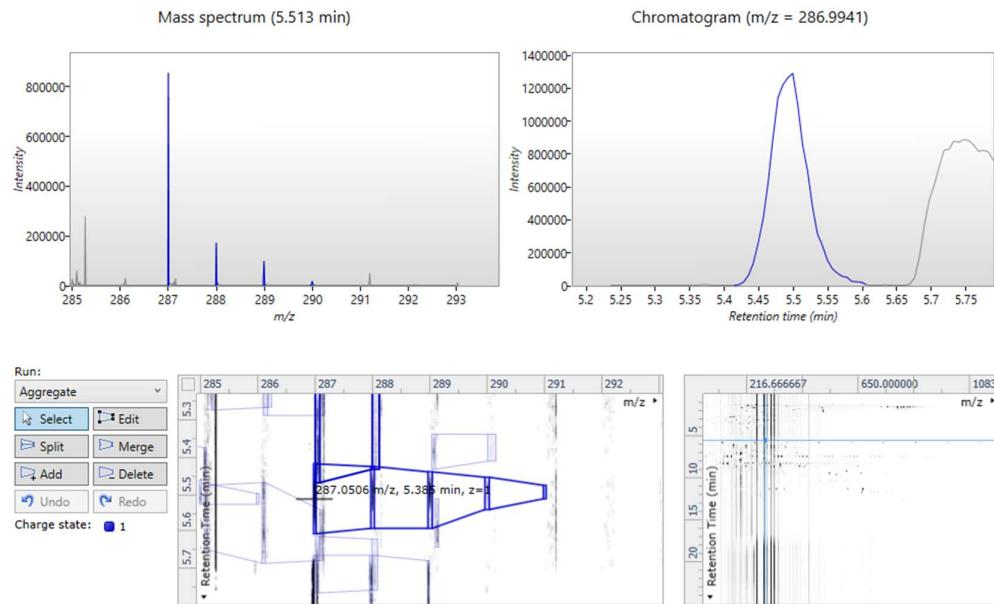


What's new in Progenesis QI v3.0?

The latest release of Progenesis QI helps scientists to overcome challenges in their research by offering some significant new developments. At the same time, attention has been paid to the usability of Progenesis QI, making it even more enjoyable to use.

Peak Editing

Peak Editing functionality has been added to Peak Picking View allowing the ability to review and then manually re-integrate, delete, split, merge and add new peak selections. This includes the ability to multi-delete peaks.



Support for Waters METLIN LC/MS/MS library 2019

Progenesis QI version 3 adds support for the forthcoming Waters METLIN LC/MS/MS library 2019.

With this second version of the industry leading metabolomic resource, all MS/MS data are now experimentally derived. We have also included support to integrate Waters CCS measurements which have been generated using a research version of our new CCS prediction algorithms which utilize machine learning approaches. With Waters ion mobility data, you will now be able to filter the Waters METLIN search results that match a CCS tolerance.

The screenshot shows the Progenesis QI software interface. On the left, there is a sidebar titled "Identify Compounds" with three steps: 1. Filter the compounds, 2. Choose search parameters, and 3. Search for identifications. Step 2 is expanded, showing a dropdown menu for "METLIN™ MS/MS Library 2019" and a "Search for identifications" button. On the right, a modal dialog box titled "Edit Search Parameters" is open, containing sections for "METLIN search parameters", "Search tolerances" (Precursor tolerance: 5 ppm, Fragment tolerance: 15 ppm), "Composition filters" (Elemental composition checkbox, Define ranges... button), "Include CCS predictions in the output table" (checkbox checked, information about CCS predictions), "Browse..." button for saving search parameters, and a "Save search parameters" button.

Adduct measurement export

We have improved the export functionality so you can now export individual adduct measurements to a CSV file.

Peak picking performance improvements

We have made some changes in the peak picking algorithm to improve the detection of peaks with long fronting or long tailing.

Improved data compatibility

- Updated Agilent plugin to support recent data format changes
- Support for importing Waters RDa data with dynamic lockmass correction from UEP files

More pathway analysis options

We have added a new plugin to export metabolite identifications to MetaCore, a Cortellis solution, which allows for comprehensive pathway analysis to be conducted for multi-omic datasets. Metabolite IDs need to be KEGG identifiers. Now matching the capabilities of Progenesis QI for proteomics.

You are entitled to the latest version of Progenesis QI if you have an [active maintenance plan](#). Please [contact us](#) if you would like to review your maintenance plan.