

Bioinformatics software for effective analysis of mass spectrometry data: *S2P*, *Mass-Up* and *LA-iMageS*

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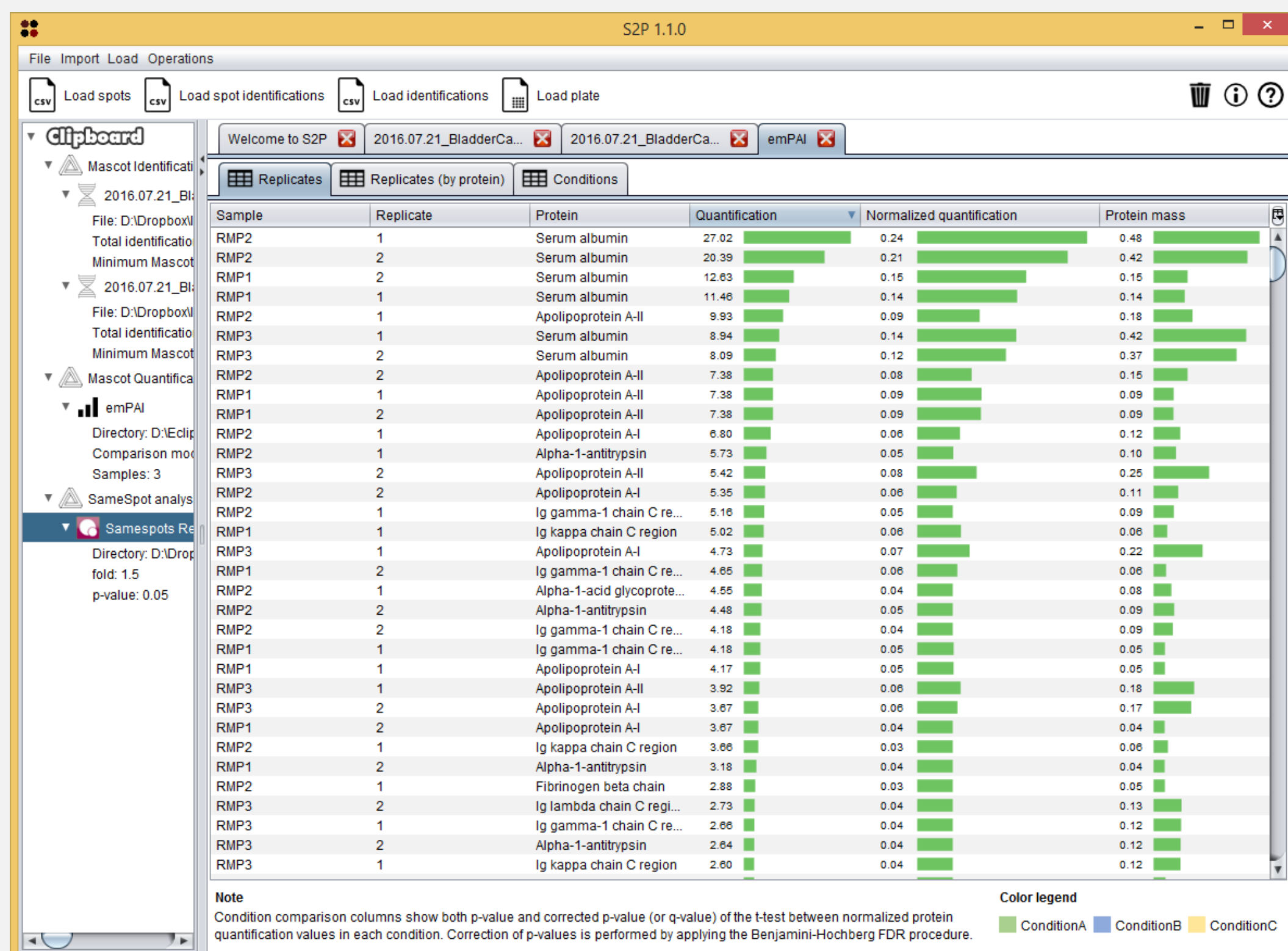
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S2P

www.sing-group.org/s2p



What is S2P? *S2P* is a desktop multiplatform application specifically created to perform fast and easy processing of 2D-gel and MS protein identification-based data.

Features: *S2P* allows researchers to:

- Import data from Progenesis SameSpots and save it as comma-separated values (CSV) files.
- Import, process and save Mascot reports.
- Create MALDI plate designs and export them as PDF or CSV files.
- Bind Mascot identifications to spots data.
- Visualize and explore spots data in different ways.

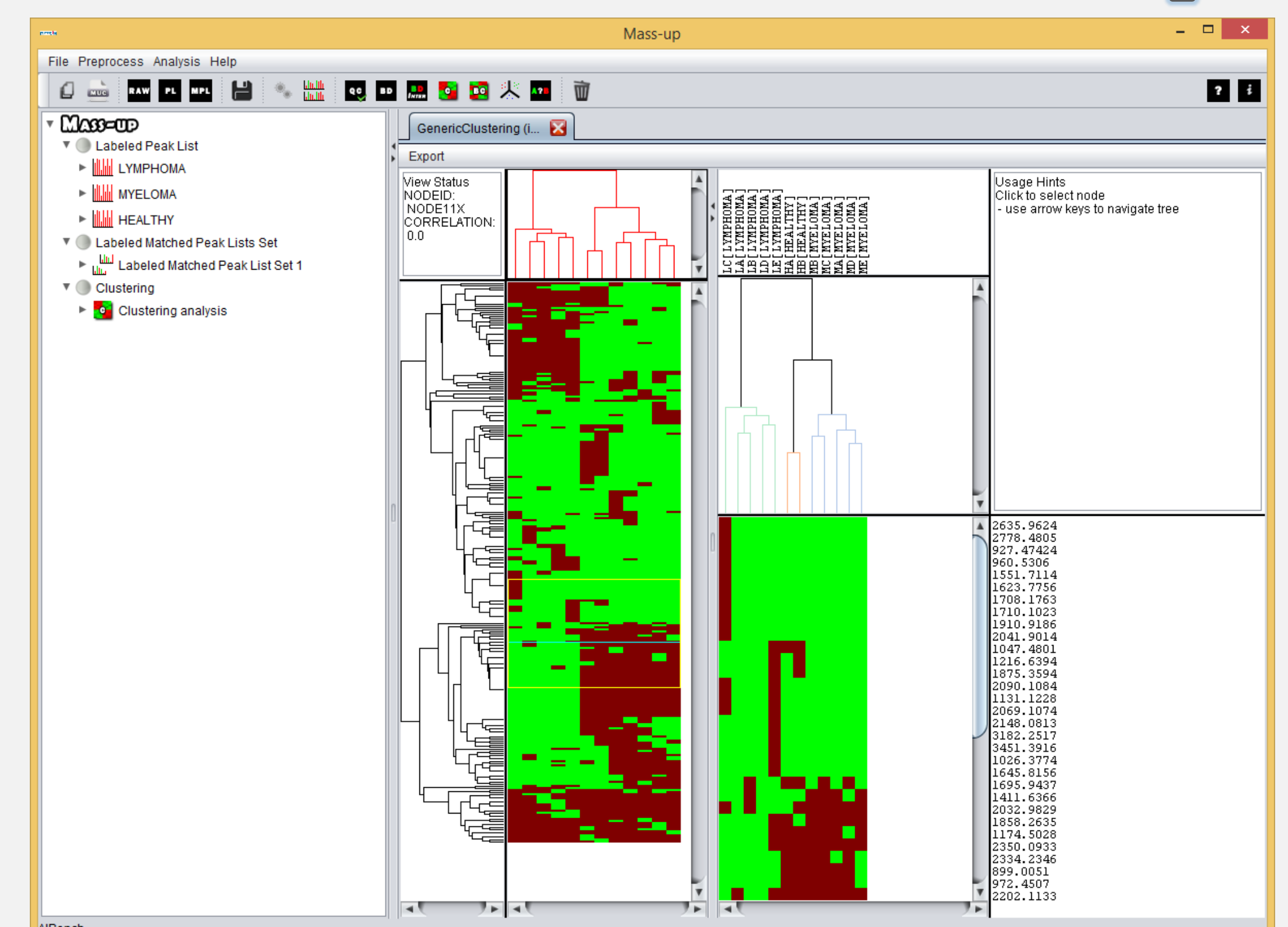
www.sing-group.org/mass-up

Mass-Up

What is Mass-Up? *Mass-Up* is an open-source software for proteomics designed to support the preprocessing and analysis of MALDI-TOF mass spectrometry data.

Features: *Mass-Up* allows researchers to:

- Load and visualize raw spectra from mzML, mzXML or CSV files.
- Preprocess raw spectra using well-known R libraries (MALDIquant and MassSpectWavelet).
- Perform different types of analysis (quality control, biomarker discovery, principal component analysis, hierarchical clustering, biclustering, and classification analysis) on the aligned peak lists.



LA-iMageS

www.la-images-net

What is LA-iMageS? *LA-iMageS* is an open source application to generate 2D/3D elemental distribution bioimages from LA-ICP-MS spectra.

Features: *LA-iMageS* allows researchers to:

- Extract the elemental distributions of elements from LA-ICP-MS spectra.
- Normalize the elements by a standard.
- Generate custom 2D/3D representations of each element.
- Export the results into images and the elemental distributions to CSV files.

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