A Novel Approach to LC-MS Expression Analysis using the Progenesis LC-MS Workflow

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Traditional LC-MS-MS Workflow

**Peptide mix**

- **LC-MS-MS**
  - Peptide separation & fragmentation (Data dependant acquisition)
  - MS-MS Spectra

- **Database Searching**
  - Protein Identification
  - Search results

- **Results Filtering**
  - Validation of identifications
  - Confident IDs

- **Data Mining**
  - Quantitation analysis
  - Results

In traditional LC-MS-MS analysis, information is discarded where data-dependent acquisition is not quick enough to probe every ion. This can result in significant protein behaviour being overlooked.

The software ranks peptides in order of p-value and fold change between groups, with the most significant at the top. Using 2- and 3-D montage views and expression profile data, peptides of interest can be selected for further analysis.

The software outputs an inclusion list enabling targeted MS-MS analysis of the selected peptides. Thus, even if a confident protein identification does not follow for a peptide of interest, you are still aware of the significant expression change and can investigate further.

Progenesis LC-MS Workflow

**Peptide mix**

- **LC-MS**
  - Peptide separation
  - MS Spectra

- **Data Analysis**
  - Locate peaks of significant expression behaviour
  - Inclusion list

- **Targeted MS-MS**
  - Peptide fragmentation
  - MS-MS Spectra

- **Protein Identification**
  - Results

To enable differential expression analysis of LC-MS data it needs to be aligned to compensate for the positional bias introduced by the LC separation technique. This is achieved using automated LC-MS alignment algorithms coupled with the software’s advanced visualisation tools.

In Progenesis LC-MS, data is analysed at the LC-MS level to locate peaks exhibiting significant expression change between experiment groups.