Progenesis LC-MS v3.0 – new features in the current release

Version 3.0 of Progenesis LC-MS will provide new features that make your results reliable and increase confidence in your protein quantification and identification. These include a workflow to analyse fractionated samples, the ability to normalise based on a sub-set of known peptide ions, import results from Scaffold (Proteome Software) and exclude non-unique peptides from protein quantification automatically.

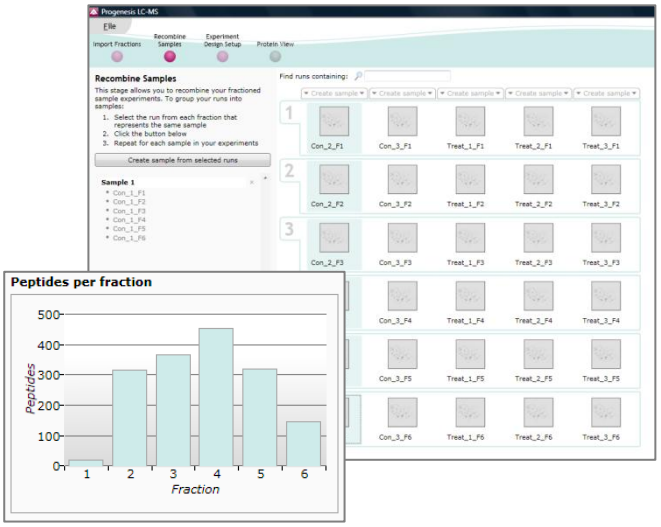
A summary of the new features and workflows are below.

Fractionated Sample Analysis

You apply an ion abundance based label-free quantification and protein identification to each fraction separately. The new fractionation workflow then combines all these fractions into a single protein based view of the experiment.

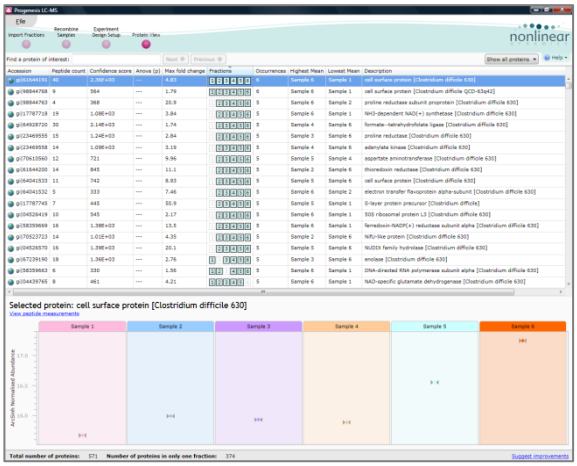
Import and recombine fractions

After importing and ordering the fractions to represent how the experiment was designed and run, a graph shows how many peptides were identified in each fraction so you can review the separation results. By telling the software which runs are fractions of the same sample you can normalise between fractions to see global results at the protein level.



Protein View

This gives you an analysis of the experiment as a whole. It reports quantification and identification at the protein level but allows you to view the peptide measurements underlying each reported protein. The table shows which fraction the data was obtained. A graph of protein abundance in each sample is automatically generated to show expression trends. The table of protein results can be exported for any external data processing needs.



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Normalisation to selected peptide ions

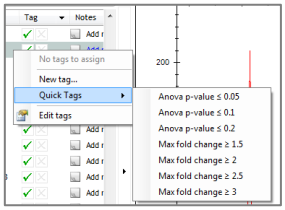
If you are using spiked proteins of fixed concentration or know the identity of any peptide ions that do not vary within your experiment you can re-normalise your data to these features. This helps you closely control an important parameter in LC-MS data analysis.

Improvements to tags & searches

Tags allow you to label a selection of peptides according to the data associated with them (e.g. p-value, fold change, identity, etc), or their expression profile (e.g. up regulated in treatment). The existing tags feature has been updated to improve usability and provide more flexibility in the way tagged data can be displayed. There is a new filter dialog that allows you to display peptide ions based on a selection of their tags.

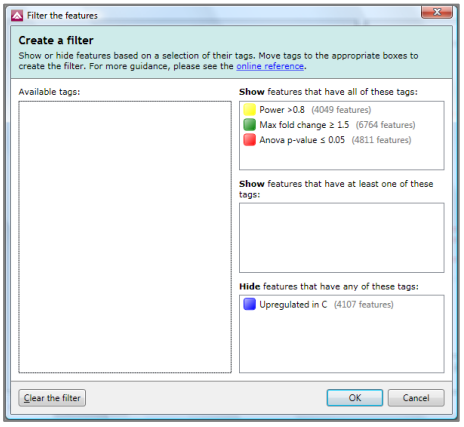
Quick Tags

Using the new Quick Tags feature, certain tags can be created without first having to multi-select the peptide ions. For example, you can quickly tag all peptide ions with a p-value of less than 0.05 and there is also the option to Quick Tag using pre-defined fold changes. You are still free to tag peptide ions manually.



Filtering your tags

Whilst labelling your peptides with tags is a helpful way to organize your data, filtering based on those tags is the more powerful analysis tool. By creating a filter, you can quickly reduce the amount of data you are viewing, enabling you to concentrate on the peptide ions of real experimental interest.



Regular expression filters

The ability to filter tables of results based on regular expression terminology has been implemented.

Link with Scaffold

Now you can use Scaffold to make sense of your indentified proteins then import results into Progenesis LC-MS. This means you can link high quality identification with high quality quantification.

Protein View

There are two major additions to the protein view that increase the reliability of your protein quantification and reduce the complexity of highlighting significant entries in a long list of proteins.

Remove non-unique peptides from quantification automatically

Quantification based on unique peptides means the results you report are more reliable. When two protein identifications share common peptides the software uses unique peptides for quantification.

Group protein identifications

Searching peptides against databases can return multiple entries that are actually the same or related protein(s). To make sense of this and help pin point interesting classes of proteins within your experiment you can automatically group similar proteins.

Protein Report

The goal of most analyses is to share results on the significant proteins you have quantified and indentified. By tagging proteins you can report a sub-set of proteins within your experiment including the peptide measurements associated with each protein.