

API 4000™ LC/MS/MS SYSTEM



Proven
quantitation
and reliability

API 4000™ LC/MS/MS SYSTEM



High-quality quantitation

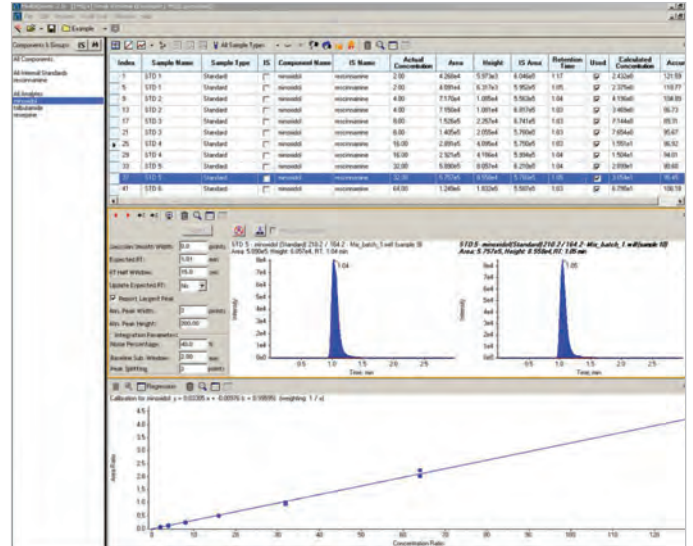
Results you can rely on

The API 4000™ LC/MS/MS System established the standard of performance, reliability, and dependability for quantitative analysis.

- Sensitive results for drug development
- Robust, high-throughput efficiency
- Low detection limits for trace analysis

Even in complex matrices

Whether you're an expert or just getting started in LC/MS/MS, the API 4000 System makes it easy to get high-quality results, with outstanding quantitation and precise identification of low abundance compounds, even in matrices such as clinical samples, pesticide/drug residues, forensic toxicology samples, environmental samples, and foods.



MultiQuant® Software: Industry-standard data review



Optimized ion path

From the advanced Turbo V™ ion source, to the reliable interface, and the patented LINAC® collision cell, the API 4000™ ion path accelerates productivity.

Plug-and-Play probes

The Turbo V™ Source

Effortless flexibility: Change quickly between APCI (atmospheric pressure chemical ionization) and TurbolonSpray® probes.

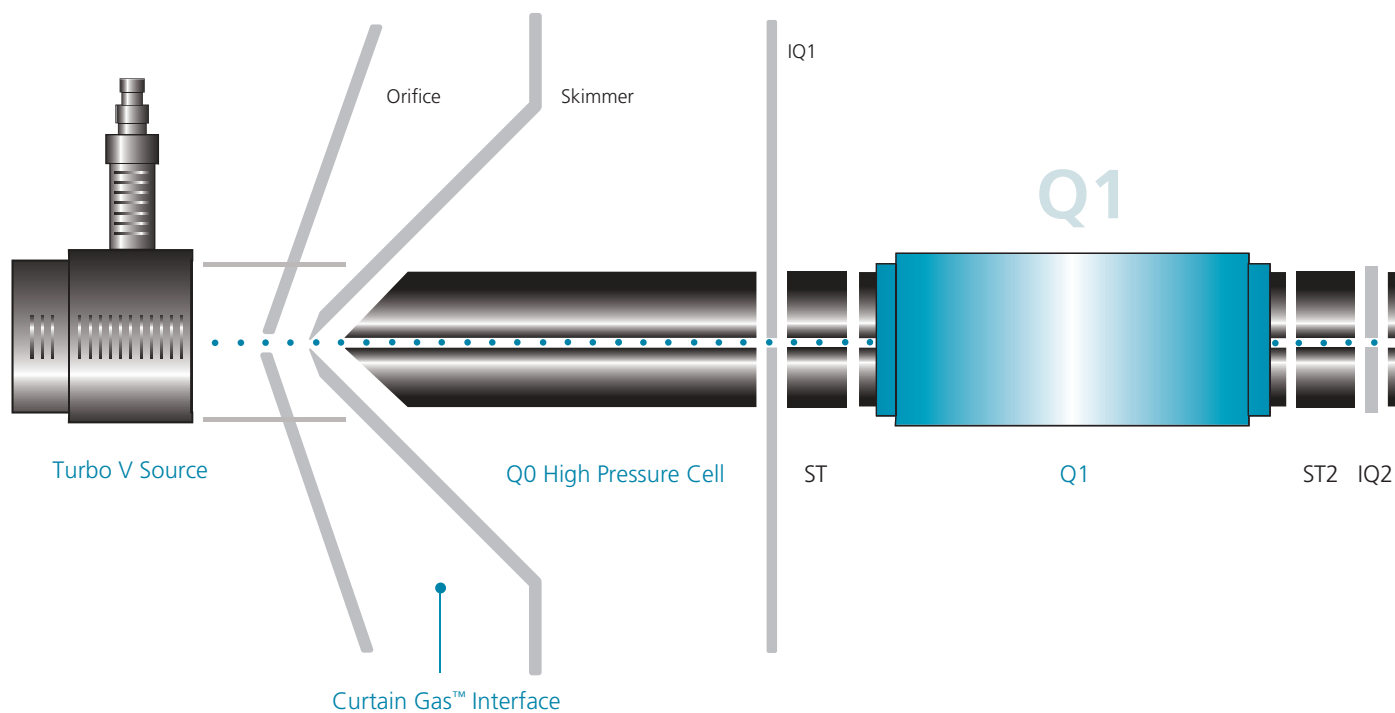
Efficient ionization: Decrease chemical noise, enhance gas dynamics, and improve quantitation levels – even at flow rates as high as 3 mL/min.

Pristine ceramic interface

Unparalleled ruggedness: Proven Curtain Gas™ interface technology combined with improved gas dynamics in the ion-source housing reduces maintenance and increases uptime.

Rugged, reliable operation

The innovative APCI probe reduces peak tailing from cross contamination and other sources of chemical noise. Absorptive residues are eliminated. So you reduce thermal degradation and ionization suppression, while increasing sensitivity and throughput – even at flow rates up to 3 mL/min. The Turbo V source's self-cleaning capability ensures uninterrupted, reproducible operation, and day-in, day-out reliability.

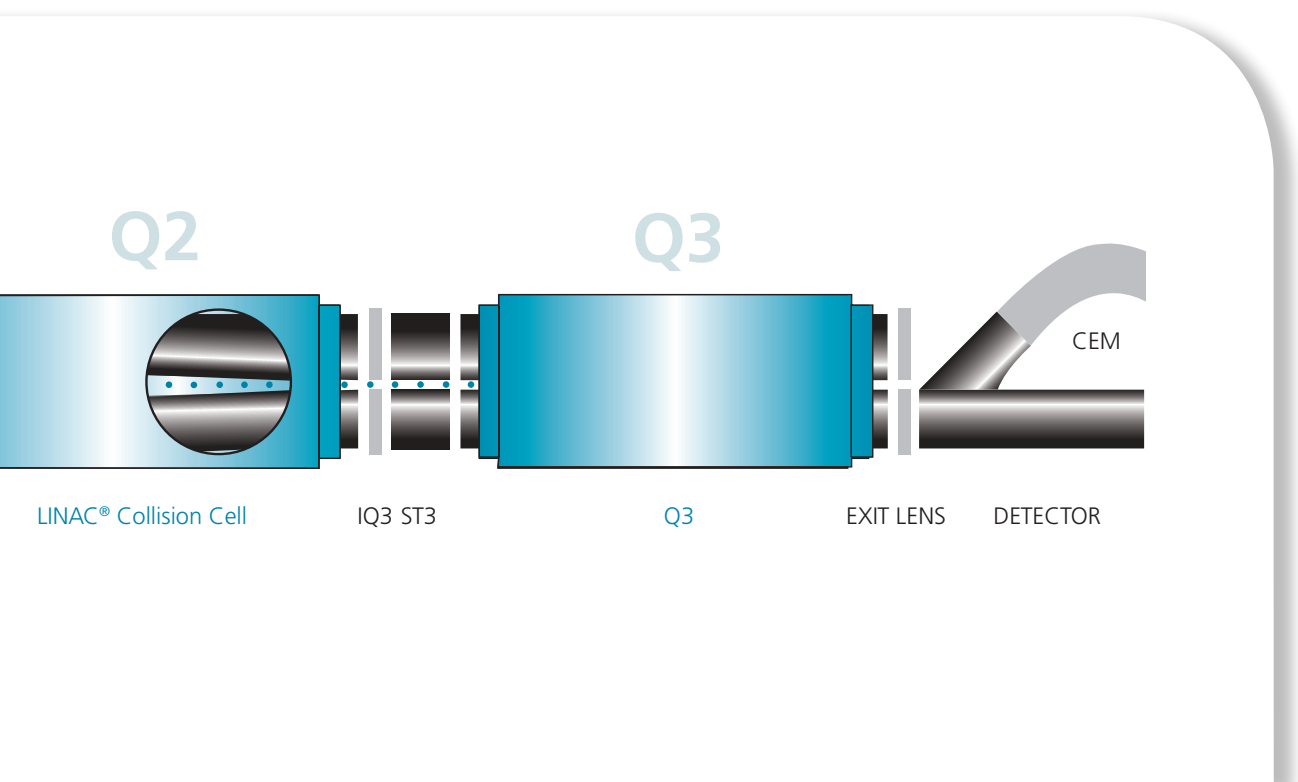


Unique collision cell design

The API 4000™ System uses patented LINAC® high-pressure collision cell technology to ensure maximum ion transfer from the interface to the detector. The LINAC collision cell enables fast scanning without compromising performance in all MS/MS modes, including multiple reaction monitoring (MRM), product ion scan, precursor ion scan, and neutral loss scan. For quantitative applications, the LINAC collision cell translates into multiple component analysis in a single-period MRM experiment. In qualitative applications, the LINAC collision cell enables faster precursor ion and neutral loss scans with excellent sensitivity and resolution.

Dependable digital pulse-counting detector

The sensitive pulse-counting detector in the API 4000 System provides consistent quantitative results over a wide dynamic range. Reproducible intra-day and inter-day results quickly validate even your most difficult assays.



Greater sensitivity and ease-of-use make all the difference

Advanced source design features highly efficient ionization probes.



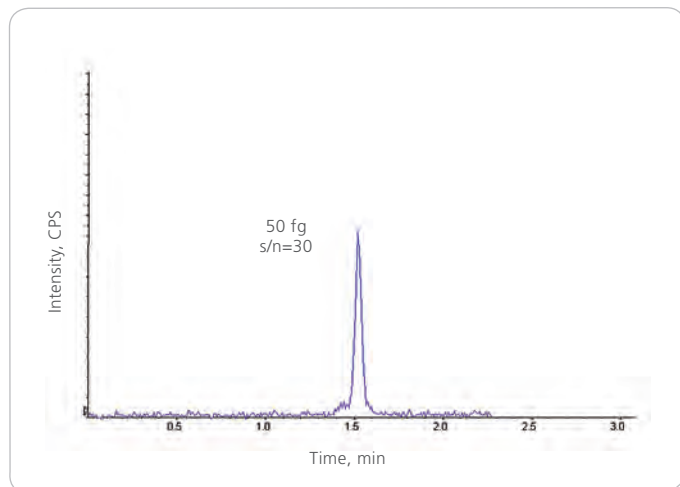
Turbo V™ Ion Source

The source for better lab results

The Turbo V™ Source for the API 4000™ System maximizes ionization efficiency by combining embedded ceramic heater technology with improved gas dynamics. The increased ion yield in the gas phase translates into greater sensitivity. The dual heaters in the Turbo V Source provide greater efficiency in ionization over the wide range of liquid flow rates used in drug metabolism and pharmacokinetic (DMPK) analysis. Improved heat transfer and gas dynamics provide a tenfold increase in sensitivity.

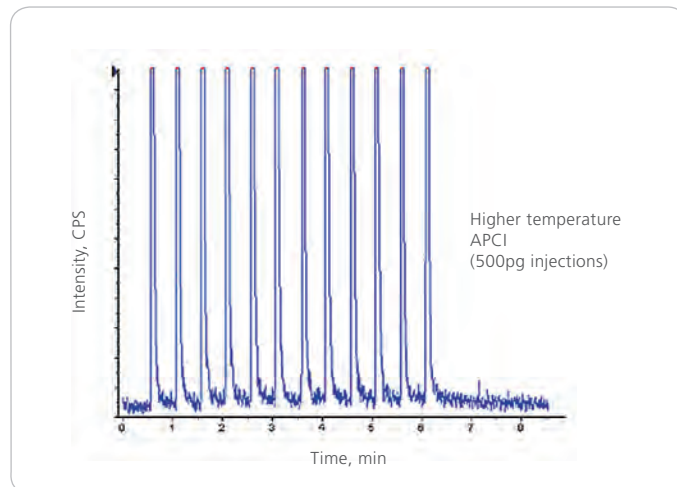
With the advanced Turbo V Source, you can switch between APCI and TurbolonSpray® probes in seconds. Determining the optimal ionization technique during method development is now simpler and faster.

Higher sensitivity



The TurbolonSpray probe increases sensitivity at flow rates up to 3 mL/min, without flow splitting.

Higher throughput



The Turbo V source virtually eliminates cross-contamination, even with large sample loads. Injection of 5-fluorouracil every 30 seconds demonstrates no discernible peak tailing.

Quantitative data processing

A new industry standard

Windows® platform-based Analyst® Software in combination with MultiQuant® Software is the new industry standard for high-throughput quantitation. MultiQuant Software was designed to improve efficiency and enable compliance through an easy-to-use interface and easy database searching, traceability, and a comprehensive suite of 21 CFR Part 11 compliance features. Core functions allow you to configure, tune, acquire, explore, and quantitate results from any matrix.

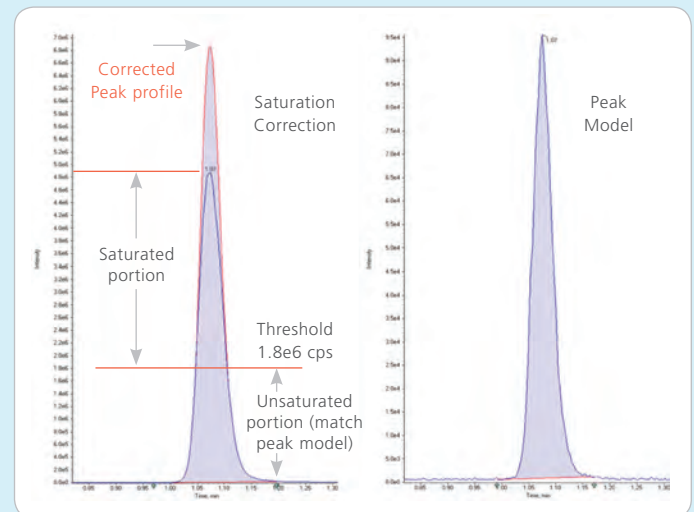
Analyst with MultiQuant Software automates method development, data analysis, review, and reporting:

- Easy-to-use interface
- Custom queries
- Centralized security management
- Detailed audit trail
- Dedicated data review
- Clear data plots of results and trends
- Enhanced data security
- Integrated workflow support – from LIMS to processing tools

Extended functionality

The API 4000™ System is compatible with the full range of automated add-on applications for Analyst software, including IDA, Lightsight, and DiscoveryQuant. The IDA application maximizes the MS and MS/MS information generated from a single run. IDA with triple quadrupole systems helps you achieve unprecedented selectivity of candidate ion species when precursor ion and neutral loss scans are used in the decision-making process. The Lightsight application automates data acquisition and processing for metabolite profiling and identification. The DiscoveryQuant application easily performs automated, unattended optimization and quantitative analyses of samples from drug discovery and development experiments.

AB SCIEX continues to develop systems and software that improve data quality. So you can make better-informed decisions and faster discoveries.



Optional Saturation correction. (Left) The unsaturated portion of the peak is used by SignalFinder to extrapolate the correct peak profile and intensity. (Right) Peak model from an unsaturated peak used to extrapolate the peak profile of the saturated peak.

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