



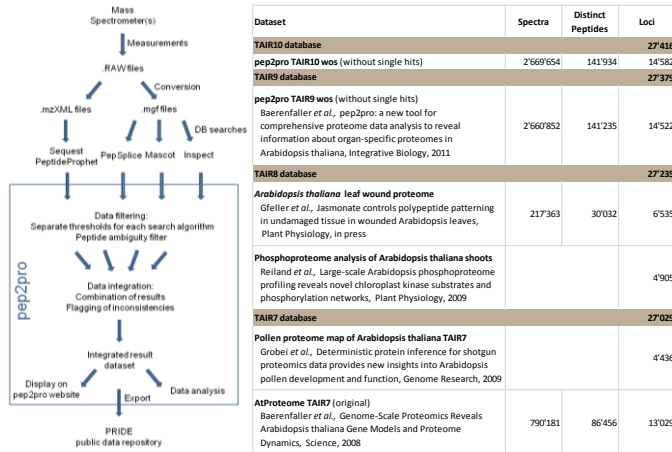
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Summary

Mass spectrometry-based proteomics has now become an important tool for obtaining qualitative and quantitative protein information. Data analysis of the proteomics data usually requires integration of search results from different experiments and search algorithms. The results are then often combined with other proteome data or compared with additional datasets like transcript data. To accomplish the integration of proteomics data at these different levels specialised tools like the pep2pro proteome analysis database, the MASCP Proteomics Aggregation Portal and the Agron-omics RDB have been developed and employed for data analysis.

pep2pro



pep2pro is a comprehensive proteome analysis database and its capacity has been demonstrated with the pep2pro genome-scale organ-specific proteome maps of Arabidopsis thaliana providing expression evidence for more than 50% of all predicted proteins. New datasets are continually added and made available through the pep2pro website in which we also provide a proteogenomic mapping of the peptides to the genome sequence.

www.pep2pro.ethz.ch

The screenshot shows the pep2pro search interface. The search results for RBR1 (AT3G12280.1) are displayed, including protein description, ID, and coverage. Below the search results, there is a detailed view of the protein structure and sequence, including a peptide browser and a sequence alignment table.

Sequence Position	Sequence	MS/MS	pI	PKS
AT3G12280.1	MEIQGPPYR EIKWHRK AELGQIKR LKQDQIKR ILLANRHR DEKQYRQYR WYLLIYR KLRWHRK LKQDQIKR	112174	7.96	1013

MASCP Gator

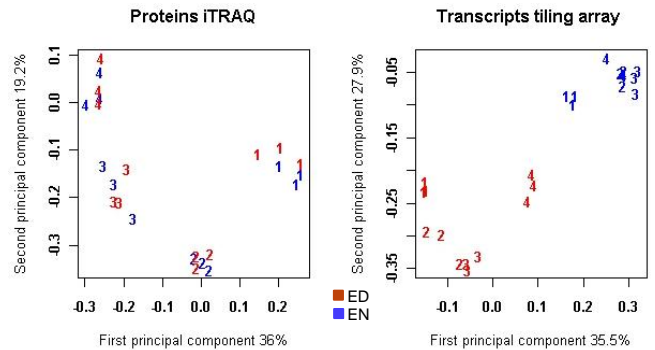
<http://gator.masc-proteomics.org>

The screenshot shows the MASCP Gator web portal. The search results for RBR1 (RETINOBLASTOMA-RELATED 1) are displayed, including protein description, ID, and coverage. The interface includes a search bar, a results table, and a detailed view of the protein structure and sequence.

The MASCP Gator portal is a simple web page that allows for retrieval of proteomics data from across the MASCP consortium, and presents it in an easy to understand, summarised view. Through a clientside approach to aggregation, the data presented by the aggregator is always up-to-date (Joshi et al., Plant Physiology, 2011).

Integration of quantitative transcript and protein data in the Agron-omics RDB

For combined analyses of the Agron-omics quantitative proteomics data on leaf 6 with additional datasets, the final proteomics result data that had been processed in pep2pro have been integrated into the AgroRDB. Querying this database followed by statistical analyses allows effective data analysis and reveals new insights into the regulation of protein and transcript levels.



Both the results from the Principal Component Analysis and the comparison of individual protein-transcript pairs indicate that many transcripts display significantly changed levels during growth and/or day-time, while proteins show a dampened response, particularly concerning day-time fluctuations.

