

Accuracy & Sensitivity



PEAKS is:

- de novo* sequencing
- database search protein identification
- homology searching (sequence tags)
- multi-engine protein identification
(compare/combine multiple search engines)
- PTM analysis
- quantification

for You!

PEAKS enables straight-forward identification of proteins and peptide sequencing.

Organized and easy to navigate results makes it simple to understand your data.

Built-in result validation tools ensure publication worthy-data.

Compatible with all major instrument vendors, PEAKS delivers accurate peptide sequences, comprehensive protein lists and precise quantification ratios.

Join the growing number of researches worldwide who depend on PEAKS for confident results.



PEAKS[®]

De Novo Sequencing

Find what you have been missing!

PEAKS provides the industry's leading *de novo* sequencing algorithm. Excelling in analyzing high mass accuracy data, PEAKS supports a wide variety of fragmentation types (CID, HCD, ECD, ETD, PSD, PQD) and easily identifies fixed and variable PTM. *De novo* sequencing identifies both known and novel peptides.

PEAKS DB (Database Searching)

Protein identification via database searching is a prominent feature of PEAKS. This highly sensitive method provides increased coverage with exceptionally low false discovery rates, making it a fundamental part of any proteomic workflow. Amongst other fragmentation types, PEAKS boasts significantly improved ETD interpretation.

Researchers in the iPRG study (ABRF2011) using PEAKS performed excellently and identified a considerably high quantity of peptides with a very low false discovery rate. This is just another study illustrating the exceptional capabilities of the PEAKS software in providing a high peptide identification rate combined with a low FDR from database searching.

Summary Reporting

Avoid the daunting task of manually summarizing the analysis by using the automated Summary pane in PEAKS 5.3.

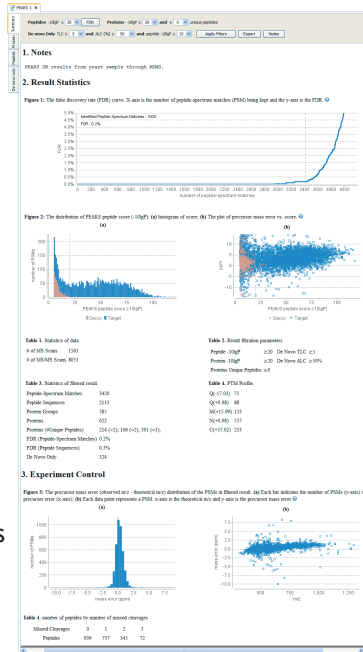
Result Statistics:

- FDR Curve
- Score Histogram
- Precursor Mass Error vs. Score Plot
- Data Statistics
- Statistics of Filtered Results
- PTM Profile

Experiment Control:

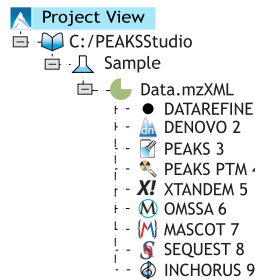
- Precursor Mass Error
- Distribution of the PSMs

inChorus Summary displays peptide spectrum matches from each search engine utilized.



inChorus (Multi-Engine Protein ID)

Quickly compare protein identification results from multiple search engines within a single window for effective result validation.

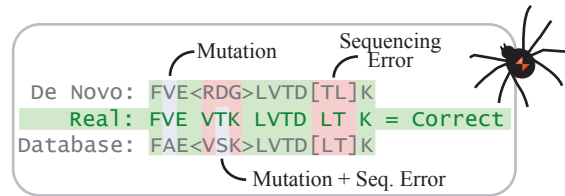


In addition to PEAKS' unique database searching approach, users can launch third-party engines (Mascot,™ Sequest,™ X!Tandem, OMSSA) to generate consensus reports. Performing this step provides unparalleled confidence and increased coverage. Already have processed data from these engines, load it in and automatically compare instantly.

SPIDER

Discover More with Homology Searching

Protein sequence databases will never be complete, cannot account for mutations between individuals and contain gene prediction errors. SPIDER is an irreplaceable homology based search tool, which allows you to find homologous peptides in the database and reconstruct the real peptide sequence. Since peptide sequence variations are common, use of this technique provides a significantly better explanation of your samples.



PEAKS Q (Quantification)

Using the latest technology, perform quantification with Label Free (with replicate analysis) and Labelled (ICAT, ICPL, ITRAQ, SILAC, O¹⁸, TMT and many more) samples.

PEAKS Online: Server Solution

To really speed up analysis, unleash PEAKS on your server. PEAKS Online allows for multi-node processing, as well as multiple client access, offering all the benefits of PEAKS Studio with the power of a server.

Share results with colleagues or customers via the free **PEAKS Viewer**.



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Everyone Wins

With the PEAKS referral program, both you and your colleague's lab are rewarded. Ask about details.

Free Training

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