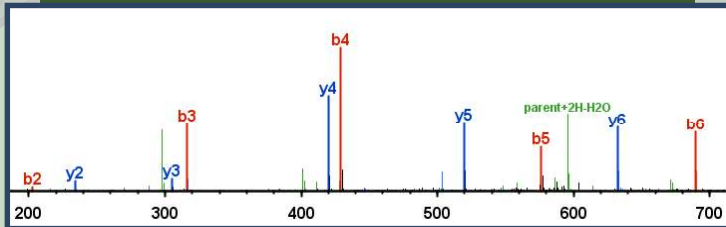


5 scaffold

The Industry Standard MS/MS Proteomics Tool

Search raw data directly with MS Fragger* integration and load precursor intensity data from FragPipe

Build a complete DDA / DIA pipeline using Scaffold 5 DDA library exports and Scaffold DIA

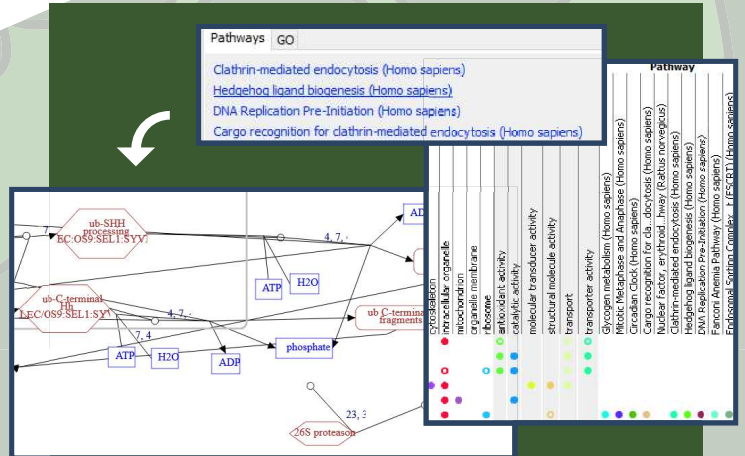


Control experiment-wide FDR using Percolator and validate peptide identifications using spectrum visualization

Load data from Mascot, Proteome Discoverer, MaxQuant, and more

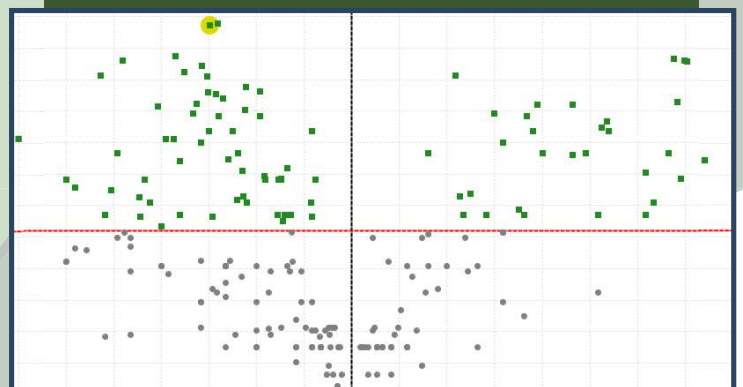
Researchers: Process raw data into results using a single program

Core facilities: collaborate using the cross-platform free Scaffold Viewer, Excel reports, and mzIdentML exports



Classify proteins by biological function with Gene Ontology (GO) and pathway annotations

Upload data to PRIDE using mzIdentML exports



Visualize differential expression and statistical significance using spectrum counting or precursor intensity

* MS Fragger license required; free for academic labs