



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^E 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