



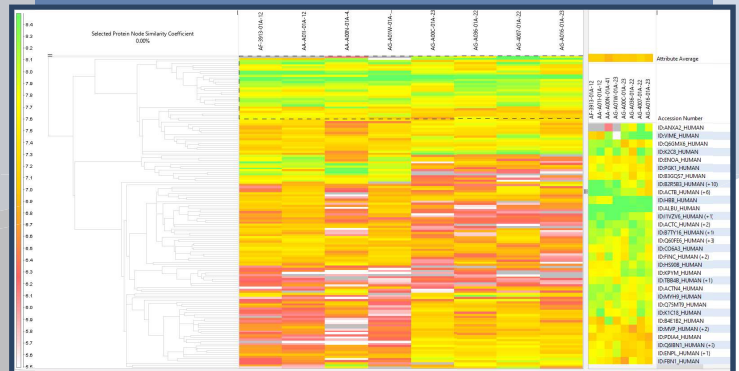
Simple, Experiment-driven Quantitative Analysis for Proteomics

Combine multiple complex Scaffold experiments, or directly load Mascot or PEAKS mzIdentML files

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

Quantify differential expression using spectral counts or precursor intensities and test for statistical significance

Assess biological meaning with gene ontology (GO) annotations



Analyze your data using PCA and heatmaps, an ideal exploratory environment with flexible organization

Normalize, roll-up, and interpret biological differences and find sources of technical variation at the fraction, technical, and biological replicate level

Select the most appropriate experimental design with easy-to-use wizards: basic, repeated measures, or two way

Share data using the free Scaffold LFQ Viewer or exportable reports and graphics



Proteome Software

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