



SpectroMine

powered by Pulsar

UNSURPASSED PERFORMANCE
FOR DDA PROTEOMICS

Deeper Coverage, Faster Analysis and Better Experience
for Quantitative Proteomics

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 and new Kuiper search engines, offering full support for ion mobility technologies and achieving more identifications thanks to deep learning augmentation.

Mass spectrometry (MS) based proteomics is evolving rapidly, with ion mobility separations and high-order isobaric multiplexing now routine. These advances enable studies once deemed impossible – from immuno-peptidomics and limited proteolysis to large cohort analyses. To harness these capabilities, researchers need software that matches the pace: versatile, high-performance platforms that integrate advanced algorithms, flexible workflows, and intuitive interfaces to deliver actionable proteomic insights.

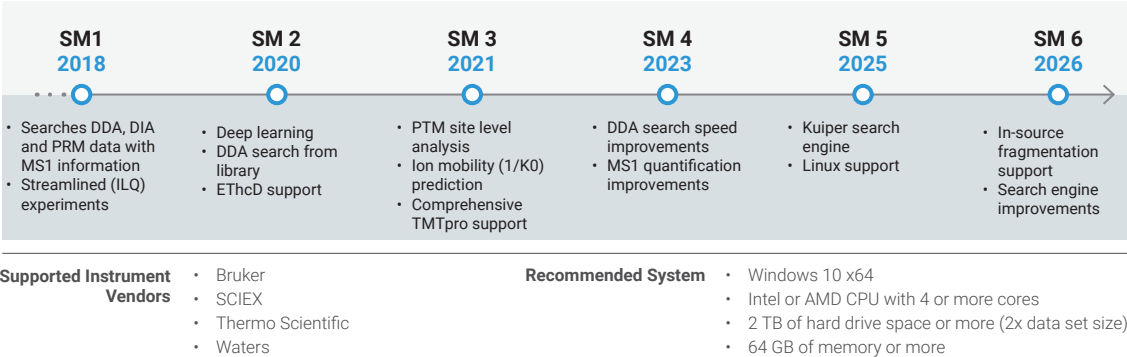
Biognosys is best known as a co-inventor and developer of technologies for the processing of data-independent acquisition (DIA) as well as our industry-leading DIA software, *Spectronaut*. Based on the powerful algorithms developed for the analysis of DIA data, we built *SpectroMine* to address the demands of modern DDA proteomics. *SpectroMine* can search various data types¹ and performs high-quality isobaric labeling quantification (ILQ)². It has been used for LiP-MS, a drug target identification pipeline and recently for label free Host Cell Proteome (HCP) analysis³.

SpectroMine brings DDA to its full potential:

- **Deep-learning augmentation**
Advanced search algorithms for unsurpassed identification and speed, including nonspecific searches such as immunopeptidomics.
- **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 Khalil et al., bioRxiv, 2024.11.03.621185

Figure 1. **Milestones in SpectroMine (SM) development**





«I have been thoroughly impressed by the capabilities of *SpectroMine*, particularly in the context of MS-based quantitative proteomics for host cell protein monitoring.»

Somar Khalil, Principal Scientist
Glaxo Smith Kline

FEATURES

Performance

Scalability

Versatility

Simplicity

Reproducibility

Usability

BENEFITS

Deep proteome coverage with deep-learning augmentation.

Fast search and quantification of large ILQ experiments with block normalization, high speed and coverage for open and nonspecific searches.

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

Complete analysis environment with 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.

Figure 2. Overview of Isobaric Labeling Quantification

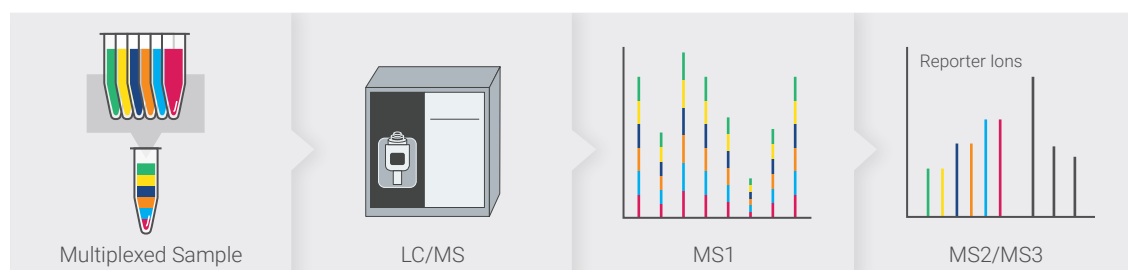
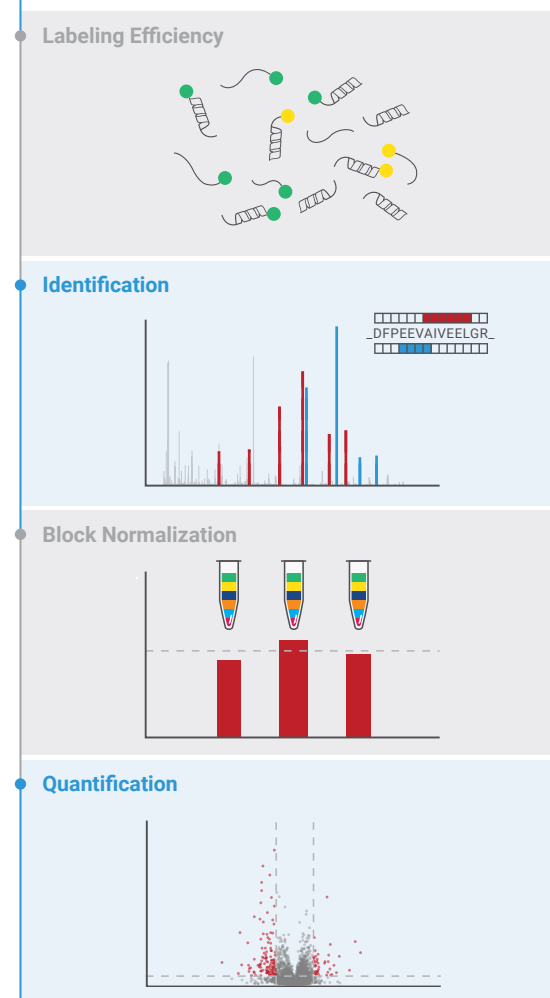


Figure 3. ILQ Processing in *SpectroMine*
(Optional Steps Shown in Grey)



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.⁴

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.

⁴ Muntel et al., J Proteome Res, 2019, 18, 1340-1351

THE MOST POWERFUL SEARCH ENGINE

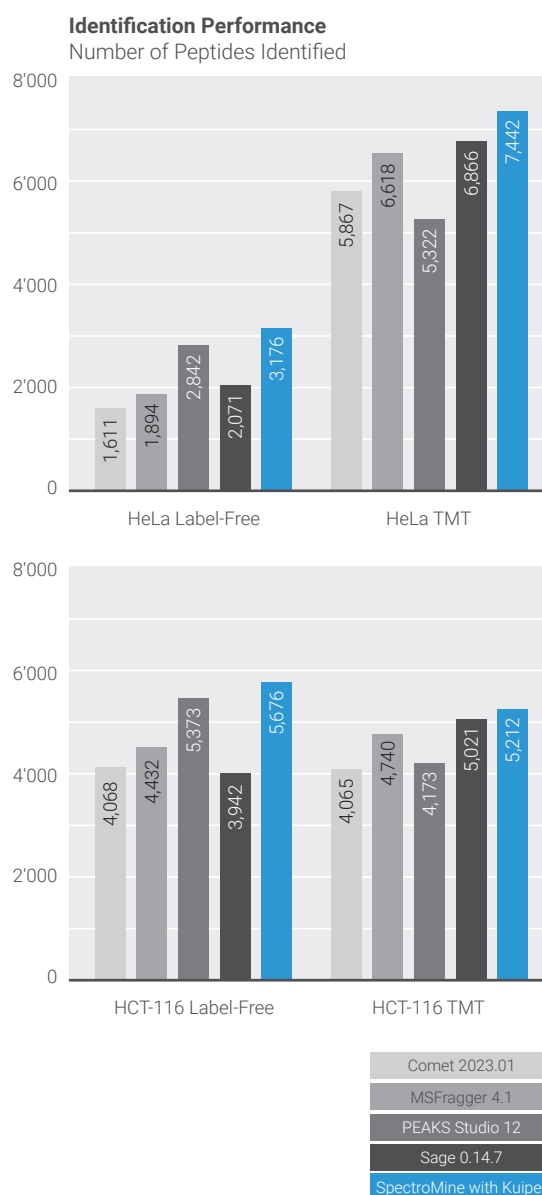
***SpectroMine* pairs our industry-leading, vendor-independent Pulsar search engine with the Kuiper engine, delivering deeper proteome coverage and lightning-fast DDA analysis for immunopeptidomics and PTM analysis applications.**

Kuiper powered immunopeptidomics data analysis delivers unmatched depth and confidence for your immunopeptidomics workflows. Harness advanced deep-learning models for indexed retention time (IRT) and fragmentation prediction, now tuned specifically for immunopeptidomics and nonspecific searches to achieve broader, more accurate peptide coverage than ever before.

In benchmarking against leading software under harmonized search-space, protein-inference, and FDR settings, *SpectroMine* with Kuiper consistently outperformed (see Figure 4) for DDA immunopeptidomics experiments.

Kuiper revolutionizes even the toughest workflows, supercharging immunopeptidomics analysis while enabling comprehensive open searches. *SpectroMine* combines upgraded Pulsar property prediction with Kuiper's advanced search indexing to deliver state-of-the-art performance and dramatically shorter turnaround times.

Figure 4. **Analysis of Published⁵ Immunopeptidomics Datasets Using *SpectroMine* and Leading Competitors**

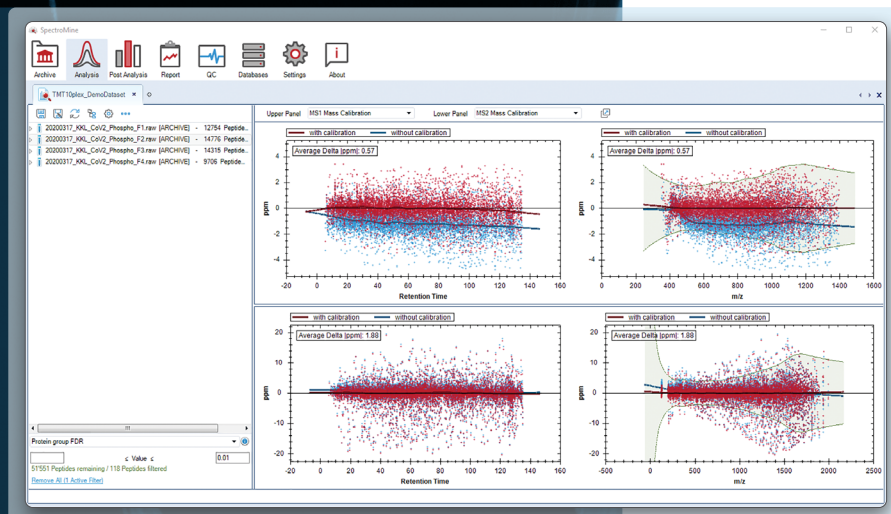


THE ALL-IN-ONE WORKFLOW

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.



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

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.

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. Therefore, 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 integrate our software and kits into your workflow. Our support team is here to ensure a great 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.

The *Biognosys Group* brings together the Bruker Corporation affiliates Biognosys, biocrates, and PreOmics to deliver integrated solutions across proteomics, metabolomics, and lipidomics. Its ecosystem spans high quality consumables, software, and contract research services. The Group enables seamlessly connected mass spectrometry workflows, making advanced multiomics technologies accessible to laboratories worldwide.

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