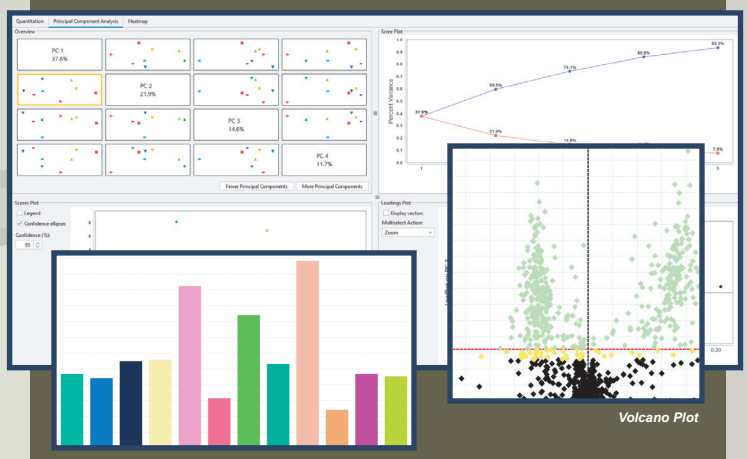
Scaffold Software Meets Small Molecule LC-MS Analysis

Identify and quantify small molecules using MS1 or MS/MS data

Import CSV files containing sample metadata to automatically configure your experimental design and organize samples

^{13}C ^{15}N ^{18}O ^{2}H

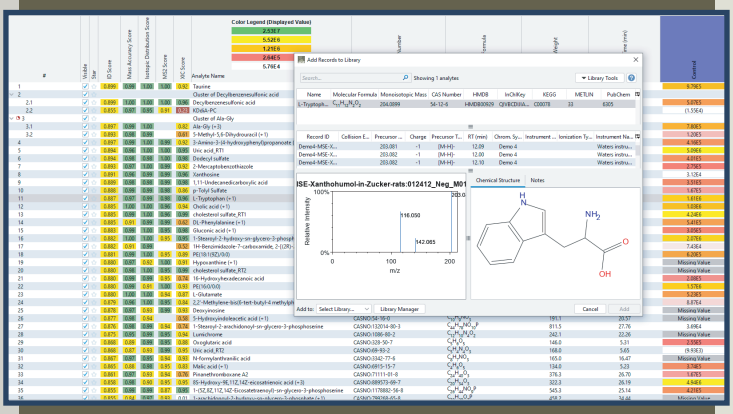
Track isotopically labeled compounds using metabolic flux experiments



Quantify, determine statistical significance, and visualize results

Load raw data* from major vendor instruments, including Thermo, Sciex, and Agilent

Search multiple spectral libraries including NIST, HMDB, and LIPID MAPS



Create personal spectral libraries using spectra from your instrument

Validate potential identifications using ID scores, fragmentation patterns, isotopic distributions, and chromatographic shapes

Share results with colleagues or customers using the free Scaffold Elements Viewer

METDB

*Windows is required to process vendor-formatted raw files

Proteome Software
www.proteomesoftware.com

Version 4.1