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

Suma Ramagiri, Ian Moore; SCIEX, Concord, ON

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 Aglient Infinity II autosamplers G7167A and G7167B) (new)** |
| **LC Systems**  
(Autosamplers) | **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** |