Scaffold PTM
Confident Site Assignment for Post Translational Modifications

Assess Site Assignments
Scaffold PTM evaluates the confidence of modification site assignment using Ascore, originally developed for analysis of phosphorylation. In Scaffold PTM, the algorithm has been adapted to work with any type of modification, including phosphorylation, oxidation, and glycosylation.

Find Motifs
Scaffold PTM searches for motifs that are over-represented in the sequences surrounding PTMs in the experiment as compared to the sequences surrounding the same amino acid in a background data set. Motifs that have been previously reported are annotated and, when known, the associated enzymes are displayed.

Evaluate Localization Probability
In addition to the Ascore, Scaffold PTM uses Bayesian analysis to calculate the probability that a PTM is located at a specific site.

Compare Samples with Modified Spectra Using Differential Expression

Scaffold PTM and its free Viewer are available for Windows, macOS/OS X, and Linux.
Perform Labeled or Precursor Intensity Quantitation of Modsites with Q+/Q+S

Export quantitative results from Scaffold Q+ or Scaffold Q+S, then analyze at the modsite level in Scaffold PTM. Statistical testing assesses the significance of differences between the modified and unmodified intensities.

Validate Peptide Assignments

Examine Details of the Ascore

Visualize matched peaks and peak depths used in Ascore calculations.

Normalize by Protein Levels

Measure the protein levels in unenriched samples and export a Protein Quantitation Report from Scaffold Q+ or Q+S. Scaffold PTM will use these values to adjust the quantitative values to properly reflect differential modification.

Export Publication-ready Graphics