SpectroMine™

powered by Pulsar

UNSURPASSED PERFORMANCE FOR DDA PROTEOMICS

Deeper Coverage · Faster Analysis · Better Experience

THE NEXT FRONTIER OF INNOVATION IN DDA PROTEOMICS

Our powerful and user-friendly solution for DDA proteomics comes with leading performance, speed, and support for the latest acquisition methods. SpectroMine integrates our state-of-the-art Pulsar search engine, offering full support for ion mobility technologies and achieving more identifications thanks to deep learning augmentation.

Recent innovations such as ion mobility (IM) in data acquisition and novel isobaric tags for higher sample multiplexity have improved the quantitative precision of data-dependent acquisition (DDA) and expanded its applications. Such technological advances demand versatile software in order to handle new types of data.

Biognosys is best known as a co-inventor and developer of technologies for the processing of data-independent acquisition (DIA) as well as our industry-leading DIA software, Spectronaut. Based on the powerful algorithms developed for the analysis of DIA data, we built SpectroMine to address the demands of modern DDA proteomics. SpectroMine can search various data types[1], performs high-quality isobaric labeling quantification (ILQ)[2], and has recently been used for LiP-MS, a new drug target identification pipeline[3].

SpectroMine brings DDA to its full potential:

- **Deep-learning augmentation**
  Advanced search algorithms for unsurpassed identification and speed
- **Isobaric labeling quantification**
  Support for the latest isobaric tags and block normalization
- **Library-based DDA search**
  Deeper proteome coverage, even for scarce biological samples
- **Ion mobility technology support**
  Compatible with PASEF and FAIMS Pro
- **Complete analysis environment**
  DDA data analysis and detailed result review in a user-friendly interface
- **First class technical support**
  Help from our scientists when you need it

1) **Bader et al.,** Mol Syst Biol, 2020 16:e9356
2) **Hörnberg et al.,** Nature, 2020 584, 252–256
3) **Piazza et al.,** Nat Commun, 2020 11, 4200

Milestones in Isobaric Labeling development

Supported Instrument Vendors
- Bruker
- SCIEX
- Thermo Scientific
- Waters

Recommended System
- Windows 10 x64
- Intel or AMD CPU with 4 or more cores
- 2 TB of hard drive space or more (2x data set size)
- 64 GB of memory or more

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BENEFITS

- Performance
- Scalability
- Versatility
- Simplicity
- Reproducibility
- Usability

«SpectroMine is a game-changer for the analysis of multiplexed proteomics experiments. The speed and quality of analysis are unsurpassed.»

Mikhail Savitski, PhD
EMBL Heidelberg

FEATURES

Deep proteome coverage with deep-learning augmentation

Fast search and quantification of large ILQ experiments with block normalization

DDA, DIA, and PRM data searchable, FAIMS Pro, and PASEF support. ILQ with TMT, iTRAQ, EASI-tag, and TMTpro

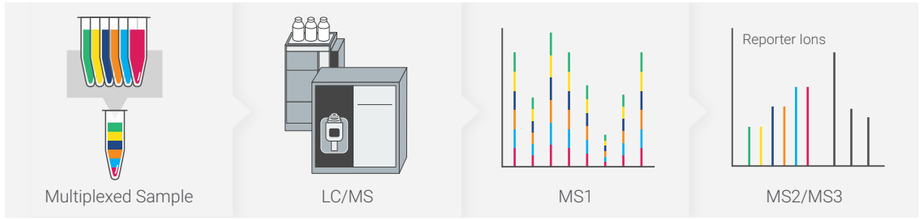
Complete analysis environment in an intuitive user interface

Reliable and robust results that are easy to share

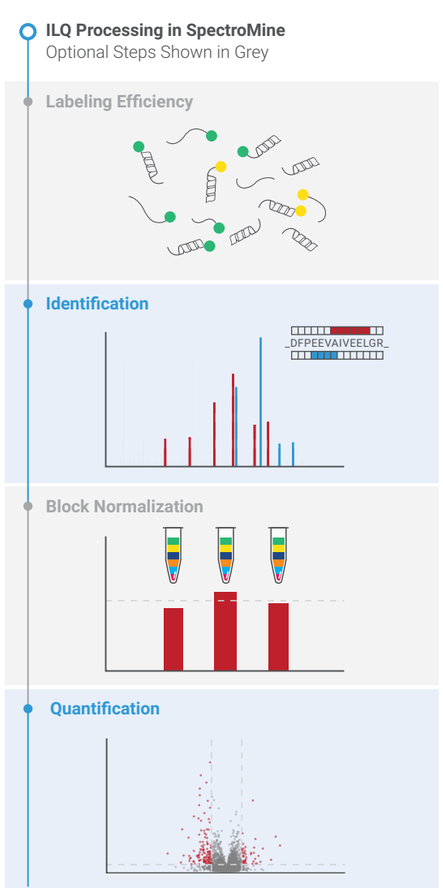
Effortless analysis with automatic optimization of parameters

EFFORTLESS ISOBARIC LABELING QUANTIFICATION

SpectroMine provides a complete platform for isobaric labeling experiments. With integrated analysis templates for all major labeling reagents including TMTpro and EASI-tag, staying on top of the latest innovations is made easy.



Overview of Isobaric Labeling Quantification



DDA combined with isobaric labeling quantification (ILQ) is a workflow of choice in discovery proteomics, enabling quantification of multiple biological samples simultaneously in a single run. ILQ delivers highly precise and reproducible quantification with deep proteome coverage.[1]

SpectroMine makes setting up of an ILQ analysis quick and efficient. With automated calibration and smart default settings, optimal results can be achieved with minimal user input. For experiments where the number of samples exceeds reporter multiplexity, samples can be organized in blocks.

SpectroMine offers experiment-wide normalization across these blocks. Moreover, workflows for assessing labeling efficiency allow you to quickly correct for sample preparation-related differences between analysis channels.

Quantification results can be viewed directly in SpectroMine, and then exported in either a customizable report format or with pre-packaged schemas for downstream processing with external tools such as MSstats.

1) Muntel et al., J Proteome Res, 2019, 18, 1340-1351

THE MOST POWERFUL SEARCH ENGINE

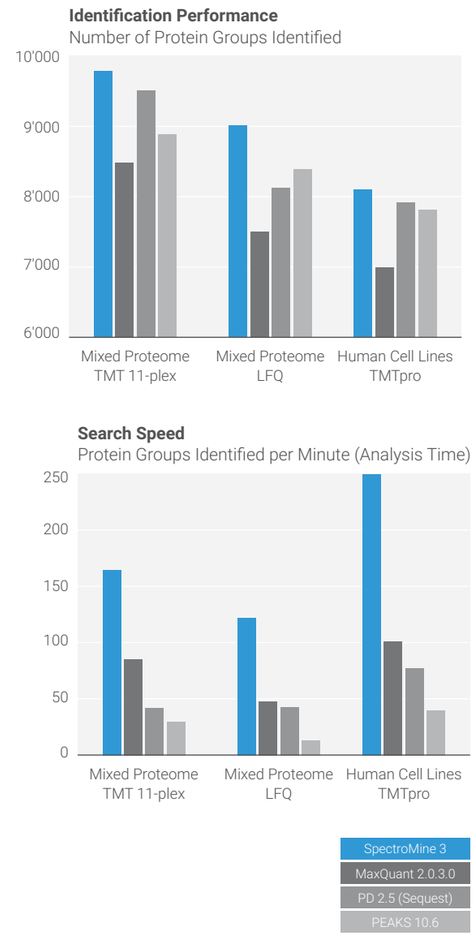
SpectroMine brings the power of Pulsar, our industry-leading and vendor-independent database search engine, to DDA proteomics for deep proteome coverage and fast analysis.

With advanced deep learning models for indexed retention time (iRT) and fragmentation prediction, SpectroMine achieves unsurpassed proteome coverage. We tested a range of software products using harmonized search space settings, protein inference, and false discovery rate (FDR) control. The results for both ILQ and label-free quantification (LFQ) demonstrate that SpectroMine provides the most identifications and fastest processing times for a wide range of DDA experiments (see Figure).

SpectroMine lets you take full advantage of the latest instrumentation from all major vendors, including FAIMS Pro and PASEF ion mobility technologies, delivering state-of-the-art identification performance and short processing times.

At the same time, SpectroMine provides an intuitive interface to ensure data integrity and enable the sharing of data. FDR is rigorously controlled at peptide-spectrum match (PSM), peptide and protein levels, and a wide range of quality control visualizations are also available. To keep your results organized, they are saved in search archives, giving you full access to annotated raw data, and making it easy to share with anyone through the free SpectroMine Viewer.

Analysis of Published Datasets[1,2] Using SpectroMine and Leading Competitors

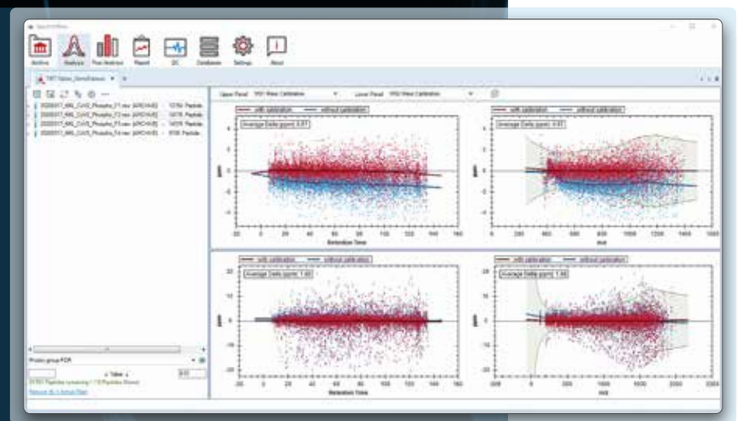


1) O'Connell et al., J. Proteome Res., 2018, 17, 1934-1942
2) Li et al., Nat. Methods, 2020, 17, 399-404

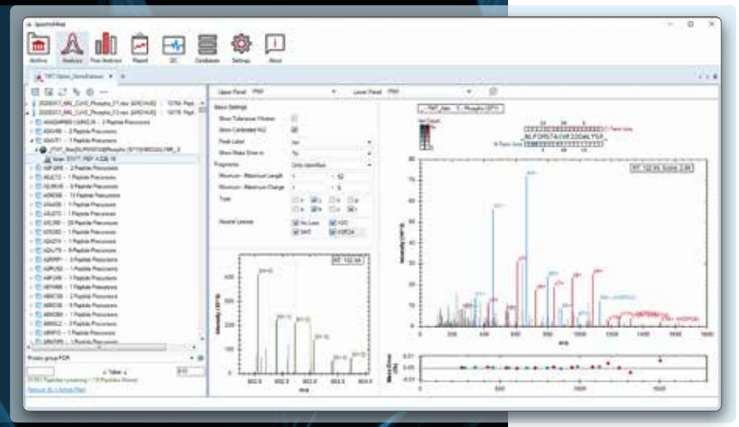
THE ALL-IN-ONE WORKFLOW

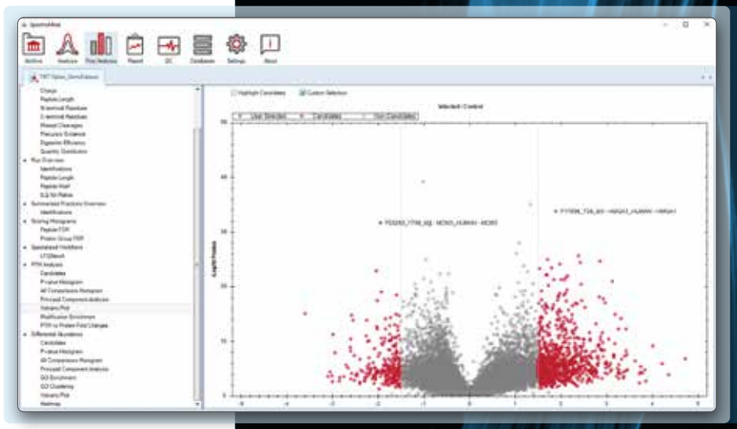
SpectroMine is an all-in-one solution with a variety of built-in functionalities for data analysis, review, interpretation, and export. The intuitive user interface comes with pre-configured wizards to guide you through the analysis setup, making it an effortless and user-friendly process.

Automated Mass Calibration
Review experiments after analysis with various visualizations, including run summary, RT calibration, and mass calibration plots. Automated mass calibration is provided at each MS level depending on the experiment at hand.

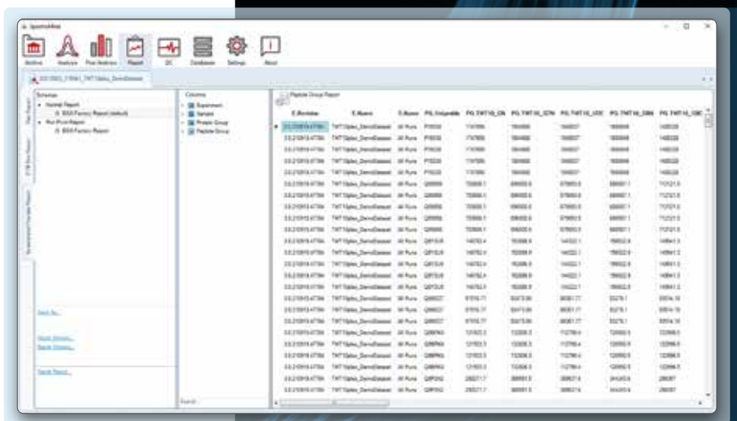


Peptide-Spectrum Match (PSM) Plots
Explore the results from run level down to scan level. PSMs are visualized with their corresponding MS spectra on all levels. SpectroMine allows setting adjustments for the best representation of your results.

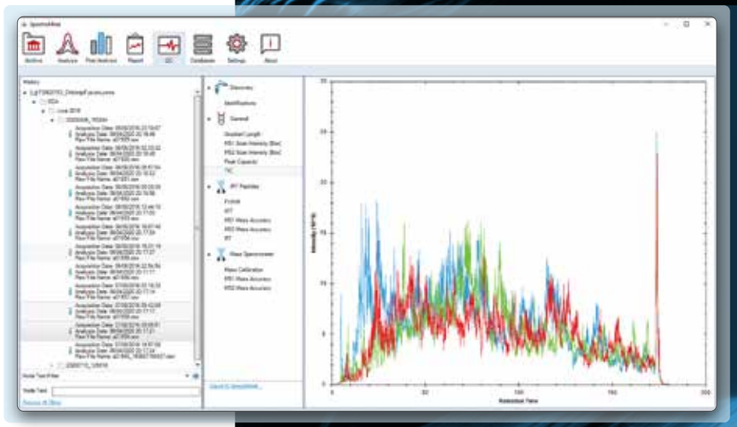




Differential Abundance Analysis
Explore experimental results with intuitive visual plots. SpectroMine routinely performs pairwise t-test comparisons of all conditions. Visually identify your differential abundance candidates in a volcano plot, and export them with just one click.



Generating Reports
Export your results in the fully customizable report perspective. Obtain information about your analysis down to the fragment ion level and build custom report templates to automate future exports. Our pre-built report schemas are compatible with external pipeline tools.



Quality Control
Utilize SpectroMine's built-in automated quality control through the iRT Kit to monitor the most important instrument parameters over time. This includes several performance indicators such as MS1 and MS2 accuracy, number of identifications, sensitivity, and more.

HOW TO GET SPECTROMINE

Here at Biognosys, we are committed to making our next-generation proteomics solutions widely available to researchers. For us to do this, we offer flexible licensing options to best fit your personal and organizational needs.

If you are interested in a SpectroMine demo, a free trial license, or you would like to proceed to purchase, contact us at **order@biognosys.com.**

FIRST CLASS SUPPORT

We are proud to offer you extensive advice and support in order to help you implement next-generation proteomics in your facility. Our support team is here to help you reach your research goals alongside a great and convenient user experience.

If you would like to have your own personal meeting with us, please feel free to contact us by emailing **support@biognosys.com**. Our average response time is less than 24 hours.

At Biognosys, we believe that deep proteome insights hold the key to breakthrough discoveries that transform science for better lives. We make the proteome actionable to empower research, drug development, and clinical decision-making with our versatile portfolio of mass spectrometry-based proteomics research services, software, and kits. These solutions provide a multi-dimensional view of protein expression, function, and structure in all biological species and sample types.

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