

Download the Free Scaffold Viewer

You can download and use the Scaffold Viewer for free.

- Download Scaffold from www.proteomesoftware.com.
- To install, click on the downloaded file (install_Scaffold.exe).
- Start Scaffold.
- During startup, you will be asked to enter a license key. At this point choose the "Free Scaffold Viewer" button.

Scaffold Viewer

The main layers of the software are accessible via the buttons at the left: Load data, Samples and so on..

In the figure below, the samples view is shown:

The screenshot shows the Scaffold Viewer software interface. On the left sidebar, there are buttons for 'Load Data', 'Samples', 'Proteins', 'Similarity', 'Quantify', 'Publish', and 'Statistics'. Arrows point from these buttons to the corresponding sections of the main window. The main window displays a heatmap of protein abundance across various samples. The 'Probability Legend' on the left indicates color coding for protein abundance: over 95% (green), 80% to 94% (yellow), 50% to 79% (orange), 20% to 49% (red), and 0% to 19% (dark red). The heatmap shows protein abundance across samples grouped by date (01-09, 09-212, 10-18, 09-212). The 'Protein Information' section at the bottom shows the 'Lookup Accession Number' as 'NCBI:gi|1351907.1|ALBU...' and 'TB10.10035', and the 'Protein Name' as 'TB10...0335 undefined product 1043258:10442'.

Load Data

All data files included in the Scaffold analysis are shown. Importantly: Only such modifications can be observed which are included in the database search

sample versus **control**
09-212-1to9 **09-212-10 to 18**

The screenshot shows the Scaffold software interface. At the top, there are two labels: "sample 09-212-1to9" and "control 09-212-10 to 18". Arrows point from these labels to a purple oval containing "09-212" in the "Files Currently Loaded" list. To the right, another arrow points from the text "Project number 09-212" to the same "09-212" entry. Below this, an arrow points from the text "gel pieces HPLC runs" to a list of file names in the "Files Currently Loaded" section, including "09-212-16.RAW (09-212-16)", "09-212-11.RAW (09-212-11)", "09-212-12.RAW (09-212-12)", "09-212-13.RAW (09-212-13)", "09-212-14.RAW (09-212-14)", "09-212-15.RAW (09-212-15)", "09-212-16.RAW (09-212-16)", "09-212-17.RAW (09-212-17)", and "09-212-18.RAW (09-212-18)".

Analysis Information:
Peptide Tolerance: 4.0 ppm (Monoisotopic)
Fragment Tolerance: 0.20 Da (Monoisotopic)
Digestion Enzyme: Trypsin
Searched Database: Trypanosoma_NCBi_genome_20070330
Original Search Date: Mascot=09/30/2009
Scaffold Version: Scaffold 2.05.01

Modification	Mass	AA
Carbam domethyl (iodoacetam...	57.0	C

Modification	Mass	AA
Deamidation	1.0	N
Trypsinolysis	1.0	Q
Oxidation	16.0	M

Amino acid modifications included in the data base search

Samples

This view provides an overview of the proteins identified in Scaffold's analysis.

Use the following standard parameters if you are not an expert:

Protein probability: 99 %

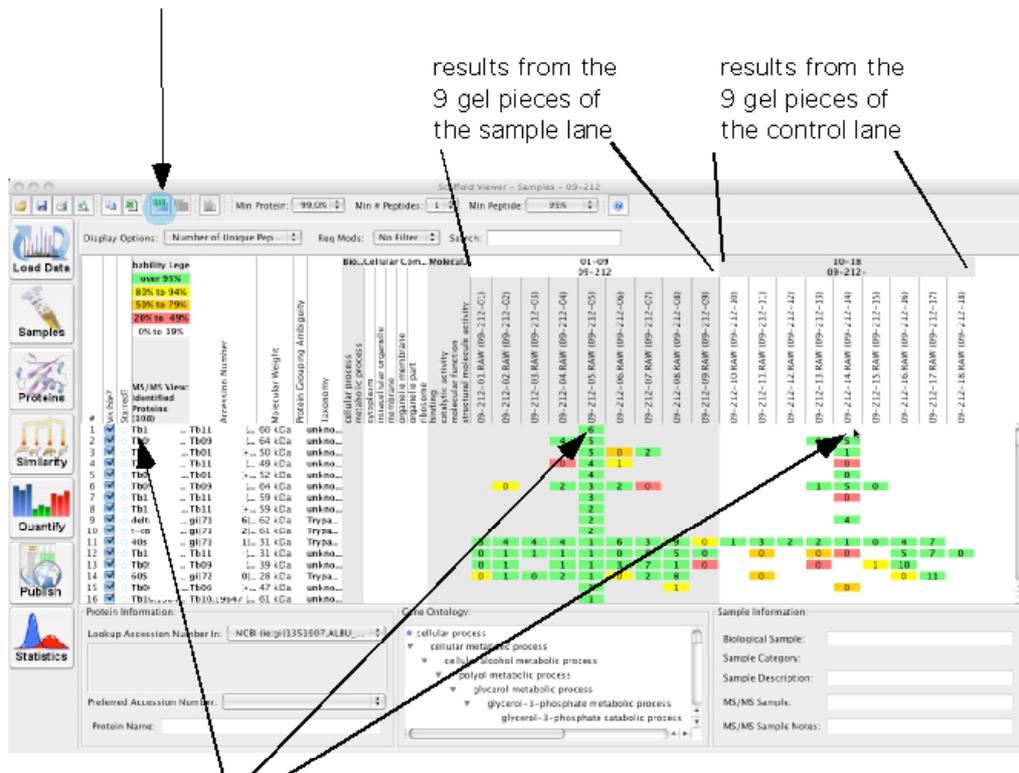
Number of peptides: 2

Peptide probability: 95 %

Biological Sample view

The screenshot displays the Scaffold software interface. At the top, the 'Display Options' section shows the following settings: 'Number of Unique Rep.' (set to 1), 'Min Protein' (99.0%), 'Min # Peptides' (2), and 'Min Peptide' (95%). A 'Probability Legend' on the left indicates color coding for protein probability: green for 'over 95%', yellow for '80% to 94%', orange for '50% to 79%', and red for '25% to 49%'. The main table lists 18 proteins with columns for Accession Number, Molecular Weight, pI, and a color-coded bar representing the number of unique peptides observed. The 10th entry, '40S ribosomal protein S4', is highlighted in green and has a bar with the number '11'. Annotations with arrows point to the 'Min Protein' and 'Min Peptide' settings, and to the '11' in the bar for protein S4. A text box on the right states: 'Number of unique peptides observed from the 40S ribosomal protein S4 in the 9 gel pieces 09-212-1 to 9'. The bottom of the interface shows 'Protein Information' and 'Gene Ontology' sections.

MSSample view



This protein is detected (6 unique peptides) in the 5th gel piece of the sample lane, but not in the corresponding gel piece of the control lane.

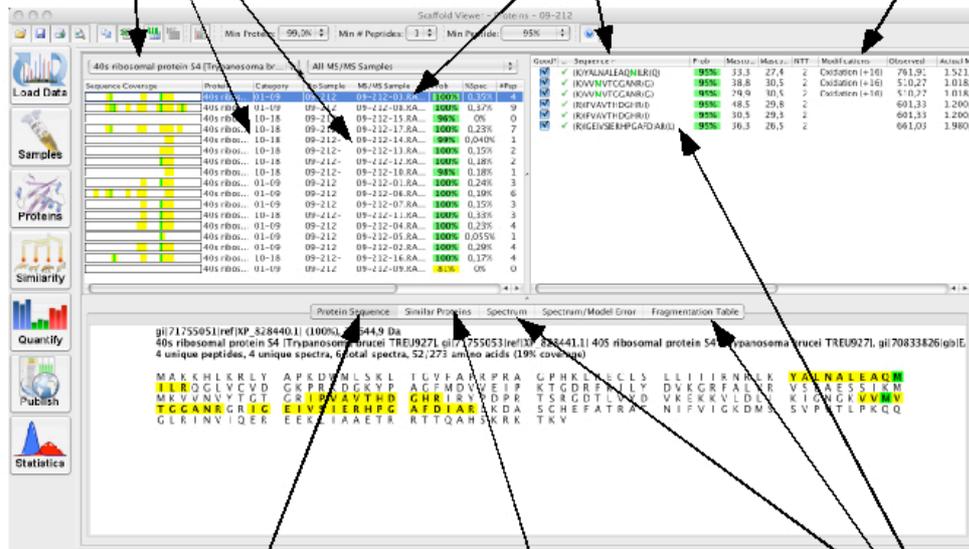
Proteins

Select a protein from the samples view by double click or from the list in the protein view

each column can be sorted by clicking in the column header which is especially useful if sorting for modifications like phosphorylation

The 40S ribosomal protein S4 is found in several gel pieces in the sample lane and in the control lane

In sample 09-212-03 S4 is detected by 6 peptides



The amino acid sequence of S4 is shown. Detected peptides are highlighted with color coded probabilities.

fragment spectra and fragmentation table of selected peptides are shown

Proteins matching the same set of identified peptides.