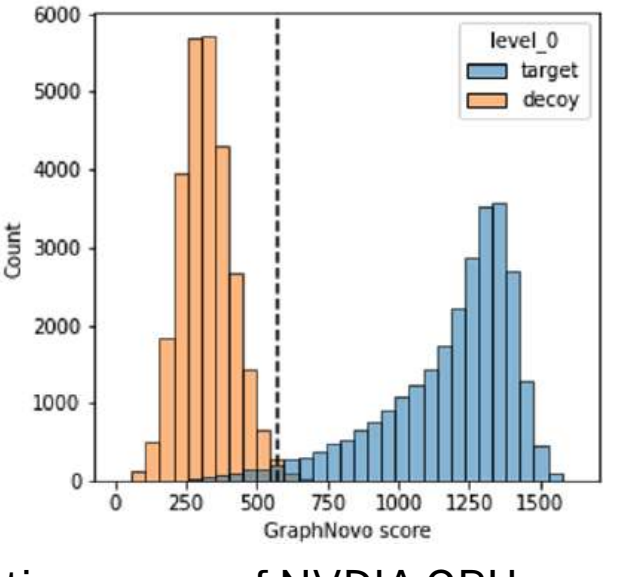


As a key technology for finding novel peptides from MS data, *DeepNovo* provides an advanced solution and will push research like antibody sequencing and neoantigen discovery further.

In PEAKS® 12, decoy spectra are used in *DeepNovo* to estimate an FDR for *de novo* peptide sequencing. The decoy generation process ensures decoy spectra has the same fragment ion distribution as target spectra. Furthermore, *DeepNovo* scoring function efficiently separates target and decoy. An FDR curve of *de novo* sequencing is now available in *DeepNovo*.



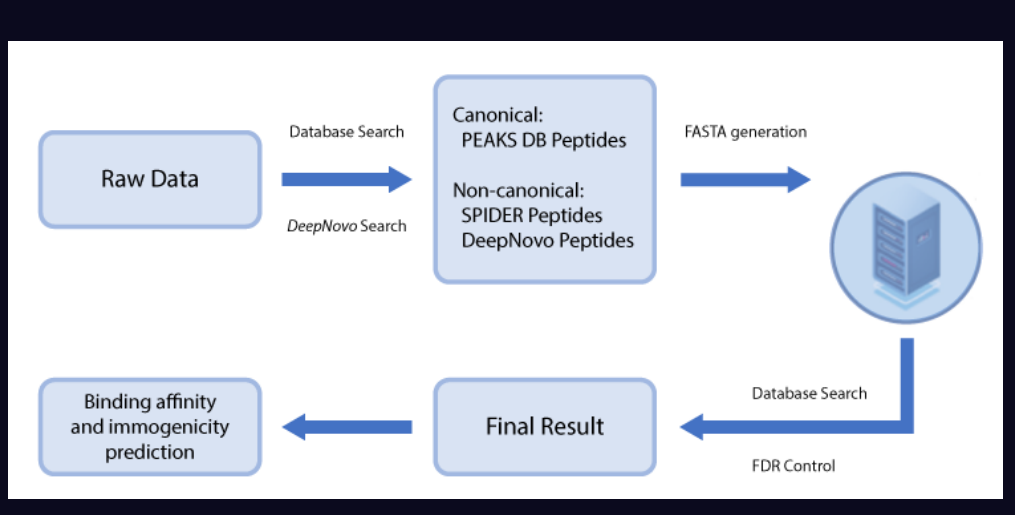




As a deep learning based solution, *DeepNovo* harnessed the computation power of NVDIA GPUs for speed. NVIDIA A100 enabled *de novo* sequencing 1200 + spectrum/s.

PEAKS® *DeepNovo* Peptidome
WORKFLOW

This new solution is a specialized workflow for peptidomics data that combines database searching, *de novo* sequencing, and identification of mutated peptides. By training *DeepNovo* deep learning model using peptidomics datasets the sensitivity and accuracy of peptide identification can significantly be improved. Furthermore, *de novo* peptides (non canonical) are combined with database peptides (canonical) for more accurate estimation of false discovery rate. The final output of peptides are categorized as Database, *DeepNovo* or Homologs (mutated peptides) and can be directly exported for binding affinity and immunogenicity predictions.



Peptide mapping to chromosome loci

To better understand non-canonical peptide biosynthesis and where in the genome each peptide is expressed, a Gene tab is integrated in the *DeepNovo* Peptidome workflow to display this information. The workflow accepts both canonical database files from predicted coding regions (Target database), as well as custom database files from next-generation sequencing (NGS). Target databases such as Uniprot are used to identify canonical peptides mapped to open reading frames of proteins and their isoforms. Custom NGS databases can be used for mapping peptides to non-coding regions and identifying non-canonical peptides. Lastly, the Gene tab also displays *DeepNovo* peptides, where only part of the peptide sequence matches to either canonical or non-canonical databases. This information is helpful in identifying post-translationally spliced peptides.

With PEAKS®, you can ensure that new instrument fragmentation methods are optimized for peptide sequence reconstruction.

Before support within the software, PEAKS® undergoes an extensive fragmentation-specific algorithm training to confidently analyze various fragmentation data. Supported Fragmentation: CID/CAD, HCD, ETD/ECD/EAD, EThcD, and mixed/complementary fragmentation.

PEAKS® provides enhanced separation of true and false hits by incorporating de novo sequencing into a database search. This unique de novo-assisted approach will allow you to identify more peptides and proteins with greater confidence.

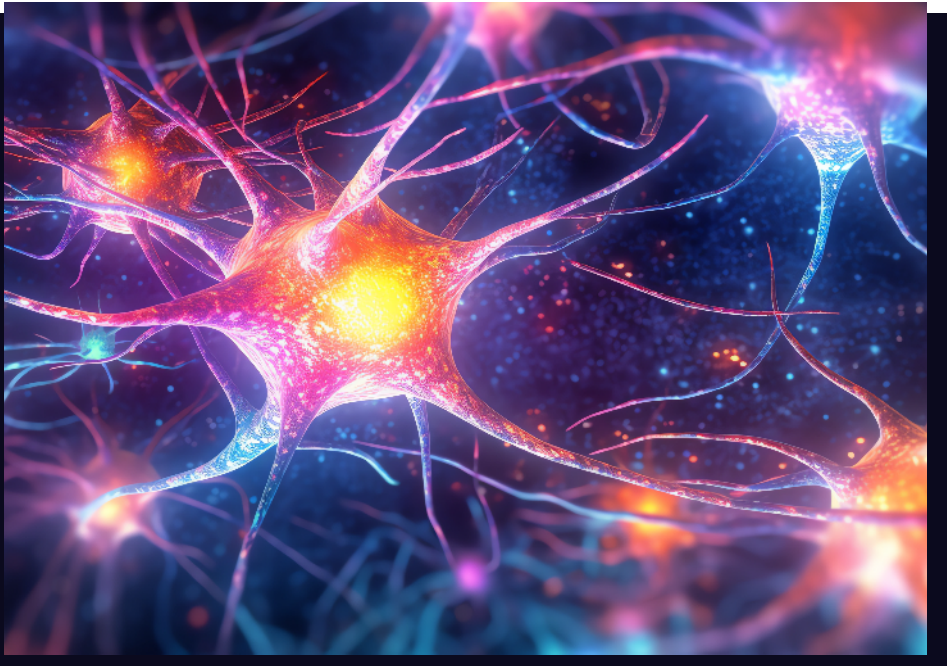
The detailed PEAKS® Studio interface allows users to quickly define, filter and visualize results as desired. With a few clicks you can specify a false discovery rate, or draw project-wide comparisons between your samples.

UNIFIED SCORING FOR EASY INTERPRETATION

PEAKS DB, PEAKS PTM, and SPIDER results are all scored using -10lgP. So, results from the three algorithms can be displayed together on the same scale.

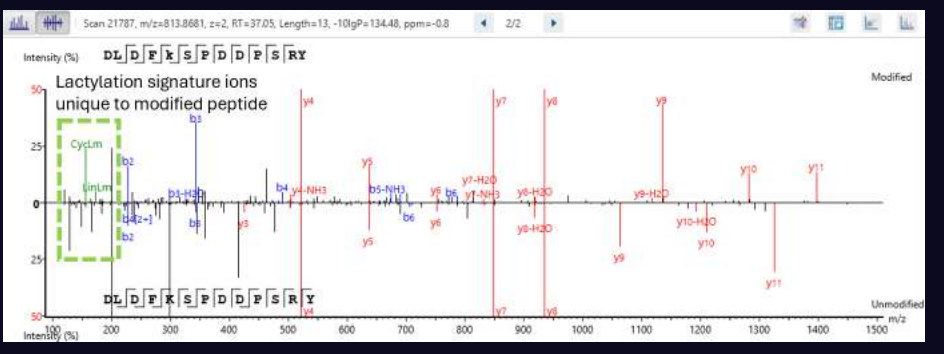
Designed to discover hidden modifications

In PEAKS® PTM and SPIDER, the highly confident spectra with a good *de novo* score are reanalyzed to assess any unknown PTMs or sequence variants. Additional confident modification algorithm and the use of Potential Signature Ions are implemented for modified peptide re-scoring and enhance accuracy in PTM and sequence variant identification.



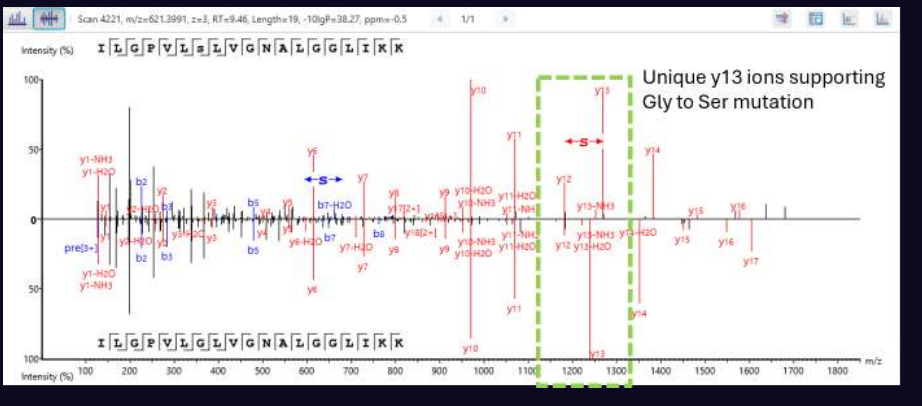
PEAKS® PTM

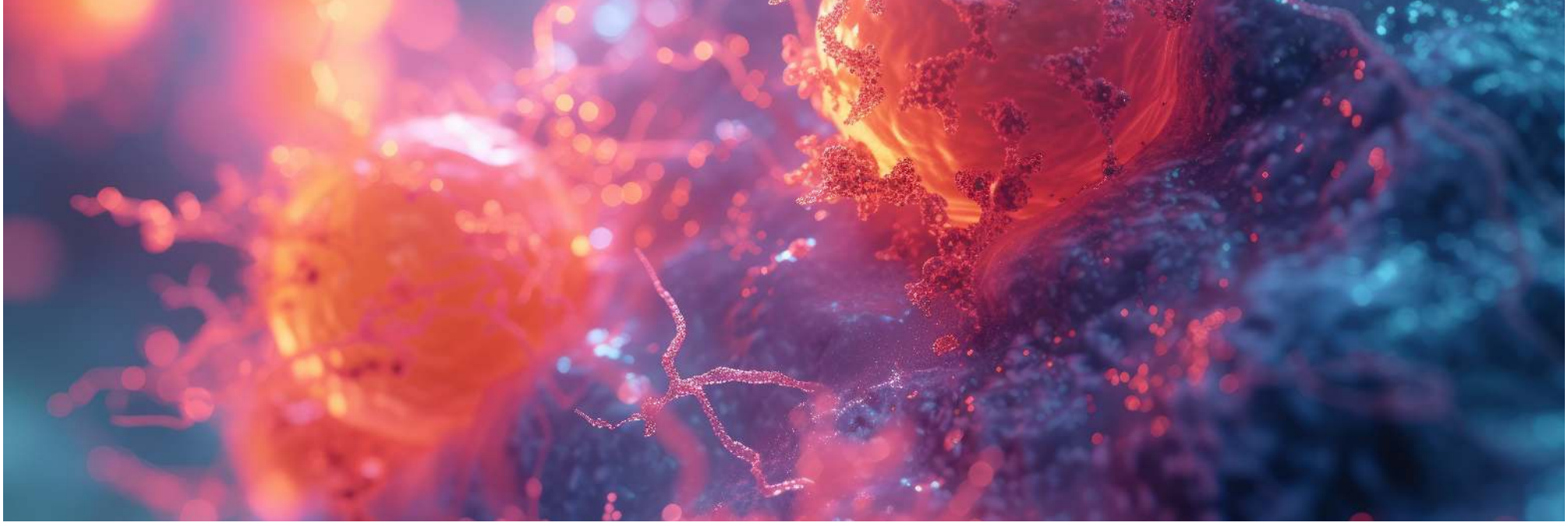
Specify the PTMs of interest or search all 313 naturally occurring biological modifications from the Unimod database in your PEAKS® PTM search.



SPIDER (peptide sequence variants and homology search)

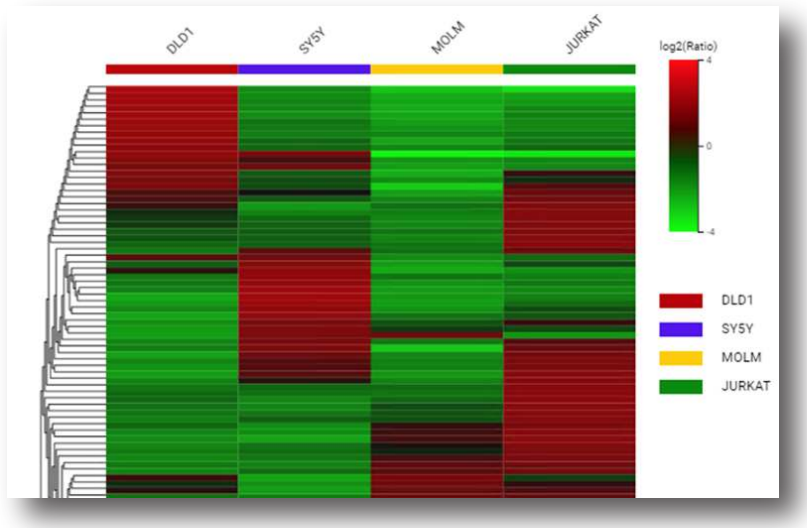
Homology search with *de novo* tags identifies amino acid mismatches between de novo and database sequences. Confident mutations are determined by the number of consecutive fragment ions at the mutation site with relative ion intensities above a threshold, each of which are user-defined. Mirror plots are provided to compare mutated vs. wild-type peptide sequences for visualization of unique fragment ions supporting the mutated amino acid.

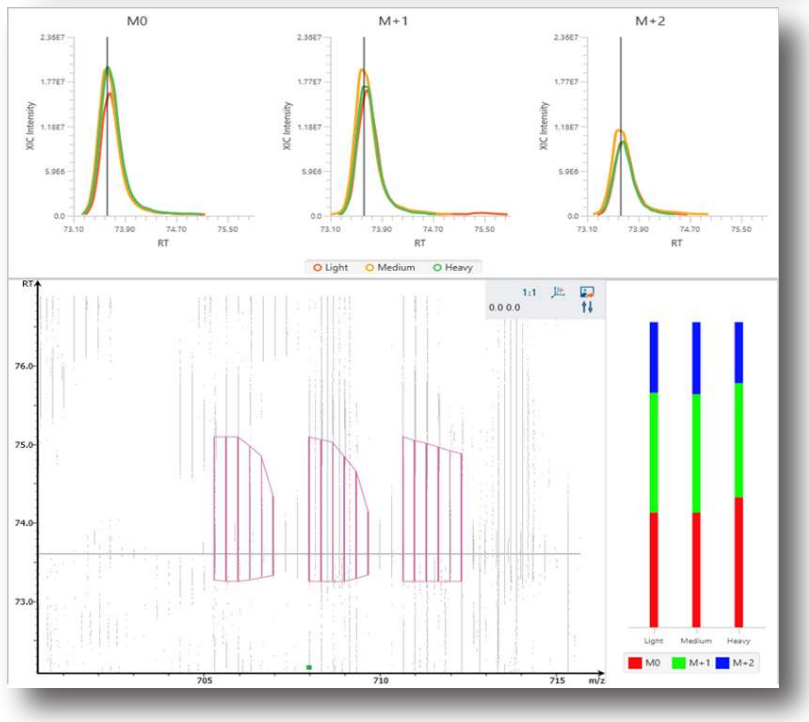




UNLEASHING
QUANTITATIVE PROTEOMICS WITH THE POWER OF PEAKS Q

Quantification provides greater insight into proteomic mysteries. Researchers need a software tool to support them as they press further in to the understanding of life sciences.





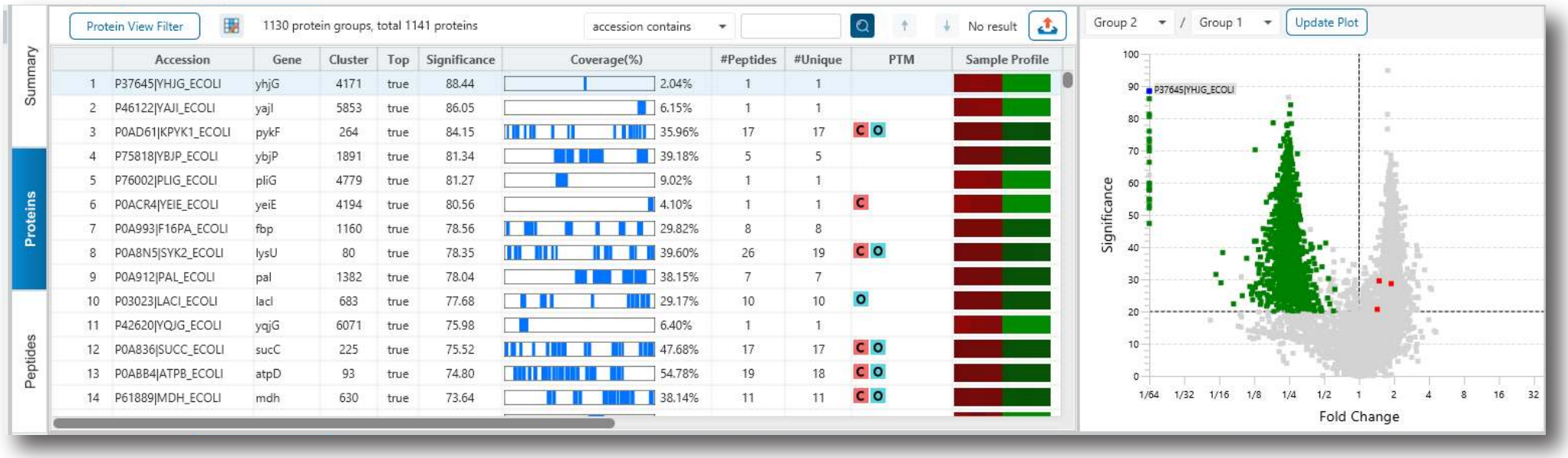
PEAKS® is equipped with not only a powerful identification algorithm, but also embraces paralleled quantification capabilities to perform:

Reporter ion quantification:

Isobaric tags (ex. TMT/iTRAQ) have identical masses and chemical properties that allow heavy and light isotopologues to co-elute. The tags are then cleaved from the peptide by collision-induced dissociation during MS/MS, which is used for quantification. For large-scale, protein quantification studies, researchers can use PEAKS® Q to expand the sample size with reference channels to enhance the accuracy of quantification.

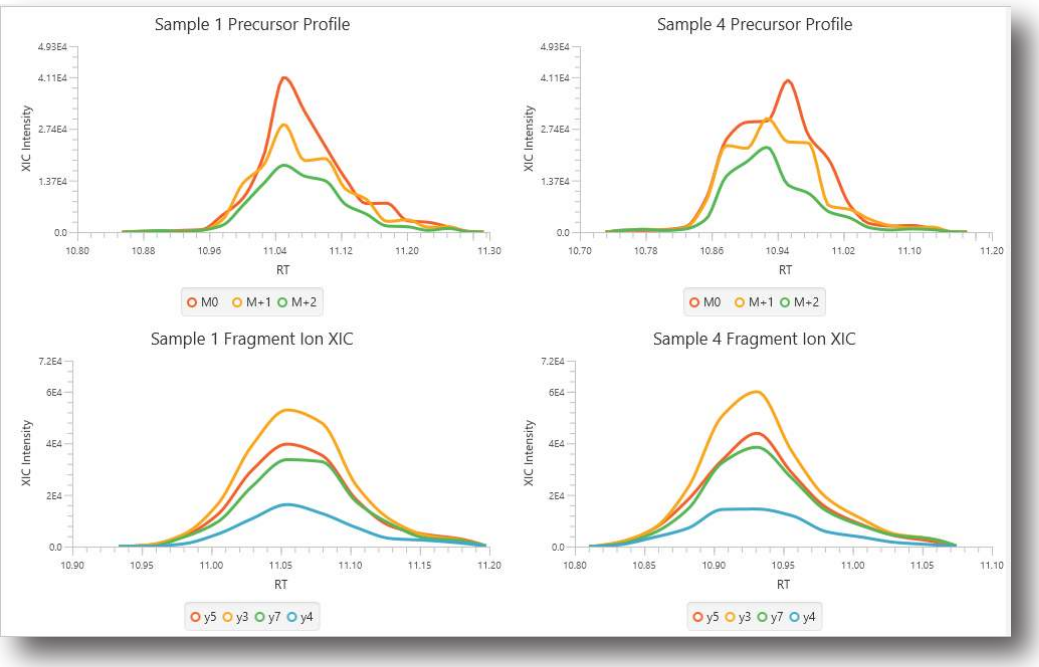
Precursor ion quantification:

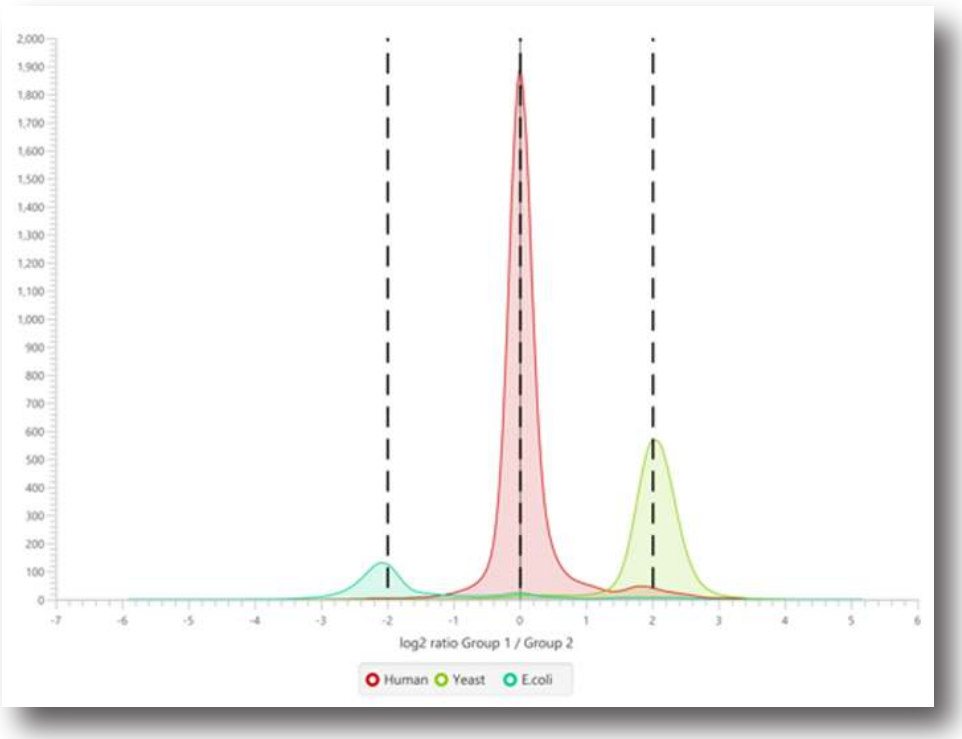
Stable Isotope Labelling by Amino Acids in Cell Culture (SILAC) is a powerful and popular approach for mass spectrometry (MS)-based quantitative proteomics. PEAKS® Q's SILAC quantification enables unsurpassed sensitivity of peptide feature detection through a novel peptide feature detection algorithm to find peptide feature pairs. Researchers can take advantage of the intuitive interface showing paired features at first glance and minimize the biases from missing values.

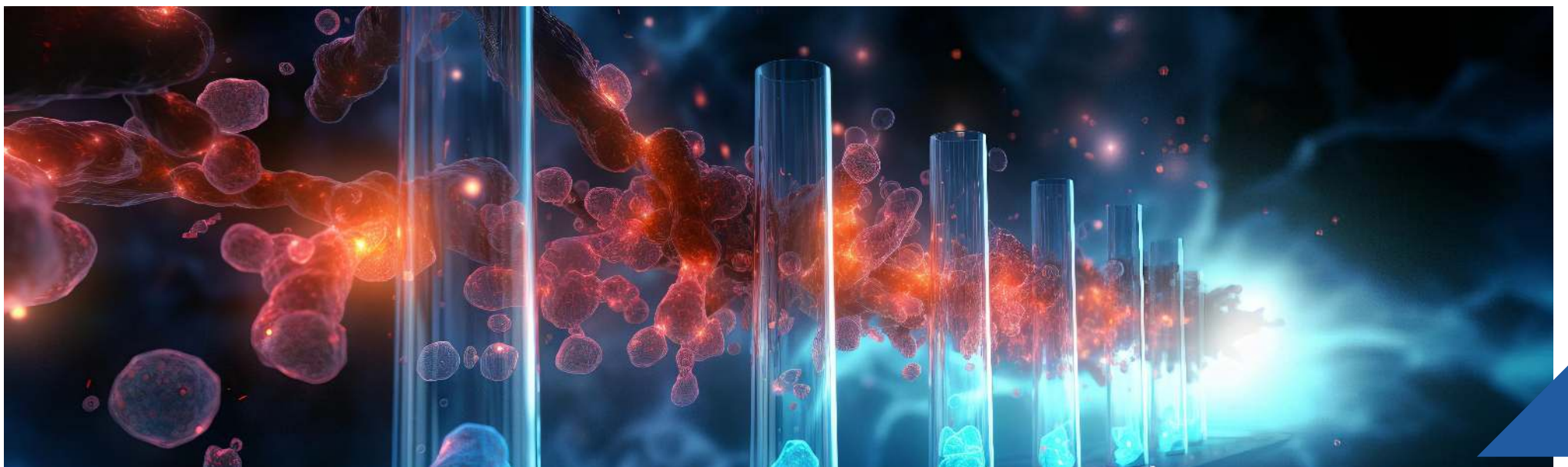


Label-free quantification (LFQ):

The ability to quantify the levels of proteins present in the samples by LFQ offers an efficient, cost-effective workflow to further understand the biological significance. PEAKS® Q 's LFQ function provides researchers with the option to calculate protein abundance either by using the well-known Top-3 peptides method or by using all unique supporting peptides. Researchers can then thoroughly investigate differences in peptide/protein abundance between samples with confident and accurate results.

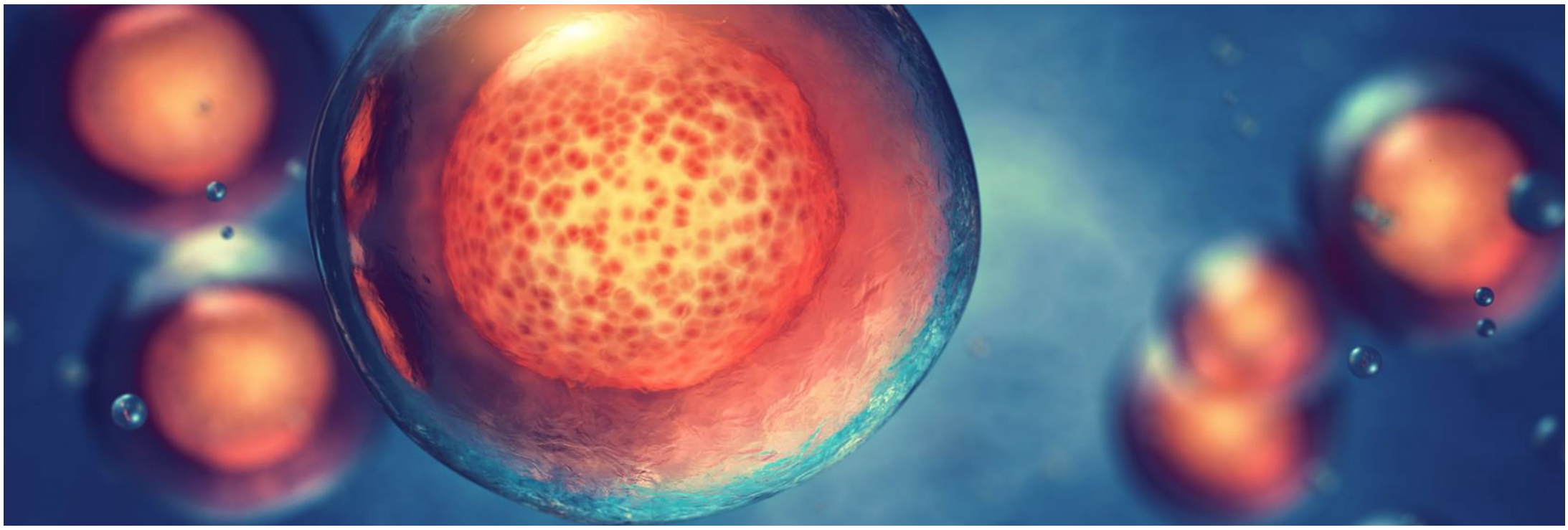






Targeted and discovery- driven clinical proteomics using

Hybrid-PRM/DIA

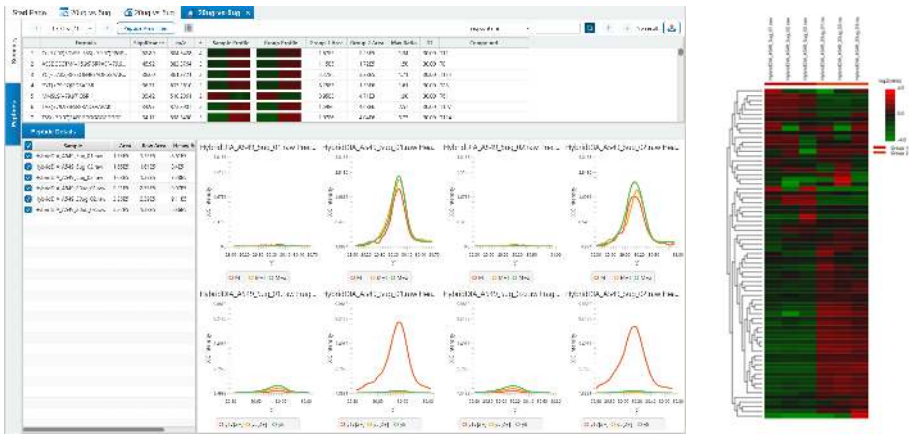


PRM analysis:

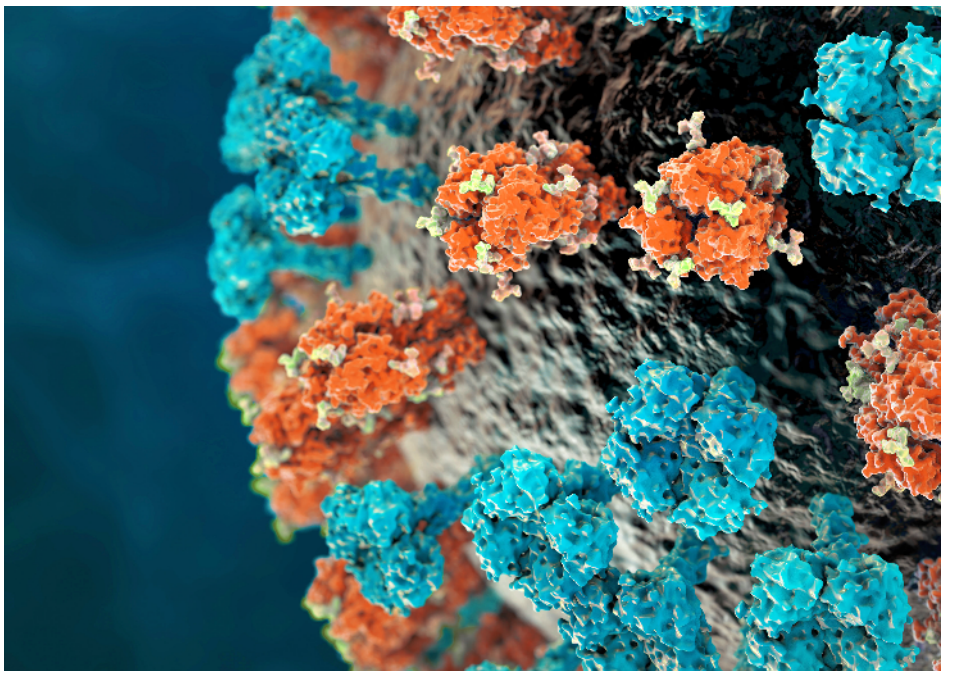
PRM provides high selectivity, high sensitivity, and high-throughput quantification with confident targeted peptide confirmation. A data-independent acquisition (DIA) / PRM workflow is suitable for discovery of biomarkers. PEAKS supports MS data analysis with data-dependent acquisition (DDA), DIA, and PRM.

Hybrid-/PRM DIA analysis:

Hybrid-PRM/DIA technology as a new intelligent data acquisition strategy enables enhanced measurement sensitivity for a specific set of analytes of current clinical interest by the intelligent triggering of multiplexed parallel reaction monitoring in combination with the discovery-driven digitization of the clinical biospecimen using DIA. Heavy-labeled reference peptides were utilized as triggers for PRM and monitoring of endogenous peptides.

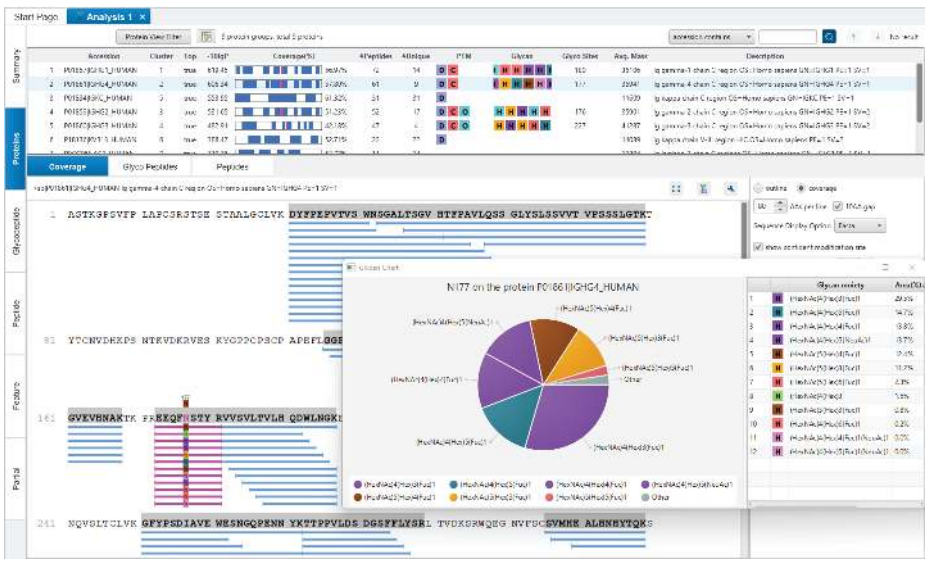


PEAKS® Glycan provides in-depth glycoproteomic analysis



Protein glycosylation is one of the most common post-translational modifications and plays a crucial role in important biological processes but is drastically understudied and deserves a specialized tool for both, N- and O-linked glycan analysis!

PEAKS® Glycan is a comprehensive data analysis tool that provides a highly sensitive and accurate glycoproteomics software solution to advance our understanding of the glycoproteome. PEAKS® Glycan search enables scientists to determine glycan site localization and glycan structures.

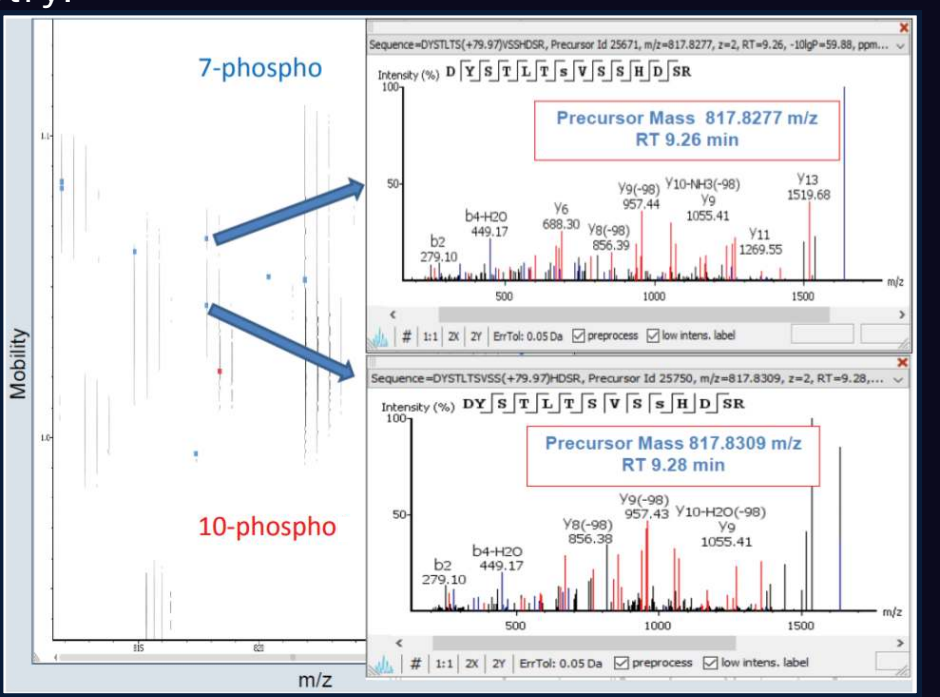


Ion Mobility Spectrometry - Mass Spectrometry (IMS-MS)

provides a compelling analytical workflow for complex biological and chemical mixtures by adding an additional dimension of ion separation; a 4th-dimension. With IMS-MS, ions are separated based on their mobility through a buffer gas, which provides the capability to differentiate ions based on their size, shape, charge and mass mobilities. Thus, it is possible to resolve ions that may be indistinguishable by traditional mass spectrometry.

Using PEAKS®, the ion mobility data can be viewed in the Mobility-LC-MS 4th-Dimension. The additional dimension enables increased identification sensitivity with smaller sample amounts.

- Analyze IMS-MS data using PEAKS® *de novo*,
- Interactive data visualization tools to view data projected on m/z-rt or m/z-1/k0 dimensions
- Vendor neutral; PEAKS® is able to support IMS data from any instrument
- Enable accurate and sensitive quantification analyses for IMS-based proteomics studies (Ex. label-free, SILAC, TMT/iTRAQ)



PEAKS® was used to analyze an extract of a HEK cell digest after a PASEF acquisition. The two co-eluting parent ions were separated in the ion mobility dimension, revealing two isobaric peptides differing only in the position of phosphorylation.

Next generation PEAKS® Studio 12

NEXT GENERATION PEAKS STUDIO WITH ENHANCED SPEED AND STABILITY

ACCURATE AND SENSITIVE IDENTIFICATION FOR BOTH, DDA AND DIA ANALYSES

ROBUST LABEL-FREE , LABELLED , AND PRM QUANTIFICATION SUPPORT

AI TECHNOLOGY INTEGRATED TO ADVANCE DE NOVO, DIA-DB, DDA-DB, AND QUANT

AUTOMATED QC TOOL FOR IN-DEPTH ANALYSIS FROM RAW DATA TO RESULTS

Deep learning technology

Deep learning enabled to improve identification accuracy and sensitivity by using algorithms to predict retention time, fragment ion intensity, mass-to-charge ratios, and ion mobility.

Updated intuitive GUI

With the updated Graphical User Interface (GUI), users still get the intuitive data visualization that PEAKS is known for but with a new look and optimized workflows to streamline your data analysis.

Increased speed & stability

The updated software architecture provides increased speed and stability for identification and quantification. Support all your discovery proteomics research with higher throughput and robust data analysis for both, DDA and DIA support.

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