DiscoveryQuant™ Software
Better and Faster LC/MS Methods for New Chemical Entities (NCEs) and New Biological Entities (NBEs)

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DiscoveryQuant™ Software reduces tedious LC/MS method development time with a fast, robust, and reliable process that optimizes methods for hundreds of small and/or large molecules. It expedites the method development process from existing database information, automates on-column optimization, and can easily analyze and process multiple samples at the same time. DiscoveryQuant™ 3.0.1 Software is supported on all AB SCIEX MS platforms and can seamlessly communicate with MultiQuant™ 3.0.2, ensuring success for everyone involved in drug discovery and development.

Challenge Today

- Manual compound optimization can occupy significant amounts of time reducing lab output
- Emergence of complicated biotherapeutics makes method development challenges even bigger
- Huge need for automated software tools to navigate through the complex LC/MS method optimization process for protein and peptide therapeutics

DiscoveryQuant™ Software was designed to address some of the key challenges in Pharma R&D and CRO bioanalytical workflows by providing

- Rapid and automated optimization of multiple MRM conditions for most sensitive quantitative assay development
- Support HT-LC/MS method building for HT-ADME screening studies to select new drug candidates with high potential for success in preclinical and clinical studies
- High quality data with fast turnaround results for screening 100s or thousands of compounds
New Features in DiscoveryQuant™ 3.0.1
Software

Single Software Program - DiscoveryQuant
Optimize and DiscoveryQuant Analyze in one unified software solution

ChromaTune - On-column MRM optimization to eliminate false positives
- Validate MRM’s from QuickTune and FineTune on column
- Screen compounds based on chromatographic properties: sensitivity, retention time, peak width and peak tailing
- Performs linear response experiments across multiple plates
- Comprehensive compound summary panel for quick and easy review

Peptide MRM optimization
- Supports HT-ADME screening of emerging new biological entities (NBEs) along with new chemical entities (NCEs)
- Improve the workflow for tuning and analysis of small peptides and large protein digests
- Optimize and fine tune MRM conditions using real time labeling of y and b ions for extra confirmation
- Handle custom amino acid side chain modifications with new peptide editor
- Import Skyline MRM transitions to the DiscoveryQuant database for FineTune optimization
- Database searches for peptide sequence and charge state

Seamless Integration with MultiQuant™ Software
- for enhanced batch processing of 100’s of samples with multiple MRM transitions

High Resolution Accurate Mass Support – All the great features of the DiscoveryQuant Analyze workflow now available for high resolution accurate mass systems- TripleTOF® 4600, TripleTOF® 5600+ and TripleTOF® 6600 Systems

DiscoveryQuant Software Features and Benefits

Fast and efficient MRM method building using the DiscoveryQuant™ global database
- Using the DiscoveryQuant™ database you can build MRM methods containing multiple compounds with multiple transitions per compound eliminating tedious method building.

Automated batch building and time saving template design
- With a visual approach, templates can be made for frequently run studies that include sample assignment, quantitative information and internal standard assignment.

Easy peak review, data analysis and report generation
- All injections from a study can be visualized on a single plot to improve trend analysis.
- Customizable tables allow tailoring of DiscoveryQuant™ Analyze to suit customer report formats.

Intuitive interface and concise plate review
- Provides a full-featured solution to the Discovery HT screening assay
- Plate-by-plate, compound-by-compound, allows the lab to meet its throughput objectives.
- Built for speed, with quick review screens for optimizations and assay results.

Enterprise-wide solution
- Import your results to your LIMS system for a final report
- Compound Library storage, sharing and retrieval
- DiscoveryQuant™ Software provides solution to multi-lab and multi-site labs and allows for a globally connected discovery environment
## DiscoveryQuant™ 3.0.1 Software Compatibility Matrix

<table>
<thead>
<tr>
<th>Operating System</th>
<th>Windows 7 32-bit and 64-bit</th>
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| **Mass Spectrometers** | API 3000™ system  
  Triple Quad™ 3500 system (new)  
  3200 QTRAP® system  
  API 4000™ and 4000 QTRAP® system  
  API 5000™ system  
  QTRAP® 5500 and AB SCIEX Triple Quad™ 5500 system  
  QTRAP® 4500 and AB SCIEX Triple Quad™ 4500 system  
  QTRAP® 6500 and AB SCIEX Triple Quad™ 6500 system  
  QTRAP® 6500+ and AB SCIEX Triple Quad™ 6500+ system (new)  
  TripleTOF® 4600 system (new)  
  TripleTOF® 5600+ system (new)  
  TripleTOF® 6600 system (new) |
| **Analyst® Software** | Analyst® 1.6.3 software (new)  
  Analyst® TF 1.7.1 software (new)  
  AnalystDeviceDriver 1.0 (required for use with Agilent Infinity II autosamplers G7167A and G7167B) (new) |
| **LC Systems** | Agilent 1100, 1200, 1260 (G1367E, New) and 1290 (G4226A, New)  
  Shimadzu HTA, HTC, SIL10, SIL20, SIL 20 ACXR, SIL 30AC (New), SIL30ACMP (New)  
  Waters Acquity (including iClass)  
  CTC-PAL  
  NanoMate  
  MPX-2 High-Throughput System  
  (New) Eksigent microLC 200, UltraLC 110, UltraLC 110XL, Ultra 110 HTC/HTS  
  Aglient Infinity II autosamplers G7167A and G7167B (new)  
  ExionLC™ AC and AD systems, and the ExionLC™ AD Multiplate Sampler (new) |
| **Free Trial Download Link** | [http://sciex.com/licensing](http://sciex.com/licensing) |