

4800 Plus

MALDI TOF/TOF™ Analyzer

Unparalleled depth of coverage. Plus. Proven Quantitation.

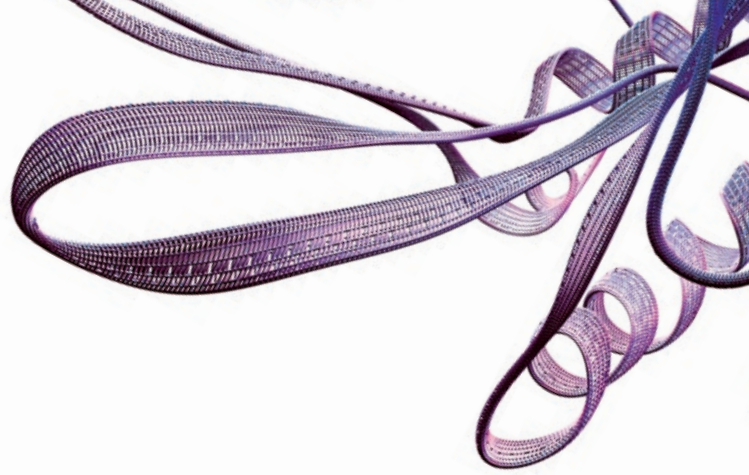


Simply *the* most powerful platform available for quantitative proteomics

Unparalleled depth of coverage plus proven, robust quantitation. The Applied Biosystems/MDS SCIEX 4800 *Plus* MALDI TOF/TOF™ Analyzer has system modifications and innovative ProteinPilot™ software, to take advantage of the powerful new 8-plex iTRAQ™ reagents. Now quantitative proteomics is within the reach of everyone.

The 4800 *Plus* MALDI TOF/TOF™ Analyzer takes TOF/TOF™ optics technology to the next level of performance and sensitivity. The integrated system features a compact vertical design and novel OptiBeam™ on-axis laser irradiation.





The Most Direct Path to the Answers

- Smart, powerful workflows help you derive more useful information from every experiment.
- Low attomole sensitivity in MS and MS/MS modes lets you confidently detect and identify peptides that other systems miss.
- Advanced, wizard-driven software allows easy setup of workflows and automatic tuning of the instrument to ensure maximum performance for every experimental run.
- Compact, vertical design minimizes floor space requirements.

Precise Quantification for Biomarker Research

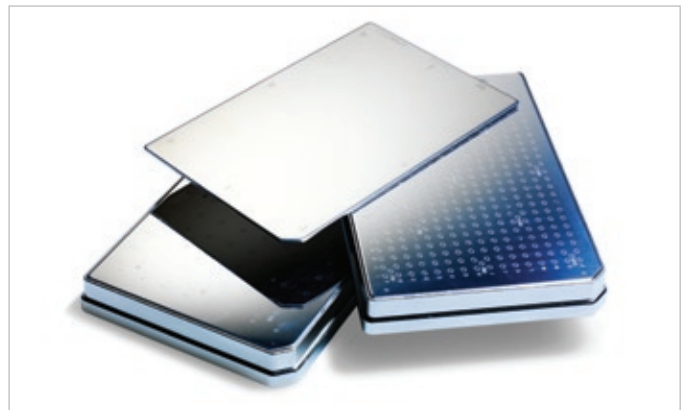
Taking full advantage of the 4800 *Plus* system's unequalled sensitivity and unique QuanTIS™ precursor ion selector, ProteinPilot™ software enables the accurate and precise quantification needed for protein biomarker discovery applications, allowing you to identify and quantify proteins relevant to a particular biological state. Plus, with multiplexed iTRAQ™ reagent technology you can compare and quantitate up to eight samples at a time.



The Tempo™ LC MALDI Spotting System provides robust, contact-free electrostatic deposition of droplets and precise mass spectrometry results.

The Ultimate LC MALDI Platform

The combination of unparalleled sensitivity and advanced, easy-to-use LC/MS software makes the 4800 *Plus* MALDI TOF/TOF™ Analyzer the ideal instrument for LC MALDI analysis. A novel peak-picking algorithm ensures that MS/MS spectra are collected at the most intense point of the chromatographic elution profile. Peak Explorer™ software lets you view the LC run in a conventional LC/MS format; the software also features advanced peak list sorting, and a “heat map” view which displays a 3D map of the entire LC MALDI chromatogram.



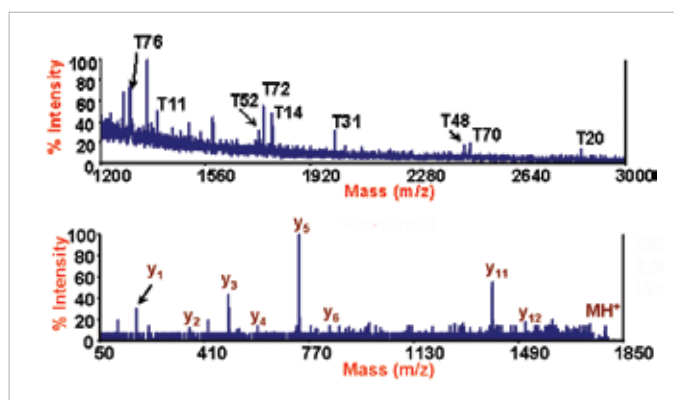
Single-use, industry-standard microtiter format Opti-TOF® sample plates simplify operation and maximize throughput, while providing convenient sample archiving.

Industry-leading TOF/TOF™ optics technology

In 2002, we introduced the world's first MALDI TOF/TOF™ Analyzer. The second generation 4800 platform took TOF/TOF™ optics performance a giant step further. Now the 4800 *Plus* has been tuned to match the performance of our industry-leading MALDI TOF/TOF™ optics with the power of our innovative 8-plex iTRAQ™ reagents.

Impressive MS and MS/MS Sensitivity

The 4800 *Plus* MALDI TOF/TOF Analyzer delivers unmatched sensitivity in both MS and MS/MS modes. This not only lets you see the ions of interest at a lower level than ever before; it means fewer laser shots are required to produce high quality spectra and faster analysis time. Higher sensitivity and fewer laser shots also conserve limited sample amounts in case further analysis is required.



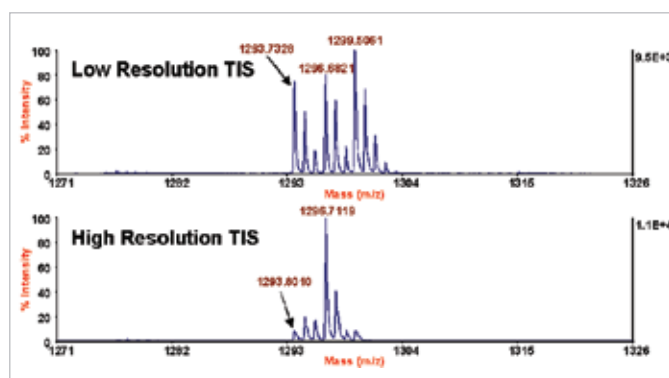
In this MS spectrum of 50 amol/μL of a tryptic digest of beta-galactosidase (top panel), 1000 laser shots were enough to confidently identify the protein by PMF. The bottom panel shows the MS/MS spectrum collected from the peptide WSDGSYLEQDMWR from a tryptic digest of beta-galactosidase at a concentration of 250 amol/μL. Both samples were prepared using standard preparation methods.

Reduce Sample Complexity by Optimizing Data Acquisition

Automated workflows utilize powerful RDA™ features of GPS Explorer™ software to give you the most useful information in the fewest experimental steps. Experimental design focuses on minimizing the number of spectra required to obtain highest confidence results—to generate more answers, not more data.

Enhanced Precursor Ion Selection

Advanced QuanTIS™ precursor selector technology offers high resolution precursor ion selection with no significant loss in sensitivity. Only the precursor of interest is transmitted, and the corresponding MS/MS spectra are not complicated by fragments from adjacent peptides.



Specific isolation of Angiotensin I (DRVYIHPFHL, m/z 1296.7) detected at m/z 1293.7 (Ac-ASQKRPSQRHG) and m/z 1299.6 (SYSMEHFRWG). Top panel demonstrates conventional precursor ion selection that can include several ions of similar mass. Bottom panel demonstrates high resolution ($r > 400$) isolation of Angiotensin I using QuanTIS precursor selector.

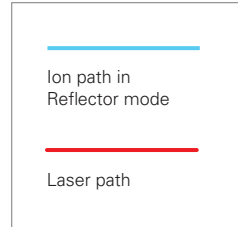
Enhanced Mass Accuracy for Increased Confidence in Results

The advanced source and plate model algorithms on the 4800 *Plus* MALDI TOF/TOF Analyzer accurately correct for fringe effects and plate flatness issues inherent in all axial TOF instruments. This assures excellent mass accuracy, sub-15 ppm, across the sample plate using default calibration. Using an internal standard, 2.5 ppm mass accuracy is easily achieved, increasing confidence in protein identifications.



Linear Detector
Linear ion optics offer unparalleled high mass performance.

Mirror Region



Source 2 Region

QuantIS™ Precursor Selector
Novel timed ion selector optics provide high resolution precursor ion selection without a significant loss in signal intensity.

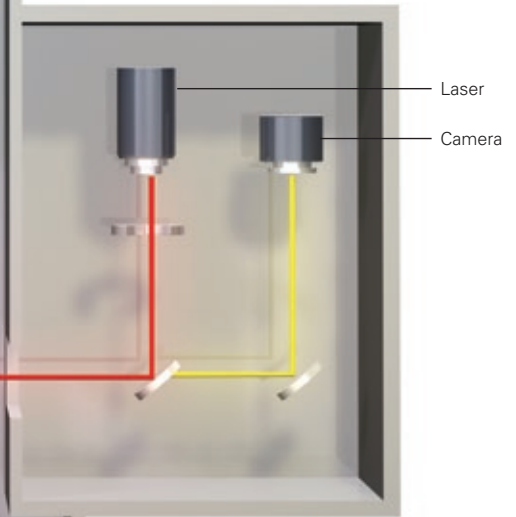
Deceleration Stack

The deceleration stack optics prior to the collision cell enable the kinetic energy of the precursor ions entering the collision cell to be tuned for controlled fragmentation. This enables the user to obtain optimum fragmentation for a wide range of applications.

Reflector Detector



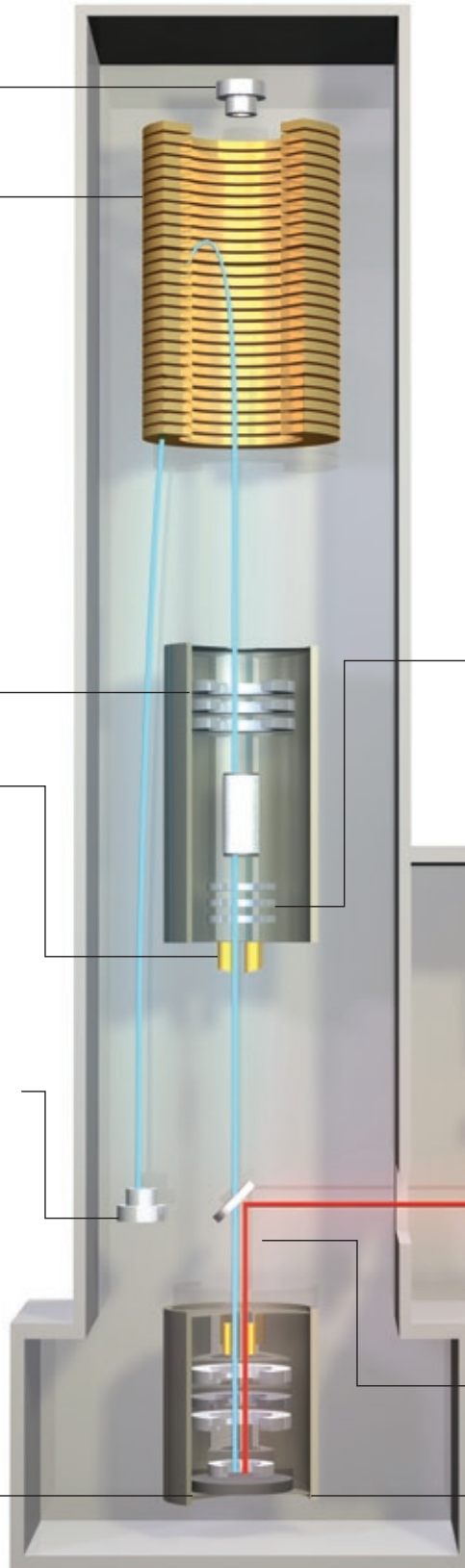
Sample Stage and Sample Plate
A unique dual-plate loading system and the use of industry-standard microtiter format sample plates simplifies operation and maximizes throughput.



OptiBeam™ On-axis Laser

Unique on-axis laser irradiation increases sensitivity in both MS and MS/MS modes.

Source 1 Region





ProteinPilot™ Software

Superior results for non-experts and experts alike

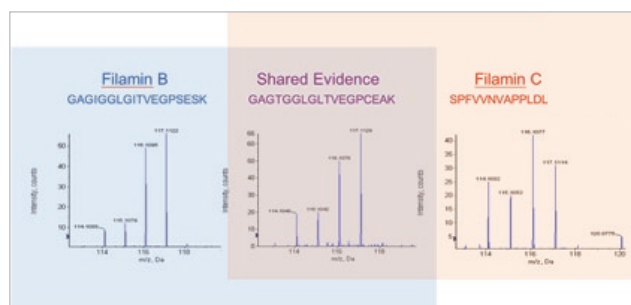
ProteinPilot™ software is “the most versatile proteomics software tool on the market” and unlike any other search engine you have used before. With the advanced Paragon™ Algorithm for database searching, the only prerequisite is knowledge of the sample. And the Pro Group™ Algorithm converts the data into biologically relevant results that conform to publishing guidelines.

Search for Everything

With the Paragon™ Algorithm over 100 post-translational modifications, up to 45 work-up modifications, and all amino acid substitutions (equivalent to 376) are searched “giving a much higher percentage of correctly assigned spectra” and a higher sequence coverage. All this is achieved with only a modest increase in search time and without the use of expensive cluster computing hardware.

Make Peptidomics a Reality

How many modifications do you typically search for when identifying endogenous peptides? Two? Five? Even ten? Try 549. ProteinPilot™ software enables routine searching of virtually every modification and amino acid substitution in difficult “no-enzyme” searches with little cost in additional search time that actually avoids rather than adding false positives.



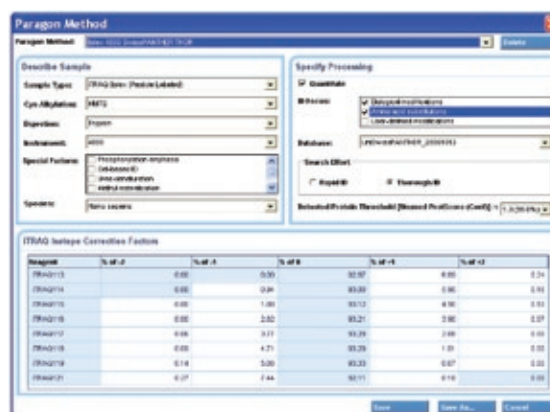
The shared evidence from Filamin peptides common to both isoforms indicates a two-fold change. The real picture, as ProteinPilot™ software reports is a five-fold change for Filamin B and no significant change for Filamin C.

Isoform-Specific Quantitation

More than ever before there is emphasis on generating proteomics results that are quantitative. With well over 50 peer-reviewed publications that use iTRAQ™ reagents for real research there has never been a better time to turn to a label-based quantitative approach. ProteinPilot™ software makes this transition painless and powerful with isoform-specific quantitation.

The Confidence to Publish

The ‘Paris Guidelines’ of 2005 give the criteria for reporting protein identifications as determined by mass spectrometry. Following these guidelines, the Pro Group™ Algorithm curates the data and reports only the proteins that can be detected with sufficient evidence.



Ideal System for Accurate Quantitative Proteomics

The 4800 *Plus* MALDI TOF/TOF™ Analyzer offers a new level of sensitivity for identifying and quantifying low abundance proteins in complex mixtures by harnessing the power of 8-plex iTRAQ™ reagents. An expanded dynamic range enables robust identification and quantitation, and powerful, easy-to-use ProteinPilot™ software means you will have the highest level of confidence in your results.

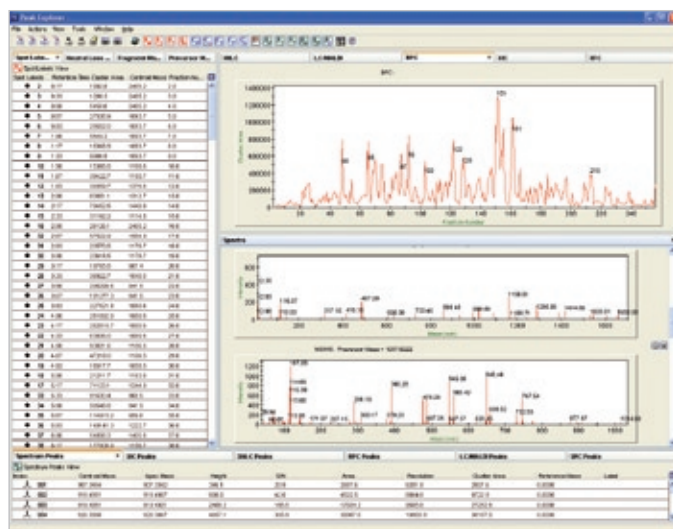


4800 *Plus* MS/MS of *VAHAVVAR peptide from Ovotransferrin showing simultaneous identification and relative quantitation of eight samples labeled with iTRAQ™ reagents.

Optimized for LC MALDI

The 4800 *Plus* system offers complete support—as well as fast, simple setup and configuration—for LC MALDI. By decoupling the mass spectral analysis from the chromatography separations, you can perform comprehensive MS and MS/MS analysis without the time constraints of LC.

- Peak Explorer™ software lets you choose how you wish to view your LC/MS data, including advanced chromatogram and peak list support.
- Unique acquisition tools automatically select precursors at the maximum point of the peak's elution profile for optimum MS/MS sensitivity.
- Remote bidirectional access triggers results-dependent analysis for targeted MS/MS selection and confident protein identification.
- New industry-standard microtiter format MALDI plates allow multiple LC separations to be deposited on a single plate



Peak Explorer™ software allows the LC run to be viewed in a conventional LC/MS format. Advanced peak list sorting and a heat-map view allow the user to create a 3D map of the entire LC MALDI chromatogram.



Explore the next generation of TOF/TOF™ optics technology today

If your research is focused on protein discovery or protein-based biomarkers of disease, the Applied Biosystems/MDS SCIEX 4800 *Plus* MALDI TOF/TOF™ Analyzer is your smartest, most direct path to confident protein identification and quantitation. To learn more, call the Applied Biosystems sales office nearest you, or visit www.appliedbiosystems.com/4800plus

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