

## What's new in Progenesis QI v2.3?

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.

### A big usability improvement

If you need to fine tune your adduct selection while running your analysis, you can now alter the set of adducts during the analysis process, saving time and making Progenesis QI more flexible.

### Symphony support

You can now initiate a Progenesis QI experiment within the [Symphony data pipeline](#). This means you can combine the efficiencies and flexibility of Symphony with the renowned user friendliness of Progenesis QI. In real terms, this means that your instrument can acquire data overnight, transfer the data to a different machine, and initiate an experiment in Progenesis QI; when you arrive in the morning, you'll be ready to get started on your data analysis!



### SONAR support

Progenesis QI v2.3 has support for [SONAR](#). This has been developed for busy omics research laboratories that need to get the answer right the first time. With efficient workflows, SONAR offers new possibilities, with an acquisition mode that collects MS/MS results from a Data Independent Acquisition (DIA) experiment. This exciting new Waters technology gives increased confidence and speed to the busy mass spec laboratory.



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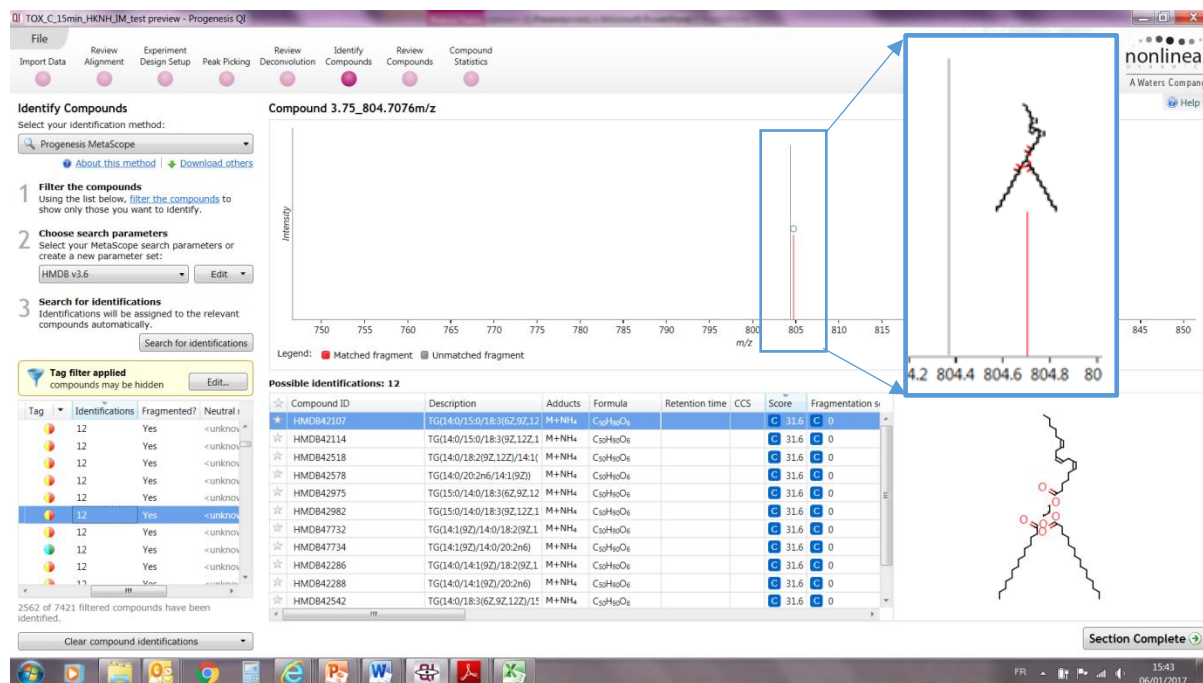
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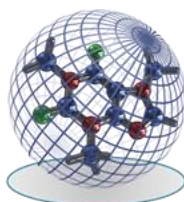
## Zooming in

You can use the zoom tool to explore differences in matched MS/MS spectra, making the data more transparent.



## Bringing ion mobility to the masses

Progenesis QI is compatible with the ion mobility capabilities of the latest Waters instruments, including Vion. This makes ion mobility measurements routine, rather than a specialist measurement. You can, of course, use Progenesis QI to search using the [Waters CCS library](#), which can be downloaded.



## Export known unknowns

Have you noticed a reproducible discovery that is not in any database? Also new is the ability to export fragment lists from unidentified compounds, allowing further exploration using tools outside Progenesis QI.

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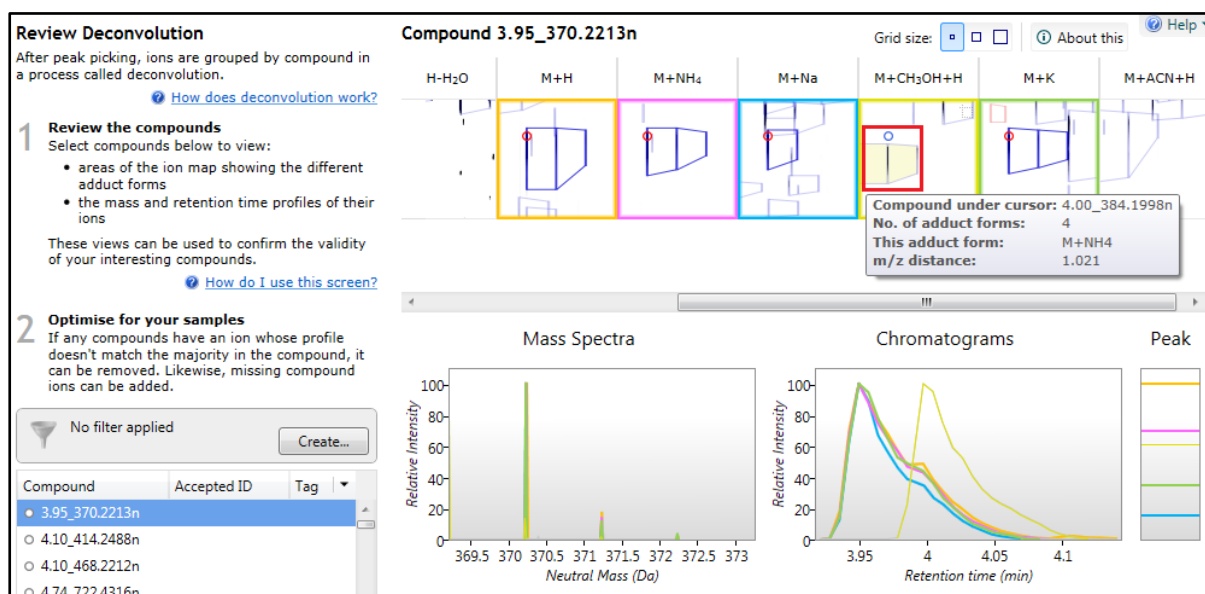
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## Better access to q-values

Q-values have now been added to the *Review Compounds* table and in both compound measurements and identifications exports, allowing you to easily and confidently focus on significant results.

## Reviewing a compound's adducts

An improved user interface providing information to help decide whether an ion belongs to a given compound. This is another usability improvement that will please Progenesis Q1 users.



**Review Deconvolution**  
After peak picking, ions are grouped by compound in a process called deconvolution.

**1 Review the compounds**  
Select compounds below to view:

- areas of the ion map showing the different adduct forms
- the mass and retention time profiles of their ions

These views can be used to confirm the validity of your interesting compounds.

**2 Optimise for your samples**  
If any compounds have an ion whose profile doesn't match the majority in the compound, it can be removed. Likewise, missing compound ions can be added.

Compound: 3.95\_370.2213n  
Accepted ID: 3.95\_370.2213n  
Tag: [dropdown]

Mass Spectra: Relative Intensity vs Neutral Mass (Da)

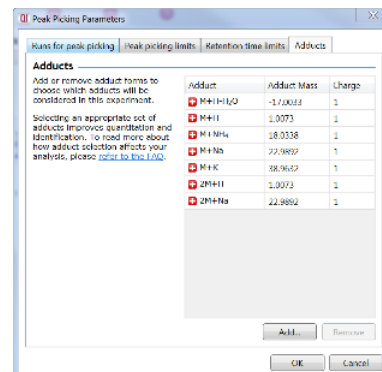
Chromatograms: Relative Intensity vs Retention time (min)

Peak: [list of peaks]

Compound under cursor: 4.00\_384.1998n  
No. of adduct forms: 4  
This adduct form: M+NH4  
m/z distance: 1.021

## Adduct selection

If you need to fine tune your adduct selection while running your analysis, you can now alter the set of adducts during the analysis process, saving time and making Progenesis Q1 more flexible.



Peak Picking Parameters

Runs for peak picking | Peak picking limits | Retention time limits | Adducts

**Adducts**  
Add or remove adduct forms to those which adducts will be considered in this experiment.

Selecting an appropriate set of adducts improves quantitation and identification. To read more about how adduct selection affects your analysis, please refer to [Exp 1.00](#).

Adduct	Adduct Mass	Charge
<input checked="" type="checkbox"/> M+H <sub>2</sub> O	-17.00013	1
<input checked="" type="checkbox"/> M+H	1.0073	1
<input checked="" type="checkbox"/> M+NH <sub>4</sub>	18.0338	1
<input checked="" type="checkbox"/> M+Na	22.9897	1
<input checked="" type="checkbox"/> M+K	38.9612	1
<input checked="" type="checkbox"/> M+H <sup>+</sup>	1.0073	1
<input checked="" type="checkbox"/> M+Na <sup>+</sup>	22.9892	1

Add Remove OK Cancel

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## **Network outages**

Improved handling of network outages where experiment data is stored on a network drive.

Just to finish, here is an independent review from one of our users; you can [read more here](#).

***"Progenesis Q1 is an easy-to-use and practicable tool in untargeted metabolite analysis. Even the students can use it without supervision. Our group uses Progenesis Q1 in versatile projects from functional genomics to perturbation analysis."*** [Agnes Fekete](#), University Würzburg

You are entitled to the latest version of Progenesis Q1 if you have an [active maintenance plan](#) .  
Please [contact us](#) if you would like to review your maintenance plan.

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