PEAKS® Online

Complete Multi-User Proteomics Solution

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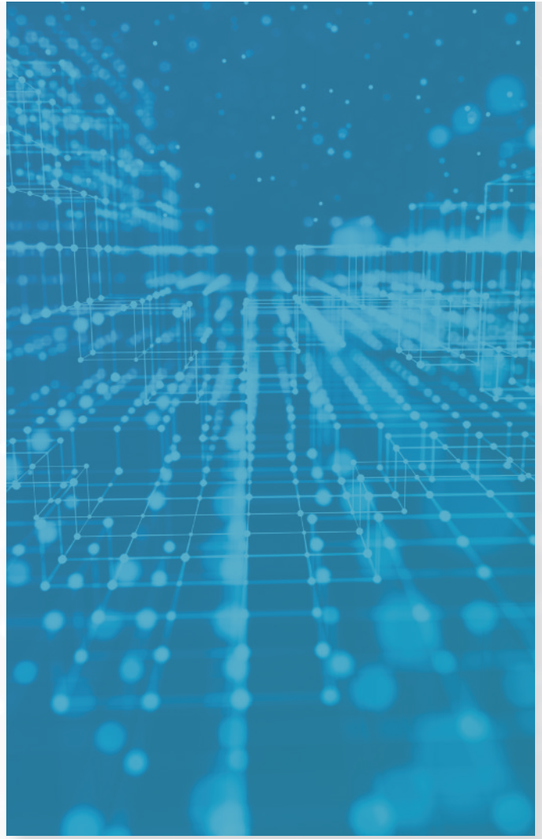


PEAKS Online users get detailed-oriented results with the advantage of using a shared resource. Users in need of an accurate quantification analysis tool can add an optional PEAKS Quantification module to their PEAKS Online platform. This proposed solution is designed to harness the power of available computing resources to perform complex algorithms on high-volume mass spectrometry data simultaneously, all while providing an easy-to-use and easy-to-access interface without the need to install local clients.

PEAKS is a specialized tool that embraces the complexity of a biological sample and maximizes the information uncovered for your discovery proteomics research.

With PEAKS DB, a unique de novo- assisted database search approach, you can expect to gain further understanding with a higher level of confidence. De novo sequence tags utilization:

- Improves database search sensitivity and accuracy
- Provide inference for new ORFs from novel peptides
- Enhances modification and sequence variant discovery

From discovering novel peptides and new biomarkers for the early detection of diseases to accurately quantitating diagnostic omics assays, PEAKS is the complete solution for your proteomics research.

PEAKS SERVER BASED SOLUTION KEY FEATURES

High performance and high accuracy algorithms to provide a complete solution for discovery proteomics, including protein identification and quantification, analysis of post-translational modifications (PTMs) and sequence variants (mutations), and peptide/protein de novo sequencing.

Quantification capabilities to perform Label-Free Quantification (LFQ) and accurately compare research groups.

Allow concurrent access from multiple users to process multiple projects in parallel.

Centralized configuration and monitoring system to easily maintain and manage all PEAKS Online data analyses.

Don’t get left in the dark! Move Together as a Cohesive Research Group

PEAKS Online means high-throughput data processing on a shared resource. This server-designed proteomics software is fully parallelized with the ability to run on a cluster of multi-CPU machine.

Users are able to run the same proven algorithms included in the PEAKS Studio solution, efficiently and on a larger scale.

By using a web interface client, users can send/retrieve data to/from the server and view the results in an intuitive manner.

Advanced System Architecture

Built on top of latest technologies to fully utilize the computing power of your hardware to provide:

High throughput solution: Allows concurrent access from multiple users to support parallelism at project and data level.

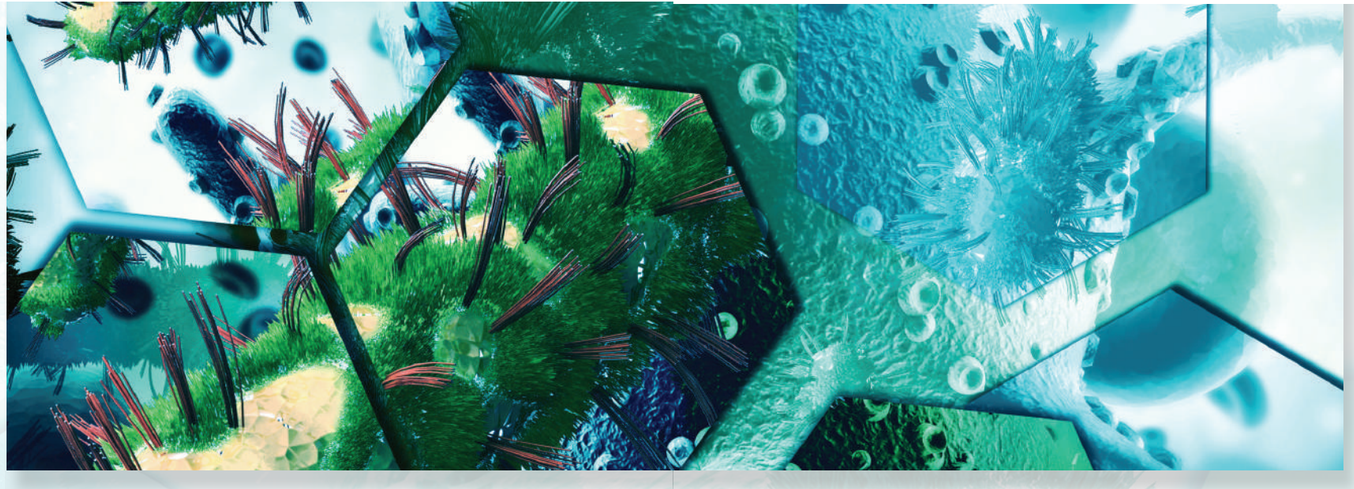
Distributed database: Yields higher I/O performance and better fault tolerance.

Ready to scale: Vertically and horizontally, add new worker node or database node to the system and see performance improvement right away.

Cross-platform deployment:
Ready to deploy on any Windows and Linux system.

Dual interfaces: The command line interface can be integrated to your existing automated workflow while the web interface provides a visualized way to configure, manage the system and review results quickly.

PEAKS' de novo peptide sequencing is world renowned and the base of all PEAKS analyses



The innovative PEAKS' de novo sequencing algorithm accurately annotate a peptide sequence without the use of a database. The sequences are then used to enhance PEAKS DB, PEAKS PTM, and SPIDER analyses.

Accuracy at the amino acid level

Local confidence scores are assigned for each amino acid. You can easily separate confident amino acid assignments from false positives.

Optimized peptide sequence reconstruction with fragmentation-specific algorithm training

De novo sequencing using spectrum-pairs that are generated in different fragmentation modes (eg.ETD/HCD) increases the precision of MS2 de novo assignments. Confident de novo sequence tags from each complementary spectrum are used to reconstruct a peptide sequence, which is optimized to both spectra.

Intuitive coverage view gives full control

De novo results from scans missed in protein databases are summarized in 'de novo only' results. Partial protein matches or "de novo tags" are also given and can be viewed directly from the coverage pane.

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.

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.

Find novel peptides not recorded in protein databases

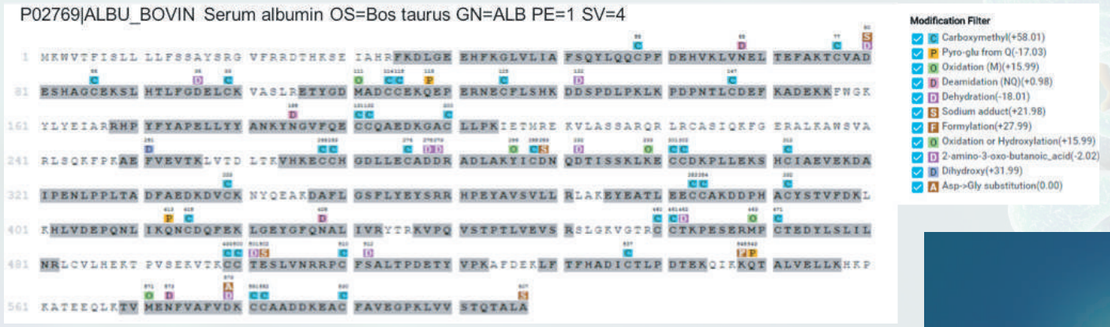
De novo results from scans missed in protein databases are summarized in 'de novo only' results. Partial protein matches or "de novo tags" are also given and can be viewed directly from the coverage pane.

Designed to discover hidden modifications

In PEAKS PTM, the highly confident spectra which have a good de novo score are reanalyzed to assess any unknown PTMs. Specify the PTMs of interest or turn on all 313 naturally occurring biological modifications from the Unimod database in your PEAKS PTM search. Don't let your computational resources limit you.

Site determination & result validations

Any identified modifications in PEAKS can be reported confidently by assessing the A-Score. Allow PEAKS to assist you with validating your results and measuring the site localization accurately before reporting them.



Cross-species homology search with SPIDER

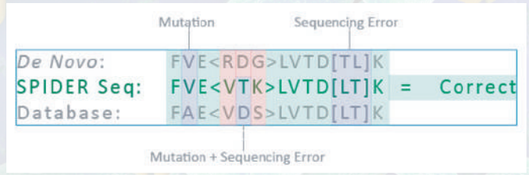
De novo tag homology search tolerates common de novo sequencing errors such as (AT/TA) and (N/GG). Find confident hits that are different from the database entry with our de novo tailored homology search.

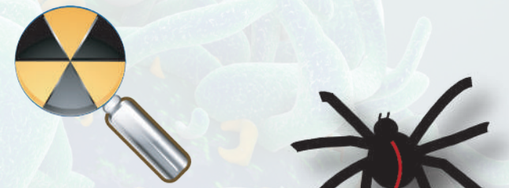
Spider provides a specialized tool for:

- Resolving database errors
- Antibody sequence confirmation
- Potential biomarker discovery
- Mutated peptide identification

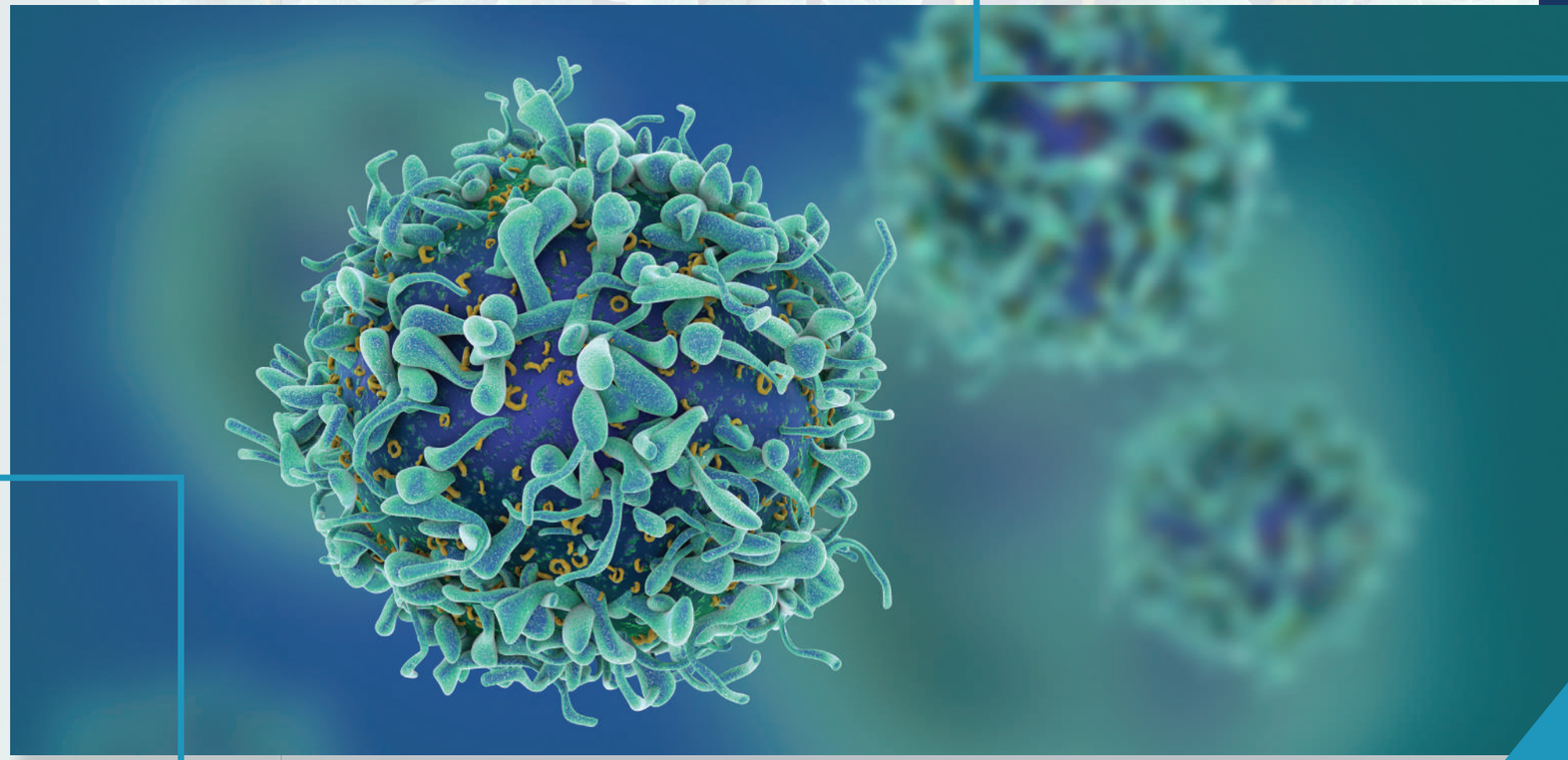
Powered by de novo sequencing to reconstruct the true sequence

The SPIDER algorithm tries to match the *de novo* sequence tags with the database proteins. By minimizing the sum of the de novo errors between the reference sequence and the *de novo* sequence, SPIDER, reconstructs a "real" sequence to find peptides with single amino acid variants.





The characterization of PTMs and sequence variants is crucial to the understanding of biological pathways.



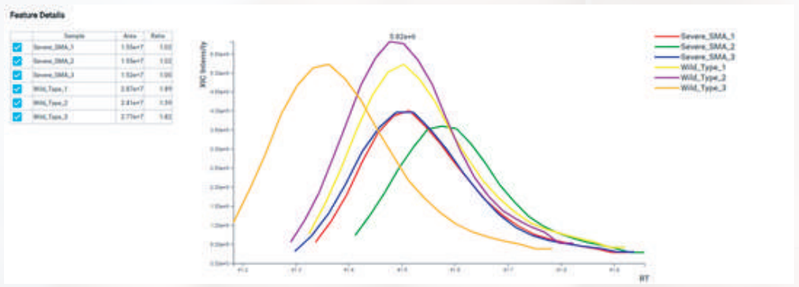
Add the PEAKS Q module to your PEAKS Online data analysis workflow for robust label-free quantification

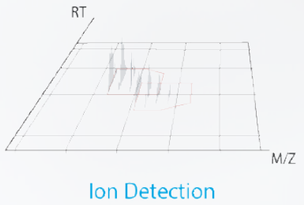
Accurate and sensitive MS1 based quantification for low abundant proteins

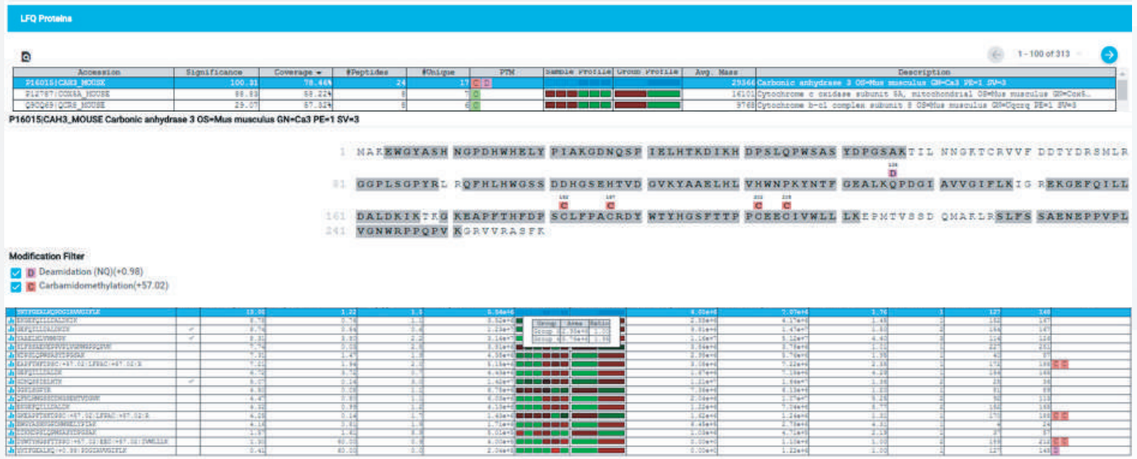
PEAKS relative protein quantification is performed based on the extracted ion chromatograms (XICs) of the whole isotopic envelope on the MS1 level. PEAKS Q also extracts and uses the LC retention time and MS features to align different runs.

Three most abundant peptides are used for protein ratio estimation

Achieve higher accuracy and smaller variance with PEAKS label-free quantification.







Organized result presentation gives you a clear representation of the proteins showing significant change between conditions.

Centralized control of analysis and users

PEAKS Online administrators can ensure deadlines are met by prioritizing data analysis and control the number of client users.

Work as team and collaborate with Ease

In PEAKS Online users can easily share projects, databases, workflows, and even parameters between your whole research team.

Developed as a platform to align your team's efforts

With PEAKS Online, administrators have centralized control and can ensure that workflows, parameters, databases are standardized from one data analysis to the next.

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