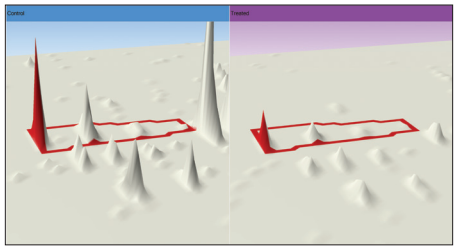
[PRODUCT SOLUTION]

nonlinear DYNAMICS
A Waters Company

The next generation in LC-MS proteomics data analysis software.

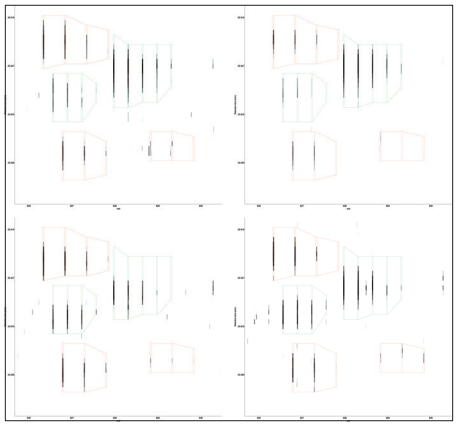
Discover the significantly changing proteins in your samples.

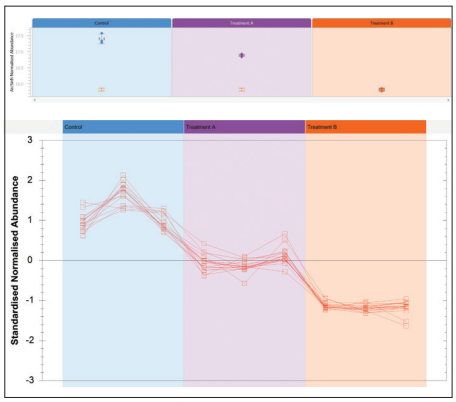
Progenesis® QI for proteomics enables you to quantify and identify proteins in your complex samples using the advantages of label-free analysis. With support for all common vendor data formats and a guided workflow, Progenesis QI software helps to overcome your data analysis challenges, enabling you to rapidly, objectively and reliably discover proteins of interest and export results for 'omics research applications.



Solving your analysis challenges

- Consistent peak picking across all runs, vital for accurate and precise quantification, using our unique approach to co-detection of peptide ions.
- No restrictions on the number of groups, samples or experimental designs you can compare within your analysis.
- Complete data matrix and no missing values, for reliable multivariate statistics.
- Query databases using common search engines to automatically combine identifications with peptide ion quantification data.
- Fully compatible with ion mobility to achieve three dimensions of resolution.
- Powerful data visualization and guided-workflow for DIA and DDA analyses as well as support for analysis of fractionated samples.





"...label free MS-based approach using Progenesis software overcomes many of the limitations of traditional proteomic methods, leading to the comparison of protein expression profiles between multiple complex mixtures, followed by a fast and effective identification of proteins of interest."

DR. ALINE ZIMMER, DR. MAXIME LE MIGNON, DR. JULIEN BOULEY
Stallergenes, Antony, France

Progenesis® QI
for proteomics

PROGENESIS QI FOR PROTEOMICS – KEY STEPS IN LC-MS DATA ANALYSIS

Quantify

Raw data import and quality control

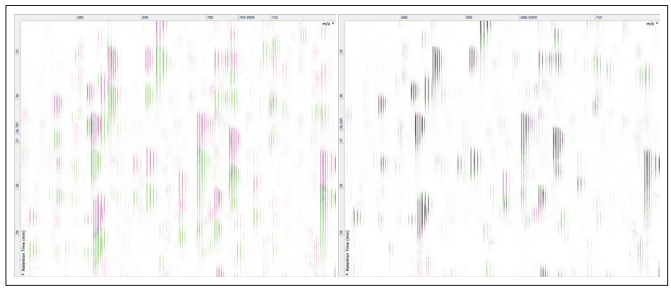
- LC-MS vendor independent, supports all major data formats plus mzXML and mzML
- Peak modelling and data reduction for fast analysis without affecting quantification
- Generate ion intensity maps of retention time (RT) vs. m/z vs. ion intensity to review raw data quality
- Automated reference run selection and RT alignment to increase objectivity
- Specific 2D-LC workflow to support analysis of fractionated samples
- Ion mobility separation adds a third dimension of resolution and increases peak capacity

"...minimize the fractions needed to achieve good peptidome coverage and so save instrument time and costs in achieving experimental goals."

DR GEUN-CHEOL GIL, DR GABRIELA CHIRICA
Systems Biology Department, Sandia National Laboratories, Livermore, CA, USA

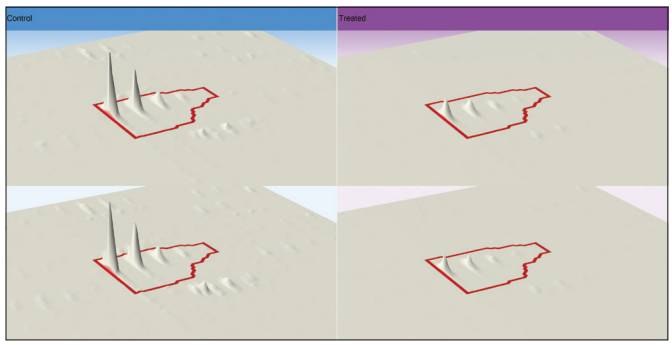
Retention time alignment

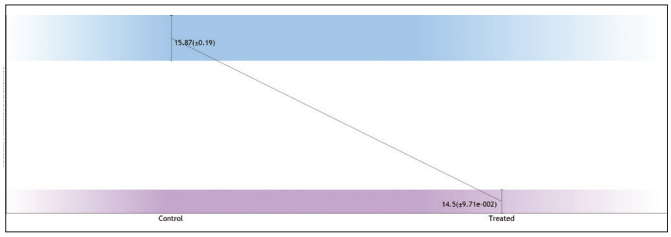
- Automatically correct for RT differences between runs and create an "aggregate run" containing every peptide to consistently detect and quantify features across all samples
- No missing values, no matter how many replicates you run
- Measure the quality of your alignment for confidence in your downstream results



Quantify peptides

- Ion abundance is measured from an isotope peak cluster detection applied consistently to every run
- Automatic normalization accounts for sample loading variation for direct comparison of up or down regulation between runs
- Quickly compare features across multiple groups within your experiment
- Visually evaluate ion mobility separated isobaric peptides
- Validate peptide quantification and expression with data tables linked to visual displays
- Simple but powerful Tagging feature to explore ions of interest in your results

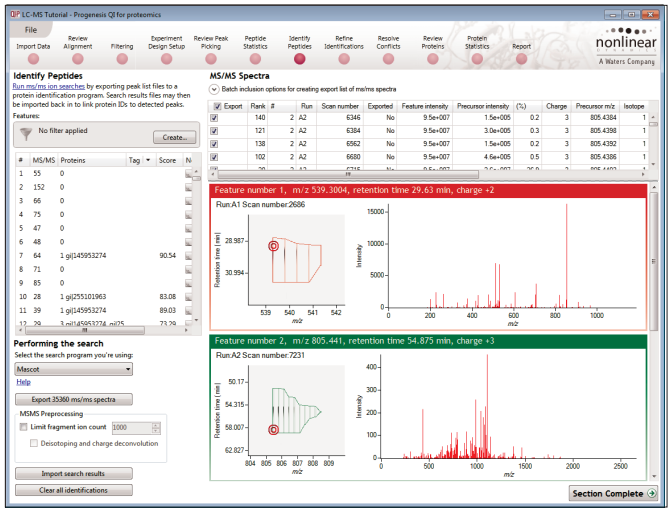




Identify

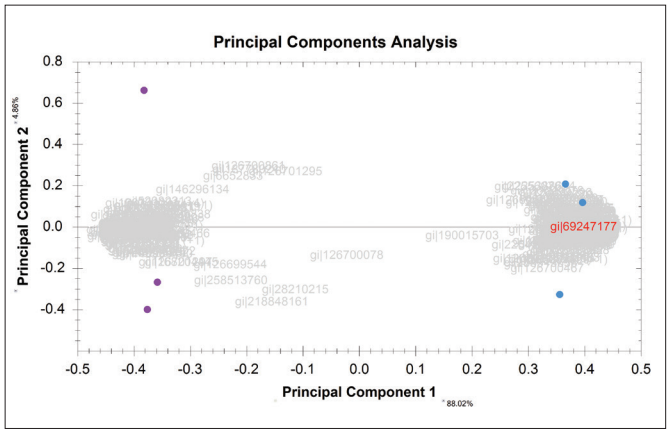
Identify peptides and proteins

- A simple, visual approach to validate and select MS/MS spectra for export
- Query using multiple search engines including MASCOT, Protein Lynx Global Server (PLGS), SEQUEST and many more
- Display imported search results alongside parent ion measurements and optionally filter to produce a peptide-based view of your experiment data
- Quantify based on unique peptides only, resolve conflicts when a sequence is associated with multiple proteins
- Easily tag and select unique peptides as candidates for MRM studies



Report interesting proteins

- Measure protein abundance from the sum of all unique normalized peptides
- Direct comparison of protein expression between groups
- Display expression profiles for selected proteins of interest
- Easy–to-use multivariate statistics including q-values to control false discovery rates, Principal Component Analysis (PCA), Correlation Analysis and Power Analysis
- Correlation Analysis allows you to find all the proteins sharing a common expression pattern
- Export protein data to any external bioinformatics package for further analysis and re-import results back into the Review Proteins table
- Report a protein and a peptide view of your experiment



"The advantage to us, of Progenesis, is the unbiased peptide-centric approach to quantitation. Significant MS1 peptides can be evaluated regardless of their identity status."

DR VALERIE WASINGER
Senior Research Scientist, Biomolecular Mass Spec. Facility (BMSF) at UNSW, Sydney, Australia

Find out how you can quickly and confidently generate results with our powerful, easy-to-use software, with the benefit of full-technical support:
www.nonlinear.com/ProgenesisQIproteomics

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