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 from single or fractionated samples.

Solving your analysis challenges

- QC Metrics to evaluate the quality of your LC-MS data.

- Consistent peak picking across all runs, vital for accurate and precise quantification, using our unique approach to co-detection of peptide ions.

- Compatible with 1D and 2D-LC and 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.

- Easy export to Pathway Analysis tools to aid biological understanding of discoveries.

"The Progenesis QI proteomics and metabolomics products are intuitive and exciting pieces of software that allows rapid identification, quantification and interpretation of your data. The presentation of data and the options to highlight features allows the user to delve deeper into the mass spectrometry data with confidence and understand the results fully."

DR. G. DON JONES AND JANICA AULUCK
Department of Cancer Studies and Molecular Medicine,
University of Leicester, UK
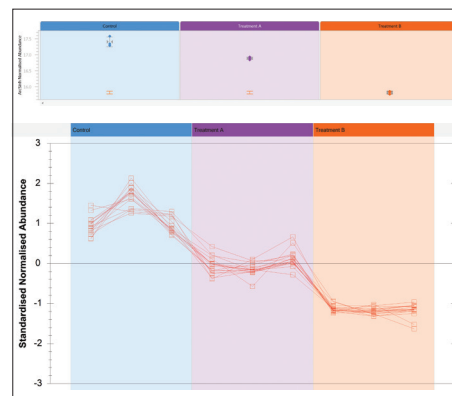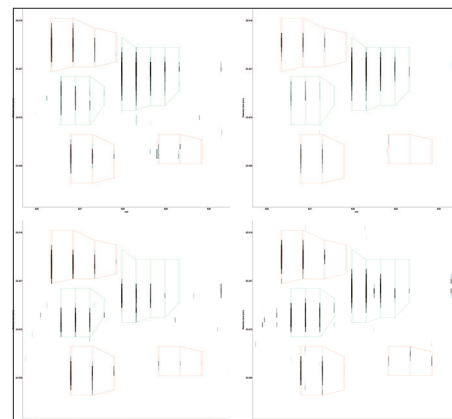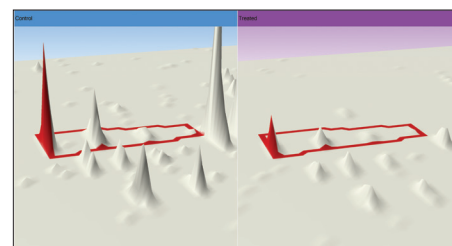
Progenesis® QI
for proteomics

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

Quantify

Automation of processing steps

- Save time with optional automation of steps from Data Import to a completed Protein Database Search

Raw data import and quality control

- LC-MS vendor independent, supports all major data formats

- Specific 2D-LC workflow for fractionated samples

- Peak modelling and data reduction for fast analysis without affecting quantification

- QC Metrics tools to evaluate the quality of LC-MS import data

- Generate ion intensity maps of retention time (RT) vs. m/z vs. ion intensity to review raw data quality

- Ion mobility separation adds a third dimension of resolution and increases peak capacity

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
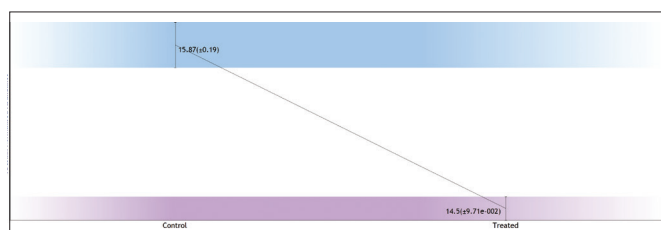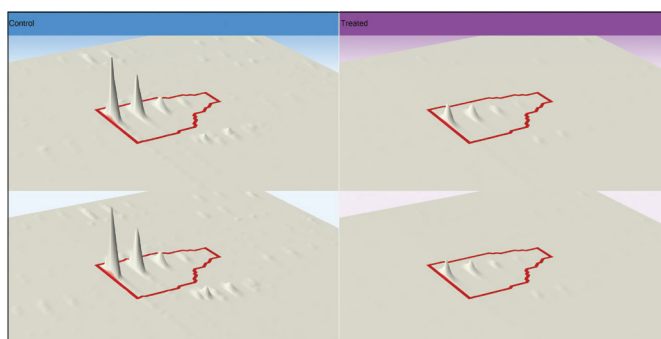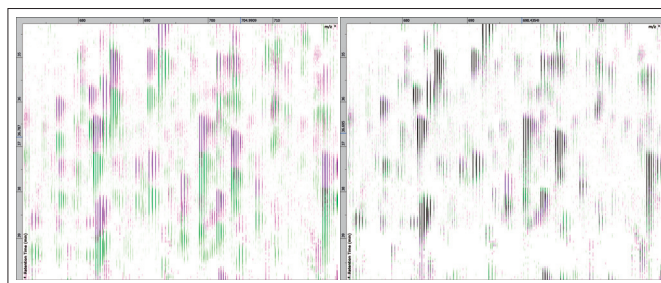
Quantify peptides

- Ion abundance is measured from an isotope peak cluster detection applied consistently to every run

- Optional use of internal standard for 'HiN' absolute quantification

- Automatic normalization accounts for sample loading variation for direct comparison 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

"Progenesis QI for proteomics has provided to our laboratory key capabilities for proper processing and analysis of label-free LC/MS/MS data including retention time alignment across injections, flexible experimental design, univariate and multivariate statistical tools, and an intuitive user interface which has enabled our students to effectively utilize the software with minimal training."

KEVIN BLACKBURN
Molecular and Structural Biochemistry,
**North Carolina State University, Raleigh, NC, USA**

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

- Simple but powerful tagging feature to focus on particular subsets of ions or for downstream MRM studies
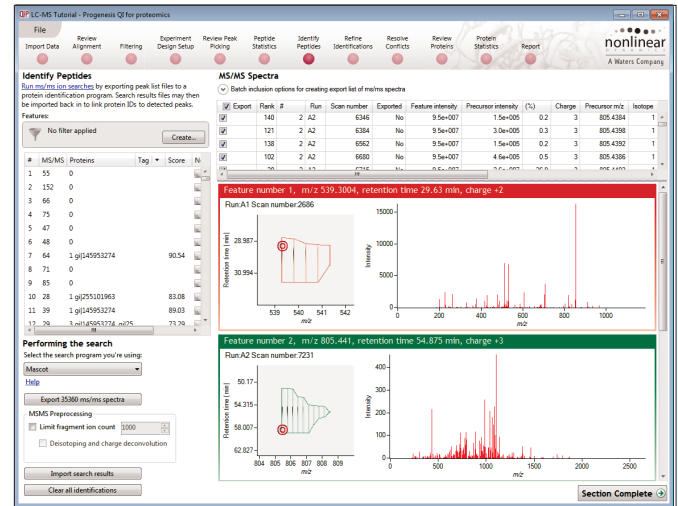
Report interesting proteins

- 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
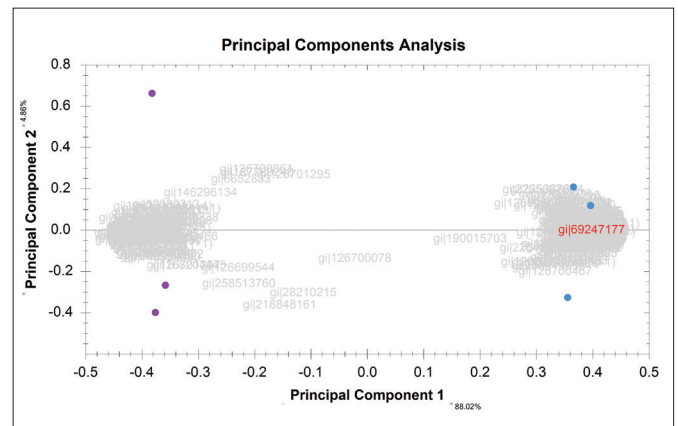
Pathway analysis

- Easily export proteins of interest to third-party Pathway Analysis tools such as IMPaLA and Panther

“…with Progenesis QI for Proteomics we practically started getting publishable data within the first few hours. As usual, Nonlinear provided wonderful technical support for us. Label-free quantitation is now a routine technique in my lab.”

DR. LAM YUN WAH
Department of Biology and Chemistry,
City University of Hong Kong

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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