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API 3000 LC/MS/MS

Unprecedented Performance: An advanced LC/MS/MS system that gives you the edge

The API 3000™ LC/MS/MS System gives you a significant edge in time-to-market with sensitivity, selectivity, and reproducibility across a wide range of applications and sample types.

- Innovative ion optics and pumping technology ensure the lowest limits of detection and quantitation, even on the most difficult matrices
- Revolutionary LINAC® collision cell technology provides fast scan times without compromising sensitivity or mass spectral quality for superior MS/MS performance
- Robust ion sources and proven Curtain Gas™ interface technology ensure reliability and uptime
- Advanced software applications, including automated method development for the routine analysis of hundreds of samples per day, deliver greater throughput
- Windows NT® platform-based Analyst® software allows you faster access to information for drug development
- Information Dependent Acquisition (IDA) enables unattended, automated MS to MS/MS acquisition, providing better structural information

Ideal for DMPK Screening

With the LINAC® collision cell, you can analyze multiple components simultaneously. Analyst® Software provides complete system control of data acquisition and post processing for the API 3000™ system. Advanced automated software applications such as Information Dependent Acquisition (IDA), Automaton, and Metabolite ID extend the functionality of the API 3000™ System for early DMPK screening in drug discovery. The system including the API 3000™ mass spectrometer, powerful Analyst® software, rugged ion sources, and fully integrated LC equipment sets the standard for dependability in the lab.

Accelerating the pace of the drug development process requires innovative technology of the highest quality. And that's exactly what the new API 3000 LC/MS/MS system from PE SCIEX, the world leader in LC/MS/MS delivers. The API 3000 gives you a significant edge in time-to-market with unmatched sensitivity, selectivity, and reproducibility while providing unrivaled performance on a wide range of demanding applications and sample types- analysis of proteins and peptides in the life sciences,

analysis of n-in-one cassette dosing experiments, and analysis of small pharmaceuticals in drug metabolism and pharmacokinetic studies. Count on the API 3000 for increased productivity, and consistent and reliable high-quality results.

- Unsurpassed sensitivity- new ion optics and pumping technology ensure the lowest limits of detection (LOD) and quantitation (LOQ) on even the most difficult matrices.
- Unparalleled MS/MS performance- revolutionary LINAC technology provides the fastest scan times without compromising sensitivity or mass spectral quality.
- Greater throughput- rapid method development for the routine analysis of hundreds of samples per day.
- Unmatched ruggedness and reliability- guaranteed by our robust source and interface technology.
- Ease of use- MassChrom and Windows NT- based TurboQuan processing software completely automate data acquisition and analysis.
- Proven PE SCIEX performance – backed by our worldwide network of service and support.
- Patented Curtain Gas technology ensures maximum uptime and productivity by protecting the interface and analyzer from contamination and degradation.

The API 3000 reaches the low limits of detection (LOD) and quantitation (LOQ). The enhanced ion optics and new pumping configuration of the API 3000 ensure maximum ion transmission into the mass spectrometer. And, the revolutionary patented LINAC high-pressure collision cell greatly enhances MS/MS performance by maximizing the transfer of ions to the detector. That's a powerful advantage in the demanding drug development environment.

- Lowest achievable LOQs-proven ion source technology, maximum ion transmission, and pulse counting detection provide optimum signal-to-noise measurements in real world analyses.
- Rapid method development- new auto-optimization software quickly maximizes instrument performance.
- Minimal sample preparation- broad dynamic range reduces the need for concentration or dilution of samples.
- The analysis of diphenhydramine by HPLC/MS/MS demonstrates the un-matched sensitivity of the new API 3000.
- Excellent linearity and wide dynamic range to accommodate diverse bioanalytical applications.

PE SCIEX's patented linearly accelerating (LINAC) high-pressure collision cell provides exceptional sensitivity and performance in all modes of MS/MS operation- including multiple reaction monitoring (MRM), neutral loss (NL), and precursor ion scan (PS) modes. This innovative technology ensures maximum transfer of ions from the interface to the detector, heightening performance.

- Quantify more compounds per analysis- LINAC allows reduced dwell times in MRM experiments without compromising sensitivity (e.g. when doing n-in-one parallel dosing experiments).
- Increase confidence in results – LINAC prevents false positives in MRM data.
- Shorten analysis times- LINAC enables faster precursor ion and neutral loss scans with excellent sensitivity and mass accuracy.
- Patented LINAC technology allows MRM dwell times to be reduced without compromising sensitivity as shown by repeated injections of diphenhydramine.
- Revolutionary LINAC technology speeds scan times without compromise.

Maximum uptime and productivity is ensured with the API 3000's patented Curtain Gas Technology, Eliminating the need for routine maintenance, Curtain Gas provides continuous operation by protecting the interface region and quadrupole analyzer from contamination. Our innovative interface design optimizes ion transfer from atmosphere to vacuum- without the need for complicated ion transfer optics that could corrupt fragile chemical compounds, such as non-covalent complexes and thermally labile species.

- Greatest uptime and reliability- patented Curtain Gas technology prevents any impurities from getting between the analyzer and your sample, ensuring minimal user intervention.
- Uncompromised sensitivity – new ion optics routinely ensure the lowest limits of detection in all biological matrices.
- Precise and accurate results- consistent performance all day.
- Maximum sample throughput – trouble-free. No daily cleaning or calibration required to maintain performance.

The API 3000 provides outstanding performance on a wide range of analytical applications- from a routine quantitative determination of drugs in the toughest biological matrices to the analysis of proteins and peptides for the life sciences. Proven quadruple technology with ultra-stable mass calibration provides maximum performance with minimal operator intervention. With the API 3000's innovative design, you get:

- Proven ion source technology- TurbolonSpray and APCI (heated nebulizer) allow for maximum performance across the widest range of flow rates and mobile phase composition.
- Simultaneous acquisition of MS and MS/MS data-state-of-the-art electronics and software allow for mixed-mode analyses.
- Minimal user intervention- precision- machined, gold-plated ceramic quadrupole rods with low thermal expansion coefficient promise ultra-stable mass calibration.
- Simplified installation and minimized operating costs- single-phase power and air-cooled, ceramic bearing turbo pumps reduce operating costs.
- Rapid method development- larger ion acceptance area allows for easy source optimization.
- The API 3000's new API interface is designed with a larger ion acceptance area.
- Proven TurbolonSpray allows for maximum performance across the widest range of flow rates and mobile phase composition.

Easy To Use Software

Our intuitive, powerful MassChrom software, developed in accordance with ISO 9001- and TickIT-certified protocols, effortlessly controls all aspects of instrument operation, data processing, and reporting. Automated mass calibration and verification facilitate easy operation, allowing even new users to generate results fast. Method development is also easier and quicker with AutoOptimize, which automatically optimizes MS/MS conditions for single or multiple analytes. Obtain maximum information from a single analysis by mixing different MS and MS/MS acquisition parameters. In addition, TurboQuan, our new processing software, available on Windows NT and Macintosh operating systems, sorts and queries the data to rapidly identify calibration standards or quality controls that have failed to meet the batch acceptance criteria.

- Rapid method development- AutoOptimize speeds sample analysis
- Fully supported- OpenMS data system enables communication with most LCs, autosamplers, and liquid handling systems.
- Saves time and samples- QuanWatch continually verifies instrument performance to protect valuable samples, 24 hours a day
- Maximum data- combine various MS and MS/MS modes of analysis for drug metabolism, post translational modification, or structural elucidation.
- Manage work flow- SQL LIMS connectivity allows seamless data transfer to LIMS systems.

Cross- platform Data Processing for Windows NT and Macintosh.

TurboQuan, the new, cross-platform quantitative data processing software from PE SCIEX, helps you convert large amounts of LC/MS/MS data into reliable, meaningful results fast. Combining the industry standard PE Nelson chromatographic peak detection algorithm with an embedded database engine, we've taken quantitative data processing to a new level of ease and performance. Sample Editor, new multi-platform software, allows you to prepare sample sequences direct from your desktop PC or Macintosh, making data acquisition easier. Upon completion of the sample batch, TurboQuan automatically processes the acquired data; moments later, all your chromatographic peaks are integrated and quantified. You get accurate, precise results in the shortest time with minimal user intervention.

- Precise and accurate integration of target compounds- made easier by PE Nelson's industry-proven, peak-finding algorithm.
- Quality control- quickly assess the accuracy and precision of your standards and quality control samples using novel summary statistics window.
- Fast identification of problem samples- TurboQuan's innovative search engine can query every aspect of your data.
- Increased flexibility- TurboQuan can quantitate all types of MS and MS/MS data.
- Customizable processing- configure the new results table to meet your specific needs.
- Managed work flow- software allows seamless data transfer to and from SQL *LIMS.

Complete Analysis Speeds Protein and Peptide Characterization.

Friendly, powerful, fast and developed by protein chemists, the optional BioToolBox software allows for easy identification and characterization of proteins and peptides. This powerful suite of software programs works with LC/MS and LC/MS/MS data to simplify the interpretation of protein and peptide mass spectral data. Automatically calculate protein or peptide molecular weight from multiply-charged ion series, search databases to identify proteins, or match peptide fragment masses against expected peptides. Data is presented in familiar formats: sequence, peptide coverage maps, molecular weights, and more. BioToolBox software lets users:

- Identify proteins in a database using intact protein masses, enzymatically-generated peptide masses, or partial amino acid sequences (sequence tags).
- Accurately determine molecular weights of proteins and peptides. Generate lists of expected peptide fragments for comparison with MS/MS data.

- Quickly identify and characterize post-translational modifications from mixed-mode data acquisition.
- Rapidly map identified sequences against original data for results comparison.



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