

DISCOVERY PROTEOMICS



Biomarker & Omics solutions

FOR DISCOVERY PROTEOMICS



Unraveling the complexity of the proteome in a cell or organism makes protein discovery research challenging. AB SCIEX has a comprehensive portfolio of cutting edge solutions that address that challenge. Our instrumentation, software, reagents, and workflows enable you to dig deeper into the proteome to identify low abundant proteins and convert complex data into biologically relevant results.

Starting with the right tools

The AB SCIEX TOF/TOF™ 5800 System combines high-sensitivity and ultimate flexibility with MALDI ease of use. The AB SCIEX TripleTOF™ 5600 System delivers uncompromising speed, sensitivity and resolution for more high-quality protein identifications than ever before. Together our solutions deliver it all with powerful, intuitive software.



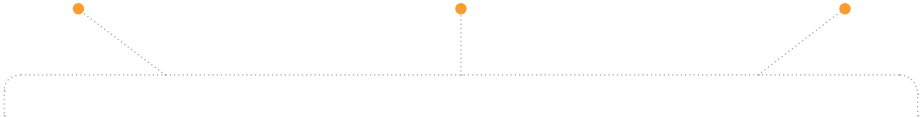
Eksigent cHiPLC™-nanoflex System



Eksigent nanoLC-Ultra™ System



AB SCIEX TripleTOF™ 5600 System



ProteinPilot™ Software



MarkerView™ Software



Eksigent nanoLC™-MALDI spotting system featuring the ekspot™ spotter

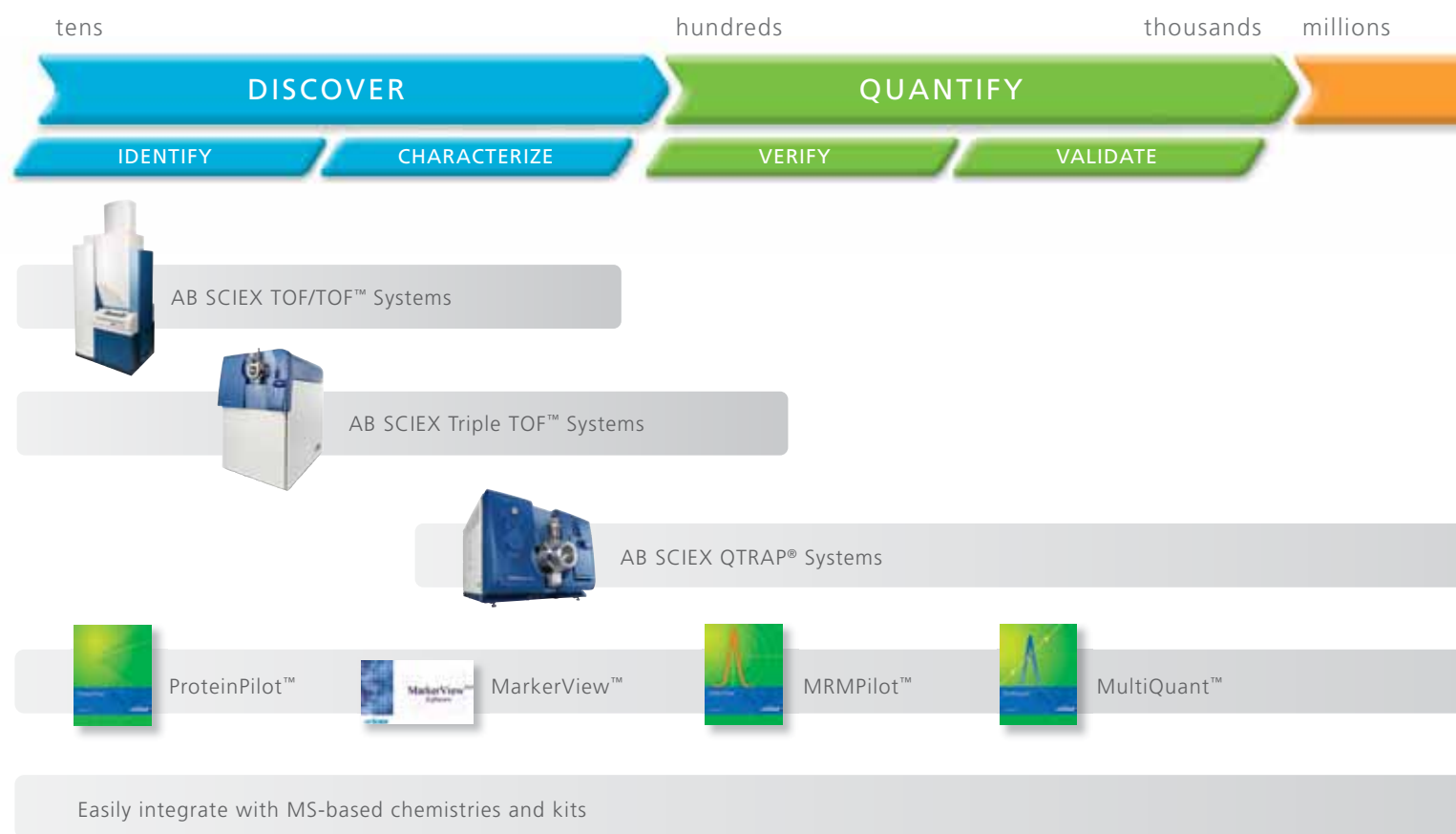


AB SCIEX TOF/TOF™ 5800 System

The protein research pipeline

Protein research is a continuous pipeline. Typically beginning with a small number of samples, hypotheses are tested and key proteins are identified and characterized. These proteins can then be verified and validated in greater numbers of samples to account for biological variation. Finally, assays are developed for routine detection of the protein.

Protein research pipeline



samples

ASSAY

HARDWARE

SOFTWARE

REAGENTS

It all starts with discovery

Powerful hardware solutions

Establish the foundation for high-quality protein discovery with the world-class performance and walk-up usability of our TripleTOF™ 5600 and TOF/TOF™ 5800 systems with Eksigent LC technologies.

Timesaving software

Identify and quantify proteins of interest, as well as their biologically relevant isoforms and PTM's with ProteinPilot™ Software.

Label-free discovery

Quickly uncover statistically interesting peptides with the powerful visualization capabilities of MarkerView™ Software.

Revealing reagents

Highlight proteins of interest in even the most complex samples with multiplexed protein discovery and expression analysis enabled by the innovative iTRAQ® reagents.

Expanded protein discovery capabilities

The AB SCIEX TOF/TOF™ 5800 System

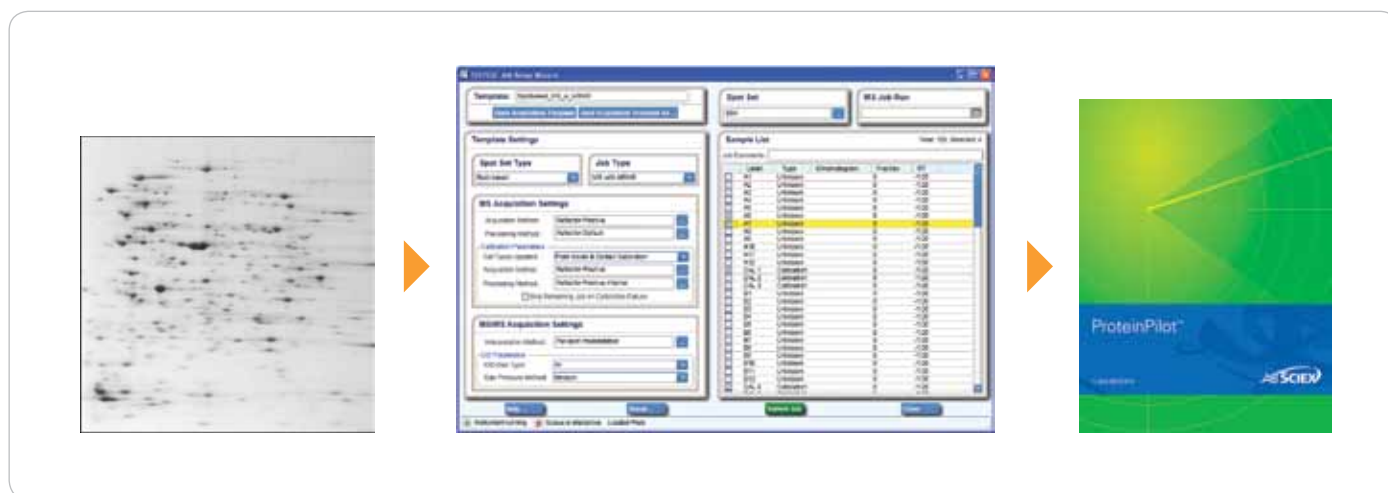
The TOF/TOF™ 5800 System is the fastest, most sensitive MALDI platform available for protein identification—from fast, automated analysis of 1D and 2D gel spots to in-depth identification and expression analysis of complex samples.

The TOF/TOF™ 5800 System features a simplified workflow for fast, definitive protein identification that is ideal for multi-user environments and gel spot analysis

- Variable rate 1000 Hz laser provides fast acquisition rates
- Self-cleaning MALDI source increases instrument uptime
- The DynamicExit™ Algorithm ensures highest MS/MS data quality through real-time spectral monitoring
- Superior QuantIS™ precursor ion selection prior to fragmentation provides clean, database-searchable MS/MS spectra and unambiguous identification of peptides and proteins.

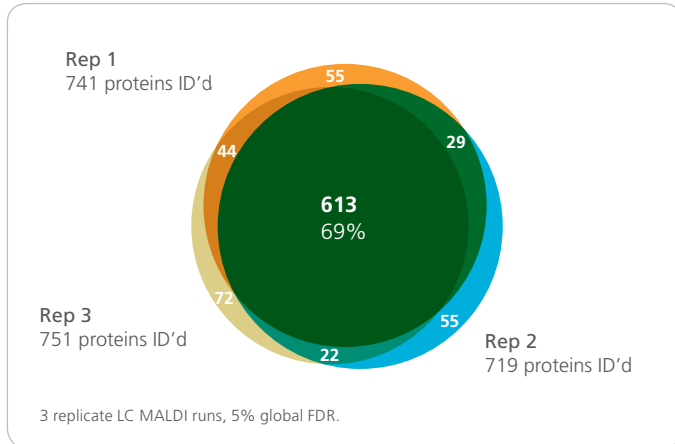


Routine gel spot analysis

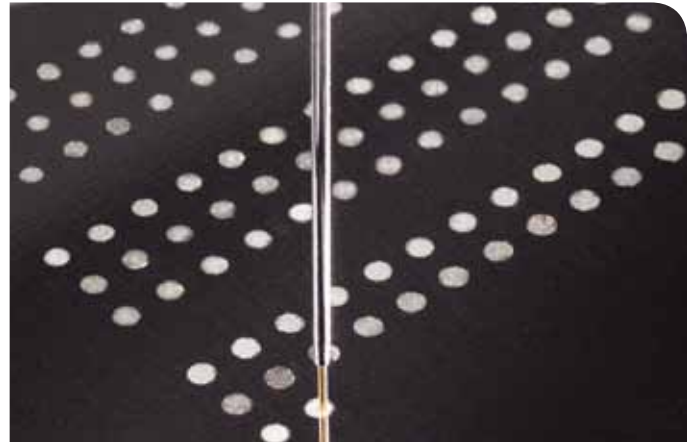


In depth identification of 1D and 2D gel spots is made fast and routine using the EasyAccess™ Wizard and ProteinPilot™ Software.

Greater depth of coverage using the LC MALDI workflow



The path to greater productivity: Innovative technology and intelligent design combine to bring new levels of efficiency and reproducibility to the LC MALDI workflow.

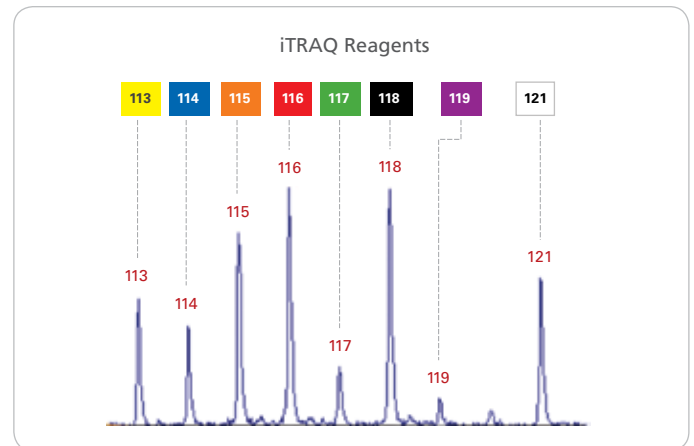


Maximum depth of coverage: The LC MALDI workflow using the Eksigent nanoLC™-MALDI spotting system and the ekspot™ spotter maximizes depth of peptide coverage by separating mass analysis from the time constraints of LC.

Compatible with industry standard labeling chemistries

Compare and quantitate protein expression changes across up to eight different biological samples in a single run with iTRAQ® reagents.

- Improve protein coverage for higher ID confidence and more accurate quantitation with amine-specific tagging of all peptides.
- Study biological fluids, tissues, and cells from any species in addition to native non-tryptic peptides in body fluids such as serum and plasma.
- Use the same workflow for 2D LC fractionation strategies.
- Solutions that fit your analytical needs: AB SCIEX mass spectrometers and ProteinPilot™ Software are optimized for iTRAQ® reagents, Cleavable ICAT® reagents and SILAC chemistry.



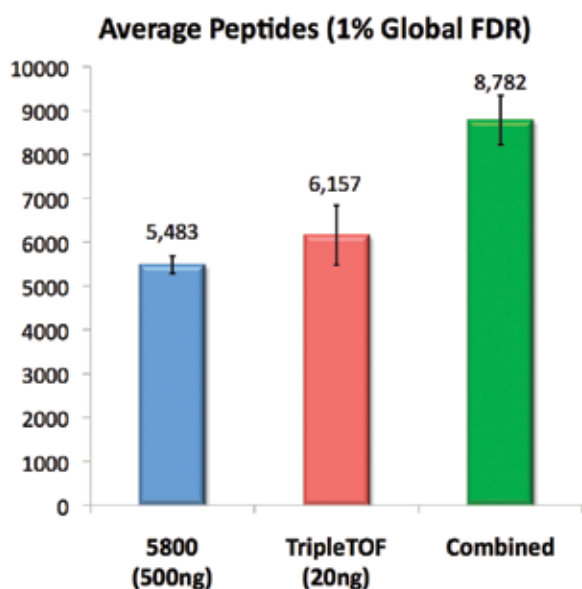
Documented performance: The breadth of publications citing the use of iTRAQ® reagents is a testament to their power.

In-depth discovery without compromise

The AB SCIEX TripleTOF™ 5600 System

The sensitivity of the TripleTOF™ 5600 System enables a new level of information-dependent acquisition (IDA) speed—and identifies a higher number of high-confidence proteins.

- Identify: Acquire up to 50 MS/MS spectra per second using SmartSpeed™ Acquisition without sacrificing resolution, mass accuracy, or dynamic range.
- Profile: Perform quant and qual in a single run using high-resolution MS with fast MS/MS confirmation.
- Quantify: Target subsets of previously detected peptides and generate initial verification data with high resolution MRM (MRM^{HR}).



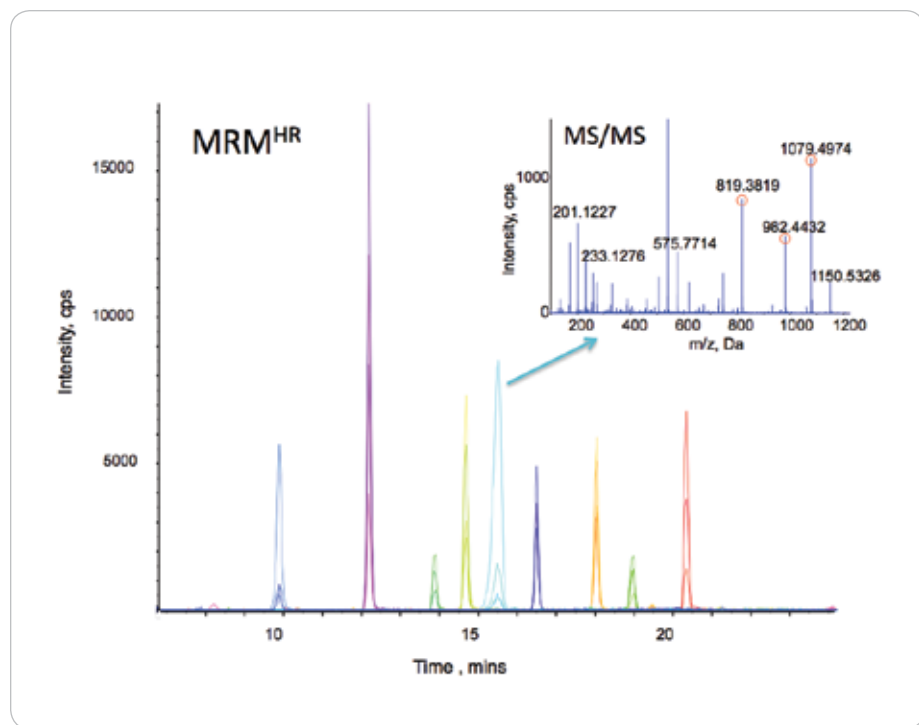
The speed and sensitivity of the TripleTOF™ 5600 System provides equivalent peptide identifications to an LC MALDI run on the TOF/TOF™ 5800 System but with 25 times less sample (E.coli digest). However, due to the complementarity of MALDI and electrospray, over 40% more peptides are identified using both techniques – and they can be processed together in ProteinPilot™ Software.

The NanoLC-Ultra—world-leading nano-chromatography

The NanoLC-Ultra uses split-less, nanoscale Microfluidic Flow Control (MFC) technology to achieve fast flow measurement in combination with automatic feedback to a regulated pressure source. As a result, the system generates accurate and reproducible flow rates with a resolution better than 1 nL/min and retention time reproducibility of less than 0.5% RSD. A maximum pressure of 10,000 psi enables the use of longer columns—or columns packed with smaller particles—for the analysis of highly complex proteomics samples.

The cHiPLC-nanoflex System

The cHiPLC-nanoflex System is an extremely simple and flexible solution for highly reproducible chromatography with chip to chip reproducibility of less than 2% for standardizing your workflows. The patented chip-to-world connection provides the lowest dead-volume, leak-free connections every time and maintains the highest data quality.



The high resolution at unparalleled speed of the TripleTOF™ 5600 System enables MRM-like quantification at up to 30,000 resolution. This MRM^{HR} provides full scan MS/MS data to allow extraction and quantification using any combination of fragment ions.

One touch productivity

ProteinPilot™ Software

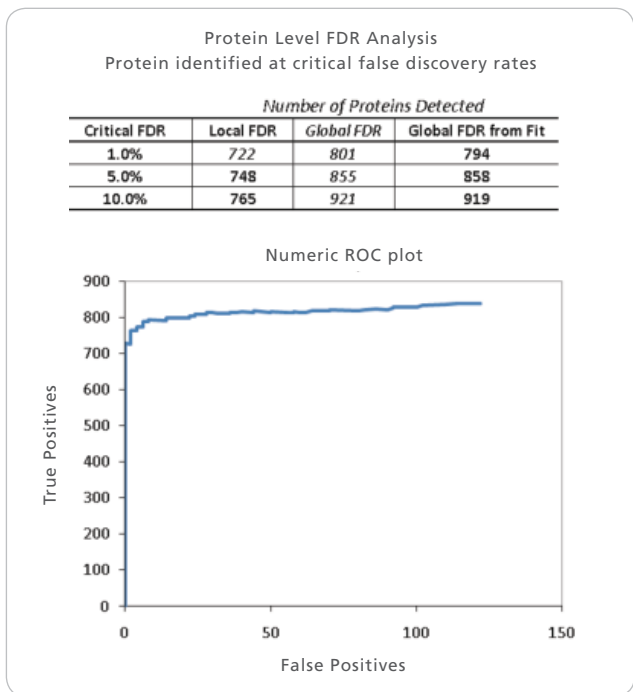
ProteinPilot™ Software sets a new standard for high-quality protein identification and biomarker discovery by enabling all users, regardless of experience to obtain reliable, understandable results.

- Get more peptide identifications in your samples using the powerful Paragon™ Algorithm.
- Report reliable, defensible protein identification results with industry leading Pro Group™ Algorithm for protein inference analysis and built-in False Discovery Rate (FDR) calculations.



Protein Group	Protein Name	Accession	Length	Score	Significance	Protein Inference	Score	Protein ID
1.0	1.0	Q1-01-01	Q1-01-01	Q1-01-01	Q1-01-01	Q1-01-01	Q1-01-01	Q1-01-01
2.0	2.0	Q2-02-02	Q2-02-02	Q2-02-02	Q2-02-02	Q2-02-02	Q2-02-02	Q2-02-02
3.0	3.0	Q3-03-03	Q3-03-03	Q3-03-03	Q3-03-03	Q3-03-03	Q3-03-03	Q3-03-03
4.0	4.0	Q4-04-04	Q4-04-04	Q4-04-04	Q4-04-04	Q4-04-04	Q4-04-04	Q4-04-04
5.0	5.0	Q5-05-05	Q5-05-05	Q5-05-05	Q5-05-05	Q5-05-05	Q5-05-05	Q5-05-05
6.0	6.0	Q6-06-06	Q6-06-06	Q6-06-06	Q6-06-06	Q6-06-06	Q6-06-06	Q6-06-06
7.0	7.0	Q7-07-07	Q7-07-07	Q7-07-07	Q7-07-07	Q7-07-07	Q7-07-07	Q7-07-07
8.0	8.0	Q8-08-08	Q8-08-08	Q8-08-08	Q8-08-08	Q8-08-08	Q8-08-08	Q8-08-08
9.0	9.0	Q9-09-09	Q9-09-09	Q9-09-09	Q9-09-09	Q9-09-09	Q9-09-09	Q9-09-09
10.0	10.0	Q10-10-10	Q10-10-10	Q10-10-10	Q10-10-10	Q10-10-10	Q10-10-10	Q10-10-10

A faster easier way to high quality results. Enter the sample information and experimental goals and ProteinPilot™ Software will do all the hard work. Results are shown in an easy to understand interface with industry-standard confidence metrics.



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.

AB SCIEX service professionals are recognized as the most highly qualified in the industry. They are certified on our instrument platforms through a rigorous 4-step certification program, with re-certification occurring every two years. This award-winning program helps to ensure that you receive the most efficient, highest-quality, and most up-to-date service available for AB SCIEX products and technology. Choose from flexible service plans and a variety of services for the right level of support for your laboratory's needs and budget.

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Whether you access our service and support team by phone, email, on-site visits, or through our innovative remote monitoring technology, you can be confident that the AB SCIEX organization will be there for you.

For more information, visit www.absciex.com

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Publication number 0041710-02



Headquarters

110 Marsh Drive | Foster City CA 94404 USA
Phone 650-627-2600
www.absciex.com

International Sales

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