

Progenesis® QI for proteomics - benefits and features of the current release

Version 1.0

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 for proteomics software enables you to rapidly, objectively and reliably discover proteins of interest and export results for 'omics research applications.

Why the new branding?

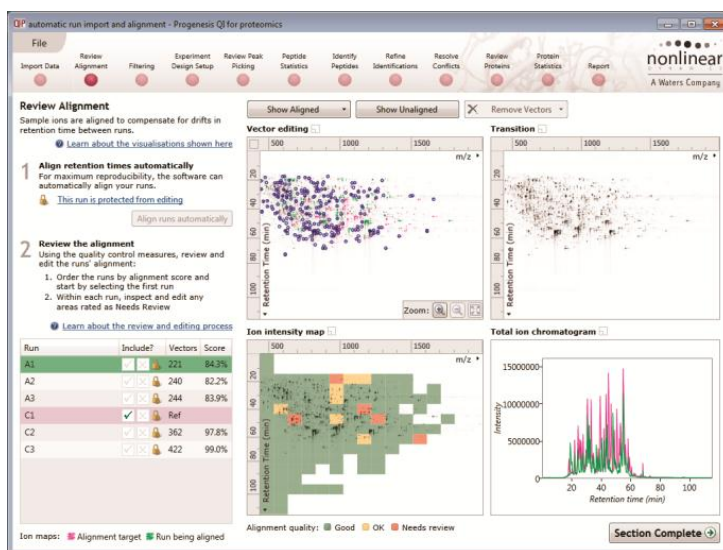
Nonlinear Dynamics was acquired by Waters Corporation in August 2013 after a successful partnership where Nonlinear supplied a customised version of Progenesis LC-MS under the TransOmics™ Informatics name to support analysis using the enhanced and unique functionality available with Synapt G2, G2-S and G2-Si high definition mass spectrometers. With this latest release we have combined the functionality of the two separately branded software products, Progenesis LC-MS and TransOmics Informatics, into one offering. Progenesis QI maintains the Progenesis heritage and focusses our resources in delivering a single world-leading informatics platform for omics data analysis. It is appreciated that modern laboratories often have instruments from multiple vendors and thus, the software will continue to support LC-MS data from the majority of sources

New features

Improved functionality in the Review Alignment step

High-quality retention-time (RT) alignment of LC-MS runs is essential first step for reliable relative quantification of peptide and proteins. In response to customer feedback we have made the Review Alignment screen more responsive, informative and interactive.

- Increased speed of updating screen views allows faster, more responsive alignment review.
- Ion intensity maps now include RT and m/z scales allowing you to focus in on areas of interest, guided by results at the review peak picking step, to manually correct areas where alignment could be improved.
- New zooming feature allows you to precisely zoom into any area of interest within the ion intensity map, even down to the feature level.



Review Alignment screen is now more responsive, informative and interactive

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Noise-reduction filter

As MS instrument performance continues to improve, we have introduced a new feature to allow user-control of the peak-modelling applied during import of raw data from high-resolution instruments. The new import filter strength tool provides more flexible control on the levels of background noise detected in your samples, which delivers faster analysis times per run and provides more reliable quantification of smaller but real features within each experiment.

Utilise Ion mobility data

Ion mobility MS separations are commercially unique to the Waters Synapt range of mass spectrometers and enable the separation of co-eluting isobaric analytes. Progenesis QI for proteomics uniquely takes advantage of this additional dimension of resolution to give improvements in accuracy and precision of identification and quantification. The highly visual nature of the software enables the user to view the full benefit of ion mobility separations for the analysis of the highly complex samples typically found in a bottom-up proteomics experiment.

Support for MS^E and HDMS^E data-independent (DIA) analysis

As well as conventional data-dependent analysis (DDA), Progenesis QI for proteomics now supports the analysis of Waters MS^E and HDMS^E data. Split-screen views show low-energy (parent ion) and high-energy (fragment ion) data functions as you import your data.

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