

Scaffold Quick Instructions

Database Search Results will either be on wi-files2 (internal) or an ftp link to the file will be emailed via SendIt (external). The program works best the file is downloaded to your hard drive/ desktop.

You'll need to download the free viewer to open the file:

<http://www.proteomesoftware.com/products/free-viewer>

The spreadsheet shows all proteins and all samples in columns. The number of peptides from each protein appears in the rows, and this can be changed in the "Display Options"

(See <http://proteome-software.wikispaces.com/Scaffold+FAQs> for further explanation of the display options, particularly the "Scaffold Pages and Displays" and "Calculations in Scaffold".)

Columns can be sorted by clicking on the column header.

The "BIO" and "MS" Icons toggle between the Biological Sample and Individual Samples. Use the "BIO" view for individual bands

Protein sequence coverage can be seen by double clicking on a protein name or clicking the big "Proteins" Icon in the left most column.

The sequence coverage for each sample can be listed vertically in the upper left panel, the individual peptides are in the upper right panel and the full sequence with identified peptides (yellow) and modified amino acids (green) are in the bottom panel.

Up to three biological samples can be compared using the Protein Venn Diagram which is in the lower left panel of the "Quantify" View. The pane contains three tabs for biological samples and shows the overlap of proteins between samples.

By double clicking on a subset in the Venn Diagram the proteins from that subset will appear in the samples view. To go back to the complete protein set, click the magnifying glass icon to the left of "Advanced..." and click "Clear"

Tutorials and FAQs can be found at <http://www.proteomesoftware.com/>

