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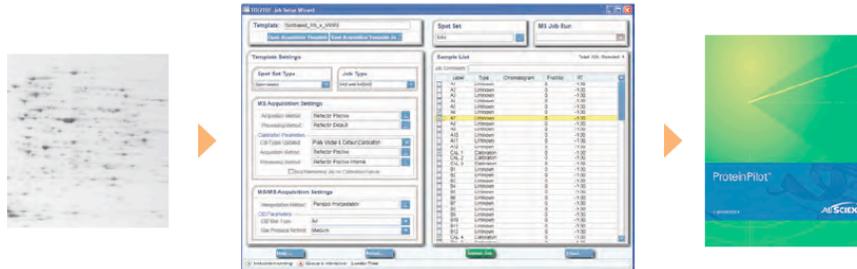
AB SCIEX TOF/TOF™ 4800 PLUS SYSTEM



It's just what you expect from the industry leader. The AB SCIEX 4800 *Plus* MALDI TOF/TOF™ Analyzer has the highest sensitivity available in MS and MS/MS modes and high resolution precursor selection. It's the most cost-effective, high-performance MALDI platform for gel spot analysis, protein biomarker discovery and MALDI mass spectrometry imaging. The perfect combination of performance and flexibility for any multi-user core laboratory.

Flexible Protein Discovery EasyAccess™ protein identification wizard

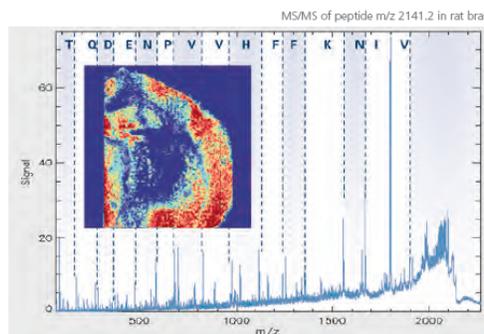
The 4800 system features a simplified workflow for fast, definitive protein identification—ideal for multi-user environments and gel spot analysis. The EasyAccess™ Wizard simplifies the selection of parameters for acquisition, and ProteinPilot™ Software makes it easy for non-experts to achieve expert results. The superior QuanTIS™ selection of precursor ions prior to fragmentation provides clean, database-searchable MS/MS spectra for the unambiguous identification of peptides and proteins.



Simplified workflows and unmatched peptide and protein coverage make the TOF/TOF™ 4800 Plus System ideal for protein identification – even in multi-user labs.

Highest sensitivity for MALDI mass spectrometry imaging

The 4800 system is the most sensitive and most flexible platform for MALDI mass spectrometry imaging (MSI). The system provides high-sensitivity MS and MS/MS data on small molecules as well as peptides and proteins, in any type of tissue.



The TOF/TOF™ 4800 system provides the highest sensitivity for MSI imaging, plus increased robustness to maximize productivity.

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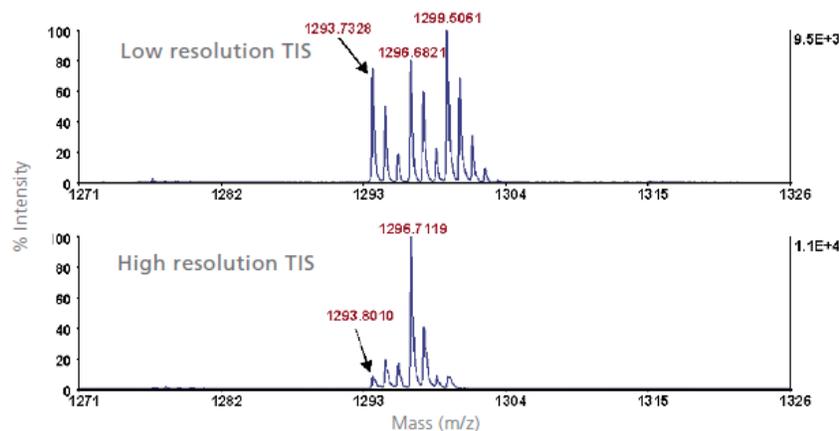
Industry-leading TOF/TOF System technology – from the company that invented it

Impressive MS and MS/MS Sensitivity

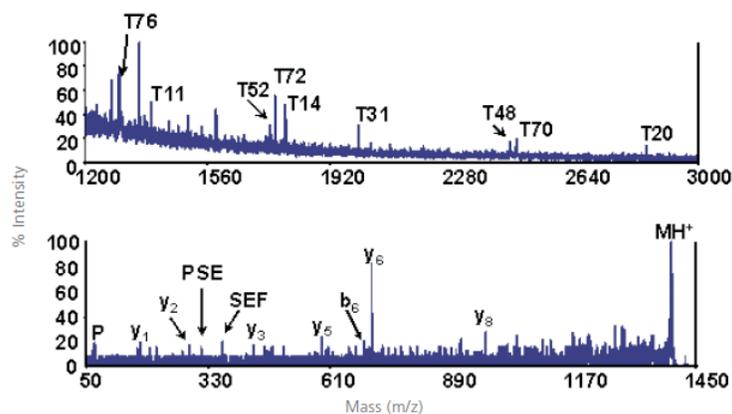
The 4800 Plus MALDI TOF/TOF Analyzer delivers unmatched sensitivity in both MS and MS/MS modes. This not only lets you see the ions of interest at a lower level than ever before; it means fewer laser shots are required to produce high quality spectra and faster analysis time. Higher sensitivity and fewer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

Enhanced Precursor Ion Selection

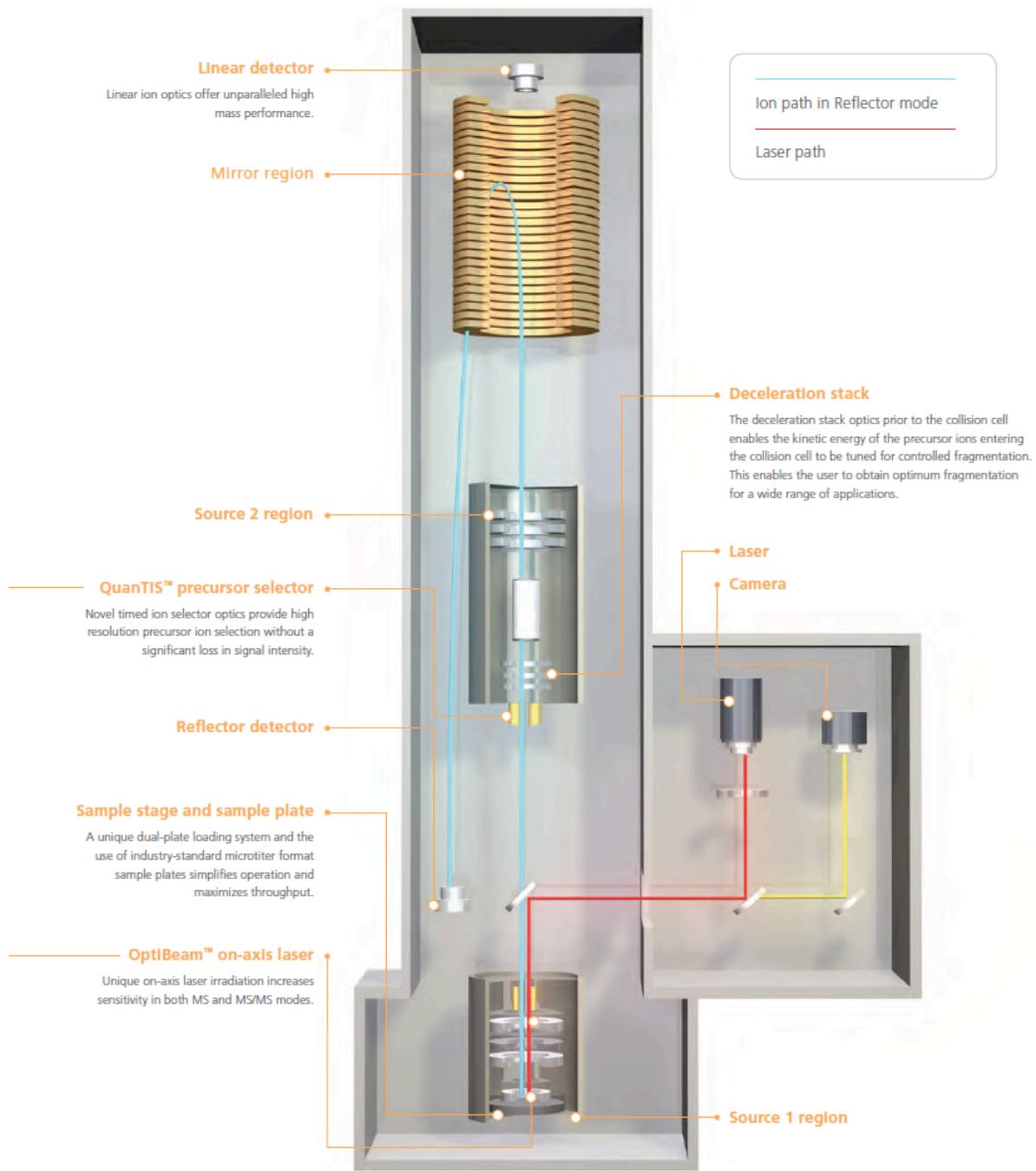
Advanced QuantIS™ precursor selector technology offers high resolution precursor ion selection with no significant loss in sensitivity. Only the precursor of interest is transmitted, and the corresponding MS/MS spectra are not complicated by fragments from adjacent peptides.



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.



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



One Touch Productivity

Powerful, easy-to-use software helps ensure that you will get meaningful results, not just data. Designed for efficiency and throughput, our software maximizes the speed and sensitivity of the 4800 system for unmatched levels of productivity and performance.

Protein identification

ProteinPilot™ Software streamlines protein identification and quantitation, allowing non-experts to obtain confident protein identifications and accurate protein quantitation. The software combines the industry-standard Mascot search engine from Matrix Science and the revolutionary new Paragon™ Algorithm with the industry-leading Pro Group™ Algorithm. The software searches for hundreds of biological and other modifications and can distinguish protein isoforms.

ProteinPilot™ Software is further optimized with improved quantitation algorithms for isobaric tagging reagents, fully integrated false discovery rate analysis, and new support for gel-based workflows. The software also extends speed and scalability, with hardware support for up to 8-core processing and 64-bit OS. ProteinPilot™ Software enables generic input for non-AB SCIEX instruments via .mgf format, allowing you to use ProteinPilot™ Software for all mass spectrometry instruments in your lab.

Tissue imaging

Designed for ease of use, TissueView™ Software displays the spatial location and intensity of proteins and small-molecule compounds in all tissue types. The software provides a seamless link between optical images, MS images, and MS and MS/MS spectra. TissueView™ Software incorporates critical features such as co-registration of images, calculation of areas, creation of multiple and layered overlays, and 3D viewing.

Carbohydrate analysis

SimGlycan® Software (a product of PREMIER Biosoft International) predicts the structure of a glycan from the MS/MS data acquired by AB SCIEX mass spectrometers, to facilitate the study of glycosylation and post-translational modifications. The software matches glycan MS/MS data with its own database of theoretical fragmentation spectra of over 8,000 glycans, using a proprietary ranking and scoring algorithm. The database can be searched using ID, sequence, composition, or mass.

Polymer analysis

Sierra Analytics Polymerix™ Software provides sophisticated tools for homopolymer composition analysis and deconvolution of homopolymer mixtures. It calculates complete

assignments of spectral features to individual series components and presents these results in complementary graphical and tabular forms. The software can import mass spectra file formats from the Data Explorer Analysis Software, and supports data from all AB SCIEX MALDI TOF and TOF/TOF™ platforms.

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.



*You invest in our technology.
We invest in your success.*

As the world leader in mass spectrometry, AB SCIEX solutions are backed by the industry's most extensive service and support organization. With a network of service professionals, experienced compliance specialists, and over 150 PhD application scientists worldwide, we are dedicated to supporting your technical needs and helping you get the most out of your AB SCIEX systems.



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