ICPL*Quant* – a directed proteomics tool for isotope labelling proteomics

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The main goal of a quantitative proteome analysis is the identification of proteins being present in different amounts in one or more biological defined proteomic states.
The high complexity of proteome samples therefore requires extensive reduction of complexity to get quantitative information also from low abundant protein species. Common data dependent acquisition methods (DDA) do not have the power to identify low intense proteins. This is based on the fact that only a certain fraction of the proteome (e.g. the 10 most intense precursor ions per MS1 spectrum) is analyzed by MS2.
To increase the analysis depth of proteomes, it is essential to quantify and identify peptides that are beyond the coverage of DDA methods, requiring a workflow which

(1) uses isotope labelling techniques like ICPL to compare several proteomic states within one single experiment
(2) performs MS1 based peptide quantification
(3) is able to specifically select peptide precursor ions for a directed protein identification

Here we present a software tool, ICPL*Quant*, comprising modules to process MS data from isotope labelled proteins.
ICPL*Quant* takes raw MS files in mzXML format as input and is able to quantify doublet, triplet or quadruplet isotopologues.
Out of that, a precursor list can be created for a targeted identification of peptides, enabling an iterative identification process of low abundant proteins. The MASCOT MS2 identification results can easily be merged with the quantitative information.
ICPL*Quant* is further able to recognize “incomplete” peptide mass pattern, which arise from the MS measurement of isotope labeled peptides being absent in one or more proteomic states.
By comparing the experimental peptide pattern to a reference dataset, which comprises complete peptide mass pattern with isoabundant peak signals, it is possible to detect and quantify extremely regulated peptide candidates.

ICPL*Quant* shows highly accurate quantification of proteins and peptides which is demonstrated with a complex protein sample.

References

Brunner A, Keidel E, Dosch D, Kellermann J, Lottspeich F. ICPL*Quant* – a software for non-isobaric isotope labeling proteomics. *Proteomics 10 (2010) , 315-323*