



### MS/MS Proteomics Validation at a Glance Scaffold 3 introduces several new features:

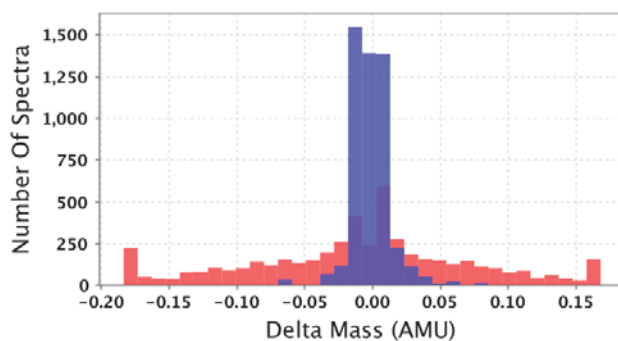
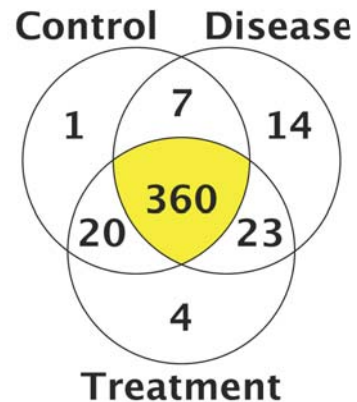


#### SF3 Format Improves Speed and Stability

Scaffold's new SF3 file format means faster data access and unlimited file size scalability. You'll load more data in less time and always be ready for the next generation of instrumentation.

#### Powerful Filtering Capabilities

Filter your data like never before. Use Venn diagrams and advanced filtering capabilities to quickly navigate your data set. New search functionality includes spectrum name, peptide sequence and even sequence motif.



#### New High Mass Accuracy Validation

Sophisticated statistical techniques improve your identification rate with high mass accuracy data. Drift and accuracy are automatically tuned for each sample. Now you can fully realize your advanced instrumentation!



# Explore What's New In Scaffold 3

### New SF3 Scaffold File Format

- SF3 utilizes a single file database to improve file access speed and reliability
- Unlimited file size scalability removes 2GB barrier of SFD files
- Open older 2.x SFDs completely transparently with no messy file conversion
- Save small changes much faster to SF3s

### Memory Usage, Speed and Stability

- Load large files faster with improved memory management
- Processing time on large data sets scales linearly with available memory and CPU power, allowing you to take advantage of large Scaffold servers

### Improved Protein Filtering Capabilities

- Single click on Venn Diagram to review proteins, peptides and spectra compared across multiple sample categories
- Double click on Venn Diagram to automatically filter proteins
- Advanced filtering options enable you to build layered queries and find proteins using regular expressions
- Search for peptide sequences and sequence motifs
- Search based on spectrum identifier name
- Search for proteins only present in specific samples
- Filter out short peptides
- Modification filter now separated from identification thresholds
- Filter using Discoverer Z-Core and Waters Identity<sup>®</sup> Scores

### Advanced High Mass Accuracy Analysis

- Perform sophisticated high mass accuracy analysis with a simple checkbox
- Improves identification rate for all instruments that can resolve the baseline between isotopes (from Q-ToF to LTQ-FT)
- Mass accuracy and drift are automatically determined on a sample by sample basis
- View mass accuracy correction factors with PeptideProphet histogram
- Based on updated PeptideProphet algorithms described by the Aebersold lab (J. Proteome Res., 2006, 5, 2241–2249)

### New Spectrum Counting Options

- New hypergeometric distribution test developed by the Tabb lab
- Set the minimum spectrum count depending on your confidence in the data set
- Up to 50% improved accuracy over t-test methodology using control data sets

### Updated MCP Publishing Guidelines Support

- New "Paris 2" guideline support with an improved publishing workflow
- Reduce distributed SF3 size up to 10x using new file size trimming tool
- Automatically upload your SF3 to the journal preferred Tranche online data storage and distribution tool
- Encrypt Tranche files with passwords while your manuscript is in press
- Upload peaklists of identified spectra to Tranche once your manuscript has been accepted
- Export results in the new HUPO-PSI mzIdentML standard

### Updated Thermo Discoverer Support

- Support for Z-Core scoring system for ETD/ECD data
- Support for Mascot run within Discoverer
- Analyze results from multiple search engines within a single MSF file
- Analyze data from alternating CID/ETD scans

### Improved Graphical Interface Details

- Estimated FDRs calculated for each MS/MS sample in new Statistics view table
- Collapse multiple MS/MS samples into a single row in the Proteins view with the Bio/MS view options
- Combine protein sequence coverages across multiple MS/MS samples with the Bio/MS view options
- Updated About Scaffold information to display 32 bit or 64 bit system

### New Scaffold Batch Features

- Support for Scaffold Q+ iTRAQ and TMT based quantitation
- Build Scaffold Batch Driver files using the Load Data queue
- Build New Scaffold Batch Packages that include all original data files using the Load Data queue