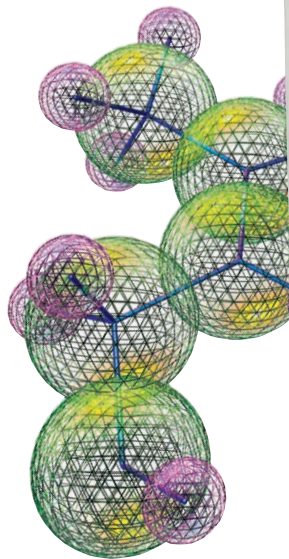


# QSTAR<sup>®</sup> Elite

Hybrid LC/MS/MS System

More performance, more reliability, more answers



# More is better—and the QSTAR® Elite LC/MS/MS system has more to offer.

## More Coverage in Less Time

Whether you are discovering or identifying protein or metabolite biomarkers, the QSTAR Elite system gives you more—up to five times more peptide, protein, and metabolite coverage—more reliably. This increase in coverage is the direct result of technology innovations in the system hardware, electronics, and software working synergistically to provide unsurpassed LC/MS/MS performance and reliability.

## More Performance

The QSTAR Elite system takes QqTOF performance to a new level by providing higher mass resolution, increased mass accuracy, greater sensitivity, faster MS/MS, and increased linear dynamic range. Along with improved workflows and more intelligent data acquisition, these performance enhancements help to ensure that you get more meaningful information from every experiment.

## More Reliability

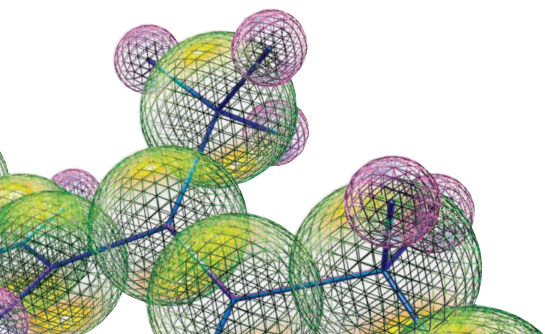
The QSTAR Elite system makes it easier to maintain day-to-day reliability at peak performance levels. Improved turbomolecular pumps, robust new Analyst® QS 2.0 software, stable ion sources, and the exceptional reproducibility of Tempo™ LC systems, combine to give you higher productivity, higher throughput, and more confidence in your results.

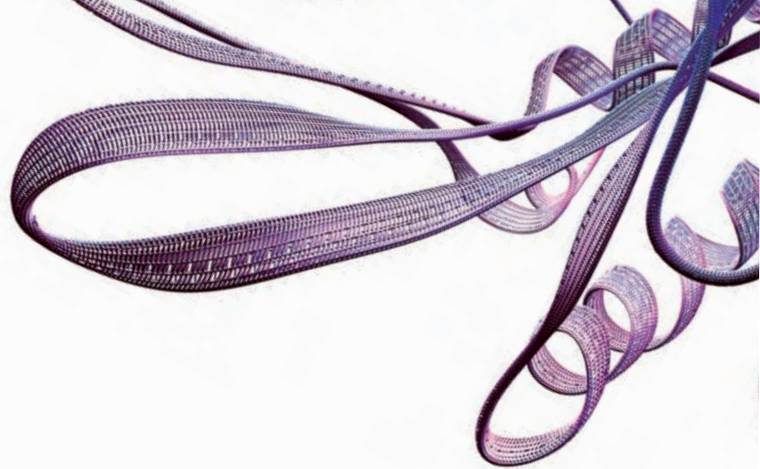
## More Answers

Robust new Analyst QS 2.0 software speeds MS/MS acquisition and intelligently selects precursor ions for MS/MS with data optimization features such as MDt™ IDA software for mass defect triggered information dependent acquisition, Dynamic Background Subtraction (DBS), Smart CE, and Smart Exit. Powerful searching, analysis, and visualization capabilities in ProteinPilot™ 1.0 software and MarkerView™ 1.1 software enhance the quality of your results for proteomics, metabolomics and metabolite identification experiments.

## More Flexibility

Interchangeable API and oMALDI™ ion sources, along with metabolite- and protein-specific biomarker workflows, make the QSTAR Elite system the ideal platform for a wide range of small molecule and proteomics applications. The system provides uncompromised performance for metabolites, drug candidates, de novo sequencing of peptides, post translational modification analysis, and the analysis of noncovalent complexes.





### Optimized Workflows

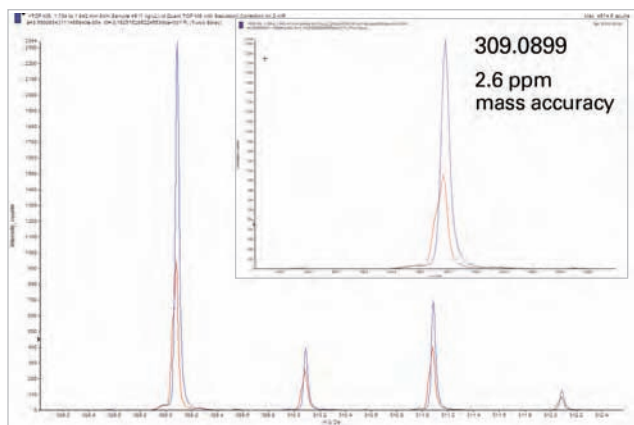
QSTAR® Elite system configurations are optimized for experimental workflows that deliver fast, high-quality answers without compromising other performance parameters. Combine the QSTAR Elite system with a Tempo™ LC system, high-speed data acquisition, and powerful software, and you have a total system solution that can discover up to 5x more proteins and metabolites, with typical increases near 3x.

### Higher Sensitivity

Sensitivity is essential for confident identification of proteins and metabolites in biological samples. The QSTAR Elite system's Razor™ detector, coupled with high-speed intelligent data collection, increase protein and metabolite coverage, and enable you to identify potential markers that were previously indistinguishable from noise.

### Higher Resolution and Mass Accuracy

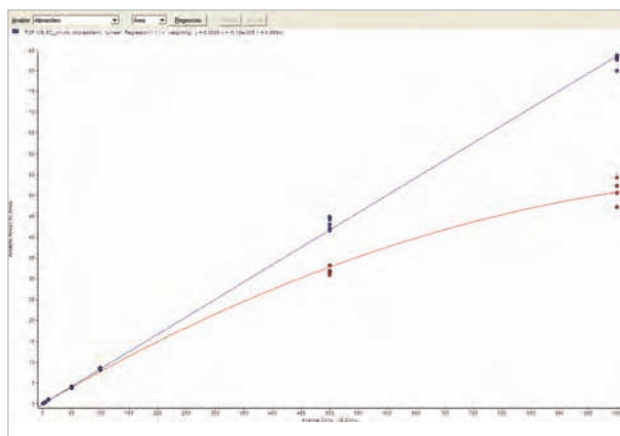
The exceptional resolution and sub-3 ppm mass accuracy of the QSTAR Elite system is achieved across a broad mass range with no low-mass cut-off. Better data improves the quality of search results and allows the user to clearly differentiate closely related metabolites or peptides.



QSTAR® Elite system (blue trace) maintains high resolution across a broad dynamic range, maintaining mass accuracy and isotopic patterns. Shown is alprazolam, [H+] exact mass=309.0907, at the point of detector saturation.

### Improved Quantitation

The QSTAR Elite system is optimized for quantitation with an increased dynamic range, making it easier to get meaningful information from peptides or metabolites that are present at a wide range of concentrations. With a dynamic range of up to four orders of magnitude in full scan mode—without signal reduction—the QSTAR Elite system accurately detects and quantifies up- and down-regulated proteins and small molecules in complex biological samples.



With a linear dynamic range of up to four orders of magnitude (in full scan mode), the QSTAR® Elite system (blue trace) combines high performance quantitation with high mass accuracy and resolution.

### Exceptional Usability

Reliability and usability add up to productivity. From the LC front-end to final reporting, the QSTAR Elite system helps non-MS experts achieve expert results—and keep reliable results coming day-to-day, week-to-week.

# Expect more.

Total system solutions provide more qualitative and quantitative information

## More Intelligent Software

Powerful, application-specific software tools provide you with efficient system control, data collection, and analysis. By combining robust reliability with ease-of-use, these software tools enable workflows that quickly uncover high-quality biomarker candidates.

### Analyst® QS 2.0 Software— A Solid Foundation for Data Collection

The new Analyst QS 2.0 software includes a set of tools that increases the speed and efficiency of data collection and processing, while also providing a stable platform for system control.

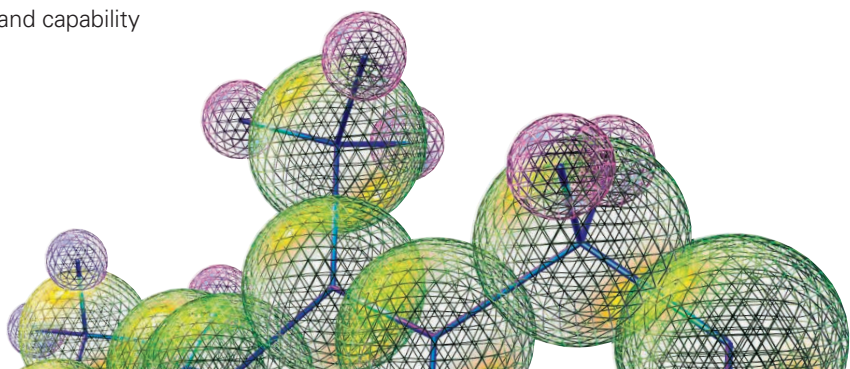
- Dynamic Background Subtraction brings added intelligence to the selection of precursor ions for MS/MS by selecting only those ions whose intensity is changing at the fastest rate.
- MDt™ IDA software focuses on compounds most likely to be metabolites by selecting only those ions for MS/MS that have a mass defect within a user-specified range.
- Smart CE allows the instrument to 'search' for the optimum collision energy based on MS/MS ion intensity.
- Smart Exit increases the total number of spectra acquired by moving to the next MS/MS experiment once sufficient fragmentation data has been collected for confident identification, minimizing wasted acquisition time.
- The Formula Finder simplifies compound identification using molecular weight, isotopic pattern and intelligent chemical logic.
- 21 CFR Part 11 Compliance tools, enhanced reporting and quantitation capabilities, and network acquisition and administration security features all expand capability beyond conventional control software.

## ProteinPilot™ Software Enables Protein ID and Expression Analysis Workflows

ProteinPilot software provides a new level of ease-of-use that allows novice users to get expert results without extensive bioinformatics training. It enables chemistry-based quantitative workflows such as iTRAQ™ and SILAC™ reagent workflows and incorporates both the revolutionary new Paragon™ search algorithm and the industry standard Mascot® search engine in a simple, yet powerful package. The innovative Pro Group™ algorithm for protein results compilation automatically groups splice variants and closely related proteins, and intelligently analyzes the peptides found to determine the true positive protein identifications for ultimate confidence in your results. Also, ProteinPilot software has been designed to conform with protein guidelines published by *Molecular and Cellular Proteomics*, so you can be confident in the results that you publish.

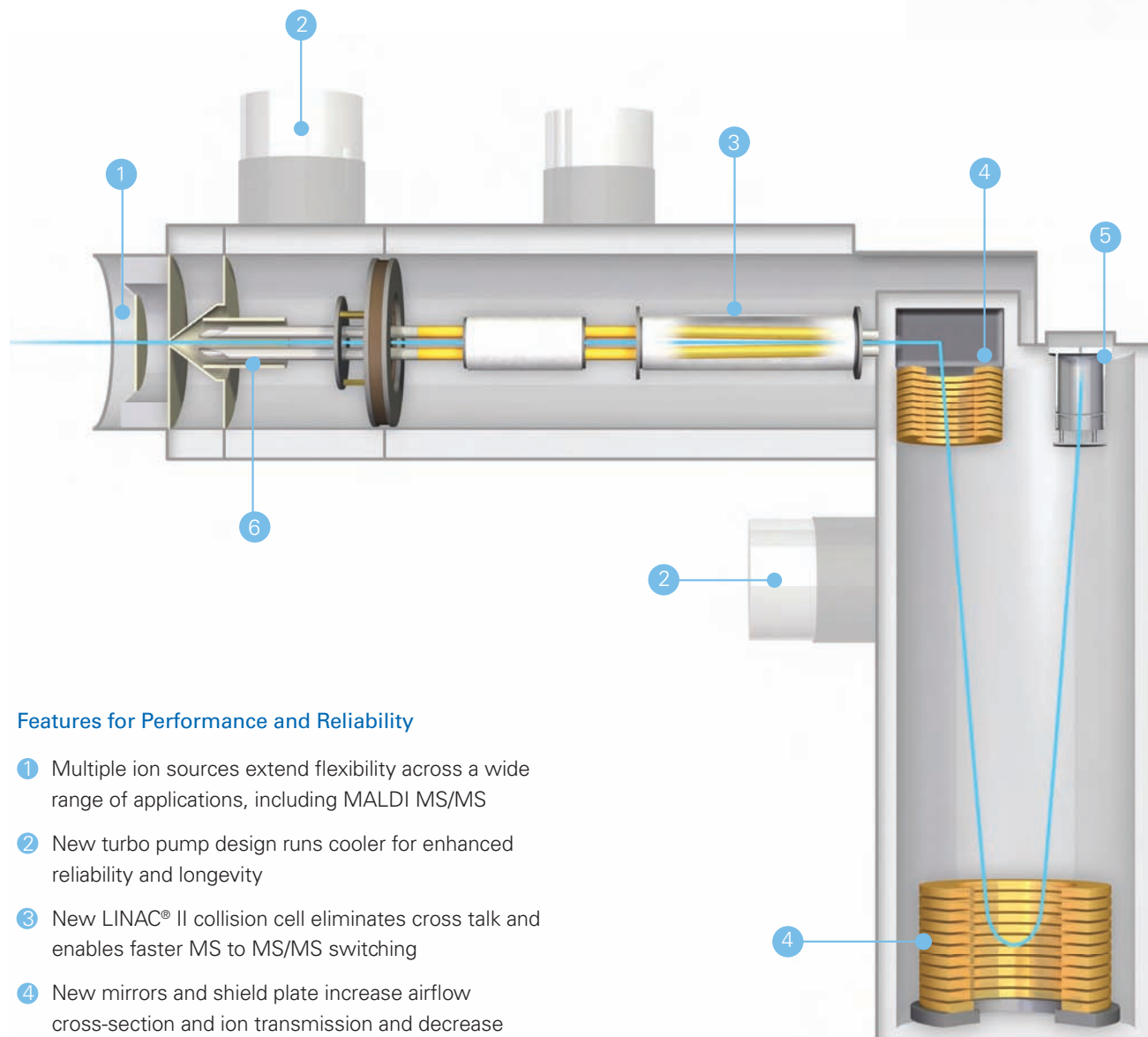
## MarkerView™ 1.1 Metabolomics and Protein Biomarker Profiling Software

MarkerView 1.1 software is the next-generation biomarker software tool that searches for masses and aligns data across multiple samples to find distinctive biomarkers using supervised and unsupervised multivariate statistical analysis tools such as T-test, Principal Components Analysis (PCA) and Principal Components Analysis-Discriminant Analysis (PCA-DA). The software can then link back to raw MS and/or MS/MS data as well as extracted ion chromatograms, and create reports on potential biomarkers. Additionally, MarkerView 1.1 software is able to create inclusion lists of potential biomarkers to target for MS/MS in subsequent IDA experiments.



# More innovation.

New technologies that drive performance



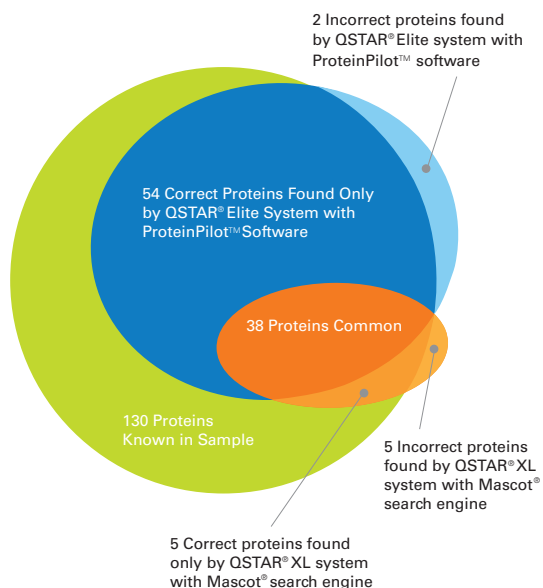
## Features for Performance and Reliability

- 1 Multiple ion sources extend flexibility across a wide range of applications, including MALDI MS/MS
- 2 New turbo pump design runs cooler for enhanced reliability and longevity
- 3 New LINAC® II collision cell eliminates cross talk and enables faster MS to MS/MS switching
- 4 New mirrors and shield plate increase airflow cross-section and ion transmission and decrease pump-down time
- 5 New Razor™ detector improves resolution, mass accuracy, robustness, linear dynamic range and ion transmission
- 6 Optional IonCooler™ Guide allows collisional cooling of large, noncovalently-bound complexes, significantly increasing the sensitivity for complexes of 0.5 MDa and above.

# Identify more proteins, discover more biomarker candidates.

## More Coverage Means More Answers and More Confidence in Your Results

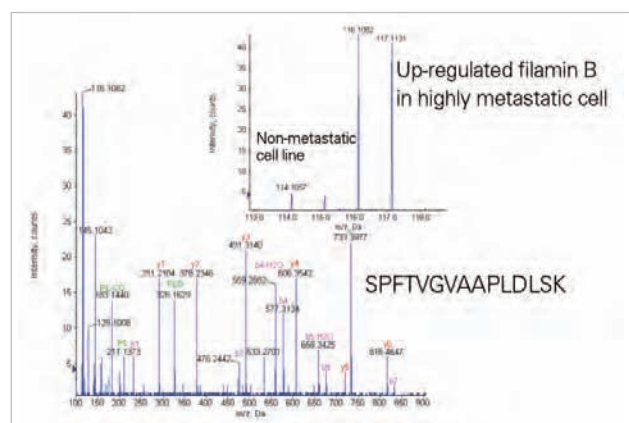
New levels of sensitivity, linear dynamic range, and speed of acquisition, combined with advanced software tools, make the QSTAR® Elite system an ideal solution for protein identification and protein biomarker discovery applications. Configured with a Tempo™ nano MDLC system and ProteinPilot™ software, featuring the novel Paragon™ search algorithm, the QSTAR® Elite system will identify more proteins in less time, increasing peptide and protein coverage, providing better protein characterization, and high confidence quantitative statistics.



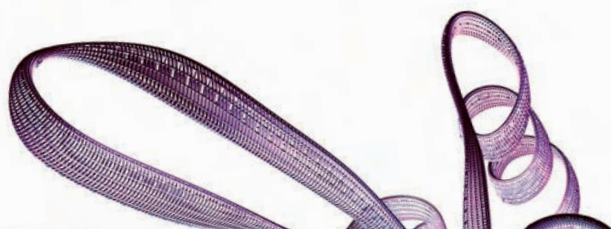
Using a well characterized complex protein digest (green circle), protein identification results from the previous QSTAR® XL system (Mascot® search engine, orange circle) were compared with the new QSTAR® Elite system using ProteinPilot™ software (blue circle). Nearly double the number of correct proteins were found in half the LC acquisition time at a minimal false positive rate. This increase was due to a 3-fold increase in the number of peptides found at 95% confidence for these proteins with the QSTAR® Elite system.

Intelligent data acquisition features such as Smart Exit and Smart CE, take advantage of the speed improvement and provide new levels of data acquisition efficiency and quality. With a minimum accumulation time of 140 msec, decisions about MS/MS signal-to-noise and fragmentation quality can be made on-the-fly to provide higher quality data as well as more data overall.

ProteinPilot™ software provides innovative tools for efficient protein identification and relative protein expression analysis and combines a new level of ease-of-use with the revolutionary new Paragon™ algorithm and the industry standard Mascot® search engine. The Paragon™ database search algorithm can efficiently and simultaneously consider over 150 biological modifications, genetic variants, sample preparation modifications and unexpected cleavages to identify more peptides from MS/MS data. The Pro Group™ algorithm performs a statistical analysis on the peptides found to determine the minimal set of confident protein identifications. The software makes maximum use of MS/MS spectra, while minimizing the reporting of false protein identifications that can be common with other tools. ProteinPilot software also supports automated chemistry-based biomarker discovery strategies including iTRAQ™ reagent and SILAC™ reagent workflows.



Increased peptide coverage for each protein provides better quantitation statistics for chemistry-based workflows such as iTRAQ™ reagent experiments (above) as well as improving the ability to differentiate between protein isoforms.



# Find more metabolites.

Smart, automated data collection quickly finds more metabolites

## Metabolite Identification

Finding and identifying all major and minor metabolites of a drug candidate is a significant challenge in drug discovery and development. The new QSTAR® Elite system provides major enhancements for this critical task. With increases in resolution, mass accuracy, sensitivity and linear dynamic range as well as significant advances in automated data acquisition, the QSTAR Elite system discovers, identifies and characterizes more metabolites faster with less irrelevant data being generated.

The QSTAR Elite system was used to identify the metabolites of propranolol from human urine samples, comparing the expected number of metabolites as described in the literature to the number identified using standard IDA, IDA with DBS, and a combination of both DBS and MDt™ IDA software. A summary of the results is shown in table 1.

Using standard IDA criteria, a total of 912 ions were selected for MS/MS data collection in the 17 minute chromatographic run. Of those 912 ions, only 32% of the 31 expected metabolites were targeted for MS/MS data acquisition.

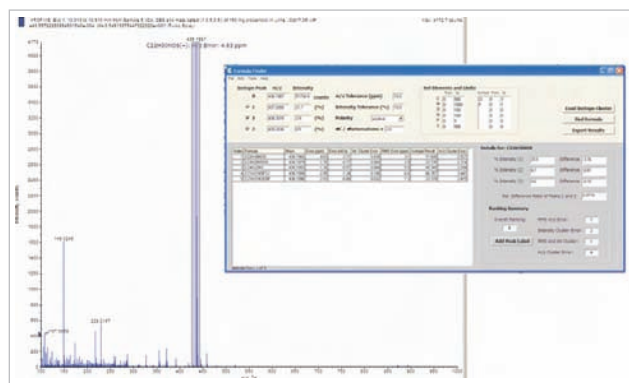
With DBS, 87% of the expected metabolites were found in the reduced set of 496 ions that had been selected for MS/MS data collection. The use of DBS filtered the data being acquired allowing for more time to be spent on relevant compounds thereby increasing the number of metabolites found.

With DBS and MDt IDA software working together, the number of metabolites identified remained at 87%, yet the number of MS/MS spectra collected was further reduced to only 288 spectra. The combination of DBS and MDt IDA software further reduced the extraneous data collected and increased the number of metabolites identified. This simplifies data processing and also permits more real-time in-depth analysis or faster HPLC separations.

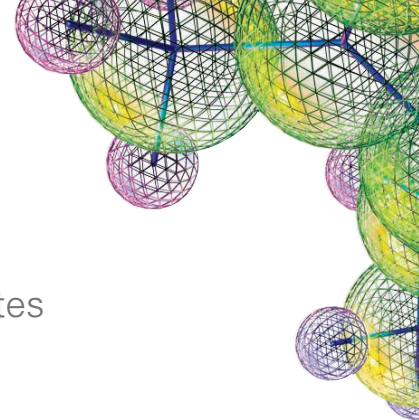
	Standard IDA	w/ DBS	w/ DBS & MDt IDA
# of ions selected	912	496	288
# of Metabolites ID'd	10	27	27

**Table 1.** Comparison of automated data collection for metabolites of propranolol. The combination of DBS and MDt IDA software significantly improves the overall efficiency of automated workflows. By greatly narrowing the search, higher quality, more relevant data are collected, yielding improved metabolite coverage and allowing additional time for more experiments.

After using DBS and MDt IDA software to find potential metabolites, the new Formula Finder adeptly identifies these potential drug metabolites as shown in figure 1. Applying the Formula Finder to the selected potential drug metabolite at mass 436.1987 resulted in only five possible elemental formulas. The number one hit is the correct chemical formula for propranolol glucuronide, one of the expected propranolol metabolites.



**Figure 1.** Formula Finder allows rapid compound identification by using compound mass, isotopic pattern and applying 'chemical sense' to minimize the list of potential elemental formulas.



# Discover more.

The QSTAR® Elite Hybrid LC/MS/MS system takes biomarker discovery to new levels of performance and productivity. Applied Biosystems/MDS SCIEX can help your laboratory reach its research goals with a single-vendor solution that combines the QSTAR Elite system with a Tempo™ LC system, powerful and efficient workflows, and expert applications support.

When you choose Applied Biosystems/MDS SCIEX as your partner, you're choosing to work with the leading developer of LC/MS/MS technologies. We are committed to remaining at the forefront of life science research by providing you with the tools you need to succeed.

## Support You Can Depend On—Whenever and Wherever You Need It

Our LC/MS/MS systems are backed by one of the world's most extensive service and support organizations staffed by professionals who are trained and dedicated to keep your system running at peak performance and productivity 24 hours a day, seven days a week.

## Maximize Instrument Uptime with Applied Biosystems BioMonitor® Service

With our BioMonitor Service, we can remotely and proactively track critical system parameters over the Internet and identify potential instrument problems before they affect your lab's efficiency. Using a combination of remote monitoring, preemptive monitoring and remote diagnostics, our award-winning BioMonitor Service is helping many of our customers achieve a significant increase in instrument uptime.

For more information about the QSTAR Elite Hybrid LC/MS/MS system, please call the sales office nearest you or visit [www.appliedbiosystems.com/QSTAR](http://www.appliedbiosystems.com/QSTAR)

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Printed in the USA, 02/2006 Publication 114BR22-01



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